

# Mapping and quantifying mammalian transcriptomes b

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Nonketotic hyperosmolar hyperglycemia during glycerol therapy for cerebral edema. <i>Neurology</i> , 1976, 26, 89-89.	1.5	29
4	Heroic Bureaucracies. <i>Administration and Society</i> , 1991, 23, 123-147.	1.2	8
6	An Integrated Genomic Analysis of Human Glioblastoma Multiforme. <i>Science</i> , 2008, 321, 1807-1812.	6.0	5,230
7	Alternative isoform regulation in human tissue transcriptomes. <i>Nature</i> , 2008, 456, 470-476.	13.7	4,508
8	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008, 456, 53-59.	13.7	3,118
9	Power sequencing. <i>Nature</i> , 2008, 453, 1197-1198.	13.7	60
10	Next-generation DNA sequencing. <i>Nature Biotechnology</i> , 2008, 26, 1135-1145.	9.4	3,609
11	What would you do if you could sequence everything?. <i>Nature Biotechnology</i> , 2008, 26, 1125-1133.	9.4	175
12	Deep surveying of alternative splicing complexity in the human transcriptome by high-throughput sequencing. <i>Nature Genetics</i> , 2008, 40, 1413-1415.	9.4	3,243
13	The beginning of the end for microarrays?. <i>Nature Methods</i> , 2008, 5, 585-587.	9.0	291
14	Hunting hidden transcripts. <i>Nature Methods</i> , 2008, 5, 587-589.	9.0	8
15	A protocol for unraveling gene regulatory networks. <i>Nature Protocols</i> , 2008, 3, 1876-1887.	5.5	38
17	Genes and environment – Striking the fine balance between sophisticated biomonitoring and true functional environmental genomics. <i>Science of the Total Environment</i> , 2008, 400, 142-161.	3.9	103
18	Single-molecule DNA sequencing technologies for future genomics research. <i>Trends in Biotechnology</i> , 2008, 26, 602-611.	4.9	191
19	Gene Expression Analysis of Neural Cells and Tissues Using DNA Microarrays. <i>Current Protocols in Neuroscience</i> , 2008, 45, Unit 4.28.	2.6	8
20	Transcriptome content and dynamics at single-nucleotide resolution. <i>Genome Biology</i> , 2008, 9, 234.	13.9	112
21	The Antisense Transcriptomes of Human Cells. <i>Science</i> , 2008, 322, 1855-1857.	6.0	489
22	A Guide to One of the Genome's Best-Kept Secrets. <i>Molecular Cell</i> , 2008, 31, 782-784.	4.5	0

#	ARTICLE	IF	CITATIONS
23	Annotating genomes with massive-scale RNA sequencing. <i>Genome Biology</i> , 2008, 9, R175.	13.9	210
24	Core Signaling Pathways in Human Pancreatic Cancers Revealed by Global Genomic Analyses. <i>Science</i> , 2008, 321, 1801-1806.	6.0	3,755
25	A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome. <i>Science</i> , 2008, 321, 956-960.	6.0	1,164
26	RNA cytosine methylation analysis by bisulfite sequencing. <i>Nucleic Acids Research</i> , 2008, 37, e12-e12.	6.5	304
27	SeqMap: mapping massive amount of oligonucleotides to the genome. <i>Bioinformatics</i> , 2008, 24, 2395-2396.	1.8	459
28	Trim24 (Tif1 $\pm$ ): An essential $\hat{\sim}$ brake $\hat{\sim}$ ™ for retinoic acid-induced transcription to prevent liver cancer. <i>Cell Cycle</i> , 2008, 7, 3647-3652.	1.3	30
29	MicroRNA target prediction by expression analysis of host genes. <i>Genome Research</i> , 2009, 19, 481-490.	2.4	168
30	Determination of tag density required for digital transcriptome analysis: Application to an androgen-sensitive prostate cancer model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20179-20184.	3.3	90
31	Deep sequencing-based expression analysis shows major advances in robustness, resolution and inter-lab portability over five microarray platforms. <i>Nucleic Acids Research</i> , 2008, 36, e141-e141.	6.5	653
32	Novel Low Abundance and Transient RNAs in Yeast Revealed by Tiling Microarrays and Ultra High $\hat{\sim}$ Throughput Sequencing Are Not Conserved Across Closely Related Yeast Species. <i>PLoS Genetics</i> , 2008, 4, e1000299.	1.5	31
33	Cross-hybridization modeling on Affymetrix exon arrays. <i>Bioinformatics</i> , 2008, 24, 2887-2893.	1.8	35
34	Next-generation sequencing: applications beyond genomes. <i>Biochemical Society Transactions</i> , 2008, 36, 1091-1096.	1.6	111
35	Variation in the Large-Scale Organization of Gene Expression Levels in the Hippocampus Relates to Stable Epigenetic Variability in Behavior. <i>PLoS ONE</i> , 2008, 3, e3344.	1.1	28
36	Genomic Convergence Analysis of Schizophrenia: mRNA Sequencing Reveals Altered Synaptic Vesicular Transport in Post-Mortem Cerebellum. <i>PLoS ONE</i> , 2008, 3, e3625.	1.1	106
37	High-throughput verification of transcriptional starting sites by Deep-RACE. <i>BioTechniques</i> , 2009, 46, 130-132.	0.8	33
38	Large-scale RACE approach for proactive experimental definition of <i>C. elegans</i> ORFeome. <i>Genome Research</i> , 2009, 19, 2334-2342.	2.4	12
39	Analyzing Gene Expression Data from Microarray and Next $\hat{\sim}$ Generation DNA Sequencing Transcriptome Profiling Assays Using GeneSifter Analysis Edition. <i>Current Protocols in Bioinformatics</i> , 2009, 27, Unit 7.14 7.14.1-35.	25.8	4
40	Detection of single nucleotide variations in expressed exons of the human genome using RNA-Seq. <i>Nucleic Acids Research</i> , 2009, 37, e106-e106.	6.5	152

#	ARTICLE	IF	CITATIONS
41	Towards Reliable Isoform Quantification Using RNA-Seq Data. , 2009, , .		2
42	Native Chromatin Preparation and Illumina/Solexa Library Construction. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5237.	0.2	26
43	Improved RNA preservation for immunolabeling and laser microdissection. Rna, 2009, 15, 2364-2374.	1.6	29
44	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3264-3269.	3.3	201
45	Overestimation of alternative splicing caused by variable probe characteristics in exon arrays. Nucleic Acids Research, 2009, 37, e107-e107.	6.5	24
46	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRRescueLite. Bioinformatics, 2009, 25, 2613-2614.	1.8	41
47	The resolution of the genetics of gene expression. Human Molecular Genetics, 2009, 18, R211-R215.	1.4	20
48	Transcriptional Regulatory Circuits: Predicting Numbers from Alphabets. Science, 2009, 325, 429-432.	6.0	168
49	Expansion Mechanisms and Functional Annotations of Hypothetical Genes in the Rice Genome. Plant Physiology, 2009, 150, 1997-2008.	2.3	19
50	Genomic determination of the glucocorticoid response reveals unexpected mechanisms of gene regulation. Genome Research, 2009, 19, 2163-2171.	2.4	460
51	Benchmarking regulatory network reconstruction with GRENDL. Bioinformatics, 2009, 25, 801-807.	1.8	25
52	Cancer Genomes on a Shoestring Budget. New England Journal of Medicine, 2009, 360, 2781-2783.	13.9	4
53	Massively parallel sequencing of the polyadenylated transcriptome of <i>C. elegans</i> . Genome Research, 2009, 19, 657-666.	2.4	169
54	An Abundance of Ubiquitously Expressed Genes Revealed by Tissue Transcriptome Sequence Data. PLoS Computational Biology, 2009, 5, e1000598.	1.5	777
55	An Integrated Strategy to Study Muscle Development and Myofilament Structure in <i>Caenorhabditis elegans</i> . PLoS Genetics, 2009, 5, e1000537.	1.5	89
56	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. Bioinformatics, 2009, 25, 2607-2608.	1.8	481
57	How eukaryotic genes are transcribed. Critical Reviews in Biochemistry and Molecular Biology, 2009, 44, 117-141.	2.3	129
58	Whole genome transcriptome analysis. RNA Biology, 2009, 6, 107-112.	1.5	44

#	ARTICLE	IF	CITATIONS
59	Automation of cDNA Synthesis and Labelling Improves Reproducibility. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-7.	3.0	13
60	Annotating non-coding transcription using functional genomics strategies. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 437-443.	3.8	5
61	A hierarchical Bayesian model for comparing transcriptomes at the individual transcript isoform level. <i>Nucleic Acids Research</i> , 2009, 37, e75-e75.	6.5	49
62	ChIP-Seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21521-21526.	3.3	312
63	Dissection of gene regulatory networks in embryonic stem cells by means of high-throughput sequencing. <i>Biological Chemistry</i> , 2009, 390, 1139-1144.	1.2	3
64	Experimental discovery of sRNAs in <i>Vibrio cholerae</i> by direct cloning, 5S/tRNA depletion and parallel sequencing. <i>Nucleic Acids Research</i> , 2009, 37, e46-e46.	6.5	148
65	Genomic Analysis of Left Ventricular Remodeling. <i>Circulation</i> , 2009, 120, 437-444.	1.6	10
66	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , 2009, 37, e148-e148.	6.5	88
67	Chimeric transcript discovery by paired-end transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12353-12358.	3.3	302
68	Complex architecture and regulated expression of the <i>Sox2</i> locus during vertebrate development. <i>Rna</i> , 2009, 15, 2013-2027.	1.6	200
69	Establishing legitimacy and function in the new transcriptome. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 424-436.	3.8	62
70	ISOLATE: a computational strategy for identifying the primary origin of cancers using high-throughput sequencing. <i>Bioinformatics</i> , 2009, 25, 2882-2889.	1.8	41
71	Transcriptome analysis by strand-specific sequencing of complementary DNA. <i>Nucleic Acids Research</i> , 2009, 37, e123-e123.	6.5	720
72	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. <i>Bioinformatics</i> , 2009, 25, 2615-2616.	1.8	45
73	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. <i>Current Opinion in Plant Biology</i> , 2009, 12, 107-118.	3.5	261
74	Characterizing natural variation using next-generation sequencing technologies. <i>Trends in Genetics</i> , 2009, 25, 463-471.	2.9	116
75	BayesPeak: Bayesian analysis of ChIP-seq data. <i>BMC Bioinformatics</i> , 2009, 10, 299.	1.2	115
76	CNV-seq, a new method to detect copy number variation using high-throughput sequencing. <i>BMC Bioinformatics</i> , 2009, 10, 80.	1.2	495

#	ARTICLE	IF	CITATIONS
77	Novel software package for cross-platform transcriptome analysis (CPTRA). BMC Bioinformatics, 2009, 10, S16.	1.2	17
78	Transcript quantification with RNA-Seq data. BMC Bioinformatics, 2009, 10, .	1.2	10
80	Determination of enriched histone modifications in non-genic portions of the human genome. BMC Genomics, 2009, 10, 143.	1.2	182
81	Estimating accuracy of RNA-Seq and microarrays with proteomics. BMC Genomics, 2009, 10, 161.	1.2	240
82	A transcriptional sketch of a primary human breast cancer by 454 deep sequencing. BMC Genomics, 2009, 10, 163.	1.2	205
83	Measuring differential gene expression by short read sequencing: quantitative comparison to 2-channel gene expression microarrays. BMC Genomics, 2009, 10, 221.	1.2	141
84	Transcriptome sequencing of the Microarray Quality Control (MAQC) RNA reference samples using next generation sequencing. BMC Genomics, 2009, 10, 264.	1.2	67
85	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	1.2	137
86	Combining next-generation pyrosequencing with microarray for large scale expression analysis in non-model species. BMC Genomics, 2009, 10, 555.	1.2	72
87	Deep RNA sequencing of <i>L. monocytogenes</i> reveals overlapping and extensive stationary phase and sigma B-dependent transcriptomes, including multiple highly transcribed noncoding RNAs. BMC Genomics, 2009, 10, 641.	1.2	160
88	BOAT: Basic Oligonucleotide Alignment Tool. BMC Genomics, 2009, 10, S2.	1.2	7
89	Non-coding RNAs and new opportunities for the private sector. Drug Discovery Today, 2009, 14, 446-452.	3.2	26
90	Developing genomic platforms for Chinese hamster ovary cells. Biotechnology Advances, 2009, 27, 1028-1035.	6.0	55
91	Next-generation sequencing approaches in genetic rodent model systems to study functional effects of human genetic variation. FEBS Letters, 2009, 583, 1668-1673.	1.3	16
92	Correlation of mRNA and protein in complex biological samples. FEBS Letters, 2009, 583, 3966-3973.	1.3	1,519
93	RNA profiling of FACS-sorted neurons from the developing zebrafish spinal cord. Developmental Dynamics, 2009, 238, 150-161.	0.8	17
94	Genomic location analysis by ChIP-Seq. Journal of Cellular Biochemistry, 2009, 107, 11-18.	1.2	153
95	Quantitative regulation of alternative splicing in evolution and development. BioEssays, 2009, 31, 40-50.	1.2	49

#	ARTICLE	IF	CITATIONS
96	RNA editing: a driving force for adaptive evolution?. <i>BioEssays</i> , 2009, 31, 1137-1145.	1.2	116
97	The evolution and application of techniques in molecular biology to human brain tumors: a 25-year perspective. <i>Journal of Neuro-Oncology</i> , 2009, 92, 261-273.	1.4	7
98	Gene Dysregulation in Huntington's Disease: REST, MicroRNAs and Beyond. <i>NeuroMolecular Medicine</i> , 2009, 11, 183-199.	1.8	104
99	Perspectives of DNA microarray and next-generation DNA sequencing technologies. <i>Science in China Series C: Life Sciences</i> , 2009, 52, 7-16.	1.3	34
100	Next-generation sequencing of vertebrate experimental organisms. <i>Mammalian Genome</i> , 2009, 20, 327-338.	1.0	34
101	Large introns in relation to alternative splicing and gene evolution: a case study of <i>Drosophila bruno-3</i> . <i>BMC Genetics</i> , 2009, 10, 67.	2.7	41
102	Stress-induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole-genome tiling arrays. <i>Plant Journal</i> , 2009, 58, 1068-1082.	2.8	273
103	Genome-wide profiling of genetic alterations in acute lymphoblastic leukemia: recent insights and future directions. <i>Leukemia</i> , 2009, 23, 1209-1218.	3.3	141
104	Direct RNA sequencing. <i>Nature</i> , 2009, 461, 814-818.	13.7	409
105	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	13.7	984
106	The digital generation. <i>Nature</i> , 2009, 458, 239-240.	13.7	74
107	How to map billions of short reads onto genomes. <i>Nature Biotechnology</i> , 2009, 27, 455-457.	9.4	257
108	Cell-specific protein phenotypes for the autoimmune locus IL2RA using a genotype-selectable human bioresource. <i>Nature Genetics</i> , 2009, 41, 1011-1015.	9.4	249
109	mRNA-Seq whole-transcriptome analysis of a single cell. <i>Nature Methods</i> , 2009, 6, 377-382.	9.0	2,736
110	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. <i>Nature Methods</i> , 2009, 6, 613-618.	9.0	149
111	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009, 6, 647-649.	9.0	160
112	Computation for ChIP-seq and RNA-seq studies. <i>Nature Methods</i> , 2009, 6, S22-S32.	9.0	489
113	Next-generation gap. <i>Nature Methods</i> , 2009, 6, S2-S5.	9.0	111

#	ARTICLE	IF	CITATIONS
114	Is sequencing enlightenment ending the dark age of the transcriptome?. Nature Methods, 2009, 6, 711-713.	9.0	28
115	Engineered fluorescent proteins: innovations and applications. Nature Methods, 2009, 6, 713-717.	9.0	108
116	Five years of Methods. Nature Methods, 2009, 6, 724-725.	9.0	0
117	Summary of the Online Focus on next-generation sequencing data analysis. Nature Methods, 2009, 6, 802-803.	9.0	0
118	RNA-Seq: a revolutionary tool for transcriptomics. Nature Reviews Genetics, 2009, 10, 57-63.	7.7	10,529
119	Genetics of human gene expression: mapping DNA variants that influence gene expression. Nature Reviews Genetics, 2009, 10, 595-604.	7.7	210
120	Under pressure: investigating the biology of plant infection by Magnaporthe oryzae. Nature Reviews Microbiology, 2009, 7, 185-195.	13.6	809
121	Application of 'next-generation' sequencing technologies to microbial genetics. Nature Reviews Microbiology, 2009, 7, 96-97.	13.6	269
122	In the News. Nature Reviews Microbiology, 2009, 7, 260-261.	13.6	158
123	Systems biology of innate immunity. Immunological Reviews, 2009, 227, 264-282.	2.8	139
124	Genomic analysis of acute leukemia. International Journal of Laboratory Hematology, 2009, 31, 384-397.	0.7	23
125	Next-generation DNA sequencing techniques. New Biotechnology, 2009, 25, 195-203.	2.4	760
126	TopHat: discovering splice junctions with RNA-Seq. Bioinformatics, 2009, 25, 1105-1111.	1.8	11,265
127	Genome-wide identification of DNA-protein interactions using chromatin immunoprecipitation coupled with flow cell sequencing. Journal of Endocrinology, 2009, 201, 1-13.	1.2	37
128	Genome-Wide Analysis in Vivo of Translation with Nucleotide Resolution Using Ribosome Profiling. Science, 2009, 324, 218-223.	6.0	3,283
129	Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12741-12746.	3.3	72
130	Epigenomic profiling of cancer cells. International Journal of Biochemistry and Cell Biology, 2009, 41, 127-135.	1.2	42
131	Towards a genome-wide reconstruction of cis-regulatory networks in the human genome. Seminars in Cell and Developmental Biology, 2009, 20, 842-848.	2.3	11



#	ARTICLE	IF	CITATIONS
132	Using ChIP-chip and ChIP-seq to study the regulation of gene expression: Genome-wide localization studies reveal widespread regulation of transcription elongation. <i>Methods</i> , 2009, 48, 398-408.	1.9	49
133	ChIP-seq: Using high-throughput sequencing to discover protein-DNA interactions. <i>Methods</i> , 2009, 48, 240-248.	1.9	455
134	RNA-Seq quantitative measurement of expression through massively parallel RNA-sequencing. <i>Methods</i> , 2009, 48, 249-257.	1.9	414
135	Virus-host interactions: from systems biology to translational research. <i>Current Opinion in Microbiology</i> , 2009, 12, 432-438.	2.3	61
136	Deep sequencing of the zebrafish transcriptome response to mycobacterium infection. <i>Molecular Immunology</i> , 2009, 46, 2918-2930.	1.0	203
137	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. <i>Genome Research</i> , 2009, 19, 521-532.	2.4	286
138	Altruistic functions for selfish DNA. <i>Cell Cycle</i> , 2009, 8, 2895-2900.	1.3	60
139	Inherited Variation in Gene Expression. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 313-332.	2.5	71
140	Institutional shared resources and translational cancer research. <i>Journal of Translational Medicine</i> , 2009, 7, 54.	1.8	16
141	Next-Generation Sequencing: From Basic Research to Diagnostics. <i>Clinical Chemistry</i> , 2009, 55, 641-658.	1.5	668
142	Statistical inferences for isoform expression in RNA-Seq. <i>Bioinformatics</i> , 2009, 25, 1026-1032.	1.8	405
144	Correlating measurements across samples improves accuracy of large-scale expression profile experiments. <i>Genome Biology</i> , 2009, 10, R143.	13.9	14
145	Searching for SNPs with cloud computing. <i>Genome Biology</i> , 2009, 10, R134.	13.9	437
146	Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts. <i>Genome Biology</i> , 2009, 10, R115.	13.9	172
147	Methods for analyzing deep sequencing expression data: constructing the human and mouse promoterome with deepCAGE data. <i>Genome Biology</i> , 2009, 10, R79.	13.9	131
148	The need for speed. <i>Genome Biology</i> , 2009, 10, 212.	13.9	12
149	Evaluation of next generation sequencing platforms for population targeted sequencing studies. <i>Genome Biology</i> , 2009, 10, R32.	13.9	510
150	Identifying protein-coding genes in genomic sequences. <i>Genome Biology</i> , 2009, 10, 201.	13.9	82

#	ARTICLE	IF	CITATIONS
151	Systems medicine: the future of medical genomics and healthcare. <i>Genome Medicine</i> , 2009, 1, 2.	3.6	333
152	Short-Read Sequencing Technologies for Transcriptional Analyses. <i>Annual Review of Plant Biology</i> , 2009, 60, 305-333.	8.6	118
153	The DNA sequencing renaissance and its implications for epigenomics. <i>Epigenomics</i> , 2009, 1, 5-8.	1.0	5
154	Genome assembly reborn: recent computational challenges. <i>Briefings in Bioinformatics</i> , 2009, 10, 354-366.	3.2	291
155	A Generalized Multivariate Approach for Correlation-Based Pattern Discovery from Replicated Molecular Profiling Data. , 2009, , .		0
156	Current-generation high-throughput sequencing: deepening insights into mammalian transcriptomes. <i>Genes and Development</i> , 2009, 23, 1379-1386.	2.7	140
157	Advantages of next-generation sequencing versus the microarray in epigenetic research. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 174-183.	3.8	218
158	Estimating an Optimal Correlation Structure from Replicated Molecular Profiling Data Using Finite Mixture Models. , 2009, , .		6
159	Mapping uniquely occurring short sequences derived from high throughput technologies to a reference genome. , 2009, , .		11
160	Quantification of the yeast transcriptome by single-molecule sequencing. <i>Nature Biotechnology</i> , 2009, 27, 652-658.	9.4	172
161	Global Genomic Characterization of Acute Lymphoblastic Leukemia. <i>Seminars in Hematology</i> , 2009, 46, 3-15.	1.8	71
162	Cancer genome sequencing: a review. <i>Human Molecular Genetics</i> , 2009, 18, R163-R168.	1.4	185
163	RECOUNT: EXPECTATION MAXIMIZATION BASED ERROR CORRECTION TOOL FOR NEXT GENERATION SEQUENCING DATA. , 2009, , .		12
164	Tagging Transcription Starting Sites with CAGE. , 2009, , 7-20.		1
165	Algorithms for mapping short degenerate and weighted sequences to a reference genome. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 385.	0.3	3
166	Novel Insights into Adipogenesis from Omics Data. <i>Current Medicinal Chemistry</i> , 2009, 16, 2952-2964.	1.2	35
167	Nuclear Origins of Cell-to-Cell Variability. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2010, 75, 87-94.	2.0	9
168	Quantifying Whole Transcriptome Size, a Prerequisite for Understanding Transcriptome Evolution Across Species: An Example from a Plant Allopolyploid. <i>Genome Biology and Evolution</i> , 2010, 2, 534-546.	1.1	110

#	ARTICLE	IF	CITATIONS
169	Functional Genomics: New Insights into the Function of Low Levels of Gene Expression in Stem Cells. <i>Current Genomics</i> , 2010, 11, 354-358.	0.7	9
170	A survey of statistical software for analysing RNA-seq data. <i>Human Genomics</i> , 2010, 5, 56.	1.4	24
171	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. <i>Nature Precedings</i> , 2010, .	0.1	13
173	Gamma-based clustering via ordered means with application to gene-expression analysis. <i>Annals of Statistics</i> , 2010, 38, 3217-3244.	1.4	1
174	Transcriptional profiling of day 12 porcine embryonic disc and trophectoderm samples using ultra-deep sequencing technologies. <i>Molecular Reproduction and Development</i> , 2010, 77, 812-819.	1.0	16
175	Improved Sensitivity of DNA Microarrays Using Photonic Crystal Enhanced Fluorescence. <i>Analytical Chemistry</i> , 2010, 82, 6854-6861.	3.2	49
176	Rapid interactome profiling by massive sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e110-e110.	6.5	62
177	Mutational analysis of the C-terminal FATC domain of <i>Saccharomyces cerevisiae</i> Tra1. <i>Current Genetics</i> , 2010, 56, 447-465.	0.8	28
178	RNA-seq: from technology to biology. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 569-579.	2.4	423
179	Transcriptomics in ecotoxicology. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 917-923.	1.9	97
180	SNP discovery in the bovine milk transcriptome using RNA-Seq technology. <i>Mammalian Genome</i> , 2010, 21, 592-598.	1.0	164
181	The next-generation sequencing technology and application. <i>Protein and Cell</i> , 2010, 1, 520-536.	4.8	112
182	Systems Biology-Based Approaches to Understand HIV-Exposed Uninfected Women. <i>Current HIV/AIDS Reports</i> , 2010, 7, 53-59.	1.1	14
183	Assigning biological functions to rice genes by genome annotation, expression analysis and mutagenesis. <i>Biotechnology Letters</i> , 2010, 32, 1753-1763.	1.1	17
184	Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. <i>Molecular Breeding</i> , 2010, 25, 553-570.	1.0	112
185	Structural annotation of equine protein-coding genes determined by mRNA sequencing. <i>Animal Genetics</i> , 2010, 41, 121-130.	0.6	46
186	Transcriptome analysis of Traf6 function in the innate immune response of zebrafish embryos. <i>Molecular Immunology</i> , 2010, 48, 179-190.	1.0	55
187	Conservation genetics in transition to conservation genomics. <i>Trends in Genetics</i> , 2010, 26, 177-187.	2.9	314

#	ARTICLE	IF	CITATIONS
188	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. <i>BMC Bioinformatics</i> , 2010, 11, 369.	1.2	94
189	SEQADAPT: an adaptable system for the tracking, storage and analysis of high throughput sequencing experiments. <i>BMC Bioinformatics</i> , 2010, 11, 377.	1.2	0
190	PeakAnalyzer: Genome-wide annotation of chromatin binding and modification loci. <i>BMC Bioinformatics</i> , 2010, 11, 415.	1.2	210
191	Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. <i>BMC Bioinformatics</i> , 2010, 11, 94.	1.2	1,421
192	Translog, a web browser for studying the expression divergence of homologous genes. <i>BMC Bioinformatics</i> , 2010, 11, S59.	1.2	0
193	The utility of mass spectrometry-based proteomic data for validation of novel alternative splice forms reconstructed from RNA-Seq data: a preliminary assessment. <i>BMC Bioinformatics</i> , 2010, 11, S14.	1.2	52
194	Digital gene expression analysis of two life cycle stages of the human-infective parasite, <i>Trypanosoma brucei gambiense</i> reveals differentially expressed clusters of co-regulated genes. <i>BMC Genomics</i> , 2010, 11, 124.	1.2	50
195	Gene-specific FACS sorting method for target selection in high-throughput amplicon sequencing. <i>BMC Genomics</i> , 2010, 11, 140.	1.2	5
196	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <i>BMC Genomics</i> , 2010, 11, 244.	1.2	45
197	A comparison of massively parallel nucleotide sequencing with oligonucleotide microarrays for global transcription profiling. <i>BMC Genomics</i> , 2010, 11, 282.	1.2	124
198	Comparison and calibration of transcriptome data from RNA-Seq and tiling arrays. <i>BMC Genomics</i> , 2010, 11, 383.	1.2	97
199	Heart transcriptome of the bank vole ( <i>Myodes glareolus</i> ): towards understanding the evolutionary variation in metabolic rate. <i>BMC Genomics</i> , 2010, 11, 390.	1.2	22
200	Incorporation of non-natural nucleotides into template-switching oligonucleotides reduces background and improves cDNA synthesis from very small RNA samples. <i>BMC Genomics</i> , 2010, 11, 413.	1.2	48
201	Deep sequencing-based transcriptome profiling analysis of bacteria-challenged <i>Lateolabrax japonicus</i> reveals insight into the immune-relevant genes in marine fish. <i>BMC Genomics</i> , 2010, 11, 472.	1.2	189
202	Assessment of orthologous splicing isoforms in human and mouse orthologous genes. <i>BMC Genomics</i> , 2010, 11, 534.	1.2	37
203	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <i>BMC Genomics</i> , 2010, 11, 663.	1.2	201
204	De novo assembled expressed gene catalog of a fast-growing Eucalyptus tree produced by Illumina mRNA-Seq. <i>BMC Genomics</i> , 2010, 11, 681.	1.2	150
205	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice ( <i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2010, 11, 683.	1.2	76

#	ARTICLE	IF	CITATIONS
206	Analysis of transcript and protein overlap in a human osteosarcoma cell line. BMC Genomics, 2010, 11, 684.	1.2	13
207	Comparison of transcriptomic landscapes of bovine embryos using RNA-Seq. BMC Genomics, 2010, 11, 711.	1.2	75
208	De novo assembly and characterization of root transcriptome using Illumina paired-end sequencing and development of cSSR markers in sweetpotato ( <i>Ipomoea batatas</i> ). BMC Genomics, 2010, 11, 726.	1.2	386
209	RNA-Seq Atlas of Glycine max: A guide to the soybean transcriptome. BMC Plant Biology, 2010, 10, 160.	1.6	634
210	ExprEssence - Revealing the essence of differential experimental data in the context of an interaction/regulation net-work. BMC Systems Biology, 2010, 4, 164.	3.0	71
211	Deep sequencing of coding and non-coding RNA in the CNS. Brain Research, 2010, 1338, 146-154.	1.1	10
212	Recent advances in DNA sequencing methods – general principles of sample preparation. Experimental Cell Research, 2010, 316, 1339-1343.	1.2	66
213	Prokaryotic whole-transcriptome analysis: deep sequencing and tiling arrays. Microbial Biotechnology, 2010, 3, 125-130.	2.0	20
214	Transcriptome sequencing, microarray, and proteomic analyses reveal cellular and metabolic impact of hepatitis C virus infection in vitro. Hepatology, 2010, 52, 443-453.	3.6	103
215	Non-coding RNAs: Meet thy masters. BioEssays, 2010, 32, 599-608.	1.2	264
216	Reaching the depth of the Chinese hamster ovary cell transcriptome. Biotechnology and Bioengineering, 2010, 105, 1002-1009.	1.7	29
217	Transcriptome study for early hematopoiesis – achievement, challenge and new opportunity. Journal of Cellular Physiology, 2010, 223, 549-552.	2.0	2
218	Transcriptome profiling in neurodegenerative disease. Journal of Neuroscience Methods, 2010, 193, 189-202.	1.3	57
219	Advances in Nutrigenomics research: Novel and future analytical approaches to investigate the biological activity of natural compounds and food functions. Journal of Pharmaceutical and Biomedical Analysis, 2010, 51, 290-304.	1.4	92
220	Towards reliable isoform quantification using RNA-SEQ data. BMC Bioinformatics, 2010, 11, S6.	1.2	32
221	ChIP-PaM: an algorithm to identify protein-DNA interaction using ChIP-Seq data. Theoretical Biology and Medical Modelling, 2010, 7, 18.	2.1	16
222	Systems analysis of alternative splicing and its regulation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 550-565.	6.6	14
223	Model-Based Quality Assessment and Base-Calling for Second-Generation Sequencing Data. Biometrics, 2010, 66, 665-674.	0.8	50

#	ARTICLE	IF	CITATIONS
224	Next generation sequencing of microbial transcriptomes: challenges and opportunities. FEMS Microbiology Letters, 2010, 302, 1-7.	0.7	158
225	Alternative splicing: global insights. FEBS Journal, 2010, 277, 856-866.	2.2	128
226	Massive parallel sequencing in animal genetics: wherefroms and wheretos. Animal Genetics, 2010, 41, 561-569.	0.6	44
227	Nucleotide divergence vs. gene expression differentiation: comparative transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. Molecular Ecology, 2010, 19, 162-175.	2.0	125
228	A genetic basis for the phenotypic differentiation between siscowet and lean lake trout ( <i>Salvelinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.0	110
229	Genome-wide analysis of alternative splicing evolution among <i>Mus</i> subspecies. Molecular Ecology, 2010, 19, 228-239.	2.0	52
230	The transcriptomics of sympatric dwarf and normal lake whitefish ( <i>Coregonus clupeaformis</i> spp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5389-5403.	2.0	93
231	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-seq. Molecular Microbiology, 2010, 76, 12-24.	1.2	374
232	Dynamic regulation of alternative splicing and chromatin structure in <i>Drosophila</i> gonads revealed by RNA-seq. Cell Research, 2010, 20, 763-783.	5.7	107
233	Interleukin-7 (IL-7) and IL-7 splice variants affect differentiation of human neural progenitor cells. Genes and Immunity, 2010, 11, 11-20.	2.2	43
234	Accurate quantification of dystrophin mRNA and exon skipping levels in Duchenne Muscular Dystrophy. Laboratory Investigation, 2010, 90, 1396-1402.	1.7	37
235	Understanding mechanisms underlying human gene expression variation with RNA sequencing. Nature, 2010, 464, 768-772.	13.7	1,200
236	Transcriptome genetics using second generation sequencing in a Caucasian population. Nature, 2010, 464, 773-777.	13.7	782
237	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
238	Mammalian microRNAs predominantly act to decrease target mRNA levels. Nature, 2010, 466, 835-840.	13.7	3,513
239	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology, 2010, 28, 503-510.	9.4	1,251
240	Advancing RNA-Seq analysis. Nature Biotechnology, 2010, 28, 421-423.	9.4	192
241	Haploidy with histones. Nature Biotechnology, 2010, 28, 423-424.	9.4	10

#	ARTICLE	IF	CITATIONS
242	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	9.4	1,504
243	The developmental dynamics of the maize leaf transcriptome. <i>Nature Genetics</i> , 2010, 42, 1060-1067.	9.4	660
244	RNA sequencing shows no dosage compensation of the active X-chromosome. <i>Nature Genetics</i> , 2010, 42, 1043-1047.	9.4	199
245	Parallel, tag-directed assembly of locally derived short sequence reads. <i>Nature Methods</i> , 2010, 7, 119-122.	9.0	144
246	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
247	Alternative expression analysis by RNA sequencing. <i>Nature Methods</i> , 2010, 7, 843-847.	9.0	283
248	Analysis and design of RNA sequencing experiments for identifying isoform regulation. <i>Nature Methods</i> , 2010, 7, 1009-1015.	9.0	1,224
249	FragSeq: transcriptome-wide RNA structure probing using high-throughput sequencing. <i>Nature Methods</i> , 2010, 7, 995-1001.	9.0	289
250	Simplifying complexity. <i>Nature Methods</i> , 2010, 7, 793-795.	9.0	1
251	RNA-Seq analysis to capture the transcriptome landscape of a single cell. <i>Nature Protocols</i> , 2010, 5, 516-535.	5.5	450
252	Next-generation genomics: an integrative approach. <i>Nature Reviews Genetics</i> , 2010, 11, 476-486.	7.7	554
253	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571.	7.7	398
254	Allied Industry Approaches to Alter Intramuscular Fat Content and Composition in Beef Animals. <i>Journal of Food Science</i> , 2010, 75, R1-8.	1.5	59
255	CHARACTERIZING THE GENOME OF WILD RELATIVES OF LIMNANTHES ALBA (MEADOWFOAM) USING MASSIVELY PARALLEL SEQUENCING. <i>Acta Horticulturae</i> , 2010, , 309-314.	0.1	7
257	Microbiome Profiling by Illumina Sequencing of Combinatorial Sequence-Tagged PCR Products. <i>PLoS ONE</i> , 2010, 5, e15406.	1.1	259
258	A Statistical Method for the Detection of Alternative Splicing Using RNA-Seq. <i>PLoS ONE</i> , 2010, 5, e8529.	1.1	36
259	Tumor Transcriptome Sequencing Reveals Allelic Expression Imbalances Associated with Copy Number Alterations. <i>PLoS ONE</i> , 2010, 5, e9317.	1.1	134
260	In-Depth Transcriptome Analysis Reveals Novel TARs and Prevalent Antisense Transcription in Human Cell Lines. <i>PLoS ONE</i> , 2010, 5, e9762.	1.1	17

#	ARTICLE	IF	CITATIONS
261	SWISS MADE: Standardized Within Class Sum of Squares to Evaluate Methodologies and Dataset Elements. PLoS ONE, 2010, 5, e9905.	1.1	12
262	Evaluation of Algorithm Performance in ChIP-Seq Peak Detection. PLoS ONE, 2010, 5, e11471.	1.1	244
263	HMMSplicer: A Tool for Efficient and Sensitive Discovery of Known and Novel Splice Junctions in RNA-Seq Data. PLoS ONE, 2010, 5, e13875.	1.1	50
264	De Novo Transcriptome Sequencing in Anopheles funestus Using Illumina RNA-Seq Technology. PLoS ONE, 2010, 5, e14202.	1.1	132
265	The Prevalence and Regulation of Antisense Transcripts in Schizosaccharomyces pombe. PLoS ONE, 2010, 5, e15271.	1.1	50
266	A Dual Platform Approach to Transcript Discovery for the Planarian Schmidtea Mediterranea to Establish RNAseq for Stem Cell and Regeneration Biology. PLoS ONE, 2010, 5, e15617.	1.1	61
267	Highly consistent, fully representative mRNA-Seq libraries from ten nanograms of total RNA. BioTechniques, 2010, 49, 898-904.	0.8	16
268	The Human Transcriptome. , 2010, , 89-103.		2
269	Statistical Analyses of Next Generation Sequence Data: A Partial Overview. Journal of Proteomics and Bioinformatics, 2010, 03, 183-190.	0.4	34
270	Scaffolding a <i>Caenorhabditis</i> nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747.	2.4	83
271	Genome-wide misexpression of X-linked versus autosomal genes associated with hybrid male sterility. Genome Research, 2010, 20, 1097-1102.	2.4	38
272	Hydroxyurea-induced global transcriptional suppression in mouse ES cells. Carcinogenesis, 2010, 31, 1661-1668.	1.3	13
273	Evolutionary history of regulatory variation in human populations. Human Molecular Genetics, 2010, 19, R197-R203.	1.4	10
274	Functional <i>cis</i> -regulatory genomics for systems biology. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3930-3935.	3.3	50
275	Computational identification of tissue-specific alternative splicing elements in mouse genes from RNA-Seq. Nucleic Acids Research, 2010, 38, 7895-7907.	6.5	15
276	Cost-Effective Sequencing of Full-Length cDNA Clones Powered by a De Novo-Reference Hybrid Assembly. PLoS ONE, 2010, 5, e10517.	1.1	11
277	Transcriptional Profiling by Deep Sequencing Identifies Differences in mRNA Transcript Abundance in In Vivo-Derived Versus In Vitro-Cultured Porcine Blastocyst Stage Embryos1. Biology of Reproduction, 2010, 83, 791-798.	1.2	66
278	Probabilistic analysis of gene expression measurements from heterogeneous tissues. Bioinformatics, 2010, 26, 2571-2577.	1.8	75



#	ARTICLE	IF	CITATIONS
279	Regulatory divergence in <i>Drosophila</i> revealed by mRNA-seq. <i>Genome Research</i> , 2010, 20, 816-825.	2.4	385
280	Into the unknown: expression profiling without genome sequence information in CHO by next generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 3999-4010.	6.5	97
281	Unconstrained mining of transcript data reveals increased alternative splicing complexity in the human transcriptome. <i>Nucleic Acids Research</i> , 2010, 38, 4740-4754.	6.5	55
282	What can whole genome expression data tell us about the ecology and evolution of personality?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 4001-4012.	1.8	95
283	A minimum of two distinct heritable factors are required to explain correlation structures in proliferating lymphocytes. <i>Journal of the Royal Society Interface</i> , 2010, 7, 1049-1059.	1.5	27
284	Deep mRNA Sequencing for In Vivo Functional Analysis of Cardiac Transcriptional Regulators. <i>Circulation Research</i> , 2010, 106, 1459-1467.	2.0	76
285	Detection, Validation, and Downstream Analysis of Allelic Variation in Gene Expression. <i>Genetics</i> , 2010, 184, 119-128.	1.2	60
286	Noncanonical transcript forms in yeast and their regulation during environmental stress. <i>Rna</i> , 2010, 16, 1256-1267.	1.6	72
287	Transcriptome and targetome analysis in MIR155 expressing cells using RNA-seq. <i>Rna</i> , 2010, 16, 1610-1622.	1.6	53
288	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	3.2	324
289	Digital Gene Expression Signatures for Maize Development. <i>Plant Physiology</i> , 2010, 154, 1024-1039.	2.3	82
290	Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1476-1481.	3.3	101
291	De novo motif identification improves the accuracy of predicting transcription factor binding sites in CHIP-Seq data analysis. <i>Nucleic Acids Research</i> , 2010, 38, e126-e126.	6.5	62
292	Evolution of alternative splicing in primate brain transcriptomes. <i>Human Molecular Genetics</i> , 2010, 19, 2958-2973.	1.4	47
293	Characterization of Transcription Start Sites of Putative Non-coding RNAs by Multifaceted Use of Massively Paralleled Sequencer. <i>DNA Research</i> , 2010, 17, 169-183.	1.5	4
294	Prediction of alternative isoforms from exon expression levels in RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2010, 38, e112-e112.	6.5	134
295	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010, 38, e178-e178.	6.5	946
296	Detection of splice junctions from paired-end RNA-seq data by SpliceMap. <i>Nucleic Acids Research</i> , 2010, 38, 4570-4578.	6.5	300

#	ARTICLE	IF	CITATIONS
297	Deep RNA sequencing at single base-pair resolution reveals high complexity of the rice transcriptome. <i>Genome Research</i> , 2010, 20, 646-654.	2.4	435
298	Polygenic and directional regulatory evolution across pathways in <i>Saccharomyces</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5058-5063.	3.3	93
299	Quantitative and Qualitative RNA-Seq-Based Evaluation of Epstein-Barr Virus Transcription in Type I Latency Burkitt's Lymphoma Cells. <i>Journal of Virology</i> , 2010, 84, 13053-13058.	1.5	43
300	Strand-specific deep sequencing of the transcriptome. <i>Genome Research</i> , 2010, 20, 989-999.	2.4	76
301	Arginine methylation mediated by the <i>Arabidopsis</i> homolog of PRMT5 is essential for proper pre-mRNA splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19114-19119.	3.3	174
302	ISOFORM ABUNDANCE INFERENCE PROVIDES A MORE ACCURATE ESTIMATION OF GENE EXPRESSION LEVELS IN RNA-SEQ. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 177-192.	0.3	33
303	A two-parameter generalized Poisson model to improve the analysis of RNA-seq data. <i>Nucleic Acids Research</i> , 2010, 38, e170-e170.	6.5	131
304	Detection of splicing events and multiread locations from RNA-seq data based on a geometric-tail (GT) distribution of intron length. , 2010, , .		0
305	System-Level Analysis of Neuroblastoma Tumor-Initiating Cells Implicates AURKB as a Novel Drug Target for Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 4572-4582.	3.2	43
306	Digital transcriptome profiling from attomole-level RNA samples. <i>Genome Research</i> , 2010, 20, 519-525.	2.4	56
307	Glucocorticoids Modulate MicroRNA Expression and Processing during Lymphocyte Apoptosis. <i>Journal of Biological Chemistry</i> , 2010, 285, 36698-36708.	1.6	81
308	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5254-5259.	3.3	168
309	Altered distributions of Gemini of coiled bodies and mitochondria in motor neurons of <i>TDP-43</i> transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16325-16330.	3.3	283
310	Genome variation discovery with high-throughput sequencing data. <i>Briefings in Bioinformatics</i> , 2010, 11, 3-14.	3.2	58
311	Genomics of medulloblastoma: from Giemsa-banding to next-generation sequencing in 20 years. <i>Neurosurgical Focus</i> , 2010, 28, E6.	1.0	48
312	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239
313	Microdissection of the gene expression codes driving nephrogenesis. <i>Organogenesis</i> , 2010, 6, 263-269.	0.4	4
314	Suppression of the Vacuolar Invertase Gene Prevents Cold-Induced Sweetening in Potato. <i>Plant Physiology</i> , 2010, 154, 939-948.	2.3	165

#	ARTICLE	IF	CITATIONS
315	Noisy Splicing Drives mRNA Isoform Diversity in Human Cells. <i>PLoS Genetics</i> , 2010, 6, e1001236.	1.5	254
316	Expression in Aneuploid <i>Drosophila</i> S2 Cells. <i>PLoS Biology</i> , 2010, 8, e1000320.	2.6	161
317	Intergenic and Repeat Transcription in Human, Chimpanzee and Macaque Brains Measured by RNA-Seq. <i>PLoS Computational Biology</i> , 2010, 6, e1000843.	1.5	62
318	Uncovering the Complexity of Transcriptomes with RNA-Seq. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-19.	3.0	315
319	The Transcriptomes of Two Heritable Cell Types Illuminate the Circuit Governing Their Differentiation. <i>PLoS Genetics</i> , 2010, 6, e1001070.	1.5	147
320	A Comprehensive, Quantitative, and Genome-Wide Model of Translation. <i>PLoS Computational Biology</i> , 2010, 6, e1000865.	1.5	80
321	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. <i>PLoS Biology</i> , 2010, 8, e1000480.	2.6	142
322	A Young <i>Drosophila</i> Duplicate Gene Plays Essential Roles in Spermatogenesis by Regulating Several Y-Linked Male Fertility Genes. <i>PLoS Genetics</i> , 2010, 6, e1001255.	1.5	68
323	Arbovirus Detection in Insect Vectors by Rapid, High-Throughput Pyrosequencing. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e878.	1.3	53
324	Genome-wide analysis of mRNA abundance in two life-cycle stages of <i>Trypanosoma brucei</i> and identification of splicing and polyadenylation sites. <i>Nucleic Acids Research</i> , 2010, 38, 4946-4957.	6.5	276
325	Control of Transcription by Cell Size. <i>PLoS Biology</i> , 2010, 8, e1000523.	2.6	108
326	PPARG: Gene Expression Regulation and Next-Generation Sequencing for Unsolved Issues. <i>PPAR Research</i> , 2010, 2010, 1-17.	1.1	52
327	mRNA-seq with agnostic splice site discovery for nervous system transcriptomics tested in chronic pain. <i>Genome Research</i> , 2010, 20, 847-860.	2.4	71
328	Application of <i>œomics</i> to Prion Biomarker Discovery. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-14.	3.0	19
329	MamPhEA: a web tool for mammalian phenotype enrichment analysis. <i>Bioinformatics</i> , 2010, 26, 2212-2213.	1.8	26
330	Both Noncoding and Protein-Coding RNAs Contribute to Gene Expression Evolution in the Primate Brain. <i>Genome Biology and Evolution</i> , 2010, 2, 67-79.	1.1	103
331	REAL. , 2010, , .		24
332	RNA-Seq Analysis of Sulfur-Deprived <i>Chlamydomonas</i> Cells Reveals Aspects of Acclimation Critical for Cell Survival. <i>Plant Cell</i> , 2010, 22, 2058-2084.	3.1	253

#	ARTICLE	IF	CITATIONS
333	Transcriptional Control of Acinar Development and Homeostasis. <i>Progress in Molecular Biology and Translational Science</i> , 2010, 97, 1-40.	0.9	40
334	Close association of RNA polymerase II and many transcription factors with Pol III genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3639-3644.	3.3	167
335	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	2.4	126
336	Gene Expression Profiling of Mouse Embryos with Microarrays. <i>Methods in Enzymology</i> , 2010, 477, 511-541.	0.4	5
337	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. <i>Bioinformatics</i> , 2010, 26, 730-736.	1.8	192
338	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
339	JASPAR 2010: the greatly expanded open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2010, 38, D105-D110.	6.5	529
340	Experimental Approaches to the Human Renal Transcriptome. <i>Seminars in Nephrology</i> , 2010, 30, 455-467.	0.6	8
341	Integrative Systems Biology for Data-Driven Knowledge Discovery. <i>Seminars in Nephrology</i> , 2010, 30, 443-454.	0.6	20
342	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010, 11, R106.	3.8	13,707
343	RNA-Seq: A Method for Comprehensive Transcriptome Analysis. <i>Current Protocols in Molecular Biology</i> , 2010, 89, Unit 4.11.1-13.	2.9	218
344	A scaling normalization method for differential expression analysis of RNA-seq data. <i>Genome Biology</i> , 2010, 11, R25.	13.9	6,234
345	Statistical Issues in the Analysis of ChIP-Seq and RNA-Seq Data. <i>Genes</i> , 2010, 1, 317-334.	1.0	17
346	Next-Generation Sequencing Techniques for Eukaryotic Microorganisms: Sequencing-Based Solutions to Biological Problems. <i>Eukaryotic Cell</i> , 2010, 9, 1300-1310.	3.4	120
347	Molecular diagnostics in transplantation. <i>Nature Reviews Nephrology</i> , 2010, 6, 614-628.	4.1	80
348	Evolutionary Analysis and Expression Profiling of Zebra Finch Immune Genes. <i>Genome Biology and Evolution</i> , 2010, 2, 781-790.	1.1	38
349	ChIP-Seq. <i>Methods in Enzymology</i> , 2010, 470, 77-104.	0.4	23
350	Genome-Wide Translational Profiling by Ribosome Footprinting. <i>Methods in Enzymology</i> , 2010, 470, 119-142.	0.4	159

#	ARTICLE	IF	CITATIONS
353	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
354	Target mRNA abundance dilutes microRNA and siRNA activity. <i>Molecular Systems Biology</i> , 2010, 6, 363.	3.2	299
355	Probabilistic Peak Calling and Controlling False Discovery Rate Estimations in Transcription Factor Binding Site Mapping from ChIP-seq. <i>Methods in Molecular Biology</i> , 2010, 674, 161-177.	0.4	3
356	FusionSeq: a modular framework for finding gene fusions by analyzing paired-end RNA-sequencing data. <i>Genome Biology</i> , 2010, 11, R104.	3.8	137
357	Identification of tumor-associated cassette exons in human cancer through EST-based computational prediction and experimental validation. <i>Molecular Cancer</i> , 2010, 9, 230.	7.9	5
358	Replacement of Rbpj With Rbpjl in the PTF1 Complex Controls the Final Maturation of Pancreatic Acinar Cells. <i>Gastroenterology</i> , 2010, 139, 270-280.	0.6	85
359	Optimization of de novo transcriptome assembly from next-generation sequencing data. <i>Genome Research</i> , 2010, 20, 1432-1440.	2.4	324
360	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010, 20, 413-427.	2.4	248
361	Unique Signatures of Long Noncoding RNA Expression in Response to Virus Infection and Altered Innate Immune Signaling. <i>MBio</i> , 2010, 1, .	1.8	237
362	Exploring plant transcriptomes using ultra high-throughput sequencing. <i>Briefings in Functional Genomics</i> , 2010, 9, 118-128.	1.3	108
363	Advances in porcine genomics and proteomics—a toolbox for developing the pig as a model organism for molecular biomedical research. <i>Briefings in Functional Genomics</i> , 2010, 9, 208-219.	1.3	140
364	Studying bacterial transcriptomes using RNA-seq. <i>Current Opinion in Microbiology</i> , 2010, 13, 619-624.	2.3	238
365	Genome-wide Identification of Polycomb-Associated RNAs by RIP-seq. <i>Molecular Cell</i> , 2010, 40, 939-953.	4.5	914
366	Exon Junction Complex Subunits Are Required to Splice <i>Drosophila</i> MAP Kinase, a Large Heterochromatic Gene. <i>Cell</i> , 2010, 143, 238-250.	13.5	102
367	Perturbation analysis analyzedâ€”mathematical modeling of intact and perturbed gene regulatory circuits for animal development. <i>Developmental Biology</i> , 2010, 344, 1110-1118.	0.9	4
368	A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. <i>Genomics</i> , 2010, 96, 259-265.	1.3	184
369	A comparative analysis of liver transcriptome suggests divergent liver function among human, mouse and rat. <i>Genomics</i> , 2010, 96, 281-289.	1.3	41
370	Genomic SELEX: A discovery tool for genomic aptamers. <i>Methods</i> , 2010, 52, 125-132.	1.9	55

#	ARTICLE	IF	CITATIONS
371	Next-generation sequencing in aging research: Emerging applications, problems, pitfalls and possible solutions. <i>Ageing Research Reviews</i> , 2010, 9, 315-323.	5.0	98
372	What can next generation sequencing do for you? Next generation sequencing as a valuable tool in plant research. <i>Plant Biology</i> , 2010, 12, 831-841.	1.8	140
373	Promiscuity of enhancer, coding and non-coding transcription functions in ultraconserved elements. <i>BMC Genomics</i> , 2010, 11, 151.	1.2	32
374	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. <i>Nature Biotechnology</i> , 2010, 28, 511-515.	9.4	13,805
375	A survey of sequence alignment algorithms for next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 473-483.	3.2	765
376	Transcriptome Analysis of <i>Pseudomonas syringae</i> Identifies New Genes, Noncoding RNAs, and Antisense Activity. <i>Journal of Bacteriology</i> , 2010, 192, 2359-2372.	1.0	121
377	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2010, 20, 45-58.	2.4	825
378	Genome-wide analysis of allelic expression imbalance in human primary cells by high-throughput transcriptome resequencing. <i>Human Molecular Genetics</i> , 2010, 19, 122-134.	1.4	197
379	Survey of the transcriptome of <i>Aspergillus oryzae</i> via massively parallel mRNA sequencing. <i>Nucleic Acids Research</i> , 2010, 38, 5075-5087.	6.5	189
380	Cell-type specific analysis of translating RNAs in developing flowers reveals new levels of control. <i>Molecular Systems Biology</i> , 2010, 6, 419.	3.2	155
381	Advances in Computational Biology. <i>Advances in Experimental Medicine and Biology</i> , 2010, , .	0.8	2
382	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	3.2	141
383	Biases in Illumina transcriptome sequencing caused by random hexamer priming. <i>Nucleic Acids Research</i> , 2010, 38, e131-e131.	6.5	573
384	DEGseq: an R package for identifying differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2010, 26, 136-138.	1.8	3,728
385	RNA-Seq gene expression estimation with read mapping uncertainty. <i>Bioinformatics</i> , 2010, 26, 493-500.	1.8	1,012
386	DNA Microarrays in Biological Discovery and Patient Care. , 2010, , 73-88.		5
387	Genomic Analyses of Hormone Signaling and Gene Regulation. <i>Annual Review of Physiology</i> , 2010, 72, 191-218.	5.6	78
388	Bioinformatics for Next Generation Sequencing Data. <i>Genes</i> , 2010, 1, 294-307.	1.0	65

#	ARTICLE	IF	CITATIONS
390	Systems Biology for Ecology. <i>Advances in Ecological Research</i> , 2010, 43, 87-149.	1.4	29
391	Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. <i>Genome Biology</i> , 2010, 11, R119.	13.9	499
392	Homoeolog-specific retention and use in allotetraploid <i>Arabidopsis suecica</i> depends on parent of origin and network partners. <i>Genome Biology</i> , 2010, 11, R125.	13.9	83
393	An atlas of bovine gene expression reveals novel distinctive tissue characteristics and evidence for improving genome annotation. <i>Genome Biology</i> , 2010, 11, R102.	3.8	46
394	Sequencing and analysis of an Irish human genome. <i>Genome Biology</i> , 2010, 11, R91.	13.9	36
395	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	159
396	Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. <i>Genome Biology</i> , 2010, 11, R86.	13.9	3,082
397	Cloud-scale RNA-sequencing differential expression analysis with Myrna. <i>Genome Biology</i> , 2010, 11, R83.	13.9	268
398	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010, 11, R87.	13.9	122
399	Identification of novel exons and transcribed regions by chimpanzee transcriptome sequencing. <i>Genome Biology</i> , 2010, 11, R78.	13.9	26
400	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
401	A mouse embryonic stem cell bank for inducible overexpression of human chromosome 21 genes. <i>Genome Biology</i> , 2010, 11, R64.	13.9	16
402	Modeling non-uniformity in short-read rates in RNA-Seq data. <i>Genome Biology</i> , 2010, 11, R50.	13.9	165
403	Monovalent and unpoised status of most genes in undifferentiated cell-enriched <i>Drosophila</i> testis. <i>Genome Biology</i> , 2010, 11, R42.	13.9	65
404	Conserved developmental transcriptomes in evolutionarily divergent species. <i>Genome Biology</i> , 2010, 11, R35.	13.9	164
405	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010, 11, R14.	13.9	5,824
406	Data mining of mRNA-Seq and small RNA-Seq data to find microRNA targets. , 2010, , .		0
407	Statistical Design and Analysis of RNA Sequencing Data. <i>Genetics</i> , 2010, 185, 405-416.	1.2	332

#	ARTICLE	IF	CITATIONS
408	Estimating the Expression of Transcript Isoforms from mRNA-Seq via Nonnegative Least Squares. , 2010, , ,		3
409	Interrogating the Transcriptome of Oocytes and Preimplantation Embryos. <i>Methods in Enzymology</i> , 2010, 477, 481-510.	0.4	3
410	rQuant.web: a tool for RNA-Seq-based transcript quantitation. <i>Nucleic Acids Research</i> , 2010, 38, W348-W351.	6.5	58
411	Comprehensive annotation of the transcriptome of the human fungal pathogen <i>Candida albicans</i> using RNA-seq. <i>Genome Research</i> , 2010, 20, 1451-1458.	2.4	191
412	Characterization of Transcriptional Complexity during Berry Development in <i>Vitis vinifera</i> Using RNA-Seq. <i>Plant Physiology</i> , 2010, 152, 1787-1795.	2.3	330
413	Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq. <i>Genome Research</i> , 2010, 20, 1238-1249.	2.4	307
414	RNADAP&#x2014;RNA-Seq data annotation pipeline. , 2011, , ,		0
415	Multiple Sequence Assembly from Reads Alignable to a Common Reference Genome. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1283-1295.	1.9	2
416	Sequencing nucleic acids: from chemistry to medicine. <i>Chemical Communications</i> , 2011, 47, 7281.	2.2	26
417	AlleleSeq: analysis of allele&#x2014;specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522.	3.2	284
418	The real cost of sequencing: higher than you think!. <i>Genome Biology</i> , 2011, 12, 125.	13.9	299
419	Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. , 2011, , ,		0
420	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	2.4	172
421	Analysis of Transcriptome Complexity Through RNA Sequencing in Normal and Failing Murine Hearts. <i>Circulation Research</i> , 2011, 109, 1332-1341.	2.0	194
422	Improved RNA-Seq Partitions in Linear Models for Isoform Quantification. , 2011, , ,		0
423	Evaluation of normalization methods for RNA-Seq gene expression estimation. , 2011, 2011, 50-57.		4
424	Gene expression patterns are correlated with genomic and genic structure in soybean. <i>Genome</i> , 2011, 54, 10-18.	0.9	23
425	Recurrent chimeric RNAs enriched in human prostate cancer identified by deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9172-9177.	3.3	169



#	ARTICLE	IF	CITATIONS
426	Discovery of non-ETS gene fusions in human prostate cancer using next-generation RNA sequencing. <i>Genome Research</i> , 2011, 21, 56-67.	2.4	179
427	Posterior Probability of Discovery and Expected Rate of Discovery for Multiple Hypothesis Testing and High Throughput Assays. <i>Journal of the American Statistical Association</i> , 2011, 106, 984-996.	1.8	3
428	A comparison of RNA-Seq and high-density exon array for detecting differential gene expression between closely related species. <i>Nucleic Acids Research</i> , 2011, 39, 578-588.	6.5	123
429	RNA-sequence analysis of human B-cells. <i>Genome Research</i> , 2011, 21, 991-998.	2.4	126
430	Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223.	2.4	1,456
431	Comparing Next-Generation Sequencing and Microarray Technologies in a Toxicological Study of the Effects of Aristolochic Acid on Rat Kidneys. <i>Chemical Research in Toxicology</i> , 2011, 24, 1486-1493.	1.7	80
432	Tissue-Specific Proteins and Functional Implications. <i>Journal of Proteome Research</i> , 2011, 10, 1893-1903.	1.8	31
433	Epigenetic mechanisms in diabetic vascular complications. <i>Cardiovascular Research</i> , 2011, 90, 421-429.	1.8	178
434	Next-Generation Sequencing and Its Potential Impact. <i>Chemical Research in Toxicology</i> , 2011, 24, 1163-1168.	1.7	6
435	De Novo Assembly of Expressed Transcripts and Global Analysis of the <i>Phalaenopsis aphrodite</i> Transcriptome. <i>Plant and Cell Physiology</i> , 2011, 52, 1501-1514.	1.5	109
436	Toward Clinical Proteomics on a Next-Generation Sequencing Platform. <i>Analytical Chemistry</i> , 2011, 83, 666-670.	3.2	18
437	Pol III binding in six mammals shows conservation among amino acid isotypes despite divergence among tRNA genes. <i>Nature Genetics</i> , 2011, 43, 948-955.	9.4	94
438	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. <i>Genes and Development</i> , 2011, 25, 1915-1927.	2.7	3,208
439	RNA Sequencing Reveals Novel Gene Clusters in Bovine Conceptuses Associated with Maternal Recognition of Pregnancy and Implantation <sup>1</sup> . <i>Biology of Reproduction</i> , 2011, 85, 1143-1151.	1.2	88
440	Regulation of nucleosome landscape and transcription factor targeting at tissue-specific enhancers by BRG1. <i>Genome Research</i> , 2011, 21, 1650-1658.	2.4	160
441	A Generalized Multivariate Approach to Pattern Discovery from Replicated and Incomplete Genome-Wide Measurements. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1153-1169.	1.9	1
442	Measuring reproducibility of high-throughput experiments. <i>Annals of Applied Statistics</i> , 2011, 5, .	0.5	868
443	Analyzing Schizophrenia by DNA Microarrays. <i>Biological Psychiatry</i> , 2011, 69, 157-162.	0.7	58

#	ARTICLE	IF	CITATIONS
444	Analysis of Transcriptome Differences between Resistant and Susceptible Strains of the Citrus Red Mite <i>Panonychus citri</i> (Acari: Tetranychidae). <i>PLoS ONE</i> , 2011, 6, e28516.	1.1	81
445	Protocol Dependence of Sequencing-Based Gene Expression Measurements. <i>PLoS ONE</i> , 2011, 6, e19287.	1.1	97
446	Transcriptome Profiling Using Single-Molecule Direct RNA Sequencing. <i>Methods in Molecular Biology</i> , 2011, 733, 51-61.	0.4	34
447	Genomic Analysis at the Single-Cell Level. <i>Annual Review of Genetics</i> , 2011, 45, 431-445.	3.2	187
448	Molecular Targets of Alcohol Action. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 98, 293-347.	0.9	15
449	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. <i>Journal of Computational Biology</i> , 2011, 18, 1693-1707.	0.8	139
450	A Strand-Specific Library Preparation Protocol for RNA Sequencing. <i>Methods in Enzymology</i> , 2011, 500, 79-98.	0.4	127
451	On Differential Gene expression Using RNA-Seq Data. <i>Cancer Informatics</i> , 2011, 10, CIN.S7473.	0.9	18
452	Sequencing transcriptomes in toto. <i>Integrative Biology (United Kingdom)</i> , 2011, 3, 522.	0.6	16
453	A Portrait of the Transcriptome of the Neglected Trematode, <i>Fasciola gigantica</i> —Biological and Biotechnological Implications. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1004.	1.3	84
454	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. <i>Nature Genetics</i> , 2011, 43, 745-752.	9.4	121
455	Sequencing technology does not eliminate biological variability. <i>Nature Biotechnology</i> , 2011, 29, 572-573.	9.4	193
456	Transcriptional activity regulates alternative cleavage and polyadenylation. <i>Molecular Systems Biology</i> , 2011, 7, 534.	3.2	111
457	An RNA-Seq Strategy to Detect the Complete Coding and Non-Coding Transcriptome Including Full-Length Imprinted Macro ncRNAs. <i>PLoS ONE</i> , 2011, 6, e27288.	1.1	97
458	The NBP Negative Binomial Model for Assessing Differential Gene Expression from RNA-Seq. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, .	0.2	117
459	Insights into Global Mechanisms and Disease by Gene Expression Profiling. <i>Methods in Molecular Biology</i> , 2011, 719, 269-298.	0.4	2
460	Identification of recurring tumor-specific somatic mutations in acute myeloid leukemia by transcriptome sequencing. <i>Leukemia</i> , 2011, 25, 821-827.	3.3	54
461	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	3.2	878

#	ARTICLE	IF	CITATIONS
462	PeakRanger: A cloud-enabled peak caller for CHIP-seq data. BMC Bioinformatics, 2011, 12, 139.	1.2	142
463	SeqGene: a comprehensive software solution for mining exome- and transcriptome- sequencing data. BMC Bioinformatics, 2011, 12, 267.	1.2	41
464	Transcriptome Analysis of the Medulla Tissue from Cattle in Response to Bovine Spongiform Encephalopathy using Digital Gene Expression Tag Profiling. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2011, 74, 127-137.	1.1	5
465	Arabidopsis REF6 is a histone H3 lysine 27 demethylase. Nature Genetics, 2011, 43, 715-719.	9.4	351
466	Yeast Systems Biology. Methods in Molecular Biology, 2011, , .	0.4	7
467	Characterizing deep sequencing analytics using BFAST. , 2011, , .		7
468	Counting individual DNA molecules by the stochastic attachment of diverse labels. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9026-9031.	3.3	140
470	Lignin metabolism has a central role in the resistance of cotton to the wilt fungus Verticillium dahliae as revealed by RNA-Seq-dependent transcriptional analysis and histochemistry. Journal of Experimental Botany, 2011, 62, 5607-5621.	2.4	389
471	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	13.7	1,428
472	RNA. Methods in Molecular Biology, 2011, , .	0.4	5
473	Neurodegeneration. Methods in Molecular Biology, 2011, , .	0.4	9
474	MicroRNAs and their isomiRs function cooperatively to target common biological pathways. Genome Biology, 2011, 12, R126.	13.9	297
475	The draft genome of the carcinogenic human liver fluke Clonorchis sinensis. Genome Biology, 2011, 12, R107.	13.9	183
476	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. Genome Biology, 2011, 12, R72.	13.9	670
477	Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads. Genome Biology, 2011, 12, R13.	13.9	224
478	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15.	13.9	118
479	Genomewide characterization of non-polyadenylated RNAs. Genome Biology, 2011, 12, R16.	13.9	365
480	Coding potential of the products of alternative splicing in human. Genome Biology, 2011, 12, R9.	3.8	38

#	ARTICLE	IF	CITATIONS
481	Identification of fusion genes in breast cancer by paired-end RNA-sequencing. <i>Genome Biology</i> , 2011, 12, R6.	13.9	301
484	Impulse Control: Temporal Dynamics in Gene Transcription. <i>Cell</i> , 2011, 144, 886-896.	13.5	227
485	An Epigenetic Signature for Monoallelic Olfactory Receptor Expression. <i>Cell</i> , 2011, 145, 555-570.	13.5	257
486	An Alternative Splicing Switch Regulates Embryonic Stem Cell Pluripotency and Reprogramming. <i>Cell</i> , 2011, 147, 132-146.	13.5	325
487	Deep sequencing of the innate immune transcriptomic response of zebrafish embryos to Salmonella infection. <i>Fish and Shellfish Immunology</i> , 2011, 31, 716-724.	1.6	79
488	Observations on novel splice junctions from RNA sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 299-303.	1.0	16
489	Linear amplification for deep sequencing. <i>Nature Protocols</i> , 2011, 6, 1026-1036.	5.5	72
490	Next-generation sequencing applied to molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 425-444.	1.5	33
491	Total RNA sequencing reveals nascent transcription and widespread co-transcriptional splicing in the human brain. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1435-1440.	3.6	294
492	Identification of novel transcripts in annotated genomes using RNA-Seq. <i>Bioinformatics</i> , 2011, 27, 2325-2329.	1.8	906
493	Design and validation issues in RNA-seq experiments. <i>Briefings in Bioinformatics</i> , 2011, 12, 280-287.	3.2	184
494	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011, 21, 1543-1551.	2.4	588
495	Functional Analysis of Protein Targets by Metabolomic Approaches. <i>Topics in Current Chemistry</i> , 2011, 324, 137-162.	4.0	0
496	Epigenetics in Male Reproduction: A Practical Introduction to the Informatics of Next Generation Sequencing. <i>Epigenetics and Human Health</i> , 2011, , 231-258.	0.2	0
497	A Pre-mRNA Degradation Pathway that Selectively Targets Intron-Containing Genes Requires the Nuclear Poly(A)-Binding Protein. <i>Molecular Cell</i> , 2011, 44, 108-119.	4.5	93
498	Pyrosequencing-based expression profiling and identification of differentially regulated genes from <i>Manduca sexta</i> , a lepidopteran model insect. <i>Insect Biochemistry and Molecular Biology</i> , 2011, 41, 733-746.	1.2	40
499	The gene regulatory networks controlled by estrogens. <i>Molecular and Cellular Endocrinology</i> , 2011, 334, 83-90.	1.6	35
500	Viral transcriptome analysis of feline immunodeficiency virus infected cells using second generation sequencing technology. <i>Veterinary Immunology and Immunopathology</i> , 2011, 143, 314-324.	0.5	8

#	ARTICLE	IF	CITATIONS
501	Transcriptome profiling and digital gene expression by deep-sequencing in normal/regenerative tissues of planarian <i>Dugesia japonica</i> . <i>Genomics</i> , 2011, 97, 364-371.	1.3	56
502	A multiplex RNA-seq strategy to profile poly(A+) RNA: Application to analysis of transcription response and 3' end formation. <i>Genomics</i> , 2011, 98, 266-271.	1.3	61
503	Looking ultra deep: Short identical sequences and transcriptional slippage. <i>Genomics</i> , 2011, 98, 90-95.	1.3	9
504	The discovery of novel protein-coding features in mouse genome based on mass spectrometry data. <i>Genomics</i> , 2011, 98, 343-351.	1.3	19
505	DNA Methylation and SETDB1/H3K9me3 Regulate Predominantly Distinct Sets of Genes, Retroelements, and Chimeric Transcripts in mESCs. <i>Cell Stem Cell</i> , 2011, 8, 676-687.	5.2	427
506	Friend or foe: using systems biology to elucidate interactions between fungi and their hosts. <i>Trends in Microbiology</i> , 2011, 19, 509-515.	3.5	22
507	Mechanisms of specificity in neuronal activity-regulated gene transcription. <i>Progress in Neurobiology</i> , 2011, 94, 259-295.	2.8	174
508	A Transcriptomic Atlas of Mouse Neocortical Layers. <i>Neuron</i> , 2011, 71, 605-616.	3.8	266
509	Proteomic and phosphoproteomic comparison of human ES and iPS cells. <i>Nature Methods</i> , 2011, 8, 821-827.	9.0	254
510	Introduction and Historical Overview of DNA Sequencing. <i>Current Protocols in Molecular Biology</i> , 2011, 96, 7.0.1.	2.9	1
511	Omics Technologies, Data and Bioinformatics Principles. <i>Methods in Molecular Biology</i> , 2011, 719, 3-30.	0.4	92
512	Predicting a Human Gut Microbiota's Response to Diet in Gnotobiotic Mice. <i>Science</i> , 2011, 333, 101-104.	6.0	480
513	GC-Content Normalization for RNA-Seq Data. <i>BMC Bioinformatics</i> , 2011, 12, 480.	1.2	712
515	Unraveling the Genetics of Cancer: Genome Sequencing and Beyond. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 407-430.	2.5	85
516	Construction of Normalized RNA-seq Libraries for Next-Generation Sequencing Using the Crab Duplex-Specific Nuclease. <i>Current Protocols in Molecular Biology</i> , 2011, 94, Unit4.12.	2.9	72
517	SNP discovery in black cottonwood ( <i>Populus trichocarpa</i> ) by population transcriptome resequencing. <i>Molecular Ecology Resources</i> , 2011, 11, 81-92.	2.2	104
518	ExpressionPlot: a web-based framework for analysis of RNA-Seq and microarray gene expression data. <i>Genome Biology</i> , 2011, 12, R69.	3.8	32
519	An Introduction to the Informatics of Next-Generation Sequencing. <i>Current Protocols in Bioinformatics</i> , 2011, 36, Unit 11.1..	25.8	12

#	ARTICLE	IF	CITATIONS
520	RNA-Seq for Plant Pathogenic Bacteria. <i>Genes</i> , 2011, 2, 689-705.	1.0	9
521	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011, 25, 1499-1509.	2.7	60
522	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
523	Designing, Performing, and Interpreting a Microarray-Based Gene Expression Study. <i>Methods in Molecular Biology</i> , 2011, 793, 417-439.	0.4	22
524	Advancing transcriptome platforms. <i>Nature Precedings</i> , 2011, , .	0.1	0
525	Non-coding RNAs in schistosomes: an unexplored world. <i>Anais Da Academia Brasileira De Ciencias</i> , 2011, 83, 673-694.	0.3	36
526	CELLULAR, MOLECULAR, GENOMICS, AND BIOMEDICAL APPROACHES   Global Gene Expression Profiling in Fish. , 2011, , 2055-2060.		0
527	Gene Expression Analysis Using RNA-Seq from Organisms Lacking Substantial Genomic Resources. , 2011, , .		0
528	Information as a Manifestation of Development. <i>Information (Switzerland)</i> , 2011, 2, 102-116.	1.7	5
529	Review Application of RNA-seq to reveal the transcript profile in bacteria. <i>Genetics and Molecular Research</i> , 2011, 10, 1707-1718.	0.3	58
530	Use of Non-normalized, Non-amplified cDNA for 454-based RNA Sequencing of Fleshy Melon Fruit. <i>Plant Genome</i> , 2011, 4, .	1.6	27
531	Gene Expression in Leaves of Susceptible Glycine max during Infection with Phakopsora pachyrhizi Using Next Generation Sequencing. <i>Sequencing</i> , 2011, 2011, 1-14.	0.5	12
532	Asymmetric Distribution of Gene Expression in the Centromeric Region of Rice Chromosome 5. <i>Frontiers in Plant Science</i> , 2011, 2, 16.	1.7	15
533	Next generation quantitative genetics in plants. <i>Frontiers in Plant Science</i> , 2011, 2, 77.	1.7	11
534	SOAPSsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. <i>Frontiers in Genetics</i> , 2011, 2, 46.	1.1	89
535	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. <i>Frontiers in Genetics</i> , 2011, 2, 69.	1.1	12
536	Thousands of Novel Transcripts Identified in Mouse Cerebrum, Testis, and ES Cells Based on ribo-minus RNA Sequencing. <i>Frontiers in Genetics</i> , 2011, 2, 93.	1.1	12
537	Genome-wide gene expression profiling of nucleus accumbens neurons projecting to ventral pallidum using both microarray and transcriptome sequencing. <i>Frontiers in Neuroscience</i> , 2011, 5, 98.	1.4	30

#	ARTICLE	IF	CITATIONS
538	Transcriptome Profiling of Bovine Milk Oligosaccharide Metabolism Genes Using RNA-Sequencing. PLoS ONE, 2011, 6, e18895.	1.1	105
539	Second-Generation Sequencing Supply an Effective Way to Screen RNAi Targets in Large Scale for Potential Application in Pest Insect Control. PLoS ONE, 2011, 6, e18644.	1.1	143
540	Genome-Wide and Phase-Specific DNA-Binding Rhythms of BMAL1 Control Circadian Output Functions in Mouse Liver. PLoS Biology, 2011, 9, e1000595.	2.6	395
541	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	1.1	17
542	Mitochondrial Genome Sequence and Expression Profiling for the Legume Pod Borer Maruca vitrata (Lepidoptera: Crambidae). PLoS ONE, 2011, 6, e16444.	1.1	55
543	A Comparative Transcriptomic Analysis of Uveal Melanoma and Normal Uveal Melanocyte. PLoS ONE, 2011, 6, e16516.	1.1	25
544	Evaluating Gene Expression in C57BL/6J and DBA/2J Mouse Striatum Using RNA-Seq and Microarrays. PLoS ONE, 2011, 6, e17820.	1.1	215
545	Massive-Scale RNA-Seq Analysis of Non Ribosomal Transcriptome in Human Trisomy 21. PLoS ONE, 2011, 6, e18493.	1.1	62
546	A Comprehensive Analysis of Gene Expression Changes Provoked by Bacterial and Fungal Infection in <i>C. elegans</i> . PLoS ONE, 2011, 6, e19055.	1.1	169
547	The First Insight into the Tissue Specific Taxus Transcriptome via Illumina Second Generation Sequencing. PLoS ONE, 2011, 6, e21220.	1.1	169
548	Scalable Transcriptome Preparation for Massive Parallel Sequencing. PLoS ONE, 2011, 6, e21910.	1.1	18
549	Differential Gene Expression in the Siphonophore <i>Nanomia bijuga</i> (Cnidaria) Assessed with Multiple Next-Generation Sequencing Workflows. PLoS ONE, 2011, 6, e22953.	1.1	43
550	RNA-Seq of Human Neurons Derived from iPS Cells Reveals Candidate Long Non-Coding RNAs Involved in Neurogenesis and Neuropsychiatric Disorders. PLoS ONE, 2011, 6, e23356.	1.1	227
551	The Transcriptome of <i>Trichuris suis</i> – First Molecular Insights into a Parasite with Curative Properties for Key Immune Diseases of Humans. PLoS ONE, 2011, 6, e23590.	1.1	43
552	Genomic Analysis of Parent-of-Origin Allelic Expression in <i>Arabidopsis thaliana</i> Seeds. PLoS ONE, 2011, 6, e23687.	1.1	178
553	Expression Profiling of Autism Candidate Genes during Human Brain Development Implicates Central Immune Signaling Pathways. PLoS ONE, 2011, 6, e24691.	1.1	65
554	Transcriptional Profiling of Endocrine Cerebro-Osteodysplasia Using Microarray and Next-Generation Sequencing. PLoS ONE, 2011, 6, e25400.	1.1	10
555	RNA-Seq Analyses Generate Comprehensive Transcriptomic Landscape and Reveal Complex Transcript Patterns in Hepatocellular Carcinoma. PLoS ONE, 2011, 6, e26168.	1.1	98

#	ARTICLE	IF	CITATIONS
556	Statistical Modeling of RNA-Seq Data. <i>Statistical Science</i> , 2011, 26, .	1.6	64
558	Advances in Whole Genome Sequencing Technology. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 293-305.	0.9	62
559	Genome Size and Transposable Element Content as Determined by High-Throughput Sequencing in Maize and <i>Zea luxurians</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 219-229.	1.1	167
560	Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. <i>Blood</i> , 2011, 118, e128-e138.	0.6	103
561	METADOMAIN: A PROFILE HMM-BASED PROTEIN DOMAIN CLASSIFICATION TOOL FOR SHORT SEQUENCES. , 2011, , .		5
564	Single Read and Paired End mRNA-Seq Illumina Libraries from 10 Nanograms Total RNA. <i>Journal of Visualized Experiments</i> , 2011, , e3340.	0.2	25
565	Characterization of Alternative Spliceforms and the RNA Splicing Machinery in Pancreatic Cancer. <i>Pancreas</i> , 2011, 40, 281-288.	0.5	13
566	<i>Pseudomonas putida</i> KT2440 genome update by cDNA sequencing and microarray transcriptomics. <i>Environmental Microbiology</i> , 2011, 13, 1309-1326.	1.8	25
567	The next generation: Using new sequencing technologies to analyse gene regulation. <i>Respirology</i> , 2011, 16, 210-222.	1.3	46
568	Developmental changes in transcriptional profiles. <i>Development Growth and Differentiation</i> , 2011, 53, 567-575.	0.6	19
569	Large-scale transcriptome analysis in chickpea ( <i>Cicer arietinum</i> L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. <i>Plant Biotechnology Journal</i> , 2011, 9, 922-931.	4.1	250
570	Profiling of short RNAs during fleshy fruit development reveals stage-specific sRNAome expression patterns. <i>Plant Journal</i> , 2011, 67, 232-246.	2.8	138
571	Ecological genetics and genomics of plant defences: evidence and approaches. <i>Functional Ecology</i> , 2011, 25, 312-324.	1.7	54
572	The RNA-Seq approach to studying the expression of mosquito mitochondrial genes. <i>Insect Molecular Biology</i> , 2011, 20, 141-152.	1.0	25
573	Responses of the pea aphid transcriptome to infection by facultative symbionts. <i>Insect Molecular Biology</i> , 2011, 20, 357-365.	1.0	42
574	Profiling gene expression responses of coral larvae ( <i>Acropora millepora</i> ) to elevated temperature and settlement inducers using a novel RNA-Seq procedure. <i>Molecular Ecology</i> , 2011, 20, no-no.	2.0	328
575	Association of OLE RNA with bacterial membranes via an RNA-protein interaction. <i>Molecular Microbiology</i> , 2011, 79, 21-34.	1.2	28
576	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , 2011, 116, 937-946.	2.1	65



#	ARTICLE	IF	CITATIONS
577	Isolation and characterization of <i>MAT</i> genes in the symbiotic ascomycete <i>Tuber melanosporum</i> . <i>New Phytologist</i> , 2011, 189, 710-722.	3.5	108
578	Deep RNA sequencing improved the structural annotation of the <i>Tuber melanosporum</i> transcriptome. <i>New Phytologist</i> , 2011, 189, 883-891.	3.5	54
579	BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1215-1224.	0.8	23
580	Survey of Genomics Approaches to Improve Bioenergy Traits in Maize, Sorghum and Sugarcane. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 105-119.	4.1	82
581	Exploring the Transcriptome Landscape of Pomegranate Fruit Peel for Natural Product Biosynthetic Gene and SSR Marker Discovery. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 800-813.	4.1	61
582	Functional genomics of the initial phase of cold adaptation of <i>Pseudomonas putida</i> KT2440. <i>FEMS Microbiology Letters</i> , 2011, 318, 47-54.	0.7	26
583	Development and applications of single-cell transcriptome analysis. <i>Nature Methods</i> , 2011, 8, S6-S11.	9.0	280
584	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
585	Long pre-mRNA depletion and RNA missplicing contribute to neuronal vulnerability from loss of TDP-43. <i>Nature Neuroscience</i> , 2011, 14, 459-468.	7.1	1,050
586	Unravelling the complexity of metastasis – molecular understanding and targeted therapies. <i>Nature Reviews Cancer</i> , 2011, 11, 735-748.	12.8	318
587	RNA sequencing: advances, challenges and opportunities. <i>Nature Reviews Genetics</i> , 2011, 12, 87-98.	7.7	1,770
588	Needles in stacks of needles: finding disease-causal variants in a wealth of genomic data. <i>Nature Reviews Genetics</i> , 2011, 12, 628-640.	7.7	531
589	Next-generation transcriptome assembly. <i>Nature Reviews Genetics</i> , 2011, 12, 671-682.	7.7	1,073
590	Transcriptome-wide sequencing reveals numerous APOBEC1 mRNA-editing targets in transcript 3' UTRs. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 230-236.	3.6	217
591	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. <i>Nature</i> , 2011, 471, 377-381.	13.7	551
592	Initial impact of the sequencing of the human genome. <i>Nature</i> , 2011, 470, 187-197.	13.7	919
593	Global quantification of mammalian gene expression control. <i>Nature</i> , 2011, 473, 337-342.	13.7	5,498
594	Advances in bacterial transcriptome and transposon insertion-site profiling using second-generation sequencing. <i>Trends in Biotechnology</i> , 2011, 29, 586-594.	4.9	25

#	ARTICLE	IF	CITATIONS
595	In vitro culture and characterization of putative porcine embryonic germ cells derived from domestic breeds and Yucatan mini pig embryos at Days 20–24 of gestation. <i>Stem Cell Research</i> , 2011, 6, 226-237.	0.3	28
596	Characterization of the abomasal transcriptome for mechanisms of resistance to gastrointestinal nematodes in cattle. <i>Veterinary Research</i> , 2011, 42, 114.	1.1	66
597	Proportion statistics to detect differentially expressed genes: a comparison with log-ratio statistics. <i>BMC Bioinformatics</i> , 2011, 12, 228.	1.2	26
598	AnyExpress: Integrated toolkit for analysis of cross-platform gene expression data using a fast interval matching algorithm. <i>BMC Bioinformatics</i> , 2011, 12, 75.	1.2	12
599	Effects of genome-wide copy number variation on expression in mammalian cells. <i>BMC Genomics</i> , 2011, 12, 562.	1.2	19
600	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. <i>BMC Genomics</i> , 2011, 12, 590.	1.2	34
601	Expression divergence measured by transcriptome sequencing of four yeast species. <i>BMC Genomics</i> , 2011, 12, 635.	1.2	26
602	Transcriptome analysis of ectopic chloroplast development in green curd cauliflower ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	1.6	25
603	New Challenges in the Analysis of Gene Transcription in Bovine Blastocysts. <i>Reproduction in Domestic Animals</i> , 2011, 46, 2-10.	0.6	8
604	Plant Y Chromosome Degeneration Is Retarded by Haploid Purifying Selection. <i>Current Biology</i> , 2011, 21, 1475-1479.	1.8	164
605	Alterations of pre-mRNA splicing in human inflammatory bowel disease. <i>European Journal of Cell Biology</i> , 2011, 90, 603-611.	1.6	41
606	Identification of housekeeping genes suitable for gene expression analysis in the zebrafish. <i>Gene Expression Patterns</i> , 2011, 11, 271-276.	0.3	78
607	Genome-wide functional annotation and structural verification of metabolic ORFeome of <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2011, 12, S4.	1.2	17
608	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011, 29, 436-442.	9.4	524
609	The integration of “omic” disciplines and systems biology in cattle breeding. <i>Animal</i> , 2011, 5, 493-505.	1.3	21
610	Determinants of nucleosome organization in primary human cells. <i>Nature</i> , 2011, 474, 516-520.	13.7	567
611	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011, 478, 343-348.	13.7	1,080
612	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. <i>Lecture Notes in Computer Science</i> , 2011, , 168-188.	1.0	25

#	ARTICLE	IF	CITATIONS
613	Ascaris suum draft genome. <i>Nature</i> , 2011, 479, 529-533.	13.7	246
614	Applications of high-throughput sequencing to symbiotic nematodes of the genus <i>Heterorhabditis</i> . <i>Symbiosis</i> , 2011, 55, 111-118.	1.2	8
615	Cleavage of rRNA ensures translational cessation in sperm at fertilization. <i>Molecular Human Reproduction</i> , 2011, 17, 721-726.	1.3	99
616	RNA Sequencing and Quantitation Using the Helicos Genetic Analysis System. <i>Methods in Molecular Biology</i> , 2011, 733, 37-49.	0.4	9
617	Local and global factors affecting RNA sequencing analysis. <i>Analytical Biochemistry</i> , 2011, 419, 317-322.	1.1	45
618	Genome-wide Studies of Copy Number Variation and Exome Sequencing Identify Rare Variants in BAG3 as a Cause of Dilated Cardiomyopathy. <i>American Journal of Human Genetics</i> , 2011, 88, 273-282.	2.6	320
619	Effects of chronic metal exposure on wild fish populations revealed by high-throughput cDNA sequencing. <i>Ecotoxicology</i> , 2011, 20, 1388-1399.	1.1	61
620	New approaches to <i>Prunus</i> transcriptome analysis. <i>Genetica</i> , 2011, 139, 755-769.	0.5	43
621	RNA-Seq analysis and de novo transcriptome assembly of <i>Hevea brasiliensis</i> . <i>Plant Molecular Biology</i> , 2011, 77, 299-308.	2.0	131
622	Defining the genetic blueprint of kidney development. <i>Pediatric Nephrology</i> , 2011, 26, 1469-1478.	0.9	6
623	Wnt gene loss in flatworms. <i>Development Genes and Evolution</i> , 2011, 221, 187-197.	0.4	59
624	RNA splicing and debranching viewed through analysis of RNA lariats. <i>Molecular Genetics and Genomics</i> , 2011, 286, 395-410.	1.0	8
625	A review of the evolution of viviparity in squamate reptiles: the past, present and future role of molecular biology and genomics. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2011, 181, 575-594.	0.7	53
626	Per-arnt-sim (PAS) domain-containing protein kinase is downregulated in human islets in type 2 diabetes and regulates glucagon secretion. <i>Diabetologia</i> , 2011, 54, 819-827.	2.9	46
627	RNA-Seq of the xylose-fermenting yeast <i>Scheffersomyces stipitis</i> cultivated in glucose or xylose. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 1237-1249.	1.7	30
628	Brain expression quantitative trait locus mapping informs genetic studies of psychiatric diseases. <i>Neuroscience Bulletin</i> , 2011, 27, 123-133.	1.5	28
629	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65.	1.7	45
630	Dual Blockade of PKA and NF- $\kappa$ B Inhibits H2 Relaxin-Mediated Castrate-Resistant Growth of Prostate Cancer Sublines and Induces Apoptosis. <i>Hormones and Cancer</i> , 2011, 2, 224-238.	4.9	32

#	ARTICLE	IF	CITATIONS
631	Overview of available methods for diverse RNA-Seq data analyses. <i>Science China Life Sciences</i> , 2011, 54, 1121-1128.	2.3	54
632	De novo transcriptome assembly of RNA-Seq reads with different strategies. <i>Science China Life Sciences</i> , 2011, 54, 1129-1133.	2.3	16
633	Observations on potential novel transcripts from RNA-Seq data. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2011, 6, 275-282.	0.6	1
634	Generate gene expression profile from high-throughput sequencing data. <i>Frontiers of Mathematics in China</i> , 2011, 6, 1131-1145.	0.4	1
635	Transcriptomics and molecular evolutionary rate analysis of the bladderwort ( <i>Utricularia</i> ), a carnivorous plant with a minimal genome. <i>BMC Plant Biology</i> , 2011, 11, 101.	1.6	50
636	Transcript profiling reveals expression differences in wild-type and glabrous soybean lines. <i>BMC Plant Biology</i> , 2011, 11, 145.	1.6	18
637	Genomic sequencing in clinical trials. <i>Journal of Translational Medicine</i> , 2011, 9, 222.	1.8	28
638	Microarrays, deep sequencing and the true measure of the transcriptome. <i>BMC Biology</i> , 2011, 9, 34.	1.7	432
639	Estimation of alternative splicing isoform frequencies from RNA-Seq data. <i>Algorithms for Molecular Biology</i> , 2011, 6, 9.	0.3	155
640	SAMMate: a GUI tool for processing short read alignments in SAM/BAM format. <i>Source Code for Biology and Medicine</i> , 2011, 6, 2.	1.7	54
641	Using next generation transcriptome sequencing to predict an ectomycorrhizal metabolome. <i>BMC Systems Biology</i> , 2011, 5, 70.	3.0	60
642	An integrative analysis of DNA methylation and RNA-Seq data for human heart, kidney and liver. <i>BMC Systems Biology</i> , 2011, 5, S4.	3.0	36
643	Functional characterization of cellulases identified from the cow rumen fungus <i>Neocallimastix patriciarum</i> W5 by transcriptomic and secretomic analyses. <i>Biotechnology for Biofuels</i> , 2011, 4, 24.	6.2	74
644	Identification of gene fusion transcripts by transcriptome sequencing in BRCA1-mutated breast cancers and cell lines. <i>BMC Medical Genomics</i> , 2011, 4, 75.	0.7	40
645	Experimental design, preprocessing, normalization and differential expression analysis of small RNA sequencing experiments. <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 2.	8.0	82
646	Differentiation and fiber type-specific activity of a muscle creatine kinase intronic enhancer. <i>Skeletal Muscle</i> , 2011, 1, 25.	1.9	28
647	NSMAP: A method for spliced isoforms identification and quantification from RNA-Seq. <i>BMC Bioinformatics</i> , 2011, 12, 162.	1.2	29
648	rnaSeqMap: a Bioconductor package for RNA sequencing data exploration. <i>BMC Bioinformatics</i> , 2011, 12, 200.	1.2	11

#	ARTICLE	IF	CITATIONS
649	An integrated ChIP-seq analysis platform with customizable workflows. BMC Bioinformatics, 2011, 12, 277.	1.2	80
650	Bias detection and correction in RNA-Sequencing data. BMC Bioinformatics, 2011, 12, 290.	1.2	135
651	IsoformEx: isoform level gene expression estimation using weighted non-negative least squares from mRNA-Seq data. BMC Bioinformatics, 2011, 12, 305.	1.2	24
652	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics, 2011, 12, 323.	1.2	16,042
653	ReCount: A multi-experiment resource of analysis-ready RNA-seq gene count datasets. BMC Bioinformatics, 2011, 12, 449.	1.2	144
654	A regression analysis of gene expression in ES cells reveals two gene classes that are significantly different in epigenetic patterns. BMC Bioinformatics, 2011, 12, S50.	1.2	18
655	Evaluation of the coverage and depth of transcriptome by RNA-Seq in chickens. BMC Bioinformatics, 2011, 12, S5.	1.2	86
656	Analysis of cancer metabolism with high-throughput technologies. BMC Bioinformatics, 2011, 12, S8.	1.2	12
657	Detection of splicing events and multiread locations from RNA-seq data based on a geometric-tail (GT) distribution of intron length. BMC Bioinformatics, 2011, 12, S2.	1.2	0
658	Genotyping common and rare variation using overlapping pool sequencing. BMC Bioinformatics, 2011, 12, S2.	1.2	5
659	STELLAR: fast and exact local alignments. BMC Bioinformatics, 2011, 12, S15.	1.2	28
660	The zebrafish transcriptome during early development. BMC Developmental Biology, 2011, 11, 30.	2.1	108
661	Genome-wide mapping of Sox6 binding sites in skeletal muscle reveals both direct and indirect regulation of muscle terminal differentiation by Sox6. BMC Developmental Biology, 2011, 11, 59.	2.1	46
662	Deep sequencing of the Camellia sinensis transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. BMC Genomics, 2011, 12, 131.	1.2	374
663	Composite transcriptome assembly of RNA-seq data in a sheep model for delayed bone healing. BMC Genomics, 2011, 12, 158.	1.2	63
664	Using RNA-Seq for gene identification, polymorphism detection and transcript profiling in two alfalfa genotypes with divergent cell wall composition in stems. BMC Genomics, 2011, 12, 199.	1.2	131
665	Transcriptome profiling of chemosensory appendages in the malaria vector Anopheles gambiae reveals tissue- and sex-specific signatures of odor coding. BMC Genomics, 2011, 12, 271.	1.2	181
666	RNA-seq: technical variability and sampling. BMC Genomics, 2011, 12, 293.	1.2	250

#	ARTICLE	IF	CITATIONS
667	A tissue-specific landscape of sense/antisense transcription in the mouse intestine. <i>BMC Genomics</i> , 2011, 12, 305.	1.2	18
668	Directional RNA deep sequencing sheds new light on the transcriptional response of <i>Anabaena</i> sp. strain PCC 7120 to combined-nitrogen deprivation. <i>BMC Genomics</i> , 2011, 12, 332.	1.2	151
669	Somatic sex-specific transcriptome differences in <i>Drosophila</i> revealed by whole transcriptome sequencing. <i>BMC Genomics</i> , 2011, 12, 364.	1.2	80
670	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. <i>BMC Genomics</i> , 2011, 12, 441.	1.2	27
671	A global view of porcine transcriptome in three tissues from a full-sib pair with extreme phenotypes in growth and fat deposition by paired-end RNA sequencing. <i>BMC Genomics</i> , 2011, 12, 448.	1.2	103
672	Single-nucleotide resolution analysis of the transcriptome structure of <i>Clostridium beijerinckii</i> NCIMB 8052 using RNA-Seq. <i>BMC Genomics</i> , 2011, 12, 479.	1.2	65
673	Comparative analysis of neural transcriptomes and functional implication of unannotated intronic expression. <i>BMC Genomics</i> , 2011, 12, 494.	1.2	3
674	Transcriptome map of mouse isochores. <i>BMC Genomics</i> , 2011, 12, 511.	1.2	6
675	The classification of mRNA expression levels by the phosphorylation state of RNAPII CTD based on a combined genome-wide approach. <i>BMC Genomics</i> , 2011, 12, 516.	1.2	36
676	Next-generation DNA sequencing-based assay for measuring allelic expression imbalance (AEI) of candidate neuropsychiatric disorder genes in human brain. <i>BMC Genomics</i> , 2011, 12, 518.	1.2	15
677	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011, 12, 552.	1.2	127
678	A de novo transcriptome of the Asian tiger mosquito, <i>Aedes albopictus</i> , to identify candidate transcripts for diapause preparation. <i>BMC Genomics</i> , 2011, 12, 619.	1.2	118
679	Transcriptomes of <i>Frankia</i> sp. strain Ccl3 in growth transitions. <i>BMC Microbiology</i> , 2011, 11, 192.	1.3	26
680	Genome-Wide Studies Reveal That Lin28 Enhances the Translation of Genes Important for Growth and Survival of Human Embryonic Stem Cells. <i>Stem Cells</i> , 2011, 29, 496-504.	1.4	176
681	Genome-wide approaches in the study of microRNA biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 491-512.	6.6	26
682	Whole transcriptome analysis: what are we still missing?. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 527-543.	6.6	22
683	Functional genomics of the brain: uncovering networks in the CNS using a systems approach. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 628-648.	6.6	11
684	Exploring genomic profiles of hepatocellular carcinoma. <i>Molecular Carcinogenesis</i> , 2011, 50, 235-243.	1.3	61

#	ARTICLE	IF	CITATIONS
685	<i>Nodal</i> -mediated epigenesis requires dynamin-mediated endocytosis. <i>Developmental Dynamics</i> , 2011, 240, 704-711.	0.8	10
686	Diabetic embryopathy: A role for the epigenome?. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2011, 91, 770-780.	1.6	37
687	Review of Cap analysis gene expression™. <i>BioEssays</i> , 2011, 33, 233-234.	1.2	0
688	Comprehensive identification and quantification of microbial transcriptomes by genome-wide unbiased methods. <i>Current Opinion in Biotechnology</i> , 2011, 22, 32-41.	3.3	60
689	MARF and Opa1 Control Mitochondrial and Cardiac Function in <i>Drosophila</i> . <i>Circulation Research</i> , 2011, 108, 12-17.	2.0	124
690	EpiRegNet: Constructing epigenetic regulatory network from high throughput gene expression data for humans. <i>Epigenetics</i> , 2011, 6, 1505-1512.	1.3	19
691	Integrating Multiple Types of Data for Signaling Research: Challenges and Opportunities. <i>Science Signaling</i> , 2011, 4, pe9.	1.6	17
692	The <i>Drosophila melanogaster</i> transcriptome by paired-end RNA sequencing. <i>Genome Research</i> , 2011, 21, 315-324.	2.4	123
693	Editing of Neurotransmitter Receptor and Ion Channel RNAs in the Nervous System. <i>Current Topics in Microbiology and Immunology</i> , 2011, 353, 61-90.	0.7	59
694	A comparison of analog and Next-Generation transcriptomic tools for mammalian studies. <i>Briefings in Functional Genomics</i> , 2011, 10, 135-150.	1.3	59
695	Silencing of Soybean Seed Storage Proteins Results in a Rebalanced Protein Composition Preserving Seed Protein Content without Major Collateral Changes in the Metabolome and Transcriptome. <i>Plant Physiology</i> , 2011, 156, 330-345.	2.3	135
696	RNA sequencing reveals two major classes of gene expression levels in metazoan cells. <i>Molecular Systems Biology</i> , 2011, 7, 497.	3.2	265
697	A method for counting PCR template molecules with application to next-generation sequencing. <i>Nucleic Acids Research</i> , 2011, 39, e81-e81.	6.5	141
698	Systematic reconstruction of splicing regulatory modules by integrating many RNA-seq datasets. , 2011, , .		0
699	Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments. <i>Journal of Computational Biology</i> , 2011, 18, 459-468.	0.8	41
700	Multimodal RNA-seq using single-strand, double-strand, and CirLigase-based capture yields a refined and extended description of the <i>C. elegans</i> transcriptome. <i>Genome Research</i> , 2011, 21, 265-275.	2.4	38
701	AREM: Aligning Short Reads from CHIP-Sequencing by Expectation Maximization. <i>Journal of Computational Biology</i> , 2011, 18, 1495-1505.	0.8	22
702	RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. , 2011, , .		3

#	ARTICLE	IF	CITATIONS
703	Whole-transcriptome RNAseq analysis from minute amount of total RNA. <i>Nucleic Acids Research</i> , 2011, 39, e120-e120.	6.5	127
704	Transcriptome Analysis. , 2011, 127, 1-25.		8
705	Classification and clustering of sequencing data using a Poisson model. <i>Annals of Applied Statistics</i> , 2011, 5, .	0.5	142
706	Deep-transcriptome and ribonome sequencing redefines the molecular networks of pluripotency and the extracellular space in human embryonic stem cells. <i>Genome Research</i> , 2011, 21, 2014-2025.	2.4	23
707	An Integrated Proteomics/Transcriptomics Approach Points to Oxygen as the Main Electron Sink for Methanol Metabolism in <i>Methylobacterium mobilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4758-4765.	1.0	22
708	Systems Biologyâ€™Biomedical Modeling. <i>Science Signaling</i> , 2011, 4, tr2.	1.6	32
709	Pyicos: a versatile toolkit for the analysis of high-throughput sequencing data. <i>Bioinformatics</i> , 2011, 27, 3333-3340.	1.8	86
710	Digital gene expression for non-model organisms. <i>Genome Research</i> , 2011, 21, 1905-1915.	2.4	50
711	Genome-wide mapping of RNA Pol-II promoter usage in mouse tissues by ChIP-seq. <i>Nucleic Acids Research</i> , 2011, 39, 190-201.	6.5	81
712	Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. <i>Nucleic Acids Research</i> , 2011, 39, 1408-1418.	6.5	19
713	HIF1 $\alpha$ synergizes with glucocorticoids to promote BFU-E progenitor self-renewal. <i>Blood</i> , 2011, 117, 3435-3444.	0.6	143
714	The role of the 5â€™-3â€™ exoribonuclease XRN1 in transcriptome-wide mRNA degradation. <i>Rna</i> , 2011, 17, 2039-2047.	1.6	48
715	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
716	Characterizing the Impact of Smoking and Lung Cancer on the Airway Transcriptome Using RNA-Seq. <i>Cancer Prevention Research</i> , 2011, 4, 803-817.	0.7	144
717	Mammalian Polycomb-Like Pcl2/Mtf2 Is a Novel Regulatory Component of PRC2 That Can Differentially Modulate Polycomb Activity both at the <i>Hox</i> Gene Cluster and at <i>Cdkn2a</i> Genes. <i>Molecular and Cellular Biology</i> , 2011, 31, 351-364.	1.1	68
718	Receptor-independent Protein Kinase C $\delta$ (PKC $\delta$ ) Signaling by Calpain-generated Free Catalytic Domains Induces HDAC5 Nuclear Export and Regulates Cardiac Transcription. <i>Journal of Biological Chemistry</i> , 2011, 286, 26943-26951.	1.6	38
719	GeneNetWeaver: <i>in silico</i> benchmark generation and performance profiling of network inference methods. <i>Bioinformatics</i> , 2011, 27, 2263-2270.	1.8	465
720	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. <i>Bioinformatics</i> , 2011, 27, 281-283.	1.8	93



#	ARTICLE	IF	CITATIONS
721	Toward knowing the whole human: next-generation sequencing for personalized medicine. <i>Personalized Medicine</i> , 2011, 8, 483-491.	0.8	6
722	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. <i>Molecular Biology and Evolution</i> , 2011, 28, 2949-2959.	3.5	74
723	Deciphering Squamous Cell Carcinoma Using Multidimensional Genomic Approaches. <i>Journal of Skin Cancer</i> , 2011, 2011, 1-16.	0.5	9
724	Rapid identification of therapeutic targets in hematologic malignancies via functional genomics. <i>Therapeutic Advances in Hematology</i> , 2011, 2, 83-93.	1.1	1
725	Genome-wide RNA-seq analysis of human and mouse platelet transcriptomes. <i>Blood</i> , 2011, 118, e101-e111.	0.6	484
726	A Survey for Novel Imprinted Genes in the Mouse Placenta by mRNA-seq. <i>Genetics</i> , 2011, 189, 109-122.	1.2	89
727	Inference of Isoforms from Short Sequence Reads. <i>Journal of Computational Biology</i> , 2011, 18, 305-321.	0.8	54
728	Histone H2B ubiquitylation and H3 lysine 4 methylation prevent ectopic silencing of euchromatic loci important for the cellular response to heat. <i>Molecular Biology of the Cell</i> , 2011, 22, 2741-2753.	0.9	13
729	RseqFlow: workflows for RNA-Seq data analysis. <i>Bioinformatics</i> , 2011, 27, 2598-2600.	1.8	25
730	RNA-Seq Analysis of a Soybean Near-Isogenic Line Carrying Bacterial Leaf Pustule-Resistant and -Susceptible Alleles. <i>DNA Research</i> , 2011, 18, 483-497.	1.5	96
731	Extracellular Aldonolactonase from <i>Myceliophthora thermophila</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 650-656.	1.4	50
732	Sequentially acting Sox transcription factors in neural lineage development. <i>Genes and Development</i> , 2011, 25, 2453-2464.	2.7	263
733	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. <i>Nucleic Acids Research</i> , 2011, 39, e9-e9.	6.5	101
734	Ultraconserved cDNA segments in the human transcriptome exhibit resistance to folding and implicate function in translation and alternative splicing. <i>Nucleic Acids Research</i> , 2011, 39, 1967-1979.	6.5	21
735	Modeling and automation of sequencing-based characterization of RNA structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11069-11074.	3.3	109
736	The BTB and CNC Homology 1 (BACH1) Target Genes Are Involved in the Oxidative Stress Response and in Control of the Cell Cycle. <i>Journal of Biological Chemistry</i> , 2011, 286, 23521-23532.	1.6	136
737	Using non-uniform read distribution models to improve isoform expression inference in RNA-Seq. <i>Bioinformatics</i> , 2011, 27, 502-508.	1.8	91
738	RISC RNA Sequencing for Context-Specific Identification of In Vivo MicroRNA Targets. <i>Circulation Research</i> , 2011, 108, 18-26.	2.0	99

#	ARTICLE	IF	CITATIONS
739	Whole Transcriptome Sequencing Reveals Gene Expression and Splicing Differences in Brain Regions Affected by Alzheimer's Disease. PLoS ONE, 2011, 6, e16266.	1.1	266
740	Programmed fluctuations in sense/antisense transcript ratios drive sexual differentiation in <i>S. pombe</i> . Molecular Systems Biology, 2011, 7, 559.	3.2	41
741	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
742	Functional Relevance of CpG Island Length for Regulation of Gene Expression. Genetics, 2011, 187, 1077-1083.	1.2	53
743	Efficiently identifying genome-wide changes with next-generation sequencing data. Nucleic Acids Research, 2011, 39, e130-e130.	6.5	29
744	Genome-scale transcriptome analysis of the desert poplar, <i>Populus euphratica</i> . Tree Physiology, 2011, 31, 452-461.	1.4	179
745	Aphid genome expression reveals host-symbiont cooperation in the production of amino acids. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2849-2854.	3.3	375
746	Genome-wide depletion of replication initiation events in highly transcribed regions. Genome Research, 2011, 21, 1822-1832.	2.4	112
747	Constant Splice-Isoform Ratios in Human Lymphoblastoid Cells Support the Concept of a Splice-Stat. Genetics, 2011, 187, 761-770.	1.2	10
748	RNA sequencing reveals the role of splicing polymorphisms in regulating human gene expression. Genome Research, 2011, 21, 545-554.	2.4	107
749	Defective photoreceptor phagocytosis in a mouse model of enhanced Sâ€cone syndrome causes progressive retinal degeneration. FASEB Journal, 2011, 25, 3157-3176.	0.2	76
750	Sparse linear modeling of next-generation mRNA sequencing (RNA-Seq) data for isoform discovery and abundance estimation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19867-19872.	3.3	135
751	<i>Stacks</i> : Building and Genotyping Loci <i>De Novo</i> From Short-Read Sequences. G3: Genes, Genomes, Genetics, 2011, 1, 171-182.	0.8	1,643
752	Widespread establishment and regulatory impact of Alu exons in human genes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2837-2842.	3.3	119
753	Nuclear Effects of G-Protein Receptor Kinase 5 on Histone Deacetylase 5-Regulated Gene Transcription in Heart Failure. Circulation: Heart Failure, 2011, 4, 659-668.	1.6	48
754	Evidence for dosage compensation between the X chromosome and autosomes in mammals. Nature Genetics, 2011, 43, 1167-1169.	9.4	81
755	Relative overexpression of X-linked genes in mouse embryonic stem cells is consistent with Ohno's hypothesis. Nature Genetics, 2011, 43, 1169-1170.	9.4	71
756	Systems Biology Approach in <i>Chlamydomonas</i> Reveals Connections between Copper Nutrition and Multiple Metabolic Steps. Plant Cell, 2011, 23, 1273-1292.	3.1	204

#	ARTICLE	IF	CITATIONS
757	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. <i>Genome Research</i> , 2011, 21, 1193-1200.	2.4	100
758	COMPARING MULTIPLE ChIP-SEQUENCING EXPERIMENTS. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 269-282.	0.3	2
759	LEX-SVM: EXPLORING THE POTENTIAL OF EXON EXPRESSION PROFILING FOR DISEASE CLASSIFICATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 299-316.	0.3	1
760	Characterization of the single-cell transcriptional landscape by highly multiplex RNA-seq. <i>Genome Research</i> , 2011, 21, 1160-1167.	2.4	828
761	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , 2011, 39, e140-e140.	6.5	100
762	Sensitive gene fusion detection using ambiguously mapping RNA-Seq read pairs. <i>Bioinformatics</i> , 2011, 27, 1068-1075.	1.8	53
763	Regulation of alternative splicing by the core spliceosomal machinery. <i>Genes and Development</i> , 2011, 25, 373-384.	2.7	181
764	Next-generation insights into regulatory T cells: expression profiling and FoxP3 occupancy in Human. <i>Nucleic Acids Research</i> , 2011, 39, 7946-7960.	6.5	81
765	ESRRA-C11orf20 Is a Recurrent Gene Fusion in Serous Ovarian Carcinoma. <i>PLoS Biology</i> , 2011, 9, e1001156.	2.6	50
766	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002111.	1.5	73
767	Genetic Rearrangements Can Modify Chromatin Features at Epialleles. <i>PLoS Genetics</i> , 2011, 7, e1002331.	1.5	22
768	A Deep Sequencing Approach to Comparatively Analyze the Transcriptome of Lifecycle Stages of the Filarial Worm, <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1409.	1.3	86
769	A High-Resolution Anatomical Atlas of the Transcriptome in the Mouse Embryo. <i>PLoS Biology</i> , 2011, 9, e1000582.	2.6	552
770	Accelerated Recruitment of New Brain Development Genes into the Human Genome. <i>PLoS Biology</i> , 2011, 9, e1001179.	2.6	139
771	Analysis of DNA Methylation in a Three-Generation Family Reveals Widespread Genetic Influence on Epigenetic Regulation. <i>PLoS Genetics</i> , 2011, 7, e1002228.	1.5	256
772	Innovative technology for cancer risk analysis. <i>Annals of Oncology</i> , 2011, 22, i37-i43.	0.6	2
773	Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling. <i>Bioinformatics</i> , 2011, 27, i383-i391.	1.8	119
774	RNA-Seq analysis in MeV. <i>Bioinformatics</i> , 2011, 27, 3209-3210.	1.8	461

#	ARTICLE	IF	CITATIONS
775	AgBase: supporting functional modeling in agricultural organisms. <i>Nucleic Acids Research</i> , 2011, 39, D497-D506.	6.5	56
776	Response to "The Reality of Pervasive Transcription". <i>PLoS Biology</i> , 2011, 9, e1001102.	2.6	30
777	An EMT-Driven Alternative Splicing Program Occurs in Human Breast Cancer and Modulates Cellular Phenotype. <i>PLoS Genetics</i> , 2011, 7, e1002218.	1.5	399
778	The transcriptional diversity of 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2011, 21, 301-314.	2.4	235
779	Sequencing-based Expression Profiling in Zebrafish. <i>Methods in Cell Biology</i> , 2011, 104, 379-399.	0.5	1
780	Length bias correction for RNA-seq data in gene set analyses. <i>Bioinformatics</i> , 2011, 27, 662-669.	1.8	49
781	Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> , 2011, 155, 1071-1080.	0.7	44
782	Retrotransposon-Induced Heterochromatin Spreading in the Mouse Revealed by Insertional Polymorphisms. <i>PLoS Genetics</i> , 2011, 7, e1002301.	1.5	129
783	Chromatin Organization in Sperm May Be the Major Functional Consequence of Base Composition Variation in the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002036.	1.5	90
784	Reshaping of global gene expression networks and sex-biased gene expression by integration of a young gene. <i>EMBO Journal</i> , 2012, 31, 2798-2809.	3.5	44
785	Transcriptome analysis of rice mature root tissue and root tips in early development by massive parallel sequencing. <i>Journal of Experimental Botany</i> , 2012, 63, 2141-2157.	2.4	41
786	Mechanisms and Evolutionary Patterns of Mammalian and Avian Dosage Compensation. <i>PLoS Biology</i> , 2012, 10, e1001328.	2.6	198
787	Translation in Giant Viruses: A Unique Mixture of Bacterial and Eukaryotic Termination Schemes. <i>PLoS Genetics</i> , 2012, 8, e1003122.	1.5	25
788	Assembly and Characterization of the European Hazelnut "Jefferson" Transcriptome. <i>Crop Science</i> , 2012, 52, 2679-2686.	0.8	35
789	RNA-Sequencing Analysis of 5' Capped RNAs Identifies Many New Differentially Expressed Genes in Acute Hepatitis C Virus Infection. <i>Viruses</i> , 2012, 4, 581-612.	1.5	42
790	Deep Sequencing of <i>Porphyromonas gingivalis</i> and Comparative Transcriptome Analysis of a LuxS Mutant. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 79.	1.8	27
791	Transcriptomic Analysis of Phenotypic Changes in Birch ( <i>Betula platyphylla</i> ) Autotetraploids. <i>International Journal of Molecular Sciences</i> , 2012, 13, 13012-13029.	1.8	52
792	Identifying small interfering RNA loci from high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 457-463.	1.8	30

#	ARTICLE	IF	CITATIONS
793	Tools for managing and analyzing microarray data. <i>Briefings in Bioinformatics</i> , 2012, 13, 46-60.	3.2	28
794	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. <i>Bioinformatics</i> , 2012, 28, 3232-3239.	1.8	154
795	Predictive Models of Gene Regulation from High-Throughput Epigenomics Data. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-13.	2.0	10
796	DNA Methyltransferases Are Required to Induce Heterochromatic Re-Replication in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2012, 8, e1002808.	1.5	67
797	Synergistic Parasite-Pathogen Interactions Mediated by Host Immunity Can Drive the Collapse of Honeybee Colonies. <i>PLoS Pathogens</i> , 2012, 8, e1002735.	2.1	364
798	Proximity of H2A.Z containing nucleosome to the transcription start site influences gene expression levels in the mammalian liver and brain. <i>Nucleic Acids Research</i> , 2012, 40, 8965-8978.	6.5	41
799	Adaptive Evolution and the Birth of CTCF Binding Sites in the <i>Drosophila</i> Genome. <i>PLoS Biology</i> , 2012, 10, e1001420.	2.6	60
800	Confidence-based Somatic Mutation Evaluation and Prioritization. <i>PLoS Computational Biology</i> , 2012, 8, e1002714.	1.5	30
801	The Ortholog Conjecture Is Untestable by the Current Gene Ontology but Is Supported by RNA Sequencing Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002784.	1.5	72
802	A Comparison of Brain Gene Expression Levels in Domesticated and Wild Animals. <i>PLoS Genetics</i> , 2012, 8, e1002962.	1.5	130
803	Polyadenylation-Dependent Control of Long Noncoding RNA Expression by the Poly(A)-Binding Protein Nuclear 1. <i>PLoS Genetics</i> , 2012, 8, e1003078.	1.5	140
804	A Histone Deacetylase Adjusts Transcription Kinetics at Coding Sequences during <i>Candida albicans</i> Morphogenesis. <i>PLoS Genetics</i> , 2012, 8, e1003118.	1.5	88
805	RNAseq Analysis of the Parasitic Nematode <i>Strongyloides stercoralis</i> Reveals Divergent Regulation of Canonical Dauer Pathways. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1854.	1.3	79
806	Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. <i>PLoS Genetics</i> , 2012, 8, e1002565.	1.5	88
807	Hominoid-Specific De Novo Protein-Coding Genes Originating from Long Non-Coding RNAs. <i>PLoS Genetics</i> , 2012, 8, e1002942.	1.5	130
808	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	1.3	400
809	Molecular Changes in <i>Opisthorchis viverrini</i> (Southeast Asian Liver Fluke) during the Transition from the Juvenile to the Adult Stage. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1916.	1.3	19
810	Global Gene Transcriptome Analysis in Vaccinated Cattle Revealed a Dominant Role of IL-22 for Protection against Bovine Tuberculosis. <i>PLoS Pathogens</i> , 2012, 8, e1003077.	2.1	91

#	ARTICLE	IF	CITATIONS
811	The Single-Nucleotide Resolution Transcriptome of <i>Pseudomonas aeruginosa</i> Grown in Body Temperature. <i>PLoS Pathogens</i> , 2012, 8, e1002945.	2.1	240
812	Global Gene Expression Analysis of the Zoonotic Parasite <i>Trichinella spiralis</i> Revealed Novel Genes in Host Parasite Interaction. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1794.	1.3	27
813	BatMis: a fast algorithm for <i>k</i> -mismatch mapping. <i>Bioinformatics</i> , 2012, 28, 2122-2128.	1.8	32
814	Evidence for Widespread Positive and Purifying Selection Across the European Rabbit ( <i>Oryctolagus</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	3.5	71
815	Uncovering the Genome-Wide Transcriptional Responses of the Filamentous Fungus <i>Aspergillus niger</i> to Lignocellulose Using RNA Sequencing. <i>PLoS Genetics</i> , 2012, 8, e1002875.	1.5	157
816	Positional differences of axon growth rates between sensory neurons encoded by <i>runx3</i> . <i>EMBO Journal</i> , 2012, 31, 3718-3729.	3.5	37
817	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. <i>Bioinformatics</i> , 2012, 28, 929-937.	1.8	6
818	Ago HITS-CLIP Expands Understanding of Kaposi's Sarcoma-associated Herpesvirus miRNA Function in Primary Effusion Lymphomas. <i>PLoS Pathogens</i> , 2012, 8, e1002884.	2.1	167
819	Persistent androgen receptor-mediated transcription in castration-resistant prostate cancer under androgen-deprived conditions. <i>Nucleic Acids Research</i> , 2012, 40, 10765-10779.	6.5	108
820	UTX and UTY Demonstrate Histone Demethylase-Independent Function in Mouse Embryonic Development. <i>PLoS Genetics</i> , 2012, 8, e1002964.	1.5	253
821	OLE RNA protects extremophilic bacteria from alcohol toxicity. <i>Nucleic Acids Research</i> , 2012, 40, 6898-6907.	6.5	23
822	5-hydroxymethyl-cytosine enrichment of non-committed cells is not a universal feature of vertebrate development. <i>Epigenetics</i> , 2012, 7, 383-389.	1.3	48
823	Assessing the Genome-Wide Effect of Promoter Region Tandem Repeat Natural Variation on Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1643-1649.	0.8	7
824	Regulatory changes contribute to the adaptive enhancement of thermogenic capacity in high-altitude deer mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8635-8640.	3.3	159
825	Age-related changes of gene expression in the neocortex: Preliminary data on RNA-Seq of the transcriptome in three functionally distinct cortical areas. <i>Development and Psychopathology</i> , 2012, 24, 1427-1442.	1.4	22
826	Loss of Cell-Surface Laminin Anchoring Promotes Tumor Growth and Is Associated with Poor Clinical Outcomes. <i>Cancer Research</i> , 2012, 72, 2578-2588.	0.4	47
827	Overexpression of <i>ShCYP51B</i> and <i>ShatrD</i> in <i>Sclerotinia homoeocarpa</i> Isolates Exhibiting Practical Field Resistance to a Demethylation Inhibitor Fungicide. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6674-6682.	1.4	85
828	Fe Sparing and Fe Recycling Contribute to Increased Superoxide Dismutase Capacity in Iron-Starved <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2012, 24, 2649-2665.	3.1	82

#	ARTICLE	IF	CITATIONS
829	LOESS correction for length variation in gene set-based genomic sequence analysis. <i>Bioinformatics</i> , 2012, 28, 1446-1454.	1.8	5
830	Genome-wide analyses of gene activity during seed development. <i>Seed Science Research</i> , 2012, 22, S15-S22.	0.8	9
831	Incomplete Sex Chromosome Dosage Compensation in the Indian Meal Moth, <i>Plodia interpunctella</i> , Based on De Novo Transcriptome Assembly. <i>Genome Biology and Evolution</i> , 2012, 4, 1118-1126.	1.1	64
832	Exploiting the Mutanome for Tumor Vaccination. <i>Cancer Research</i> , 2012, 72, 1081-1091.	0.4	706
833	Transcriptome survey reveals increased complexity of the alternative splicing landscape in <i>Arabidopsis</i> . <i>Genome Research</i> , 2012, 22, 1184-1195.	2.4	750
834	Cell type-specific genomics of <i>Drosophila</i> neurons. <i>Nucleic Acids Research</i> , 2012, 40, 9691-9704.	6.5	138
835	Global Transcriptome Changes Underlying Colony Growth in the Opportunistic Human Pathogen <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2012, 11, 68-78.	3.4	107
836	A new approach to bias correction in RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 921-928.	1.8	28
837	Correcting for the bias due to expression specificity improves the estimation of constrained evolution of expression between mouse and human. <i>Bioinformatics</i> , 2012, 28, 1865-1872.	1.8	19
838	Genome-wide alternative polyadenylation in animals: insights from high-throughput technologies. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 352-361.	1.5	41
839	RNA-Seq Mapping and Detection of Gene Fusions with a Suffix Array Algorithm. <i>PLoS Computational Biology</i> , 2012, 8, e1002464.	1.5	45
840	Research Resource: Whole Transcriptome RNA Sequencing Detects Multiple 1 $\alpha$ ,25-Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Developing Zebrafish. <i>Molecular Endocrinology</i> , 2012, 26, 1630-1642.	3.7	41
841	The <i>Pseudomonas aeruginosa</i> Transcriptome in Planktonic Cultures and Static Biofilms Using RNA Sequencing. <i>PLoS ONE</i> , 2012, 7, e31092.	1.1	212
842	Impact of Oxidative Stress on Ascorbate Biosynthesis in <i>Chlamydomonas</i> via Regulation of the VTC2 Gene Encoding a GDP-l-galactose Phosphorylase. <i>Journal of Biological Chemistry</i> , 2012, 287, 14234-14245.	1.6	93
843	Identification of allele-specific alternative mRNA processing via transcriptome sequencing. <i>Nucleic Acids Research</i> , 2012, 40, e104-e104.	6.5	74
844	Direct and Indirect Involvement of MicroRNA-499 in Clinical and Experimental Cardiomyopathy. <i>Circulation Research</i> , 2012, 111, 521-531.	2.0	133
845	Accurate identification of A-to-I RNA editing in human by transcriptome sequencing. <i>Genome Research</i> , 2012, 22, 142-150.	2.4	297
846	A robust model for read count data in exome sequencing experiments and implications for copy number variant calling. <i>Bioinformatics</i> , 2012, 28, 2747-2754.	1.8	534

#	ARTICLE	IF	CITATIONS
847	dKDM5/LID regulates H3K4me3 dynamics at the transcription-start site (TSS) of actively transcribed developmental genes. <i>Nucleic Acids Research</i> , 2012, 40, 9493-9505.	6.5	47
848	RNA-Seq Analysis of Frontal Cortex and Cerebellum from 5XFAD Mice at Early Stage of Disease Pathology. <i>Journal of Alzheimer's Disease</i> , 2012, 29, 793-808.	1.2	43
849	Functional transcriptomics of a migrating cell in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16246-16251.	3.3	39
850	Characterization of the RpoN regulon reveals differential regulation of T6SS and new flagellar operons in <i>Vibrio cholerae</i> O37 strain V52. <i>Nucleic Acids Research</i> , 2012, 40, 7766-7775.	6.5	101
851	Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. <i>Briefings in Bioinformatics</i> , 2012, 13, 696-710.	3.2	70
852	fus/TLS orchestrates splicing of developmental regulators during gastrulation. <i>Genes and Development</i> , 2012, 26, 1351-1363.	2.7	41
853	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads. , 2012, , .		15
854	DNA Methylation Rebalances Gene Dosage after Mammalian Gene Duplications. <i>Molecular Biology and Evolution</i> , 2012, 29, 133-144.	3.5	50
855	Research Resource: RNA-Seq Reveals Unique Features of the Pancreatic Î²-Cell Transcriptome. <i>Molecular Endocrinology</i> , 2012, 26, 1783-1792.	3.7	95
856	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , 2012, 22, 528-538.	2.4	59
857	Motor Neuron Diseases. , 2012, , 801-814.		3
858	Comparative Genomics and Systems Biology of Malaria Parasites <i>Plasmodium</i> . <i>Current Bioinformatics</i> , 2012, 7, 478-489.	0.7	8
859	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012, 22, 1173-1183.	2.4	557
860	Analysis of <i>C. elegans</i> intestinal gene expression and polyadenylation by fluorescence-activated nuclei sorting and 3' end-seq. <i>Nucleic Acids Research</i> , 2012, 40, 6304-6318.	6.5	69
861	A transgenic zebrafish liver tumor model with inducible <i>Myc</i> expression reveals conserved <i>Myc</i> signatures with mammalian liver tumors. <i>DMM Disease Models and Mechanisms</i> , 2013, 6, 414-23.	1.2	69
862	Revealing stable processing products from ribosome-associated small RNAs by deep-sequencing data analysis. <i>Nucleic Acids Research</i> , 2012, 40, 4013-4024.	6.5	53
863	Systematic measurement of mismatch effect for designing inter-species microarray. , 2012, , .		0
864	Widespread Transcription in an Amphibian Oocyte Relates to Its Reprogramming Activity on Transplanted Somatic Nuclei. <i>Stem Cells and Development</i> , 2012, 21, 181-190.	1.1	15



#	ARTICLE	IF	CITATIONS
865	Removing technical variability in RNA-seq data using conditional quantile normalization. <i>Biostatistics</i> , 2012, 13, 204-216.	0.9	532
866	Transposase mediated construction of RNA-seq libraries. <i>Genome Research</i> , 2012, 22, 134-141.	2.4	85
867	Workshop: Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. , 2012, , .		0
868	Incorporating RNA-seq data into the zebrafish Ensembl genebuild. <i>Genome Research</i> , 2012, 22, 2067-2078.	2.4	96
869	easyRNASeq: a bioconductor package for processing RNA-Seq data. <i>Bioinformatics</i> , 2012, 28, 2532-2533.	1.8	98
870	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. <i>Bioinformatics</i> , 2012, 28, 2914-2921.	1.8	87
871	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. <i>American Journal of Botany</i> , 2012, 99, 383-396.	0.8	80
872	A new strategy to reduce allelic bias in RNA-Seq readmapping. <i>Nucleic Acids Research</i> , 2012, 40, e127-e127.	6.5	86
873	Breast cancer signatures for invasiveness and prognosis defined by deep sequencing of microRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3024-3029.	3.3	334
874	RNA editing in the human ENCODE RNA-seq data. <i>Genome Research</i> , 2012, 22, 1626-1633.	2.4	139
875	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , 2012, 40, 10073-10083.	6.5	264
876	Identification of hundreds of novel UPF1 target transcripts by direct determination of whole transcriptome stability. <i>RNA Biology</i> , 2012, 9, 1370-1379.	1.5	153
877	Complementary Proteome and Transcriptome Profiling in Phosphate-deficient Arabidopsis Roots Reveals Multiple Levels of Gene Regulation. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1156-1166.	2.5	266
878	Application of the whole-transcriptome shotgun sequencing approach to the study of Philadelphia-positive acute lymphoblastic leukemia. <i>Blood Cancer Journal</i> , 2012, 2, e61-e61.	2.8	8
879	Response to Copper Stress in <i>Streptomyces lividans</i> Extends beyond Genes under Direct Control of a Copper-sensitive Operon Repressor Protein (CsoR). <i>Journal of Biological Chemistry</i> , 2012, 287, 17833-17847.	1.6	50
880	Comparative Analysis of <i>Lactobacillus plantarum</i> WCFS1 Transcriptomes by Using DNA Microarray and Next-Generation Sequencing Technologies. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4141-4148.	1.4	24
881	Identification of a <i>p</i> -Coumarate Degradation Regulon in <i>Rhodospseudomonas palustris</i> by Xpression, an Integrated Tool for Prokaryotic RNA-Seq Data Processing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6812-6818.	1.4	15
882	Glycosylation of Human Milk Lactoferrin Exhibits Dynamic Changes During Early Lactation Enhancing Its Role in Pathogenic Bacteria-Host Interactions. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015248.	2.5	143

#	ARTICLE	IF	CITATIONS
883	Copy number variation detection and genotyping from exome sequence data. <i>Genome Research</i> , 2012, 22, 1525-1532.	2.4	550
884	Distinct phytochrome actions in nonvascular plants revealed by targeted inactivation of phytyl biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8310-8315.	3.3	52
885	The Role of CYP3A4 mRNA Transcript with Shortened 3' Untranslated Region in Hepatocyte Differentiation, Liver Development, and Response to Drug Induction. <i>Molecular Pharmacology</i> , 2012, 81, 86-96.	1.0	10
886	Impact of experience-dependent and -independent factors on gene expression in songbird brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17245-17252.	3.3	55
887	Identification and Properties of 1,119 Candidate LincRNA Loci in the <i>Drosophila melanogaster</i> Genome. <i>Genome Biology and Evolution</i> , 2012, 4, 427-442.	1.1	217
888	Complex effects of nucleotide variants in a mammalian cis-regulatory element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19498-19503.	3.3	245
889	What are the determinants of gene expression levels and breadths in the human genome?. <i>Human Molecular Genetics</i> , 2012, 21, 46-56.	1.4	38
890	Deep Sequencing Identifies Viral and Wasp Genes with Potential Roles in Replication of <i>Microplitis demolitor</i> Bracovirus. <i>Journal of Virology</i> , 2012, 86, 3293-3306.	1.5	73
891	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012, 22, 2315-2327.	2.4	177
892	Digging in the RNA-seq Garbage: Evaluating the Characteristics of Unmapped RNA-seq Reads in Normal Tissues. , 2012, , .		1
893	SHAPE-Seq: High-Throughput RNA Structure Analysis. <i>Current Protocols in Chemical Biology</i> , 2012, 4, 275-297.	1.7	67
894	Read-mapping using personalized diploid reference genome for RNA sequencing data reduced bias for detecting allele-specific expression. , 2012, 2012, 718-724.		13
895	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses. , 2012, , .		5
896	De Novo Sequencing and Characterization of the Floral Transcriptome of <i>Dendrocalamus latiflorus</i> (Poaceae: Bambusoideae). <i>PLoS ONE</i> , 2012, 7, e42082.	1.1	111
897	RNA-Seq and RNA Immunoprecipitation Analyses of the Transcriptome of <i>Streptomyces coelicolor</i> Identify Substrates for RNase III. <i>Journal of Bacteriology</i> , 2012, 194, 2228-2237.	1.0	36
898	Pediatric Biomedical Informatics. <i>Translational Bioinformatics</i> , 2012, , .	0.0	3
899	Picking ChIP-seq peak detectors for analyzing chromatin modification experiments. <i>Nucleic Acids Research</i> , 2012, 40, e70-e70.	6.5	64
900	Dynamic Evolution of Toll-Like Receptor Multigene Families in Echinoderms. <i>Frontiers in Immunology</i> , 2012, 3, 136.	2.2	116

#	ARTICLE	IF	CITATIONS
901	Alternative Splicing: A Potential Source of Functional Innovation in the Eukaryotic Genome. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	66
902	PLEXdb: gene expression resources for plants and plant pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D1194-D1201.	6.5	244
903	A Next-Generation Sequencing Approach to Study the Transcriptomic Changes during the Differentiation of <i>Physarum</i> at the Single-Cell Level. <i>Gene Regulation and Systems Biology</i> , 2012, 6, GRSB.S10224.	2.3	7
904	Genomic Analysis of the Hydrocarbon-Producing, Cellulolytic, Endophytic Fungus <i>Ascocoryne sarcoides</i> . <i>PLoS Genetics</i> , 2012, 8, e1002558.	1.5	76
905	Systems and Trans-System Level Analysis Identifies Conserved Iron Deficiency Responses in the Plant Lineage. <i>Plant Cell</i> , 2012, 24, 3921-3948.	3.1	142
906	Whole Transcriptome RNA-Seq Analysis of Breast Cancer Recurrence Risk Using Formalin-Fixed Paraffin-Embedded Tumor Tissue. <i>PLoS ONE</i> , 2012, 7, e40092.	1.1	70
907	RecountDB: a database of mapped and count corrected transcribed sequences. <i>Nucleic Acids Research</i> , 2012, 40, D1089-D1092.	6.5	0
908	Identification and characterization of a kunzeaol synthase from <i>Thapsia garganica</i> : implications for the biosynthesis of the pharmaceutical thapsigargin. <i>Biochemical Journal</i> , 2012, 448, 261-271.	1.7	51
909	Gene expression changes in a tumor xenograft by a pyrrole-imidazole polyamide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16041-16045.	3.3	42
910	Epitranscriptional orchestration of genetic reprogramming is an emergent property of stress-regulated cardiac microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19864-19869.	3.3	57
911	Using Poisson mixed-effects model to quantify transcript-level gene expression in RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 63-68.	1.8	29
912	MolBioLib: a C++11 framework for rapid development and deployment of bioinformatics tasks. <i>Bioinformatics</i> , 2012, 28, 2412-2416.	1.8	9
913	Contributions of mRNA abundance, ribosome loading, and post- or peri-translational effects to temporal repression of <i>C. elegans</i> heterochronic miRNA targets. <i>Genome Research</i> , 2012, 22, 2418-2426.	2.4	56
914	Identification of Candidate Genes Underlying an Iron Efficiency Quantitative Trait Locus in Soybean. <i>Plant Physiology</i> , 2012, 158, 1745-1754.	2.3	60
915	The effect of human genome annotation complexity on RNA-Seq gene expression quantification. , 2012, 2012, 712-717.		7
916	AutismKB: an evidence-based knowledgebase of autism genetics. <i>Nucleic Acids Research</i> , 2012, 40, D1016-D1022.	6.5	157
917	RNASEQ—a streamlined and accurate RNA-seq sequence analysis program. <i>Nucleic Acids Research</i> , 2012, 40, e42-e42.	6.5	33
918	Novel insight into the non-coding repertoire through deep sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, e86-e86.	6.5	17

#	ARTICLE	IF	CITATIONS
919	Expression Dynamics of the <i>Medicago truncatula</i> Transcriptome during the Symbiotic Interaction with <i>Sinorhizobium meliloti</i> : Which Role for Nitric Oxide? <i>Plant Physiology</i> , 2012, 161, 425-439.	2.3	87
920	Transcriptomic landscape of breast cancers through mRNA sequencing. <i>Scientific Reports</i> , 2012, 2, 264.	1.6	83
921	Methods, Challenges and Potentials of Single Cell RNA-seq. <i>Biology</i> , 2012, 1, 658-667.	1.3	53
922	Dynamic Nucleotide-Binding Site and Leucine-Rich Repeat-Encoding Genes in the Grass Family <i>Plant Physiology</i> , 2012, 159, 197-210.	2.3	132
923	Characterizing Regulatory and Functional Differentiation between Maize Mesophyll and Bundle Sheath Cells by Transcriptomic Analysis <i>Plant Physiology</i> , 2012, 160, 165-177.	2.3	156
924	Minireview: Applications of Next-Generation Sequencing on Studies of Nuclear Receptor Regulation and Function. <i>Molecular Endocrinology</i> , 2012, 26, 1651-1659.	3.7	9
925	Comparison of Parallel High-Throughput RNA Sequencing Between Knockout of TDP-43 and Its Overexpression Reveals Primarily Nonreciprocal and Nonoverlapping Gene Expression Changes in the Central Nervous System of <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 789-802.	0.8	71
927	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410
928	GenomicTools: an open source platform for developing high-throughput analytics in genomics. , 2012, , 189-220.		0
929	Challenges in Feasible Problem Construction in Nutritional Genomics: An Empirical Study. , 2012, , 136-157.		4
930	Genomics of Fruit Quality and Disorders. , 2012, , 180-217.		0
931	Biomarkers of Diabetic Nephropathy, the Present and the Future. <i>Current Diabetes Reviews</i> , 2012, 8, 317-328.	0.6	33
932	Molecular Functions of Long Non-Coding RNAs in Plants. <i>Genes</i> , 2012, 3, 176-190.	1.0	139
933	Genotyping-by-Sequencing in Plants. <i>Biology</i> , 2012, 1, 460-483.	1.3	315
934	Genomic Analysis Indicates the Presence of an Asymmetric Bilayer Outer Membrane in Planctomycetes and Verrucomicrobia. <i>Frontiers in Microbiology</i> , 2012, 3, 304.	1.5	51
935	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. <i>IPSI Transactions on Bioinformatics</i> , 2012, 5, 27-33.	0.2	0
936	Study of Cnidarian-Algal Symbiosis in the <i>Age</i> . <i>Biological Bulletin</i> , 2012, 223, 44-65.	0.7	82
937	ChIP-Seq Analytics: Methods and Systems to Improve ChIP-Seq Peak Identification. , 2012, , 87-112.		4

#	ARTICLE	IF	CITATIONS
938	The Application of the Next-Generation Sequencing Technologies in Cancer Research. , 2012, , 227-258.		0
939	Site-Specific Silencing of Regulatory Elements as a Mechanism of X Inactivation. <i>Cell</i> , 2012, 151, 951-963.	13.5	176
940	RNA Sequencing Reveals Dynamic Changes of mRNA Abundance of Cytochromes P450 and Their Alternative Transcripts during Mouse Liver Development. <i>Drug Metabolism and Disposition</i> , 2012, 40, 1198-1209.	1.7	52
941	STATs Shape the Active Enhancer Landscape of T Cell Populations. <i>Cell</i> , 2012, 151, 981-993.	13.5	325
942	Genome-wide analysis of histone H3.1 and H3.3 variants in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5370-5375.	3.3	211
943	Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.	0.4	56
944	Coverage-based consensus calling (CbCC) of short sequence reads and comparison of CbCC results to identify SNPs in chickpea ( <i>Cicer arietinum</i> ; Fabaceae), a crop species without a reference genome. <i>American Journal of Botany</i> , 2012, 99, 186-192.	0.8	34
945	A Deep Exploration of the Transcriptome and Excretory/Secretory Proteome of Adult <i>Fascioloides magna</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1340-1353.	2.5	35
946	Two sides of the coin. <i>Nature Genetics</i> , 2012, 44, 1287-1287.	9.4	1
947	Genome-wide Transcription Factor Gene Prediction and their Expressional Tissue Specificities in Maize. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 616-630.	4.1	82
948	Gene-expression measurement: variance-modeling considerations for robust data analysis. <i>Nature Immunology</i> , 2012, 13, 199-203.	7.0	26
949	Divergent roles of ALS-linked proteins FUS/TLS and TDP-43 intersect in processing long pre-mRNAs. <i>Nature Neuroscience</i> , 2012, 15, 1488-1497.	7.1	628
950	Transcriptome Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2012, 923, 221-239.	0.4	35
951	Online Tools for Bioinformatics Analyses in Nutrition Sciences. <i>Advances in Nutrition</i> , 2012, 3, 654-665.	2.9	13
952	Facilitators and Impediments of the Pluripotency Reprogramming Factors' Initial Engagement with the Genome. <i>Cell</i> , 2012, 151, 994-1004.	13.5	789
953	The expanding scope of DNA sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1084-1094.	9.4	280
954	Transcriptional Silencing of Transposons by Piwi and Maelstrom and Its Impact on Chromatin State and Gene Expression. <i>Cell</i> , 2012, 151, 964-980.	13.5	548
955	Hsp70 and small Hsps are the major heat shock protein members involved in midgut metamorphosis in the common cutworm, <i>Spodoptera litura</i> . <i>Insect Molecular Biology</i> , 2012, 21, 535-543.	1.0	54

#	ARTICLE	IF	CITATIONS
956	<i>GenomicTools</i> : a computational platform for developing high-throughput analytics in genomics. <i>Bioinformatics</i> , 2012, 28, 282-283.	1.8	42
957	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. <i>Nucleic Acids Research</i> , 2012, 40, 4288-4297.	6.5	4,474
958	Emerging real-time technologies in molecular medicine and the evolution of integrated "pharmacomics" approaches to personalized medicine and drug discovery. , 2012, 136, 295-304.		14
959	Genome-wide Epigenetic Data Facilitate Understanding of Disease Susceptibility Association Studies. <i>Journal of Biological Chemistry</i> , 2012, 287, 30932-30940.	1.6	49
960	Sporadic autism exomes reveal a highly interconnected protein network of de novo mutations. <i>Nature</i> , 2012, 485, 246-250.	13.7	1,960
961	Comprehensive structural annotation of <i>Pichia pastoris</i> transcriptome and the response to various carbon sources using deep paired-end RNA sequencing. <i>BMC Genomics</i> , 2012, 13, 738.	1.2	59
962	Rab25 Is a Tumor Suppressor Gene with Antiangiogenic and Anti-Invasive Activities in Esophageal Squamous Cell Carcinoma. <i>Cancer Research</i> , 2012, 72, 6024-6035.	0.4	110
963	Circadian Oscillations of Protein-Coding and Regulatory RNAs in a Highly Dynamic Mammalian Liver Epigenome. <i>Cell Metabolism</i> , 2012, 16, 833-845.	7.2	230
964	Protection from Feed-Forward Amplification in an Amplified RNAi Mechanism. <i>Cell</i> , 2012, 151, 885-899.	13.5	70
965	A potential role for an extracellular methanol oxidase secreted by <i>Moniliophthora perniciosa</i> in Witches' broom disease in cacao. <i>Fungal Genetics and Biology</i> , 2012, 49, 922-932.	0.9	17
966	Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. <i>Bioinformatics</i> , 2012, 28, 464-469.	1.8	1,029
967	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
968	Identification of Metabolic Biomarkers for Personalized Nutrition. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2012, 5, I-II.	1.8	5
969	FX: an RNA-Seq analysis tool on the cloud. <i>Bioinformatics</i> , 2012, 28, 721-723.	1.8	66
970	The transcriptional landscape and mutational profile of lung adenocarcinoma. <i>Genome Research</i> , 2012, 22, 2109-2119.	2.4	524
971	Functional screening identifies miRNAs inducing cardiac regeneration. <i>Nature</i> , 2012, 492, 376-381.	13.7	922
973	How to Analyze Gene Expression Using RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 802, 259-274.	0.4	23
974	Stable intronic sequence RNA (sisRNA), a new class of noncoding RNA from the oocyte nucleus of <i>Xenopus tropicalis</i> . <i>Genes and Development</i> , 2012, 26, 2550-2559.	2.7	124

#	ARTICLE	IF	CITATIONS
975	Independent Domestication of Asian Rice Followed by Gene Flow from japonica to indica. <i>Molecular Biology and Evolution</i> , 2012, 29, 1471-1479.	3.5	70
976	Retrograde Signaling and Photoprotection in a gun4 Mutant of <i>Chlamydomonas reinhardtii</i> . <i>Molecular Plant</i> , 2012, 5, 1242-1262.	3.9	52
977	Distinct Contributions of Replication and Transcription to Mutation Rate Variation of Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 4-10.	3.0	31
978	The Transcript-centric Mutations in Human Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 11-22.	3.0	21
979	Gene2DGE: A Perl Package for Gene Model Renewal with Digital Gene Expression Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 51-54.	3.0	4
980	Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	38
981	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. <i>Genome Biology</i> , 2012, 13, R4.	13.9	140
982	Defining the molecular profile of planarian pluripotent stem cells using a combinatorial RNA-seq, RNA interference and irradiation approach. <i>Genome Biology</i> , 2012, 13, R19.	13.9	135
983	Efficient and robust RNA-seq process for cultured bacteria and complex community transcriptomes. <i>Genome Biology</i> , 2012, 13, r23.	13.9	197
984	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	157
985	Mediation of <i>Drosophila</i> autosomal dosage effects and compensation by network interactions. <i>Genome Biology</i> , 2012, 13, R28.	13.9	98
986	Proteogenomic characterization and mapping of nucleosomes decoded by Brd and HP1 proteins. <i>Genome Biology</i> , 2012, 13, R68.	13.9	81
987	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012, 13, R48.	13.9	233
988	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	9.4	785
989	The Evolutionary Imprint of Domestication on Genome Variation and Function of the Filamentous Fungus <i>Aspergillus oryzae</i> . <i>Current Biology</i> , 2012, 22, 1403-1409.	1.8	177
990	Analysis of the transcriptome of differentiating and non-differentiating preadipocytes from rats and humans by next generation sequencing. <i>Molecular and Cellular Biochemistry</i> , 2012, 369, 175-181.	1.4	5
991	Building an mRNA transcriptome from the shoots of <i>Betula platyphylla</i> by using Solexa technology. <i>Tree Genetics and Genomes</i> , 2012, 8, 1031-1040.	0.6	10
993	Mutation of a U2 snRNA Gene Causes Global Disruption of Alternative Splicing and Neurodegeneration. <i>Cell</i> , 2012, 148, 296-308.	13.5	123

#	ARTICLE	IF	CITATIONS
994	A Validated Regulatory Network for Th17 Cell Specification. <i>Cell</i> , 2012, 151, 289-303.	13.5	1,010
995	The Cellular EJC Interactome Reveals Higher-Order mRNP Structure and an EJC-SR Protein Nexus. <i>Cell</i> , 2012, 151, 750-764.	13.5	287
996	Revisiting Global Gene Expression Analysis. <i>Cell</i> , 2012, 151, 476-482.	13.5	526
997	MeCP2 Binds to 5hmC Enriched within Active Genes and Accessible Chromatin in the Nervous System. <i>Cell</i> , 2012, 151, 1417-1430.	13.5	837
998	FACS Purification and Transcriptome Analysis of Drosophila Neural Stem Cells Reveals a Role for Klumpfuss in Self-Renewal. <i>Cell Reports</i> , 2012, 2, 407-418.	2.9	122
999	Mpn1, Mutated in Poikiloderma with Neutropenia Protein 1, Is a Conserved 3' to 5' RNA Exonuclease Processing U6 Small Nuclear RNA. <i>Cell Reports</i> , 2012, 2, 855-865.	2.9	63
1000	A defect in iron uptake enhances the susceptibility of <i>Cryptococcus neoformans</i> to azole antifungal drugs. <i>Fungal Genetics and Biology</i> , 2012, 49, 955-966.	0.9	48
1001	Living with the enemy or uninvited guests: Functional genomics approaches to investigating host resistance or tolerance traits to a protozoan parasite, <i>Theileria annulata</i> , in cattle. <i>Veterinary Immunology and Immunopathology</i> , 2012, 148, 178-189.	0.5	36
1002	Id2a functions to limit Notch pathway activity and thereby influence the transition from proliferation to differentiation of retinoblasts during zebrafish retinogenesis. <i>Developmental Biology</i> , 2012, 371, 280-292.	0.9	18
1003	A unified framework of overlapping genes: Towards the origination and endogenic regulation. <i>Genomics</i> , 2012, 100, 231-239.	1.3	23
1004	Gastrocnemius transcriptome analysis reveals domestication induced gene expression changes between wild and domestic chickens. <i>Genomics</i> , 2012, 100, 314-319.	1.3	25
1005	RNA-seq transcriptome analysis of male and female zebra finch cell lines. <i>Genomics</i> , 2012, 100, 363-369.	1.3	23
1006	De novo transcriptome sequencing of <i>Momordica cochinchinensis</i> to identify genes involved in the carotenoid biosynthesis. <i>Plant Molecular Biology</i> , 2012, 79, 413-427.	2.0	66
1007	An RNA-seq-based Gene Expression Profiling of Radiation-induced Tumorigenic Mammary Epithelial Cells. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 326-335.	3.0	10
1008	Transcriptome Mapping of pAR060302, <i>abaCMY-2</i> -Positive Broad-Host-Range IncA/C Plasmid. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3379-3386.	1.4	40
1009	SKIP Is a Component of the Spliceosome Linking Alternative Splicing and the Circadian Clock in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 3278-3295.	3.1	198
1010	Pharmacogene regulatory elements: from discovery to applications. <i>Genome Medicine</i> , 2012, 4, 45.	3.6	18
1011	Perturbation of Flil Interferes with <i>Proteus mirabilis</i> Swarmer Cell Gene Expression and Differentiation. <i>Journal of Bacteriology</i> , 2012, 194, 437-447.	1.0	47



#	ARTICLE	IF	CITATIONS
1012	GenomeView: a next-generation genome browser. <i>Nucleic Acids Research</i> , 2012, 40, e12-e12.	6.5	126
1013	Identification of Representative Genes of the Central Nervous System of the Locust, <i>Locusta migratoria manilensis</i> by Deep Sequencing. <i>Journal of Insect Science</i> , 2012, 12, 1-15.	0.9	9
1014	Fluorescent Protein Candidate Genes in the Coral <i>Acropora digitifera</i> Genome. <i>Zoological Science</i> , 2012, 29, 260.	0.3	20
1015	R-SAP: a multi-threading computational pipeline for the characterization of high-throughput RNA-sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, e67-e67.	6.5	6
1016	BAsplice: Bi-direction alignment for detecting splice junctions. , 2012, , .		0
1017	Information theoretic methods for modeling of gene regulatory networks. , 2012, , .		4
1018	HDAC8 mutations in Cornelia de Lange syndrome affect the cohesin acetylation cycle. <i>Nature</i> , 2012, 489, 313-317.	13.7	488
1019	Deep sequencing reveals persistence of intra- and inter-host genetic diversity in natural and greenhouse populations of zucchini yellow mosaic virus. <i>Journal of General Virology</i> , 2012, 93, 1831-1840.	1.3	32
1020	Transcriptome-Wide Changes in <i>Chlamydomonas reinhardtii</i> Gene Expression Regulated by Carbon Dioxide and the CO <sub>2</sub> -Concentrating Mechanism Regulator <i>CIA5/CCM1</i> . <i>Plant Cell</i> , 2012, 24, 1876-1893.	3.1	180
1021	Next-generation sequencing technologies for gene expression profiling in plants. <i>Briefings in Functional Genomics</i> , 2012, 11, 63-70.	1.3	135
1022	Transcriptome Characterization and Sequencing-Based Identification of Salt-Responsive Genes in <i>Millettia pinnata</i> , a Semi-Mangrove Plant. <i>DNA Research</i> , 2012, 19, 195-207.	1.5	68
1023	Miniature Inverted-Repeat Transposable Elements (MITEs) Have Been Accumulated through Amplification Bursts and Play Important Roles in Gene Expression and Species Diversity in <i>Oryza sativa</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1005-1017.	3.5	191
1024	Identifying differentially expressed transcripts from RNA-seq data with biological variation. <i>Bioinformatics</i> , 2012, 28, 1721-1728.	1.8	182
1025	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , 2012, 22, 1231-1242.	2.4	143
1026	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789.	2.4	4,428
1027	<i>Oases</i> : robust <i>de novo</i> RNA-seq assembly across the dynamic range of expression levels. <i>Bioinformatics</i> , 2012, 28, 1086-1092.	1.8	1,351
1028	Application of the Gini Correlation Coefficient to Infer Regulatory Relationships in Transcriptome Analysis. <i>Plant Physiology</i> , 2012, 160, 192-203.	2.3	65
1029	Retinal Transcriptome Profiling by Directional Next-Generation Sequencing Using 100 ng of Total RNA. <i>Methods in Molecular Biology</i> , 2012, 884, 319-334.	0.4	24

#	ARTICLE	IF	CITATIONS
1030	Exploring long non-coding RNAs through sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 200-205.	2.3	108
1031	The evolution of gene expression and the transcriptome-phenotype relationship. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 222-229.	2.3	89
1032	A new branch on the tree: Next-generation sequencing in the study of cancer evolution. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 237-242.	2.3	33
1033	Parkinson's disease-linked leucine-rich repeat kinase 2(R1441G) mutation increases proinflammatory cytokine release from activated primary microglial cells and resultant neurotoxicity. <i>Neuroscience</i> , 2012, 208, 41-48.	1.1	187
1034	Grass phenylpropanoids: Regulate before using!. <i>Plant Science</i> , 2012, 184, 112-120.	1.7	79
1035	Transcriptome-wide survey and expression analysis of stress-responsive NAC genes in <i>Chrysanthemum lavandulifolium</i> . <i>Plant Science</i> , 2012, 193-194, 18-27.	1.7	48
1036	Exploring the application of high-throughput genomics technologies in the field of maternal-embryo communication. <i>Theriogenology</i> , 2012, 77, 717-737.	0.9	6
1037	Genome-wide transcriptome analysis in murine neural retina using high-throughput RNA sequencing. <i>Genomics</i> , 2012, 99, 44-51.	1.3	36
1038	The research strategies for probing the function of long noncoding RNAs. <i>Genomics</i> , 2012, 99, 76-80.	1.3	50
1039	Developmental and insecticide-resistant insights from the de novo assembled transcriptome of the diamondback moth, <i>Plutella xylostella</i> . <i>Genomics</i> , 2012, 99, 169-177.	1.3	75
1040	Transcriptome analysis of rosette and folding leaves in Chinese cabbage using high-throughput RNA sequencing. <i>Genomics</i> , 2012, 99, 299-307.	1.3	48
1041	Identification of small non-coding RNAs in the planarian <i>Dugesia japonica</i> via deep sequencing. <i>Genomics</i> , 2012, 99, 315-321.	1.3	9
1042	Next-generation sequencing-based transcriptome analysis of <i>Cryptolaemus montrouzieri</i> under insecticide stress reveals resistance-relevant genes in ladybirds. <i>Genomics</i> , 2012, 100, 35-41.	1.3	42
1043	Combined deep microRNA and mRNA sequencing identifies protective transcriptomal signature of enhanced PI3K signaling in cardiac hypertrophy. <i>Journal of Molecular and Cellular Cardiology</i> , 2012, 53, 101-112.	0.9	39
1044	Technical considerations for functional sequencing assays. <i>Nature Immunology</i> , 2012, 13, 802-807.	7.0	35
1045	GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2012, 28, 2782-2788.	1.8	376
1046	Three Acyltransferases and Nitrogen-responsive Regulator Are Implicated in Nitrogen Starvation-induced Triacylglycerol Accumulation in <i>Chlamydomonas</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 15811-15825.	1.6	379
1047	Airway Epithelial Expression of TLR5 Is Downregulated in Healthy Smokers and Smokers with Chronic Obstructive Pulmonary Disease. <i>Journal of Immunology</i> , 2012, 189, 2217-2225.	0.4	28

#	ARTICLE	IF	CITATIONS
1048	SF3B1 haploinsufficiency leads to formation of ring sideroblasts in myelodysplastic syndromes. <i>Blood</i> , 2012, 120, 3173-3186.	0.6	173
1049	Molecular and developmental contributions to divergent pigment patterns in marine and freshwater sticklebacks. <i>Evolution &amp; Development</i> , 2012, 14, 351-362.	1.1	30
1050	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , 2012, 13, R53.	13.9	231
1051	The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. <i>Nature Protocols</i> , 2012, 7, 1534-1550.	5.5	1,045
1052	Coordinated regulation of neuronal mRNA steady-state levels through developmentally controlled intron retention. <i>Genes and Development</i> , 2012, 26, 1209-1223.	2.7	247
1053	Genome-wide <i>in silico</i> prediction of gene expression. <i>Bioinformatics</i> , 2012, 28, 2789-2796.	1.8	50
1054	What are we learning from the cancer genome?. <i>Nature Reviews Clinical Oncology</i> , 2012, 9, 621-630.	12.5	50
1055	SNP Discovery and Genotyping for Evolutionary Genetics Using RAD Sequencing. <i>Methods in Molecular Biology</i> , 2012, 772, 157-178.	0.4	311
1056	Dual RNA-seq of pathogen and host. <i>Nature Reviews Microbiology</i> , 2012, 10, 618-630.	13.6	660
1057	Transcriptomics Using Next Generation Sequencing Technologies. <i>Methods in Molecular Biology</i> , 2012, 917, 293-317.	0.4	12
1058	A comparison of statistical methods for detecting differentially expressed genes from RNA-seq data. <i>American Journal of Botany</i> , 2012, 99, 248-256.	0.8	235
1059	The Hypersensitive Glucocorticoid Response Specifically Regulates Period 1 and Expression of Circadian Genes. <i>Molecular and Cellular Biology</i> , 2012, 32, 3756-3767.	1.1	122
1060	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2012, 195, 97-112.	3.5	193
1061	Dynamic MicroRNA Gene Transcription and Processing during T Cell Development. <i>Journal of Immunology</i> , 2012, 188, 3257-3267.	0.4	80
1062	Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 253-260.	9.4	461
1063	Detection and Quantification of Alternative Splicing Variants Using RNA-seq. <i>Methods in Molecular Biology</i> , 2012, 883, 97-110.	0.4	22
1064	Cis- and trans-regulatory divergence between progenitor species determines gene-expression novelty in Arabidopsis allopolyploids. <i>Nature Communications</i> , 2012, 3, 950.	5.8	186
1065	Differential expression—the next generation and beyond. <i>Briefings in Functional Genomics</i> , 2012, 11, 57-62.	1.3	31

#	ARTICLE	IF	CITATIONS
1066	Genomics of DNA cytosine methylation in <i>Escherichia coli</i> reveals its role in stationary phase transcription. <i>Nature Communications</i> , 2012, 3, 886.	5.8	131
1067	Dinoflagellate tandem array gene transcripts are highly conserved and not polycistronic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15793-15798.	3.3	73
1068	Analyzing ChIP-seq Data: Preprocessing, Normalization, Differential Identification, and Binding Pattern Characterization. <i>Methods in Molecular Biology</i> , 2012, 802, 275-291.	0.4	10
1069	Massively Parallel Sequencing Technology in Pathogenic Microbes. <i>Methods in Molecular Biology</i> , 2012, 835, 271-294.	0.4	5
1070	Gene Expression Variations in Microsatellite Stable and Unstable Colon Cancer Cells. <i>Journal of Surgical Research</i> , 2012, 174, 1-6.	0.8	22
1071	Comparative assessment of fungal cellobiohydrolase I richness and composition in cDNA generated using oligo(dT) primers or random hexamers. <i>Journal of Microbiological Methods</i> , 2012, 88, 224-228.	0.7	4
1072	MicroRNAs in inner ear biology and pathogenesis. <i>Hearing Research</i> , 2012, 287, 6-14.	0.9	26
1073	Next-generation sequencing identifies TGF- $\beta$ 1-associated gene expression profiles in renal epithelial cells reiterated in human diabetic nephropathy. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2012, 1822, 589-599.	1.8	80
1074	A simple strand-specific RNA-Seq library preparation protocol combining the Illumina TruSeq RNA and the dUTP methods. <i>Biochemical and Biophysical Research Communications</i> , 2012, 422, 643-646.	1.0	62
1075	Differential impact of nutrition on developmental and metabolic gene expression during fruiting body development in <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 405-413.	0.9	33
1076	The age of the "ome" Genome, transcriptome and proteome data set collection and analysis. <i>Brain Research Bulletin</i> , 2012, 88, 294-301.	1.4	13
1077	Characterizing short read sequencing for gene discovery and RNA-Seq analysis in <i>Crassostrea gigas</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 94-99.	0.4	21
1078	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. <i>Cell</i> , 2012, 148, 335-348.	13.5	528
1079	Spt4 Is Selectively Required for Transcription of Extended Trinucleotide Repeats. <i>Cell</i> , 2012, 148, 690-701.	13.5	86
1080	Dynamic Transformations of Genome-wide Epigenetic Marking and Transcriptional Control Establish T Cell Identity. <i>Cell</i> , 2012, 149, 467-482.	13.5	313
1081	The Pan-ErbB Negative Regulator Lrig1 Is an Intestinal Stem Cell Marker that Functions as a Tumor Suppressor. <i>Cell</i> , 2012, 149, 146-158.	13.5	580
1082	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. <i>Cell</i> , 2012, 149, 307-321.	13.5	637
1083	Cell-free Formation of RNA Granules: Bound RNAs Identify Features and Components of Cellular Assemblies. <i>Cell</i> , 2012, 149, 768-779.	13.5	698

#	ARTICLE	IF	CITATIONS
1084	Transcript Dynamics of Proinflammatory Genes Revealed by Sequence Analysis of Subcellular RNA Fractions. <i>Cell</i> , 2012, 150, 279-290.	13.5	407
1085	Frequent Recent Origination of Brain Genes Shaped the Evolution of Foraging Behavior in <i>Drosophila</i> . <i>Cell Reports</i> , 2012, 1, 118-132.	2.9	30
1086	Integrative Genome-wide Analysis Reveals Cooperative Regulation of Alternative Splicing by hnRNP Proteins. <i>Cell Reports</i> , 2012, 1, 167-178.	2.9	420
1087	RNA-Seq Atlas—a reference database for gene expression profiling in normal tissue by next-generation sequencing. <i>Bioinformatics</i> , 2012, 28, 1184-1185.	1.8	178
1088	New genes expressed in human brains: Implications for annotating evolving genomes. <i>BioEssays</i> , 2012, 34, 982-991.	1.2	54
1089	A simple and novel method for RNA-seq library preparation of single cell cDNA analysis by hyperactive Tn5 transposase. <i>Developmental Dynamics</i> , 2012, 241, 1584-1590.	0.8	20
1090	Computational analysis of noncoding RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 759-778.	3.2	50
1091	VAMP8 is a vesicle SNARE that regulates mucin secretion in airway goblet cells. <i>Journal of Physiology</i> , 2012, 590, 545-562.	1.3	50
1092	Investigating the molecular basis of local adaptation to thermal stress: population differences in gene expression across the transcriptome of the copepod <i>Tigriopus californicus</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 170.	3.2	150
1093	Genome-wide dynamic transcriptional profiling in <i>clostridium beijerinckii</i> NCIMB 8052 using single-nucleotide resolution RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 102.	1.2	72
1094	Transcriptome landscape of the human placenta. <i>BMC Genomics</i> , 2012, 13, 115.	1.2	83
1095	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	1.2	80
1096	Characterization and gene expression analysis of the cir multi-gene family of <i>plasmodium chabaudi</i> <i>chabaudi</i> (AS). <i>BMC Genomics</i> , 2012, 13, 125.	1.2	26
1097	De novo sequencing and characterization of <i>Picrorhiza kurroa</i> transcriptome at two temperatures showed major transcriptome adjustments. <i>BMC Genomics</i> , 2012, 13, 126.	1.2	124
1098	De novo assembly and characterization of the root transcriptome of <i>Aegilops variabilis</i> during an interaction with the cereal cyst nematode. <i>BMC Genomics</i> , 2012, 13, 133.	1.2	63
1099	Enhancer identification in mouse embryonic stem cells using integrative modeling of chromatin and genomic features. <i>BMC Genomics</i> , 2012, 13, 152.	1.2	60
1100	Transcriptomic analysis of Chinese bayberry ( <i>Myrica rubra</i> ) fruit development and ripening using RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 19.	1.2	199
1101	De novo assembly and characterization of bark transcriptome using Illumina sequencing and development of EST-SSR markers in rubber tree ( <i>Hevea brasiliensis</i> Muell. Arg.). <i>BMC Genomics</i> , 2012, 13, 192.	1.2	228

#	ARTICLE	IF	CITATIONS
1102	RNA-seq analysis of differential gene expression in liver from lactating dairy cows divergent in negative energy balance. BMC Genomics, 2012, 13, 193.	1.2	98
1103	Genetic variation and metabolic pathway intricacy govern the active compound content and quality of the Chinese medicinal plant <i>Lonicera japonica</i> thunb. BMC Genomics, 2012, 13, 195.	1.2	74
1104	Transcriptome profiling of the demosponge <i>Amphimedon queenslandica</i> reveals genome-wide events that accompany major life cycle transitions. BMC Genomics, 2012, 13, 209.	1.2	47
1105	Horizontal transfer of expressed genes in a parasitic flowering plant. BMC Genomics, 2012, 13, 227.	1.2	90
1106	Use of mRNA-seq to discriminate contributions to the transcriptome from the constituent genomes of the polyploid crop species <i>Brassica napus</i> . BMC Genomics, 2012, 13, 247.	1.2	91
1107	Dynamic DNA cytosine methylation in the <i>Populus trichocarpa</i> genome: tissue-level variation and relationship to gene expression. BMC Genomics, 2012, 13, 27.	1.2	136
1108	Identification of genes specifically or preferentially expressed in maize silk reveals similarity and diversity in transcript abundance of different dry stigmas. BMC Genomics, 2012, 13, 294.	1.2	33
1109	Transcriptional profile of <i>Taxus chinensis</i> cells in response to methyl jasmonate. BMC Genomics, 2012, 13, 295.	1.2	87
1110	Technical and biological variance structure in mRNA-Seq data: life in the real world. BMC Genomics, 2012, 13, 304.	1.2	42
1111	Sequencing and comparative genomic analysis of 1227 <i>Felis catus</i> cDNA sequences enriched for developmental, clinical and nutritional phenotypes. BMC Genomics, 2012, 13, 31.	1.2	9
1112	The venom-gland transcriptome of the eastern diamondback rattlesnake ( <i>Crotalus adamanteus</i> ). BMC Genomics, 2012, 13, 312.	1.2	250
1113	Development and validation of genic-SSR markers in sesame by RNA-seq. BMC Genomics, 2012, 13, 316.	1.2	122
1114	Quantitative RNA-Seq analysis in non-model species: assessing transcriptome assemblies as a scaffold and the utility of evolutionary divergent genomic reference species. BMC Genomics, 2012, 13, 361.	1.2	79
1115	MicroRNAs in metamorphic and non-metamorphic transitions in hemimetabolan insect metamorphosis. BMC Genomics, 2012, 13, 386.	1.2	51
1116	Detecting transcription of ribosomal protein pseudogenes in diverse human tissues from RNA-seq data. BMC Genomics, 2012, 13, 412.	1.2	52
1117	Transcriptome profiling in conifers and the PiceaGenExpress database show patterns of diversification within gene families and interspecific conservation in vascular gene expression. BMC Genomics, 2012, 13, 434.	1.2	60
1118	Genetic module and miRNome trait analyses reflect the distinct biological features of endothelial progenitor cells from different anatomic locations. BMC Genomics, 2012, 13, 447.	1.2	24
1119	Transcriptional profiling of bovine milk using RNA sequencing. BMC Genomics, 2012, 13, 45.	1.2	237

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1120	Whole transcriptome analyses of six thoroughbred horses before and after exercise using RNA-Seq. BMC Genomics, 2012, 13, 473.	1.2	73
1121	Genome sequencing and genetic breeding of a bioethanol <i>Saccharomyces cerevisiae</i> strain YJS329. BMC Genomics, 2012, 13, 479.	1.2	36
1122	Whole transcriptome analysis of a reversible neurodegenerative process in <i>Drosophila</i> reveals potential neuroprotective genes. BMC Genomics, 2012, 13, 483.	1.2	10
1123	Comparison of transcriptome technologies in the pathogenic fungus <i>Aspergillus fumigatus</i> reveals novel insights into the genome and MpkA dependent gene expression. BMC Genomics, 2012, 13, 519.	1.2	35
1124	SERE: Single-parameter quality control and sample comparison for RNA-Seq. BMC Genomics, 2012, 13, 524.	1.2	161
1125	Analysis of a native whitefly transcriptome and its sequence divergence with two invasive whitefly species. BMC Genomics, 2012, 13, 529.	1.2	54
1126	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. BMC Genomics, 2012, 13, 547.	1.2	118
1127	De novo assembly of the pepper transcriptome ( <i>Capsicum annuum</i> ): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. BMC Genomics, 2012, 13, 571.	1.2	109
1128	Comparison of total and cytoplasmic mRNA reveals global regulation by nuclear retention and miRNAs. BMC Genomics, 2012, 13, 574.	1.2	35
1129	Sequencing of the needle transcriptome from Norway spruce ( <i>Picea abies</i> Karst L.) reveals lower substitution rates, but similar selective constraints in gymnosperms and angiosperms. BMC Genomics, 2012, 13, 589.	1.2	60
1130	Resolving candidate genes of mouse skeletal muscle QTL via RNA-Seq and expression network analyses. BMC Genomics, 2012, 13, 592.	1.2	26
1131	RNA-seq and microarray complement each other in transcriptome profiling. BMC Genomics, 2012, 13, 629.	1.2	131
1132	Transcriptome database resource and gene expression atlas for the rose. BMC Genomics, 2012, 13, 638.	1.2	76
1133	Downy mildew resistance induced by <i>Trichoderma harzianum</i> T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. BMC Genomics, 2012, 13, 660.	1.2	132
1134	Next generation sequencing and de novo transcriptome analysis of <i>Costus pictus</i> D. Don, a non-model plant with potent anti-diabetic properties. BMC Genomics, 2012, 13, 663.	1.2	66
1135	Comparative genomics and transcriptomics of trait-gene association. BMC Genomics, 2012, 13, 669.	1.2	16
1136	Transcriptome analysis at four developmental stages of grape berry ( <i>Vitis vinifera</i> cv. Shiraz) provides insights into regulated and coordinated gene expression. BMC Genomics, 2012, 13, 691.	1.2	125
1137	De novo reconstruction of the <i>Toxoplasma gondii</i> transcriptome improves on the current genome annotation and reveals alternatively spliced transcripts and putative long non-coding RNAs. BMC Genomics, 2012, 13, 696.	1.2	38

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1138	De novo assembly and Characterisation of the Transcriptome during seed development, and generation of genic-SSR markers in Peanut ( <i>Arachis hypogaea</i> L.). <i>BMC Genomics</i> , 2012, 13, 90.	1.2	231
1139	Cutoffs and k-mers: implications from a transcriptome study in allopolyploid plants. <i>BMC Genomics</i> , 2012, 13, 92.	1.2	52
1140	Global transcriptome analysis reveals distinct expression among duplicated genes during sorghum-Bipolaris sorghicolainteraction. <i>BMC Plant Biology</i> , 2012, 12, 121.	1.6	42
1141	Sequence mining and transcript profiling to explore differentially expressed genes associated with lipid biosynthesis during soybean seed development. <i>BMC Plant Biology</i> , 2012, 12, 122.	1.6	40
1142	Transcriptome analysis of stem development in the tumourous stem mustard <i>Brassica juncea</i> var. <i>tumida</i> Tsen et Lee by RNA sequencing. <i>BMC Plant Biology</i> , 2012, 12, 53.	1.6	49
1143	Efficient recovery of whole blood RNA - a comparison of commercial RNA extraction protocols for high-throughput applications in wildlife species. <i>BMC Biotechnology</i> , 2012, 12, 33.	1.7	36
1144	HERV-H RNA is abundant in human embryonic stem cells and a precise marker for pluripotency. <i>Retrovirology</i> , 2012, 9, 111.	0.9	188
1145	Improving metabolic flux predictions using absolute gene expression data. <i>BMC Systems Biology</i> , 2012, 6, 73.	3.0	126
1146	Potential role of multiple carbon fixation pathways during lipid accumulation in <i>Phaeodactylum tricornutum</i> . <i>Biotechnology for Biofuels</i> , 2012, 5, 40.	6.2	185
1147	Transcriptomic analysis of the oleaginous microalga <i>Neochloris oleoabundans</i> reveals metabolic insights into triacylglyceride accumulation. <i>Biotechnology for Biofuels</i> , 2012, 5, 74.	6.2	178
1148	A systematic comparison and evaluation of high density exon arrays and RNA-seq technology used to unravel the peripheral blood transcriptome of sickle cell disease. <i>BMC Medical Genomics</i> , 2012, 5, 28.	0.7	71
1149	BowStrap v1.0: Assigning statistical significance to expressed genes using short-read transcriptome data. <i>BMC Research Notes</i> , 2012, 5, 275.	0.6	6
1150	The bench scientist's guide to statistical analysis of RNA-Seq data. <i>BMC Research Notes</i> , 2012, 5, 506.	0.6	30
1151	Rapid genome-scale mapping of chromatin accessibility in tissue. <i>Epigenetics and Chromatin</i> , 2012, 5, 10.	1.8	30
1152	Statistical methods for identifying differentially expressed genes in RNA-Seq experiments. <i>Cell and Bioscience</i> , 2012, 2, 26.	2.1	41
1153	An anatomically comprehensive atlas of the adult human brain transcriptome. <i>Nature</i> , 2012, 489, 391-399.	13.7	2,321
1154	Metalloproteinases and Their Associated Genes Contribute to the Functional Integrity and Noise-Induced Damage in the Cochlear Sensory Epithelium. <i>Journal of Neuroscience</i> , 2012, 32, 14927-14941.	1.7	41
1156	Next Generation Microarray Bioinformatics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	8



#	ARTICLE	IF	CITATIONS
1157	HLA typing from RNA-Seq sequence reads. <i>Genome Medicine</i> , 2012, 4, 102.	3.6	204
1158	Gene network analyses of first service conception in Brangus heifers: Use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors <sup>1</sup> . <i>Journal of Animal Science</i> , 2012, 90, 2894-2906.	0.2	66
1159	Genome-wide determination of RNA stability reveals hundreds of short-lived noncoding transcripts in mammals. <i>Genome Research</i> , 2012, 22, 947-956.	2.4	364
1160	Gene expression profiling in human neurodegenerative disease. <i>Nature Reviews Neurology</i> , 2012, 8, 518-530.	4.9	183
1161	A Statistical Framework for eQTL Mapping Using RNA-Seq Data. <i>Biometrics</i> , 2012, 68, 1-11.	0.8	140
1162	Temperature-dependent, behavioural, and transcriptional variability of a tritrophic interaction consisting of bean, herbivorous mite, and predator. <i>Molecular Ecology</i> , 2012, 21, 5624-5635.	2.0	25
1163	Systematic comparison of RNA-Seq normalization methods using measurement error models. <i>Bioinformatics</i> , 2012, 28, 2584-2591.	1.8	25
1165	An Introduction to Personalized Medicine. , 2012, , 121-142.		3
1166	Gene structure in the sea urchin <i>Strongylocentrotus purpuratus</i> based on transcriptome analysis. <i>Genome Research</i> , 2012, 22, 2079-2087.	2.4	138
1167	What does our genome encode?. <i>Genome Research</i> , 2012, 22, 1602-1611.	2.4	107
1168	Deciphering the Plant Splicing Code: Experimental and Computational Approaches for Predicting Alternative Splicing and Splicing Regulatory Elements. <i>Frontiers in Plant Science</i> , 2012, 3, 18.	1.7	78
1169	Protein Identification Using Customized Protein Sequence Databases Derived from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2012, 11, 1009-1017.	1.8	156
1170	Using Genome-Wide Expression Profiling to Define Gene Networks Relevant to the Study of Complex Traits. <i>International Review of Neurobiology</i> , 2012, 104, 91-133.	0.9	21
1171	Mapping Protein-DNA Interactions Using ChIP-Sequencing. <i>Methods in Molecular Biology</i> , 2012, 809, 157-173.	0.4	20
1172	Omics Investigations of HIV and SIV Pathogenesis and Innate Immunity. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 87-116.	0.7	3
1173	Single-neuron RNA-Seq: technical feasibility and reproducibility. <i>Frontiers in Genetics</i> , 2012, 3, 124.	1.1	61
1174	The Human Pancreatic Islet Transcriptome: Expression of Candidate Genes for Type 1 Diabetes and the Impact of Pro-Inflammatory Cytokines. <i>PLoS Genetics</i> , 2012, 8, e1002552.	1.5	398
1175	Personalizing rare disease research: how genomics is revolutionizing the diagnosis and treatment of rare disease. <i>Personalized Medicine</i> , 2012, 9, 805-819.	0.8	8

#	ARTICLE	IF	CITATIONS
1178	Conceptus-Endometrium Crosstalk During Maternal Recognition of Pregnancy in Cattle1. <i>Biology of Reproduction</i> , 2012, 87, 6, 1-9.	1.2	56
1179	The Human Salivary RNA Transcriptome Revealed by Massively Parallel Sequencing. <i>Clinical Chemistry</i> , 2012, 58, 1314-1321.	1.5	57
1180	Identification of PTK6, via RNA Sequencing Analysis, as a Suppressor of Esophageal Squamous Cell Carcinoma. <i>Gastroenterology</i> , 2012, 143, 675-686.e12.	0.6	68
1181	Transcriptomic changes in the bovine conceptus between the blastocyst stage and initiation of implantation. <i>Animal Reproduction Science</i> , 2012, 134, 56-63.	0.5	19
1182	A Global Transcriptome Analysis of a Dog Model of Congestive Heart Failure With the Human Genome as a Reference. <i>Journal of Cardiac Failure</i> , 2012, 18, 872-878.	0.7	8
1183	Identification of novel transcripts deregulated in buccal cancer by RNA-seq. <i>Gene</i> , 2012, 507, 152-158.	1.0	18
1184	A global view of gene activity at the flowering transition phase in precocious trifoliolate orange and its wild-type [ <i>Poncirus trifoliata</i> (L.) Raf.] by transcriptome and proteome analysis. <i>Gene</i> , 2012, 510, 47-58.	1.0	12
1185	De novo sequencing and comparative analysis of the blueberry transcriptome to discover putative genes related to antioxidants. <i>Gene</i> , 2012, 511, 54-61.	1.0	86
1186	The Association Between H3K4me3 and Antisense Transcription. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 74-81.	3.0	12
1187	Comparative Analyses of H3K4 and H3K27 Trimethylations Between the Mouse Cerebrum and Testis. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 82-93.	3.0	22
1188	Neurodegeneration as an RNA disorder. <i>Progress in Neurobiology</i> , 2012, 99, 293-315.	2.8	52
1189	The physiology of sterol nutrition in the pea aphid <i>Acyrtosiphon pisum</i> . <i>Journal of Insect Physiology</i> , 2012, 58, 1383-1389.	0.9	32
1190	Transcriptome comparison between honey bee queen- and worker-destined larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 665-673.	1.2	82
1191	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. <i>Methods in Enzymology</i> , 2012, 513, 297-313.	0.4	24
1192	Genetic analyses of nickel tolerance in a North American serpentine endemic plant, <i>Caulanthus amplexicaulis</i> var. <i>barbarae</i> (Brassicaceae). <i>American Journal of Botany</i> , 2012, 99, 1875-1883.	0.8	20
1193	Using Genomic Tools to Study Regulatory Evolution. <i>Methods in Molecular Biology</i> , 2012, 856, 335-361.	0.4	6
1194	Boolean modeling in systems biology: an overview of methodology and applications. <i>Physical Biology</i> , 2012, 9, 055001.	0.8	353
1195	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , 2012, 9, 609-614.	9.0	156

#	ARTICLE	IF	CITATIONS
1197	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <i>Nature Biotechnology</i> , 2012, 30, 777-782.	9.4	1,347
1198	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	9.4	383
1199	Global gene expression responses to waterlogging in roots of sesame ( <i>Sesamum indicum</i> L.). <i>Acta Physiologiae Plantarum</i> , 2012, 34, 2241-2249.	1.0	45
1200	Measurement of mRNA abundance using RNA-seq data: RPKM measure is inconsistent among samples. <i>Theory in Biosciences</i> , 2012, 131, 281-285.	0.6	1,737
1201	Role of Genomics and RNA-seq in Studies of Fungal Virulence. <i>Current Fungal Infection Reports</i> , 2012, 6, 267-274.	0.9	3
1202	<i>Xenopus</i> Protocols. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	6
1203	Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2012, 40, 553-568.	6.5	145
1204	Modeling RNA degradation for RNA-Seq with applications. <i>Biostatistics</i> , 2012, 13, 734-747.	0.9	25
1206	Application of Genomic and Molecular Methods to Fundamental Questions in Canine and Feline Reproductive Health. <i>Reproduction in Domestic Animals</i> , 2012, 47, 309-312.	0.6	1
1207	Current status and future perspectives for sequencing livestock genomes. <i>Journal of Animal Science and Biotechnology</i> , 2012, 3, 8.	2.1	41
1208	A comparative analysis of tissue gene expression data from high-throughput studies. <i>Science Bulletin</i> , 2012, 57, 2920-2927.	1.7	4
1209	A transforming <i>KIF5B</i> and <i>RET</i> gene fusion in lung adenocarcinoma revealed from whole-genome and transcriptome sequencing. <i>Genome Research</i> , 2012, 22, 436-445.	2.4	433
1210	Synchronization of the flowering transition by the tomato TERMINATING FLOWER gene. <i>Nature Genetics</i> , 2012, 44, 1393-1398.	9.4	122
1211	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, 10084-10097.	6.5	285
1212	Reduced Representation Methods for Subgenomic Enrichment and Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2012, 772, 85-103.	0.4	21
1213	Omics Era in Stem Cell Research: Data Integration of Multi-regulatory Layers. , 2012, , 119-137.		0
1215	Direct isolation and RNA-seq reveal environment-dependent properties of engrafted neural stem/progenitor cells. <i>Nature Communications</i> , 2012, 3, 1140.	5.8	65
1216	Transcription Factors in the Central Nervous System. , 2012, , 514-530.		1

#	ARTICLE	IF	CITATIONS
1217	Improving the flexibility of RNA-Seq data analysis pipelines. , 2012, 2012, 70-73.		1
1219	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
1220	Transcriptome profiling of UIP3B/NMD-deficient lymphoblastoid cells from patients with various forms of intellectual disability. <i>Molecular Psychiatry</i> , 2012, 17, 1103-1115.	4.1	97
1221	Next-generation sequencing and large genome assemblies. <i>Pharmacogenomics</i> , 2012, 13, 901-915.	0.6	120
1223	Genetic and Epigenomic Footprints of Folate. <i>Progress in Molecular Biology and Translational Science</i> , 2012, 108, 129-158.	0.9	50
1224	Transcriptome analyses of <i>Bactericera cockerelli</i> adults in response to <i>Candidatus Liberibacter solanacearum</i> infection. <i>Molecular Genetics and Genomics</i> , 2012, 287, 803-817.	1.0	53
1225	RNA-seq analysis of synovial fibroblasts brings new insights into rheumatoid arthritis. <i>Cell and Bioscience</i> , 2012, 2, 43.	2.1	40
1226	Solexa sequencing based transcriptome analysis of <i>Helicoverpa armigera</i> larvae. <i>Molecular Biology Reports</i> , 2012, 39, 11051-11059.	1.0	8
1227	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	1.2	542
1228	Accuracy of RNA-Seq and its dependence on sequencing depth. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	25
1229	Prediction of novel long non-coding RNAs based on RNA-Seq data of mouse <i>Klf1</i> knockout study. <i>BMC Bioinformatics</i> , 2012, 13, 331.	1.2	117
1230	An algorithm for chemical genomic profiling that minimizes batch effects: bucket evaluations. <i>BMC Bioinformatics</i> , 2012, 13, 245.	1.2	2
1231	Steps to ensure accuracy in genotype and SNP calling from Illumina sequencing data. <i>BMC Genomics</i> , 2012, 13, S8.	1.2	97
1232	DFI: gene feature discovery in RNA-seq experiments from multiple sources. <i>BMC Genomics</i> , 2012, 13, S11.	1.2	4
1233	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	6
1234	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. <i>BMC Genomics</i> , 2012, 13, S2.	1.2	63
1235	Combining multiple ChIP-seq peak detection systems using combinatorial fusion. <i>BMC Genomics</i> , 2012, 13, S12.	1.2	24
1236	Transcriptome analysis of <i>Sacha Inchi</i> ( <i>Plukenetia volubilis</i> L.) seeds at two developmental stages. <i>BMC Genomics</i> , 2012, 13, 716.	1.2	62

#	ARTICLE	IF	CITATIONS
1237	Transcriptomic analysis of "Suli" pear ( <i>Pyrus pyrifolia</i> white pear group) buds during the dormancy by RNA-Seq. <i>BMC Genomics</i> , 2012, 13, 700.	1.2	143
1238	Transcriptome characterization and gene expression of <i>Epinephelus</i> spp in endoplasmic reticulum stress-related pathway during betanodavirus infection in vitro. <i>BMC Genomics</i> , 2012, 13, 651.	1.2	54
1239	De novo characterization of the Chinese fir ( <i>Cunninghamia lanceolata</i> ) transcriptome and analysis of candidate genes involved in cellulose and lignin biosynthesis. <i>BMC Genomics</i> , 2012, 13, 648.	1.2	72
1240	Efficient experimental design and analysis strategies for the detection of differential expression using RNA-Sequencing. <i>BMC Genomics</i> , 2012, 13, 484.	1.2	179
1241	Deciphering the complex leaf transcriptome of the allotetraploid species <i>Nicotiana tabacum</i> : a phylogenomic perspective. <i>BMC Genomics</i> , 2012, 13, 406.	1.2	39
1242	The regulatory effect of miRNAs is a heritable genetic trait in humans. <i>BMC Genomics</i> , 2012, 13, 383.	1.2	23
1243	High yield derivation of enriched glutamatergic neurons from suspension-cultured mouse ESCs for neurotoxicology research. <i>BMC Neuroscience</i> , 2012, 13, 127.	0.8	26
1244	Deep-sequencing transcriptome analysis of chilling tolerance mechanisms of a subnival alpine plant, <i>Chorispora bungeana</i> . <i>BMC Plant Biology</i> , 2012, 12, 222.	1.6	84
1245	Development of a computational strategy to compare repetitive element enrichment between experimental conditions from high-throughput sequencing datasets. <i>BMC Proceedings</i> , 2012, 6, .	1.8	0
1246	Retinal Development. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	4
1247	A normalization strategy for comparing tag count data. <i>Algorithms for Molecular Biology</i> , 2012, 7, 5.	0.3	76
1248	A Powerful Method for Transcriptional Profiling of Specific Cell Types in Eukaryotes: Laser-Assisted Microdissection and RNA Sequencing. <i>PLoS ONE</i> , 2012, 7, e29685.	1.1	104
1249	Automated Workflow for Preparation of cDNA for Cap Analysis of Gene Expression on a Single Molecule Sequencer. <i>PLoS ONE</i> , 2012, 7, e30809.	1.1	22
1250	Transcriptome-Wide Survey of Mouse CNS-Derived Cells Reveals Monoallelic Expression within Novel Gene Families. <i>PLoS ONE</i> , 2012, 7, e31751.	1.1	50
1251	Genetic Divergence between Freshwater and Marine Morphs of Alewife ( <i>Alosa pseudoharengus</i> ): A "Next-Generation" Sequencing Analysis. <i>PLoS ONE</i> , 2012, 7, e31803.	1.1	27
1252	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. <i>PLoS ONE</i> , 2012, 7, e34286.	1.1	8
1253	Discovery of Novel MicroRNAs in Rat Kidney Using Next Generation Sequencing and Microarray Validation. <i>PLoS ONE</i> , 2012, 7, e34394.	1.1	19
1254	Complete Genome and Transcriptomes of <i>Streptococcus parasanguinis</i> FW213: Phylogenic Relations and Potential Virulence Mechanisms. <i>PLoS ONE</i> , 2012, 7, e34769.	1.1	16

#	ARTICLE	IF	CITATIONS
1255	Transcriptome Responses of Insect Fat Body Cells to Tissue Culture Environment. PLoS ONE, 2012, 7, e34940.	1.1	15
1256	Non-Overlapping Progesterone Receptor Cistromes Contribute to Cell-Specific Transcriptional Outcomes. PLoS ONE, 2012, 7, e35859.	1.1	67
1257	Concordant Signaling Pathways Produced by Pesticide Exposure in Mice Correspond to Pathways Identified in Human Parkinson's Disease. PLoS ONE, 2012, 7, e36191.	1.1	49
1258	Biased Gene Fractionation and Dominant Gene Expression among the Subgenomes of Brassica rapa. PLoS ONE, 2012, 7, e36442.	1.1	240
1259	Digital Gene Expression Profiling by 5' End Sequencing of cDNAs during Reprogramming in the Moss Physcomitrella patens. PLoS ONE, 2012, 7, e36471.	1.1	27
1260	Transcriptomic Analysis of the Salivary Glands of an Invasive Whitefly. PLoS ONE, 2012, 7, e39303.	1.1	103
1261	Transcriptome Sequencing and Comparative Analysis of Saccharina japonica (Laminariales, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502 T	1.1	93
1262	Avian Resistance to Campylobacter jejuni Colonization Is Associated with an Intestinal Immunogene Expression Signature Identified by mRNA Sequencing. PLoS ONE, 2012, 7, e40409.	1.1	46
1263	RNA-Seq Approach for Genetic Improvement of Meat Quality in Pig and Evolutionary Insight into the Substrate Specificity of Animal Carbonyl Reductases. PLoS ONE, 2012, 7, e42198.	1.1	47
1264	Selective Depletion of rRNA Enables Whole Transcriptome Profiling of Archival Fixed Tissue. PLoS ONE, 2012, 7, e42882.	1.1	168
1265	Transcriptome Analysis of Nicotiana tabacum Infected by Cucumber mosaic virus during Systemic Symptom Development. PLoS ONE, 2012, 7, e43447.	1.1	107
1266	Epigenetic Modification of Gene Expression in Honey Bees by Heterospecific Gland Secretions. PLoS ONE, 2012, 7, e43727.	1.1	25
1267	Comparative Transcript Profiling of a Male Sterile Cybrid Pummelo and Its Fertile Type Revealed Altered Gene Expression Related to Flower Development. PLoS ONE, 2012, 7, e43758.	1.1	56
1268	Analysis of the Transcriptomes Downstream of Eyeless and the Hedgehog, Decapentaplegic and Notch Signaling Pathways in Drosophila melanogaster. PLoS ONE, 2012, 7, e44583.	1.1	12
1269	Two Origins of Blastemal Progenitors Define Blastemal Regeneration of Zebrafish Lower Jaw. PLoS ONE, 2012, 7, e45380.	1.1	32
1270	High-Resolution Transcriptome of Human Macrophages. PLoS ONE, 2012, 7, e45466.	1.1	238
1271	Detailed Transcriptome Description of the Neglected Cestode Taenia multiceps. PLoS ONE, 2012, 7, e45830.	1.1	27
1272	De Novo Foliar Transcriptome of Chenopodium amaranticolor and Analysis of Its Gene Expression During Virus-Induced Hypersensitive Response. PLoS ONE, 2012, 7, e45953.	1.1	30

#	ARTICLE	IF	CITATIONS
1273	Deep RNA Sequencing Reveals Novel Cardiac Transcriptomic Signatures for Physiological and Pathological Hypertrophy. PLoS ONE, 2012, 7, e35552.	1.1	87
1274	Gene and Genome Parameters of Mammalian Liver Circadian Genes (LCGs). PLoS ONE, 2012, 7, e46961.	1.1	10
1275	Trigeminal Ganglion Neurons of Mice Show Intracellular Chloride Accumulation and Chloride-Dependent Amplification of Capsaicin-Induced Responses. PLoS ONE, 2012, 7, e48005.	1.1	26
1276	Reconstruction and Comparison of the Metabolic Potential of Cyanobacteria <i>Cyanothece</i> sp. ATCC 51142 and <i>Synechocystis</i> sp. PCC 6803. PLoS ONE, 2012, 7, e48285.	1.1	79
1277	Accurate Diagnostics for Bovine tuberculosis Based on High-Throughput Sequencing. PLoS ONE, 2012, 7, e50147.	1.1	24
1278	RNA-Seq vs Dual- and Single-Channel Microarray Data: Sensitivity Analysis for Differential Expression and Clustering. PLoS ONE, 2012, 7, e50986.	1.1	71
1279	Estimation of Copy Number Alterations from Exome Sequencing Data. PLoS ONE, 2012, 7, e51422.	1.1	18
1280	The Human Transcriptome: An Unfinished Story. <i>Genes</i> , 2012, 3, 344-360.	1.0	121
1281	Improving RNA-Seq Precision with MapAl. <i>Frontiers in Genetics</i> , 2012, 3, 28.	1.1	3
1282	Dark Matter RNA: Existence, Function, and Controversy. <i>Frontiers in Genetics</i> , 2012, 3, 60.	1.1	75
1283	Global Approaches to the Role of miRNAs in Drug-Induced Changes in Gene Expression. <i>Frontiers in Genetics</i> , 2012, 3, 109.	1.1	21
1284	Non-coding RNA and pseudogenes in neurodegenerative diseases: â€œThe (un)Usual Suspectsâ€• <i>Frontiers in Genetics</i> , 2012, 3, 231.	1.1	40
1285	Estimation of Gene Expression at Isoform Level from mRNA-Seq Data by Bayesian Hierarchical Modeling. <i>Frontiers in Genetics</i> , 2012, 3, 239.	1.1	0
1286	An Interspecies Regulatory Network Inferred from Simultaneous RNA-seq of <i>Candida albicans</i> Invading Innate Immune Cells. <i>Frontiers in Microbiology</i> , 2012, 3, 85.	1.5	123
1287	Metabolic Regulation of â€œCa. <i>Methylacidiphilum Fumariolicum</i> â€• SolV Cells Grown Under Different Nitrogen and Oxygen Limitations. <i>Frontiers in Microbiology</i> , 2012, 3, 266.	1.5	35
1288	Genomic and Physiological Analysis of Carbon Storage in the Verrucomicrobial Methanotroph â€œCa. <i>Methylacidiphilum Fumariolicum</i> â€• SolV. <i>Frontiers in Microbiology</i> , 2012, 3, 345.	1.5	61
1289	Omics strategies for revealing <i>Yersinia pestis</i> virulence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 157.	1.8	13
1290	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	21

#	ARTICLE	IF	CITATIONS
1291	Characteristics of nucleosomes and linker DNA regions on the genome of the basidiomycete <i>Mixia osmundae</i> revealed by mono- and dinucleosome mapping. <i>Open Biology</i> , 2012, 2, 120043.	1.5	11
1292	The Tissue Specific Role of Estrogen and Progesterone in Human Endometrium and Mammary Gland. , 2012, , .		2
1293	Expression Profiling of a Heterogeneous Population of ncRNAs Employing a Mixed DNA/LNA Microarray. <i>Journal of Nucleic Acids</i> , 2012, 2012, 1-10.	0.8	2
1294	Chemical Genomics and Emerging DNA Technologies in the Identification of Drug Mechanisms and Drug Targets. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1331-1345.	1.0	8
1295	Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress. , 0, , .		16
1296	The context of gene expression regulation. <i>F1000 Biology Reports</i> , 2012, 4, 8.	4.0	24
1297	Transcriptome and Proteome Research in Veterinary Science: What Is Possible and What Questions Can Be Asked?. <i>Scientific World Journal</i> , The, 2012, 2012, 1-14.	0.8	19
1298	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , 2012, 3, 1308-1319.	0.8	127
1299	IGFBP-4 tumor and serum levels are increased across all stages of epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , 2012, 5, 3.	1.3	23
1300	FiRePatâ€”Finding Regulatory Patterns between sRNAs and Genes. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 273-284.	4.6	6
1301	Analyzing genomic data: understanding the genome. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 116-137.	4.6	0
1302	Genome-Wide Analysis of N1ICD/RBPJ Targets In Vivo Reveals Direct Transcriptional Regulation of Wnt, SHH, and Hippo Pathway Effectors by Notch1. <i>Stem Cells</i> , 2012, 30, 741-752.	1.4	144
1303	Integrative Genomics Identifies the Corepressor SMRT as a Gatekeeper of Adipogenesis through the Transcription Factors C/EBP $\beta$ and KAISO. <i>Molecular Cell</i> , 2012, 46, 335-350.	4.5	96
1304	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012, 7, 562-578.	5.5	11,433
1305	Genetical Genomics for Evolutionary Studies. <i>Methods in Molecular Biology</i> , 2012, 856, 469-485.	0.4	2
1306	Ultrashort and progressive 4sU-tagging reveals key characteristics of RNA processing at nucleotide resolution. <i>Genome Research</i> , 2012, 22, 2031-2042.	2.4	132
1307	A unifying model for mTORC1-mediated regulation of mRNA translation. <i>Nature</i> , 2012, 485, 109-113.	13.7	1,245
1308	HOT regions function as patterned developmental enhancers and have a distinct cis-regulatory signature. <i>Genes and Development</i> , 2012, 26, 908-913.	2.7	130



#	ARTICLE	IF	CITATIONS
1309	A beginner's guide to eukaryotic genome annotation. <i>Nature Reviews Genetics</i> , 2012, 13, 329-342.	7.7	553
1310	RNA-SeQC: RNA-seq metrics for quality control and process optimization. <i>Bioinformatics</i> , 2012, 28, 1530-1532.	1.8	746
1311	Integrating Genomes. <i>Science</i> , 2012, 336, 179-182.	6.0	18
1312	EST and transcriptome analysis of cephalochordate amphioxus—past, present and future. <i>Briefings in Functional Genomics</i> , 2012, 11, 96-106.	1.3	5
1313	Digital RNA sequencing minimizes sequence-dependent bias and amplification noise with optimized single-molecule barcodes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1347-1352.	3.3	254
1314	Nprl3 is required for normal development of the cardiovascular system. <i>Mammalian Genome</i> , 2012, 23, 404-415.	1.0	38
1315	Chromatin state signatures associated with tissue-specific gene expression and enhancer activity in the embryonic limb. <i>Genome Research</i> , 2012, 22, 1069-1080.	2.4	121
1316	RNA-Seq Analysis of the Transcriptome of <i>Trypanosoma brucei</i> . <i>Nucleic Acids and Molecular Biology</i> , 2012, , 237-265.	0.2	1
1317	Gene set enrichment analysis: performance evaluation and usage guidelines. <i>Briefings in Bioinformatics</i> , 2012, 13, 281-291.	3.2	217
1318	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. <i>Cell</i> , 2012, 150, 264-278.	13.5	1,365
1319	High-throughput assessment of microRNA activity and function using microRNA sensor and decoy libraries. <i>Nature Methods</i> , 2012, 9, 840-846.	9.0	379
1320	De Novo Assembly of the Manila Clam <i>Ruditapes philippinarum</i> Transcriptome Provides New Insights into Expression Bias, Mitochondrial Doubly Uniparental Inheritance and Sex Determination. <i>Molecular Biology and Evolution</i> , 2012, 29, 771-786.	3.5	98
1321	Comparative Analysis of Different Label-Free Mass Spectrometry Based Protein Abundance Estimates and Their Correlation with RNA-Seq Gene Expression Data. <i>Journal of Proteome Research</i> , 2012, 11, 2261-2271.	1.8	150
1322	Modular regulatory principles of large non-coding RNAs. <i>Nature</i> , 2012, 482, 339-346.	13.7	2,036
1323	BCL2 mutations in diffuse large B-cell lymphoma. <i>Leukemia</i> , 2012, 26, 1383-1390.	3.3	135
1324	A comparative study of cell-free apoptotic and genomic DNA using FISH and massive parallel sequencing. <i>Expert Opinion on Biological Therapy</i> , 2012, 12, S11-S17.	1.4	14
1325	The B-cell identity factor Pax5 regulates distinct transcriptional programmes in early and late B lymphopoiesis. <i>EMBO Journal</i> , 2012, 31, 3130-3146.	3.5	202
1326	Normalization, testing, and false discovery rate estimation for RNA-sequencing data. <i>Biostatistics</i> , 2012, 13, 523-538.	0.9	308

#	ARTICLE	IF	CITATIONS
1327	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012, 22, 860-869.	2.4	150
1328	Applications of High-Throughput Sequencing. , 2012, , 27-53.		1
1329	DNA-Protein Interaction Analysis (ChIP-Seq). , 2012, , 127-149.		0
1330	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
1331	MicroRNA Expression Profiling and Discovery. , 2012, , 191-208.		0
1332	Designing a transcriptome next-generation sequencing project for a nonmodel plant species. <i>American Journal of Botany</i> , 2012, 99, 257-266.	0.8	192
1333	Integrated cross-species transcriptional network analysis of metastatic susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3184-3189.	3.3	50
1334	Genome Regulation by Long Noncoding RNAs. <i>Annual Review of Biochemistry</i> , 2012, 81, 145-166.	5.0	3,665
1335	AMPK Modulation in Cancer Progression: Multilayer Integrative Analysis of the Whole Transcriptome in Asian Gastric Cancer. <i>Cancer Research</i> , 2012, 72, 2512-2521.	0.4	91
1336	Single-cell systems biology by super-resolution imaging and combinatorial labeling. <i>Nature Methods</i> , 2012, 9, 743-748.	9.0	394
1337	Transcription factor redundancy and tissue-specific regulation: Evidence from functional and physical network connectivity. <i>Genome Research</i> , 2012, 22, 1907-1919.	2.4	16
1338	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. <i>Science</i> , 2012, 336, 1448-1451.	6.0	279
1339	Highly multiplexed and strand-specific single-cell RNA end sequencing. <i>Nature Protocols</i> , 2012, 7, 813-828.	5.5	262
1340	An Overview of the Analysis of Next Generation Sequencing Data. <i>Methods in Molecular Biology</i> , 2012, 802, 249-257.	0.4	22
1341	A new subtype of bone sarcoma defined by BCOR-CCNB3 gene fusion. <i>Nature Genetics</i> , 2012, 44, 461-466.	9.4	406
1342	CEDER: Accurate Detection of Differentially Expressed Genes by Combining Significance of Exons Using RNA-Seq. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1281-1292.	1.9	17
1343	Organogenesis and functional genomics of the endocrine pancreas. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2109-2123.	2.4	10
1344	De novo characterization of the antler tip of Chinese Sika deer transcriptome and analysis of gene expression related to rapid growth. <i>Molecular and Cellular Biochemistry</i> , 2012, 364, 93-100.	1.4	41

#	ARTICLE	IF	CITATIONS
1345	RNA-sequencing tag profiling of the placenta and pericarp of pungent pepper provides robust candidates contributing to capsaicinoid biosynthesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 110, 111-121.	1.2	30
1346	De novo characterization of the root transcriptome of a traditional Chinese medicinal plant <i>Polygonum cuspidatum</i> . <i>Science China Life Sciences</i> , 2012, 55, 452-466.	2.3	80
1347	Transcriptome analysis of the roots at early and late seedling stages using Illumina paired-end sequencing and development of EST-SSR markers in radish. <i>Plant Cell Reports</i> , 2012, 31, 1437-1447.	2.8	96
1348	De novo sequencing and a comprehensive analysis of purple sweet potato ( <i>Ipomoea batatas</i> L.) transcriptome. <i>Planta</i> , 2012, 236, 101-113.	1.6	118
1349	A genomewide survey of bHLH transcription factors in the coral <i>Acropora digitifera</i> identifies three novel orthologous families, pearl, amber, and peridot. <i>Development Genes and Evolution</i> , 2012, 222, 63-76.	0.4	18
1350	Cytoskeleton remodeling and alterations in smooth muscle contractility in the bovine jejunum during nematode infection. <i>Functional and Integrative Genomics</i> , 2012, 12, 35-44.	1.4	26
1351	Sequencing and de novo analysis of the Chinese Sika deer antler-tip transcriptome during the ossification stage using Illumina RNA-Seq technology. <i>Biotechnology Letters</i> , 2012, 34, 813-822.	1.1	40
1352	Identification of genes expressed by <i>Phakopsora pachyrhizi</i> , the pathogen causing soybean rust, at a late stage of infection of susceptible soybean leaves. <i>Plant Pathology</i> , 2012, 61, 773-786.	1.2	18
1353	Repetitive DNA and next-generation sequencing: computational challenges and solutions. <i>Nature Reviews Genetics</i> , 2012, 13, 36-46.	7.7	1,382
1354	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	1.3	55
1355	Interrogating genomic and epigenomic data to understand prostate cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2012, 1825, 186-196.	3.3	14
1356	Genomics in mammalian cell culture bioprocessing. <i>Biotechnology Advances</i> , 2012, 30, 629-638.	6.0	53
1357	A <i>de novo</i> transcriptome assembly of <i>Lucilia sericata</i> (Diptera: Calliphoridae) with predicted alternative splices, single nucleotide polymorphisms and transcript expression estimates. <i>Insect Molecular Biology</i> , 2012, 21, 205-221.	1.0	52
1358	Comparison of the transcriptional profiles of head and body lice. <i>Insect Molecular Biology</i> , 2012, 21, 257-268.	1.0	47
1359	Transcriptome analysis of the citrus red mite, <i>Panonychus citri</i> , and its gene expression by exposure to insecticide/acaricide. <i>Insect Molecular Biology</i> , 2012, 21, 422-436.	1.0	30
1360	Genomic toolboxes for conservation biologists. <i>Evolutionary Applications</i> , 2012, 5, 130-143.	1.5	78
1361	Quantitative analysis of 5HT2C receptor RNA editing patterns in psychiatric disorders. <i>Neurobiology of Disease</i> , 2012, 45, 8-13.	2.1	33
1362	A novel DNaseq program for enhanced analysis of Illumina GAI data: a case study on antibody complementarity-determining regions. <i>New Biotechnology</i> , 2012, 29, 271-278.	2.4	1

#	ARTICLE	IF	CITATIONS
1363	Developmental Gene Regulation by an Ancient Intercellular Communication System in Social Amoebae. <i>Protist</i> , 2012, 163, 25-37.	0.6	25
1364	RNA-Seq defines novel genes, RNA processing patterns and enhancer maps for the early stages of nephrogenesis: Hox supergenes. <i>Developmental Biology</i> , 2012, 368, 4-17.	0.9	37
1365	Tracking nickel-adaptive biomarkers in <i>Pisolithus albus</i> from New Caledonia using a transcriptomic approach. <i>Molecular Ecology</i> , 2012, 21, 2208-2223.	2.0	22
1366	Genomics and population biology of <i>Cryptosporidium</i> species. <i>Parasite Immunology</i> , 2012, 34, 61-71.	0.7	69
1367	Genomics and transcriptomics across the diversity of the Nematoda. <i>Parasite Immunology</i> , 2012, 34, 108-120.	0.7	22
1368	Functional genomics of trypanosomatids. <i>Parasite Immunology</i> , 2012, 34, 72-79.	0.7	22
1369	Transcriptome analysis and gene expression atlas for <i>Panicum hallii</i> var. <i>filipes</i> , a diploid model for biofuel research. <i>Plant Journal</i> , 2012, 70, 879-890.	2.8	37
1370	Gene expression in the developing aleurone and starchy endosperm of wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 668-679.	4.1	75
1371	Correlation Pursuit: Forward Stepwise Variable Selection for Index Models. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 849-870.	1.1	27
1372	Isoform diversity and its importance for axon regeneration. <i>Neuropathology</i> , 2012, 32, 420-431.	0.7	4
1373	Challenges in estimating percent inclusion of alternatively spliced junctions from RNA-seq data. <i>BMC Bioinformatics</i> , 2012, 13, S11.	1.2	53
1374	A context-based approach to identify the most likely mapping for RNA-seq experiments. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	14
1375	RNA-Seq quantification of the human small airway epithelium transcriptome. <i>BMC Genomics</i> , 2012, 13, 82.	1.2	107
1376	Combining SNP discovery from next-generation sequencing data with bulked segregant analysis (BSA) to fine-map genes in polyploid wheat. <i>BMC Plant Biology</i> , 2012, 12, 14.	1.6	265
1377	An ovary transcriptome for all maturational stages of the striped bass ( <i>Morone saxatilis</i> ), a highly advanced perciform fish. <i>BMC Research Notes</i> , 2012, 5, 111.	0.6	47
1378	Application of RNA-Seq transcriptome analysis: CD151 is an Invasion/Migration target in all stages of epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , 2012, 5, 4.	1.3	19
1379	Hippocampal gene profiling: Toward a systems biology of the hippocampus. <i>Hippocampus</i> , 2012, 22, 929-941.	0.9	11
1380	Assessing the Enrichment Performance in Targeted Resequencing Experiments. <i>Human Mutation</i> , 2012, 33, 635-641.	1.1	27

#	ARTICLE	IF	CITATIONS
1381	Large-scale sequencing of normalized full-length cDNA library of soybean seed at different developmental stages and analysis of the gene expression profiles based on ESTs. <i>Molecular Biology Reports</i> , 2012, 39, 2867-2874.	1.0	11
1382	Finding consistent patterns: A nonparametric approach for identifying differential expression in RNA-Seq data. <i>Statistical Methods in Medical Research</i> , 2013, 22, 519-536.	0.7	393
1383	eQTL Mapping Using RNA-seq Data. <i>Statistics in Biosciences</i> , 2013, 5, 198-219.	0.6	73
1384	High throughput investigative dermatology in 2012 and beyond: A new era beckons. <i>Australasian Journal of Dermatology</i> , 2013, 54, 1-8.	0.4	3
1385	High-throughput sequencing of cytosine methylation in plant DNA. <i>Plant Methods</i> , 2013, 9, 16.	1.9	19
1386	Using an ensemble of statistical metrics to quantify large sets of plant transcription factor binding sites. <i>Plant Methods</i> , 2013, 9, 12.	1.9	2
1387	Mapping gene activity of Arabidopsis root hairs. <i>Genome Biology</i> , 2013, 14, R67.	3.8	89
1388	TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. <i>Genome Biology</i> , 2013, 14, R36.	13.9	11,713
1389	SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. <i>Genome Biology</i> , 2013, 14, R12.	13.9	197
1390	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2013, 14, R7.	13.9	180
1391	TIMPs of parasitic helminths – a large-scale analysis of high-throughput sequence datasets. <i>Parasites and Vectors</i> , 2013, 6, 156.	1.0	18
1392	MeCP2 binds to 5hmc enriched within active genes and accessible chromatin in the nervous system. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	5
1393	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERVL in mouse ES cells. <i>Epigenetics and Chromatin</i> , 2013, 6, 15.	1.8	153
1394	Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. <i>Genome Medicine</i> , 2013, 5, 29.	3.6	96
1395	An efficient rRNA removal method for RNA sequencing in GC-rich bacteria. <i>Microbial Informatics and Experimentation</i> , 2013, 3, 1.	7.6	44
1396	Characteristics of cross-hybridization and cross-alignment of expression in pseudo-xenograft samples by RNA-Seq and microarrays. <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 8.	1.2	4
1397	Research progress in allele-specific expression and its regulatory mechanisms. <i>Journal of Applied Genetics</i> , 2013, 54, 271-283.	1.0	70
1398	Differential gene expression analysis between anagen and telogen of <i>Capra hircus</i> skin based on the de novo assembled transcriptome sequence. <i>Gene</i> , 2013, 520, 30-38.	1.0	37

#	ARTICLE	IF	CITATIONS
1399	Exploring the zebrafish embryo as an alternative model for the evaluation of liver toxicity by histopathology and expression profiling. Archives of Toxicology, 2013, 87, 807-823.	1.9	77
1400	Comparative analysis of differentially expressed genes in Sika deer antler at different stages. Molecular Biology Reports, 2013, 40, 1665-1676.	1.0	29
1401	RNA-seq Analysis Reveals Ethylene-Mediated Reproductive Organ Development and Abscission in Soybean ( <i>Glycine max</i> L. Merr.). Plant Molecular Biology Reporter, 2013, 31, 607-619.	1.0	26
1402	Independent specialization of the human and mouse X chromosomes for the male germ line. Nature Genetics, 2013, 45, 1083-1087.	9.4	164
1403	Human housekeeping genes, revisited. Trends in Genetics, 2013, 29, 569-574.	2.9	1,091
1405	High-throughput <i>scRNA</i> sequencing of a formalin-fixed, paraffin-embedded autopsy lung tissue sample from the 1918 influenza pandemic. Journal of Pathology, 2013, 229, 535-545.	2.1	74
1406	Ultra-deep profiling of alternatively spliced <i>Drosophila</i> Dscam isoforms by circularization-assisted multi-segment sequencing. EMBO Journal, 2013, 32, 2029-2038.	3.5	61
1407	Genetic programs in human and mouse early embryos revealed by single-cell RNA-seq. Nature, 2013, 500, 593-597.	13.7	859
1408	An Optimal Test with Maximum Average Power While Controlling FDR with Application to RNA-seq Data. Biometrics, 2013, 69, 594-605.	0.8	33
1409	Complex Models and Computational Methods in Statistics. Contributions To Statistics, 2013, , .	0.2	1
1410	A stable transcription factor complex nucleated by oligomeric AML1-ETO controls leukaemogenesis. Nature, 2013, 500, 93-97.	13.7	134
1411	Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods – Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314.		1
1412	Translation-dependent displacement of UPF1 from coding sequences causes its enrichment in 3' UTRs. Nature Structural and Molecular Biology, 2013, 20, 936-943.	3.6	155
1413	Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. Age, 2013, 35, 763-776.	3.0	94
1414	Transcriptomic profiling of <i>Aspergillus flavus</i> in response to 5-azacytidine. Fungal Genetics and Biology, 2013, 56, 78-86.	0.9	75
1415	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. Nature Protocols, 2013, 8, 1494-1512.	5.5	7,054
1416	Proteomics of model and crop plant species: Status, current limitations and strategic advances for crop improvement. Journal of Proteomics, 2013, 93, 5-19.	1.2	81
1417	Introduction to Next-Generation Nucleic Acid Sequencing in Cardiovascular Disease Research. Methods in Molecular Biology, 2013, 1027, 157-179.	0.4	1

#	ARTICLE	IF	CITATIONS
1418	Plant Meiosis. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	7
1419	PM-Seq: Using Finite Poisson Mixture Models for RNA-Seq Data Analysis and Transcript Expression Level Quantification. <i>Statistics in Biosciences</i> , 2013, 5, 71-87.	0.6	4
1420	A Hierarchical Bayesian Model for Estimating and Inferring Differential Isoform Expression for Multi-sample RNA-Seq Data. <i>Statistics in Biosciences</i> , 2013, 5, 119-137.	0.6	8
1421	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. <i>Statistics in Biosciences</i> , 2013, 5, 138-155.	0.6	11
1422	State of art fusion-finder algorithms are suitable to detect transcription-induced chimeras in normal tissues?. <i>BMC Bioinformatics</i> , 2013, 14, S2.	1.2	56
1423	A mixture model for expression deconvolution from RNA-seq in heterogeneous tissues. <i>BMC Bioinformatics</i> , 2013, 14, S11.	1.2	31
1424	A novel min-cost flow method for estimating transcript expression with RNA-Seq. <i>BMC Bioinformatics</i> , 2013, 14, S15.	1.2	65
1425	Gene set enrichment analysis of RNA-Seq data: integrating differential expression and splicing. <i>BMC Bioinformatics</i> , 2013, 14, S16.	1.2	43
1426	NURD: an implementation of a new method to estimate isoform expression from non-uniform RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 220.	1.2	15
1427	TCC: an R package for comparing tag count data with robust normalization strategies. <i>BMC Bioinformatics</i> , 2013, 14, 219.	1.2	477
1428	ChIPXpress: using publicly available gene expression data to improve ChIP-seq and ChIP-chip target gene ranking. <i>BMC Bioinformatics</i> , 2013, 14, 188.	1.2	15
1429	PASTA: splice junction identification from RNA-Sequencing data. <i>BMC Bioinformatics</i> , 2013, 14, 116.	1.2	19
1430	Differential expression analysis for paired RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 110.	1.2	22
1431	A comparison of methods for differential expression analysis of RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 91.	1.2	743
1432	Estimation of data-specific constitutive exons with RNA-Seq data. <i>BMC Bioinformatics</i> , 2013, 14, 31.	1.2	6
1433	FUSIM: a software tool for simulating fusion transcripts. <i>BMC Bioinformatics</i> , 2013, 14, 13.	1.2	22
1434	GSVA: gene set variation analysis for microarray and RNA-Seq data. <i>BMC Bioinformatics</i> , 2013, 14, 7.	1.2	7,876
1435	Phylogeny and evolutionary history of glycogen synthase kinase 3/SHAGGY-like kinase genes in land plants. <i>BMC Evolutionary Biology</i> , 2013, 13, 143.	3.2	21

#	ARTICLE	IF	CITATIONS
1436	De novo sequencing and transcriptome analysis of the desert shrub, <i>Ammopiptanthus mongolicus</i> , during cold acclimation using Illumina/Solexa. <i>BMC Genomics</i> , 2013, 14, 488.	1.2	80
1437	Genome-wide identification of binding sites for NAC and YABBY transcription factors and co-regulated genes during soybean seedling development by ChIP-Seq and RNA-Seq. <i>BMC Genomics</i> , 2013, 14, 477.	1.2	72
1438	Analysis and annotation of the hexaploid oat seed transcriptome. <i>BMC Genomics</i> , 2013, 14, 471.	1.2	62
1439	The genesis of an exceptionally lethal venom in the timber rattlesnake ( <i>Crotalus horridus</i> ) revealed through comparative venom-gland transcriptomics. <i>BMC Genomics</i> , 2013, 14, 394.	1.2	95
1440	RNA-seq analysis of single bovine blastocysts. <i>BMC Genomics</i> , 2013, 14, 350.	1.2	61
1441	Insights into organ-specific pathogen defense responses in plants: RNA-seq analysis of potato tuber- <i>Phytophthora infestans</i> interactions. <i>BMC Genomics</i> , 2013, 14, 340.	1.2	101
1442	Transcriptional pathways associated with the slow growth phenotype of transformed <i>Anaplasma marginale</i> . <i>BMC Genomics</i> , 2013, 14, 272.	1.2	13
1443	A zebrafish high throughput screening system used for <i>Staphylococcus epidermidis</i> infection marker discovery. <i>BMC Genomics</i> , 2013, 14, 255.	1.2	57
1444	Transcriptional landscape of <i>Aspergillus niger</i> at breaking of conidial dormancy revealed by RNA-sequencing. <i>BMC Genomics</i> , 2013, 14, 246.	1.2	54
1445	Integrated <i>œomics</i> -profiling indicates that miRNAs are modulators of the ontogenetic venom composition shift in the Central American rattlesnake, <i>Crotalus simus simus</i> . <i>BMC Genomics</i> , 2013, 14, 234.	1.2	164
1446	The transcriptome of <i>Leishmania major</i> in the axenic promastigote stage: transcript annotation and relative expression levels by RNA-seq. <i>BMC Genomics</i> , 2013, 14, 223.	1.2	75
1447	Species and condition specific adaptation of the transcriptional landscapes in <i>Candida albicans</i> and <i>Candida dubliniensis</i> . <i>BMC Genomics</i> , 2013, 14, 212.	1.2	43
1448	Xylem transcription profiles indicate potential metabolic responses for economically relevant characteristics of <i>Eucalyptus</i> species. <i>BMC Genomics</i> , 2013, 14, 201.	1.2	28
1449	Determination of dosage compensation of the mammalian X chromosome by RNA-seq is dependent on analytical approach. <i>BMC Genomics</i> , 2013, 14, 150.	1.2	35
1450	Systematic analysis of palatal transcriptome to identify cleft palate genes within TGF $\beta$ 3-knockout mice alleles: RNA-Seq analysis of TGF $\beta$ 3 Mice. <i>BMC Genomics</i> , 2013, 14, 113.	1.2	38
1451	Global analyses of <i>Ceratocystis cacaofunesta</i> mitochondria: from genome to proteome. <i>BMC Genomics</i> , 2013, 14, 91.	1.2	17
1452	Characterisation of the wheat ( <i>triticum aestivum</i> L.) transcriptome by de novo assembly for the discovery of phosphate starvation-responsive genes: gene expression in Pi-stressed wheat. <i>BMC Genomics</i> , 2013, 14, 77.	1.2	121
1453	Genome-wide identification, characterization, and expression analysis of lineage-specific genes within zebrafish. <i>BMC Genomics</i> , 2013, 14, 65.	1.2	39



#	ARTICLE	IF	CITATIONS
1454	Transcriptional profiling of the Arabidopsis abscission mutant hsl2 by RNA-Seq. BMC Genomics, 2013, 14, 37.	1.2	78
1455	Adjustment method for microarray data generated using two-cycle RNA labeling protocol. BMC Genomics, 2013, 14, 31.	1.2	6
1456	Transcriptomic profiling of the salt-stress response in the wild recretehalophyte Reaumuria trigyna. BMC Genomics, 2013, 14, 29.	1.2	147
1457	Vasohibin-1 is identified as a master-regulator of endothelial cell apoptosis using gene network analysis. BMC Genomics, 2013, 14, 23.	1.2	20
1458	RNA-Seq analysis reveals new gene models and alternative splicing in the fungal pathogen Fusarium graminearum. BMC Genomics, 2013, 14, 21.	1.2	79
1459	Improved moderation for gene-wise variance estimation in RNA-Seq via the exploitation of external information. BMC Genomics, 2013, 14, S9.	1.2	2
1460	Transcriptome analysis of embryo maturation in maize. BMC Plant Biology, 2013, 13, 19.	1.6	38
1461	Mutation spectrum in human colorectal cancers and potential functional relevance. BMC Medical Genetics, 2013, 14, 32.	2.1	13
1462	Exome profiling of primary, metastatic and recurrent ovarian carcinomas in a BRCA1-positive patient. BMC Cancer, 2013, 13, 146.	1.1	14
1463	Single-cell sequencing-based technologies will revolutionize whole-organism science. Nature Reviews Genetics, 2013, 14, 618-630.	7.7	1,012
1464	A novel metatranscriptomic approach to identify gene expression dynamics during extracellular electron transfer. Nature Communications, 2013, 4, 1601.	5.8	162
1465	Personal genomes, quantitative dynamic omics and personalized medicine. Quantitative Biology, 2013, 1, 71-90.	0.3	29
1466	Secretome Prediction and Analysis in Sacred Lotus (Nelumbo nucifera Gaertn.). Tropical Plant Biology, 2013, 6, 131-137.	1.0	6
1467	Regulation of phenylalanine ammonia-lyase (PAL) gene family in wood forming tissue of Populus trichocarpa. Planta, 2013, 238, 487-497.	1.6	53
1468	Transcriptome-wide identification of R2R3-MYB transcription factors in barley with their boron responsive expression analysis. Molecular Genetics and Genomics, 2013, 288, 141-155.	1.0	87
1469	A novel rearrangement of occludin causes brain calcification and renal dysfunction. Human Genetics, 2013, 132, 1223-1234.	1.8	24
1470	The landscape of alternative splicing in buccal mucosa squamous cell carcinoma. Oral Oncology, 2013, 49, 604-610.	0.8	10
1471	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	4.5	62

#	ARTICLE	IF	CITATIONS
1472	The p38 MAPK PMK-1 shows heat-induced nuclear translocation, supports chaperone expression, and affects the heat tolerance of <i>Caenorhabditis elegans</i> . <i>Cell Stress and Chaperones</i> , 2013, 18, 293-306.	1.2	43
1473	Transcriptome of Atlantic Cod ( <i>Gadus morhua</i> L.) Early Embryos from Farmed and Wild Broodstocks. <i>Marine Biotechnology</i> , 2013, 15, 677-694.	1.1	43
1474	Directional RNA-seq reveals highly complex condition-dependent transcriptomes in <i>E. coli</i> K12 through accurate full-length transcripts assembling. <i>BMC Genomics</i> , 2013, 14, 520.	1.2	31
1475	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. <i>Biotechnology Advances</i> , 2013, 31, 1109-1119.	6.0	23
1476	Design, construction and characterisation of a synthetic promoter library for fine-tuned gene expression in actinomycetes. <i>Metabolic Engineering</i> , 2013, 19, 98-106.	3.6	172
1477	Heterogeneity of the biological properties and gene expression profiles of murine bone marrow stromal cells. <i>International Journal of Biochemistry and Cell Biology</i> , 2013, 45, 2431-2443.	1.2	29
1478	Integrative analysis revealed the molecular mechanism underlying $\text{RBM}10$ -mediated splicing regulation. <i>EMBO Molecular Medicine</i> , 2013, 5, 1431-1442.	3.3	106
1479	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1131-1139.	3.6	1,416
1480	Plant Microbe Symbiosis: Fundamentals and Advances. , 2013, , .		25
1481	Ribosomal RNA Depletion for Efficient Use of RNA-Seq Capacity. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 4.19.	2.9	101
1482	A Long Noncoding RNA Mediates Both Activation and Repression of Immune Response Genes. <i>Science</i> , 2013, 341, 789-792.	6.0	925
1483	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	9.4	334
1484	Next Generation Sequencing in Cancer Research. , 2013, , .		5
1485	Contribution of subgenomes to the transcriptome and their intertwined regulation in the allopolyploid <i>Coffea arabica</i> grown at contrasted temperatures. <i>New Phytologist</i> , 2013, 200, 251-260.	3.5	79
1486	Characterization of MHC class I in a long-distance migrant shorebird suggests multiple transcribed genes and intergenic recombination. <i>Immunogenetics</i> , 2013, 65, 211-225.	1.2	19
1487	Tumor Suppressors Status in Cancer Cell Line Encyclopedia. <i>Molecular Oncology</i> , 2013, 7, 791-798.	2.1	28
1488	Transcriptome analysis of candidate genes and signaling pathways associated with light-induced brown film formation in <i>Lentinula edodes</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4977-4989.	1.7	74
1489	Impact of the next-generation sequencing data depth on various biological result inferences. <i>Science China Life Sciences</i> , 2013, 56, 104-109.	2.3	11

#	ARTICLE	IF	CITATIONS
1490	Transcriptome profiling of the developing postnatal mouse testis using next-generation sequencing. <i>Science China Life Sciences</i> , 2013, 56, 1-12.	2.3	42
1491	Epigenetic regulation of cholinergic receptor M1 (CHRM1) by histone H3K9me3 impairs Ca <sup>2+</sup> signaling in Huntington's disease. <i>Acta Neuropathologica</i> , 2013, 125, 727-739.	3.9	48
1492	Early role for IL-6 signalling during generation of induced pluripotent stem cells revealed by heterokaryon RNA-Seq. <i>Nature Cell Biology</i> , 2013, 15, 1244-1252.	4.6	88
1493	New Trends in Image Analysis and Processing – ICIAP 2013. <i>Lecture Notes in Computer Science</i> , 2013, , .	1.0	4
1494	The role of desaturases in the biosynthesis of marking pheromones in bumblebee males. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 724-731.	1.2	25
1495	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.	5.5	1,124
1496	Assessing Differential Expression Measurements by Highly Parallel Pyrosequencing and DNA Microarrays: A Comparative Study. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 53-59.	1.0	2
1497	The Contribution of New Technologies Toward Understanding Plant-Fungus Symbioses. , 2013, , 201-214.		2
1498	SSP: An interval integer linear programming for de novo transcriptome assembly and isoform discovery of RNA-seq reads. <i>Genomics</i> , 2013, 102, 507-514.	1.3	11
1499	Key Role for the Alternative Sigma Factor, SigH, in the Intracellular Life of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> during Macrophage Stress. <i>Infection and Immunity</i> , 2013, 81, 2242-2257.	1.0	28
1500	Genetic control of primary microRNA insight into cis- and trans-regulatory variations by RNA-seq. <i>Gene</i> , 2013, 517, 224-229.	1.0	3
1501	Infection Structure-Specific Expression of $\beta$ -1,3-Glucan Synthase Is Essential for Pathogenicity of <i>Colletotrichum graminicola</i> and Evasion of $\beta$ -Glucan-Triggered Immunity in Maize. <i>Plant Cell</i> , 2013, 25, 2356-2378.	3.1	82
1502	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4
1503	Benchmarking RNA-Seq quantification tools. , 2013, 2013, 647-50.		33
1505	Cytological and Molecular Characterization of Quantitative Trait Locus <i>qRfg1</i> , Which Confers Resistance to <i>Gibberella</i> Stalk Rot in Maize. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1417-1428.	1.4	37
1506	Genomics and proteomics in solving brain complexity. <i>Molecular BioSystems</i> , 2013, 9, 1807.	2.9	19
1507	DNMT1-interacting RNAs block gene-specific DNA methylation. <i>Nature</i> , 2013, 503, 371-376.	13.7	446
1508	Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <i>Nature Genetics</i> , 2013, 45, 1459-1463.	9.4	400

#	ARTICLE	IF	CITATIONS
1509	Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> , 2013, 4, 2612.	5.8	5,788
1510	Stochastic ERK Activation Induced by Noise and Cell-to-Cell Propagation Regulates Cell Density-Dependent Proliferation. <i>Molecular Cell</i> , 2013, 52, 529-540.	4.5	275
1511	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , 2013, 10, 1177-1184.	9.0	679
1512	Identification of the C3a Receptor (C3AR1) as the Target of the VGF-derived Peptide TLQP-21 in Rodent Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 27434-27443.	1.6	88
1513	Roles of the GacA/Rsm pathway in the regulation of phenazine biosynthesis in <i>Pseudomonas chlororaphis</i> 30A84. <i>MicrobiologyOpen</i> , 2013, 2, 505-524.	1.2	77
1514	The microglial sensome revealed by direct RNA sequencing. <i>Nature Neuroscience</i> , 2013, 16, 1896-1905.	7.1	1,244
1515	Suitability of Illumina deep mRNA sequencing for reliable gene expression profiling in a non-model conifer species ( <i>Pseudotsuga menziesii</i> ). <i>Tree Genetics and Genomes</i> , 2013, 9, 1513-1527.	0.6	2
1516	Systems-Level Analysis of Nitrogen Starvation-Induced Modifications of Carbon Metabolism in a <i>Chlamydomonas reinhardtii</i> Starchless Mutant. <i>Plant Cell</i> , 2013, 25, 4305-4323.	3.1	176
1517	Cell-type, allelic, and genetic signatures in the human pancreatic beta cell transcriptome. <i>Genome Research</i> , 2013, 23, 1554-1562.	2.4	161
1518	Dynamic transcriptomes of human myeloid leukemia cells. <i>Genomics</i> , 2013, 102, 250-256.	1.3	32
1519	A novel peroxinectin involved in antiviral and antibacterial immunity of mud crab, <i>Scylla paramamosain</i> . <i>Molecular Biology Reports</i> , 2013, 40, 6873-6881.	1.0	21
1520	RNA-sequencing from single nuclei. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19802-19807.	3.3	321
1521	Whole-transcriptome analysis of hepatocellular carcinoma. <i>Medical Oncology</i> , 2013, 30, 736.	1.2	7
1522	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16562-16567.	3.3	268
1523	Genome-wide Mapping of Transcriptional Start Sites Defines an Extensive Leaderless Transcriptome in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2013, 5, 1121-1131.	2.9	283
1524	Chemoproteomic Discovery of Cysteine-Containing Human Short Open Reading Frames. <i>Journal of the American Chemical Society</i> , 2013, 135, 16750-16753.	6.6	34
1525	Extended Self-Renewal and Accelerated Reprogramming in the Absence of Kdm5b. <i>Molecular and Cellular Biology</i> , 2013, 33, 4793-4810.	1.1	58
1526			

#	ARTICLE	IF	CITATIONS
1527	SplicingCompass: differential splicing detection using RNA-Seq data. <i>Bioinformatics</i> , 2013, 29, 1141-1148.	1.8	61
1528	Nanopore-Based Identification of Individual Nucleotides for Direct RNA Sequencing. <i>Nano Letters</i> , 2013, 13, 6144-6150.	4.5	103
1529	Metabolic Mechanisms of Epigenetic Regulation. <i>ACS Chemical Biology</i> , 2013, 8, 2607-2621.	1.6	63
1530	Comprehensive Analysis of Human Endogenous Retrovirus Group HERV-W Locus Transcription in Multiple Sclerosis Brain Lesions by High-Throughput Amplicon Sequencing. <i>Journal of Virology</i> , 2013, 87, 13837-13852.	1.5	59
1531	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
1532	The genome of the hydatid tapeworm <i>Echinococcus granulosus</i> . <i>Nature Genetics</i> , 2013, 45, 1168-1175.	9.4	260
1533	Jasmonate Signaling. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	5
1534	Extracellular Vesicle-Mediated Transfer of a Novel Long Noncoding RNA TUC339: A Mechanism of Intercellular Signaling in Human Hepatocellular Cancer. <i>Genes and Cancer</i> , 2013, 4, 261-272.	0.6	277
1535	Ribosomal proteins as novel players in tumorigenesis. <i>Cancer and Metastasis Reviews</i> , 2014, 33, 115-41.	2.7	63
1536	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	3.2	1,064
1537	Male-specific Fruitless isoforms have different regulatory roles conferred by distinct zinc finger DNA binding domains. <i>BMC Genomics</i> , 2013, 14, 659.	1.2	57
1538	RNA-seq analyses of gene expression in the microsclerotia of <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2013, 14, 607.	1.2	75
1539	Identifying potential RNAi targets in grain aphid ( <i>Sitobion avenae</i> F.) based on transcriptome profiling of its alimentary canal after feeding on wheat plants. <i>BMC Genomics</i> , 2013, 14, 560.	1.2	54
1540	Integrated detection of natural antisense transcripts using strand-specific RNA sequencing data. <i>Genome Research</i> , 2013, 23, 1730-1739.	2.4	58
1541	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013, 31, 1009-1014.	9.4	600
1542	Proteomic and Transcriptomic Analyses of Fecundity in the Brown Planthopper <i>Nilaparvata lugens</i> (Stål). <i>Journal of Proteome Research</i> , 2013, 12, 5199-5212.	1.8	58
1543	De novo assembly and characterization of spotted seal <i>Phoca largha</i> transcriptome using Illumina paired-end sequencing. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 103-110.	0.4	8
1544	Transcriptome dynamics during human erythroid differentiation and development. <i>Genomics</i> , 2013, 102, 431-441.	1.3	22

#	ARTICLE	IF	CITATIONS
1545	Deep Transcriptome Profiling of Ovarian Cancer Cells Using Next-Generation Sequencing Approach. <i>Methods in Molecular Biology</i> , 2013, 1049, 139-169.	0.4	4
1546	EPITRANS: A Database that Integrates Epigenome and Transcriptome Data. <i>Molecules and Cells</i> , 2013, 36, 472-475.	1.0	6
1547	Metabolomics and Transcriptomics of Metabolic Disorders. <i>Current Nutrition Reports</i> , 2013, 2, 199-206.	2.1	2
1548	The non-coding snRNA 7SK controls transcriptional termination, poising, and bidirectionality in embryonic stem cells. <i>Genome Biology</i> , 2013, 14, R98.	13.9	48
1549	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2013, 14, 689.	1.2	172
1550	Monitoring the immune response to vaccination with an inactivated vaccine associated to bovine neonatal pancytopenia by deep sequencing transcriptome analysis in cattle. <i>Veterinary Research</i> , 2013, 44, 93.	1.1	36
1551	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. <i>BMC Medical Genomics</i> , 2013, 6, 33.	0.7	31
1552	Towards the integration, annotation and association of historical microarray experiments with RNA-seq. <i>BMC Bioinformatics</i> , 2013, 14, S4.	1.2	14
1553	Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene. <i>Genome Biology</i> , 2013, 14, R70.	13.9	219
1554	Comparative studies of differential gene calling using RNA-Seq data. <i>BMC Bioinformatics</i> , 2013, 14, S7.	1.2	16
1555	A flexible count data model to fit the wide diversity of expression profiles arising from extensively replicated RNA-seq experiments. <i>BMC Bioinformatics</i> , 2013, 14, 254.	1.2	48
1556	Transcriptomics: Advances and approaches. <i>Science China Life Sciences</i> , 2013, 56, 960-967.	2.3	83
1557	Function of lncRNAs and approaches to lncRNA-protein interactions. <i>Science China Life Sciences</i> , 2013, 56, 876-885.	2.3	290
1558	Effects of supplementary butyrate on butanol production and the metabolic switch in <i>Clostridium beijerinckii</i> NCIMB 8052: genome-wide transcriptional analysis with RNA-Seq. <i>Biotechnology for Biofuels</i> , 2013, 6, 138.	6.2	50
1559	Model of gene expression in extreme cold - reference transcriptome for the high-Antarctic cryopelagic notothenioid fish <i>Pagothenia borchgrevinki</i> . <i>BMC Genomics</i> , 2013, 14, 634.	1.2	43
1560	Whole transcriptome sequencing identifies tumor-specific mutations in human oral squamous cell carcinoma. <i>BMC Medical Genomics</i> , 2013, 6, 28.	0.7	26
1561	Mapping genome-wide transcription factor binding sites in frozen tissues. <i>Epigenetics and Chromatin</i> , 2013, 6, 30.	1.8	29
1562	Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial <i>Wolbachia</i> endosymbiont to its host filarial nematode <i>Brugia malayi</i> . <i>BMC Genomics</i> , 2013, 14, 639.	1.2	37

#	ARTICLE	IF	CITATIONS
1563	Analysis of <i>Phakopsora pachyrhizi</i> transcript abundance in critical pathways at four time-points during infection of a susceptible soybean cultivar using deep sequencing. <i>BMC Genomics</i> , 2013, 14, 614.	1.2	30
1564	Insights into food preference in hybrid F1 of <i>Siniperca chuatsi</i> (♀) × <i>Siniperca scherzeri</i> (♂), mandarin fish through transcriptome analysis. <i>BMC Genomics</i> , 2013, 14, 601.	1.2	72
1565	The importance of tissue specificity for RNA-seq: highlighting the errors of composite structure extractions. <i>BMC Genomics</i> , 2013, 14, 586.	1.2	48
1566	Identification of differential expression genes associated with host selection and adaptation between two sibling insect species by transcriptional profile analysis. <i>BMC Genomics</i> , 2013, 14, 582.	1.2	30
1567	De novo characterization of <i>Larix gmelinii</i> (Rupr.) Rupr. transcriptome and analysis of its gene expression induced by jasmonates. <i>BMC Genomics</i> , 2013, 14, 548.	1.2	23
1568	Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data. <i>BMC Genomics</i> , 2013, 14, 584.	1.2	6
1569	NPEBseq: nonparametric empirical bayesian-based procedure for differential expression analysis of RNA-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 262.	1.2	28
1570	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . <i>BMC Genomics</i> , 2013, 14, 563.	1.2	115
1571	Analysis of the global transcriptome of longan ( <i>Dimocarpus longan</i> Lour.) embryogenic callus using Illumina paired-end sequencing. <i>BMC Genomics</i> , 2013, 14, 561.	1.2	71
1572	Gene-based single nucleotide polymorphism discovery in bovine muscle using next-generation transcriptomic sequencing. <i>BMC Genomics</i> , 2013, 14, 307.	1.2	32
1573	Sources of bias in measures of allele-specific expression derived from RNA-seq data aligned to a single reference genome. <i>BMC Genomics</i> , 2013, 14, 536.	1.2	123
1574	Comparative genomic and transcriptome analyses of pathotypes of <i>Xanthomonas citri</i> subsp. <i>citri</i> provide insights into mechanisms of bacterial virulence and host range. <i>BMC Genomics</i> , 2013, 14, 551.	1.2	88
1575	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. <i>BMC Genomics</i> , 2013, 14, 546.	1.2	22
1576	Genome-wide transcriptional response of <i>Trichoderma reesei</i> to lignocellulose using RNA sequencing and comparison with <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2013, 14, 541.	1.2	86
1577	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <i>BMC Genomics</i> , 2013, 14, 530.	1.2	111
1578	Insight into the specific virulence related genes and toxin-antitoxin virulent pathogenicity islands in swine streptococcosis pathogen <i>Streptococcus equi</i> ssp. <i>zooepidemicus</i> strain ATCC35246. <i>BMC Genomics</i> , 2013, 14, 377.	1.2	23
1579	Detection of phase-dependent transcriptomic changes and Rubisco-mediated CO <sub>2</sub> fixation into poly (3-hydroxybutyrate) under heterotrophic condition in <i>Ralstonia eutropha</i> H16 based on RNA-seq and gene deletion analyses. <i>BMC Microbiology</i> , 2013, 13, 169.	1.3	63
1580	Next-generation sequencing analysis of gene regulation in the rat model of retinopathy of prematurity. <i>Documenta Ophthalmologica</i> , 2013, 127, 13-31.	1.0	4

#	ARTICLE	IF	CITATIONS
1581	Pollen transcriptome analysis of <i>Solanum tuberosum</i> (2n=4x=48), <i>S. demissum</i> (2n=6x=72), and their reciprocal F1 hybrids. <i>Plant Cell Reports</i> , 2013, 32, 623-636.	2.8	7
1582	Bulk segregant RNA-seq reveals expression and positional candidate genes and allele-specific expression for disease resistance against enteric septicemia of catfish. <i>BMC Genomics</i> , 2013, 14, 929.	1.2	79
1583	Assessment of hematopoietic failure due to Rpl11 deficiency in a zebrafish model of Diamond-Blackfan anemia by deep sequencing. <i>BMC Genomics</i> , 2013, 14, 896.	1.2	22
1584	Fragment assignment in the cloud with eXpress-D. <i>BMC Bioinformatics</i> , 2013, 14, 358.	1.2	22
1585	Global transcriptome analysis of <i>Clostridium thermocellum</i> ATCC 27405 during growth on dilute acid pretreated <i>Populus</i> and switchgrass. <i>Biotechnology for Biofuels</i> , 2013, 6, 179.	6.2	62
1586	A multi-omic analysis of an <i>Enterococcus faecium</i> mutant reveals specific genetic mutations and dramatic changes in mRNA and protein expression. <i>BMC Microbiology</i> , 2013, 13, 304.	1.3	14
1587	Transcriptome-wide profiling and expression analysis of transcription factor families in a liverwort, <i>Marchantia polymorpha</i> . <i>BMC Genomics</i> , 2013, 14, 915.	1.2	24
1588	The nucleosome regulates the usage of polyadenylation sites in the human genome. <i>BMC Genomics</i> , 2013, 14, 912.	1.2	18
1589	Blind spots of quantitative RNA-seq: the limits for assessing abundance, differential expression, and isoform switching. <i>BMC Bioinformatics</i> , 2013, 14, 370.	1.2	38
1590	Unraveling the characteristics of microRNA regulation in the developmental and aging process of the human brain. <i>BMC Medical Genomics</i> , 2013, 6, 55.	0.7	15
1591	Global RNA sequencing reveals that genotype-dependent allele-specific expression contributes to differential expression in rice F1 hybrids. <i>BMC Plant Biology</i> , 2013, 13, 221.	1.6	43
1592	Detoxification and stress response genes expressed in a western North American bumble bee, <i>Bombus huntii</i> (Hymenoptera: Apidae). <i>BMC Genomics</i> , 2013, 14, 874.	1.2	49
1593	Analysis of sea-island cotton and upland cotton in response to <i>Verticillium dahliae</i> infection by RNA sequencing. <i>BMC Genomics</i> , 2013, 14, 852.	1.2	78
1594	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. <i>BMC Genomics</i> , 2013, 14, 843.	1.2	98
1595	Midgut transcriptome profiling of <i>Anoplophora glabripennis</i> , a lignocellulose degrading cerambycid beetle. <i>BMC Genomics</i> , 2013, 14, 850.	1.2	65
1596	Fermentation stage-dependent adaptations of <i>Bacillus licheniformis</i> during enzyme production. <i>Microbial Cell Factories</i> , 2013, 12, 120.	1.9	19
1597	HSA: A Heuristic Splice Alignment Tool. <i>BMC Systems Biology</i> , 2013, 7, S10.	3.0	7
1598	PGC-1 $\beta$ supports glutamine metabolism in breast cancer. <i>Cancer &amp; Metabolism</i> , 2013, 1, 22.	2.4	130



#	ARTICLE	IF	CITATIONS
1599	Comparative transcriptional profiling analysis of olive ripe-fruit pericarp and abscission zone tissues shows expression differences and distinct patterns of transcriptional regulation. BMC Genomics, 2013, 14, 866.	1.2	37
1600	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. BMC Genomics, 2013, 14, 855.	1.2	7
1601	Sample size calculation based on exact test for assessing differential expression analysis in RNA-seq data. BMC Bioinformatics, 2013, 14, 357.	1.2	34
1602	Evaluation of read count based RNAseq analysis methods. BMC Genomics, 2013, 14, S2.	1.2	53
1603	Selection of reference genes for quantitative real-time PCR in six oil-tea camellia based on RNA-seq. Molecular Biology, 2013, 47, 836-851.	0.4	19
1604	DNA from dead cancer cells induces TLR9-mediated invasion and inflammation in living cancer cells. Breast Cancer Research and Treatment, 2013, 142, 477-487.	1.1	31
1605	Comprehensive transcriptomic study on horse gram (Macrotyloma uniflorum): De novo assembly, functional characterization and comparative analysis in relation to drought stress. BMC Genomics, 2013, 14, 647.	1.2	71
1606	Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.2	50
1607	Finding the active genes in deep RNA-seq gene expression studies. BMC Genomics, 2013, 14, 778.	1.2	193
1608	De novo assembly and characterization of tissue specific transcriptomes in the emerald notothen, Trematomus bernacchii. BMC Genomics, 2013, 14, 805.	1.2	54
1609	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. Molecular Cancer, 2013, 12, 140.	7.9	59
1610	Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. BMC Biotechnology, 2013, 13, 99.	1.7	47
1611	Transcriptional profiling of feline infectious peritonitis virus infection in CRFK cells and in PBMCs from FIP diagnosed cats. Virology Journal, 2013, 10, 329.	1.4	31
1612	Design of RNA splicing analysis null models for post hoc filtering of Drosophila head RNA-Seq data with the splicing analysis kit (Spanki). BMC Bioinformatics, 2013, 14, 320.	1.2	40
1613	Assessing the impact of human genome annotation choice on RNA-seq expression estimates. BMC Bioinformatics, 2013, 14, S8.	1.2	49
1614	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	9.4	251
1615	Cracking the ENCODE: From transcription to therapeutics. Hepatology, 2013, 57, 2532-2535.	3.6	12
1616	Epigenetic Modifications in the Pathogenesis of Diabetic Nephropathy. Seminars in Nephrology, 2013, 33, 341-353.	0.6	80

#	ARTICLE	IF	CITATIONS
1617	A Fresh Look at the Male-specific Region of the Human Y Chromosome. <i>Journal of Proteome Research</i> , 2013, 12, 6-22.	1.8	52
1618	Investigating transcriptional states at single-cell-resolution. <i>Current Opinion in Biotechnology</i> , 2013, 24, 69-78.	3.3	30
1619	Argonaute 1 is indispensable for juvenile hormone mediated oogenesis in the migratory locust, <i>Locusta migratoria</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 879-887.	1.2	39
1620	Selective regulation of lymphopoiesis and leukemogenesis by individual zinc fingers of Ikaros. <i>Nature Immunology</i> , 2013, 14, 1073-1083.	7.0	97
1621	RNA-Seq in Prostate Cancer Research. , 2013, , 263-286.		0
1622	Dampening of expression oscillations by synchronous regulation of a microRNA and its target. <i>Nature Genetics</i> , 2013, 45, 1337-1344.	9.4	96
1623	First Proteomic Exploration of Protein-Encoding Genes on Chromosome 1 in Human Liver, Stomach, and Colon. <i>Journal of Proteome Research</i> , 2013, 12, 67-80.	1.8	20
1624	Cancer omics: From regulatory networks to clinical outcomes. <i>Cancer Letters</i> , 2013, 340, 277-283.	3.2	10
1625	The regulation of cambial activity in Chinese fir ( <i> Cunninghamia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	3.5	69
1626	Promiscuous RNA binding by Polycomb repressive complex 2. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1250-1257.	3.6	404
1627	Transcriptional profiling by RNA-Seq of peri-attachment porcine embryos generated by a variety of assisted reproductive technologies. <i>Physiological Genomics</i> , 2013, 45, 577-589.	1.0	19
1628	A model based criterion for gene expression calls using RNA-seq data. <i>Theory in Biosciences</i> , 2013, 132, 159-164.	0.6	160
1629	Early Transcriptomic Adaptation to Na <sub>2</sub> CO <sub>3</sub> Stress Altered the Expression of a Quarter of the Total Genes in the Maize Genome and Exhibited Shared and Distinctive Profiles with NaCl and High pH Stresses. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1147-1165.	4.1	22
1630	Learning a nonlinear dynamical system model of gene regulation: A perturbed steady-state approach. <i>Annals of Applied Statistics</i> , 2013, 7, .	0.5	19
1631	Microarray resources for genetic and genomic studies in chicken: A review. <i>Genesis</i> , 2013, 51, 337-356.	0.8	27
1632	The centrality of RNA for engineering gene expression. <i>Biotechnology Journal</i> , 2013, 8, 1379-1395.	1.8	76
1633	Machine learning and genome annotation: a match meant to be?. <i>Genome Biology</i> , 2013, 14, 205.	13.9	72
1634	RNA-Sequencing Quantification of Hepatic Ontogeny of Phase-I Enzymes in Mice. <i>Drug Metabolism and Disposition</i> , 2013, 41, 2175-2186.	1.7	28

#	ARTICLE	IF	CITATIONS
1635	Non-Coding RNAs: The "Dark Matter" of Cardiovascular Pathophysiology. <i>International Journal of Molecular Sciences</i> , 2013, 14, 19987-20018.	1.8	63
1636	NucleoFinder: a statistical approach for the detection of nucleosome positions. <i>Bioinformatics</i> , 2013, 29, 711-716.	1.8	20
1637	Build A Braveheart: The Missing Linc (RNA). <i>Circulation Research</i> , 2013, 112, 1532-1534.	2.0	18
1638	Metabolic Labeling of Newly Transcribed RNA for High Resolution Gene Expression Profiling of RNA Synthesis, Processing and Decay in Cell Culture. <i>Journal of Visualized Experiments</i> , 2013, , .	0.2	75
1639	Complexity of the Alternative Splicing Landscape in Plants " " . <i>Plant Cell</i> , 2013, 25, 3657-3683.	3.1	731
1640	Genomic Divergence during Speciation Driven by Adaptation to Altitude. <i>Molecular Biology and Evolution</i> , 2013, 30, 2553-2567.	3.5	91
1641	A Local Poisson Graphical Model for Inferring Networks From Sequencing Data. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 189-198.	2.2	65
1642	Long non-coding RNAs function annotation: a global prediction method based on bi-colored networks. <i>Nucleic Acids Research</i> , 2013, 41, e35-e35.	6.5	174
1643	Genome-wide analysis of the rat colon reveals proximal-distal differences in histone modifications and proto-oncogene expression. <i>Physiological Genomics</i> , 2013, 45, 1229-1243.	1.0	19
1644	An approach for assessing RNA-seq quantification algorithms in replication studies. , 2013, 2013, 15-18.		2
1645	SpliceGrapherXT. , 2013, , .		1
1646	Asymmetric thymocyte death underlies the CD4:CD8 T-cell ratio in the adaptive immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2905-14.	3.3	77
1647	Arabidopsis <i>Enhanced Drought Tolerance1/HOMEODOMAIN GLABROUS11</i> Confers Drought Tolerance in Transgenic Rice without Yield Penalty " " . <i>Plant Physiology</i> , 2013, 162, 1378-1391.	2.3	194
1648	The cytochromes P450 of <i>Grosmannia clavigera</i> : Genome organization, phylogeny, and expression in response to pine host chemicals. <i>Fungal Genetics and Biology</i> , 2013, 50, 72-81.	0.9	41
1649	Type of noise defines global attractors in bistable molecular regulatory systems. <i>Journal of Theoretical Biology</i> , 2013, 317, 140-151.	0.8	23
1650	Complete mitochondrial genome of <i>Concholepas concholepas</i> inferred by 454 pyrosequencing and mtDNA expression in two mollusc populations. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 17-23.	0.4	3
1651	Resequencing rice genomes: an emerging new era of rice genomics. <i>Trends in Genetics</i> , 2013, 29, 225-232.	2.9	108
1652	Comparative RNA-sequencing of the acarbose producer <i>Actinoplanes</i> sp. SE50/110 cultivated in different growth media. <i>Journal of Biotechnology</i> , 2013, 167, 166-177.	1.9	20

#	ARTICLE	IF	CITATIONS
1653	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013, 31, 46-53.	9.4	3,256
1654	Bias Correction in RNA-Seq Short-Read Counts Using Penalized Regression. <i>Statistics in Biosciences</i> , 2013, 5, 88-99.	0.6	1
1655	Recurrent SETBP1 mutations in atypical chronic myeloid leukemia. <i>Nature Genetics</i> , 2013, 45, 18-24.	9.4	359
1656	Transcriptomics in the RNA-seq era. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 4-11.	2.8	273
1657	Transcriptome Analysis of Mature Fruit Abscission Control in Olive. <i>Plant and Cell Physiology</i> , 2013, 54, 244-269.	1.5	75
1658	Gene Expression in the Human Brain: The Current State of the Study of Specificity and Spatiotemporal Dynamics. <i>Child Development</i> , 2013, 84, 76-88.	1.7	59
1659	Qualitative and Quantitative Expression Status of the Human Chromosome 20 Genes in Cancer Tissues and the Representative Cell Lines. <i>Journal of Proteome Research</i> , 2013, 12, 151-161.	1.8	19
1660	Dynamic DNA methylation across diverse human cell lines and tissues. <i>Genome Research</i> , 2013, 23, 555-567.	2.4	614
1661	Next-generation sequencing in the clinic: Promises and challenges. <i>Cancer Letters</i> , 2013, 340, 284-295.	3.2	272
1662	Minicircle DNA Vectors Achieve Sustained Expression Reflected by Active Chromatin and Transcriptional Level. <i>Molecular Therapy</i> , 2013, 21, 131-138.	3.7	103
1663	Achieving high throughput sequencing of a cDNA library utilizing an alternative protocol for the bench top next-generation sequencing system. <i>Journal of Microbiological Methods</i> , 2013, 92, 122-126.	0.7	2
1664	Diagnostic Applications of High-Throughput DNA Sequencing. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2013, 8, 381-410.	9.6	58
1665	Reference gene selection for RT-qPCR analysis of <i>Chrysanthemum lavandulifolium</i> during its flowering stages. <i>Molecular Breeding</i> , 2013, 31, 205-215.	1.0	31
1666	Genome-wide profiling of histone H3K4-tri-methylation and gene expression in rice under drought stress. <i>Plant Molecular Biology</i> , 2013, 81, 175-188.	2.0	164
1667	Gene Regulatory Networks. , 2013, , 65-88.		4
1668	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	13.5	325
1669	Transcriptome analysis using next-generation sequencing. <i>Current Opinion in Biotechnology</i> , 2013, 24, 22-30.	3.3	448
1670	Piwi induces piRNA-guided transcriptional silencing and establishment of a repressive chromatin state. <i>Genes and Development</i> , 2013, 27, 390-399.	2.7	429

#	ARTICLE	IF	CITATIONS
1671	Biostatistical approaches for the reconstruction of gene co-expression networks based on transcriptomic data. <i>Briefings in Functional Genomics</i> , 2013, 12, 457-467.	1.3	43
1672	Small open reading frames associated with morphogenesis are hidden in plant genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2395-2400.	3.3	178
1673	Genome-wide profiling of bone reveals differentially methylated regions in osteoporosis and osteoarthritis. <i>Arthritis and Rheumatism</i> , 2013, 65, 197-205.	6.7	133
1674	Systems biology approaches to finding novel pain mediators. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 11-35.	6.6	42
1675	Long noncoding RNAs regulate adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3387-3392.	3.3	371
1676	Assessment of the stromal contribution to Sonic Hedgehog-dependent pancreatic adenocarcinoma. <i>Molecular Oncology</i> , 2013, 7, 1031-1042.	2.1	38
1677	Transcriptomic analysis of purple leaf determination in birch. <i>Gene</i> , 2013, 526, 251-258.	1.0	13
1678	Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. <i>Developmental Biology</i> , 2013, 380, 351-362.	0.9	54
1679	Gene Expression Profiling Related to Hyphal Growth in a Temperature-Sensitive Mutant of <i>Magnaporthe oryzae</i> . <i>Journal of Integrative Agriculture</i> , 2013, 12, 2189-2196.	1.7	1
1680	Regional differences in gene expression and promoter usage in aged human brains. <i>Neurobiology of Aging</i> , 2013, 34, 1825-1836.	1.5	30
1681	Global gene expression profiling of monocyte-derived macrophages from red deer ( <i>Cervus elaphus</i> ) genotypically resistant or susceptible to <i>Mycobacterium avium</i> subspecies paratuberculosis infection. <i>Developmental and Comparative Immunology</i> , 2013, 40, 210-217.	1.0	24
1682	Evaluation of higher plant virus resistance genes in the green alga, <i>Chlorella variabilis</i> NC64A, during the early phase of infection with <i>Paramecium bursaria chlorella virus-1</i> . <i>Virology</i> , 2013, 442, 101-113.	1.1	10
1683	The function and properties of the transcriptional regulator COS1 in <i>Magnaporthe oryzae</i> . <i>Fungal Biology</i> , 2013, 117, 239-249.	1.1	22
1684	Oligonucleotide microarray-based gene expression analysis of pine sawyer ( <i>Monochamus alternatus</i> ) after treatment with a sublethal dose of diflubenzuron. <i>Journal of Asia-Pacific Entomology</i> , 2013, 16, 489-495.	0.4	3
1685	Expression profile analyses of human HCT-116 colon cancer cell line before and after serum induction. <i>Gene</i> , 2013, 517, 236-239.	1.0	0
1686	Modeling and inference of genetic interactions. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2013, 3, 453-466.	4.6	0
1687	Transcriptomic analysis of incised leaf-shape determination in birch. <i>Gene</i> , 2013, 531, 263-269.	1.0	15
1688	Axl Mediates Acquired Resistance of Head and Neck Cancer Cells to the Epidermal Growth Factor Receptor Inhibitor Erlotinib. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 2541-2558.	1.9	132

#	ARTICLE	IF	CITATIONS
1689	The Hologenomic Basis of Speciation: Gut Bacteria Cause Hybrid Lethality in the Genus <i>Nasonia</i> . <i>Science</i> , 2013, 341, 667-669.	6.0	379
1690	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1709-1722.	2.5	204
1691	Gene Networks and Chromatin and Transcriptional Regulation of the Phaseolin Promoter in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 2601-2617.	3.1	20
1692	Signal transduction involved in GnRH2-stimulation of identified LH-producing gonadotropes from <i>lhb-GFP</i> transgenic medaka ( <i>Oryzias latipes</i> ). <i>Molecular and Cellular Endocrinology</i> , 2013, 372, 128-139.	1.6	33
1693	Transcriptional responses of male fathead minnows exposed to oil sands process-affected water. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2013, 157, 227-235.	1.3	44
1694	Identification of Molecular Tumor Markers in Renal Cell Carcinomas with TFE3 Protein Expression by RNA Sequencing. <i>Neoplasia</i> , 2013, 15, 1231-1240.	2.3	45
1695	De novo characterization of transcriptome and gene expression dynamics in <i>A. epidermis</i> during the larval-pupal metamorphosis of a common cutworm. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 794-808.	1.2	57
1696	Zinc-mediated RNA fragmentation allows robust transcript reassembly upon whole transcriptome RNA-Seq. <i>Methods</i> , 2013, 63, 25-31.	1.9	27
1697	Transcriptome analysis of normal and mantled developing oil palm flower and fruit. <i>Genomics</i> , 2013, 101, 306-312.	1.3	36
1698	Transcriptome characterization by RNA-Seq reveals the involvement of the complement components in noise-traumatized rat cochleae. <i>Neuroscience</i> , 2013, 248, 1-16.	1.1	35
1699	The challenge of gene expression profiling in heterogeneous clinical samples. <i>Methods</i> , 2013, 59, 47-58.	1.9	18
1700	RNA sequencing to study gene expression and single nucleotide polymorphism variation associated with citrate content in cow milk. <i>Journal of Dairy Science</i> , 2013, 96, 2637-2648.	1.4	68
1701	Recent transcriptomics advances and emerging applications in food science. <i>TrAC - Trends in Analytical Chemistry</i> , 2013, 52, 142-154.	5.8	54
1702	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	2.9	64
1703	Indexing hypertext. <i>Journal of Discrete Algorithms</i> , 2013, 18, 113-122.	0.7	15
1704	De-novo characterization of the soft-shelled turtle <i>Pelodiscus sinensis</i> transcriptome using Illumina RNA-Seq technology. <i>Journal of Zhejiang University: Science B</i> , 2013, 14, 58-67.	1.3	18
1705	Progress and Prospects for the Ecological Genetics of Mycoheterotrophs. , 2013, , 245-266.		8
1706	In the Spotlight: Bioinformatics. <i>IEEE Reviews in Biomedical Engineering</i> , 2013, 6, 3-8.	13.1	2

#	ARTICLE	IF	CITATIONS
1707	High-throughput sequencing for biology and medicine. <i>Molecular Systems Biology</i> , 2013, 9, 640.	3.2	251
1708	NOT2 Proteins Promote Polymerase II-Dependent Transcription and Interact with Multiple MicroRNA Biogenesis Factors in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 715-727.	3.1	147
1709	Single molecule molecular inversion probes for targeted, high-accuracy detection of low-frequency variation. <i>Genome Research</i> , 2013, 23, 843-854.	2.4	292
1710	Comparative study of RNA-seq- and Microarray-derived coexpression networks in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2013, 29, 717-724.	1.8	128
1711	High-throughput sequencing of the melanoma genome. <i>Experimental Dermatology</i> , 2013, 22, 10-17.	1.4	33
1712	Genes, behavior and next-generation RNA sequencing. <i>Genes, Brain and Behavior</i> , 2013, 12, 1-12.	1.1	74
1713	Transcriptome analysis of rice root heterosis by RNA-Seq. <i>BMC Genomics</i> , 2013, 14, 19.	1.2	120
1714	The Coding and the Non-coding Transcriptome. , 2013, , 27-41.		3
1715	Application of next generation qPCR and sequencing platforms to mRNA biomarker analysis. <i>Methods</i> , 2013, 59, 89-100.	1.9	55
1716	RNA-Seq: revelation of the messengers. <i>Trends in Plant Science</i> , 2013, 18, 175-179.	4.3	155
1717	Effects of cocaine and withdrawal on the mouse nucleus accumbens transcriptome. <i>Genes, Brain and Behavior</i> , 2013, 12, 21-33.	1.1	49
1718	Differential hippocampal gene expression is associated with climate-related natural variation in memory and the hippocampus in food-caching chickadees. <i>Molecular Ecology</i> , 2013, 22, 397-408.	2.0	29
1719	Regulon controlled by the GppX hybrid two component system in <i>Porphyromonas gingivalis</i> . <i>Molecular Oral Microbiology</i> , 2013, 28, 70-81.	1.3	16
1720	Deep sequencing analysis of the transcriptomes of peanut aerial and subterranean young pods identifies candidate genes related to early embryo abortion. <i>Plant Biotechnology Journal</i> , 2013, 11, 115-127.	4.1	75
1721	Protein-Coding cis-Natural Antisense Transcripts Have High and Broad Expression in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 2171-2180.	2.3	18
1722	Repurposing CRISPR as an RNA-Guided Platform for Sequence-Specific Control of Gene Expression. <i>Cell</i> , 2013, 152, 1173-1183.	13.5	4,090
1723	Transcriptome profiling of <i>Xanthomonas campestris</i> pv. <i>campestris</i> grown in minimal medium MMX and rich medium NYC. <i>Research in Microbiology</i> , 2013, 164, 466-479.	1.0	35
1724	Estradiol supports in vitro development of bovine early antral follicles. <i>Reproduction</i> , 2013, 145, 85-96.	1.1	30

#	ARTICLE	IF	CITATIONS
1725	Braveheart, a Long Noncoding RNA Required for Cardiovascular Lineage Commitment. <i>Cell</i> , 2013, 152, 570-583.	13.5	839
1726	Epigenomics: Sequencing the Methylome. <i>Methods in Molecular Biology</i> , 2013, 973, 39-54.	0.4	3
1727	A global approach to analysis and interpretation of metabolic data for plant natural product discovery. <i>Natural Product Reports</i> , 2013, 30, 565.	5.2	104
1728	Contribution of copy number variants involving nonsense-mediated mRNA decay pathway genes to neuro-developmental disorders. <i>Human Molecular Genetics</i> , 2013, 22, 1816-1825.	1.4	120
1729	SIBER: systematic identification of bimodally expressed genes using RNAseq data. <i>Bioinformatics</i> , 2013, 29, 605-613.	1.8	26
1730	Long Noncoding RNAs: Past, Present, and Future. <i>Genetics</i> , 2013, 193, 651-669.	1.2	1,641
1731	The draft genome of sweet orange ( <i>Citrus sinensis</i> ). <i>Nature Genetics</i> , 2013, 45, 59-66.	9.4	837
1732	Opportunities and methods for studying alternative splicing in cancer with RNA-Seq. <i>Cancer Letters</i> , 2013, 340, 179-191.	3.2	107
1733	Cumulus and granulosa cell markers of oocyte and embryo quality. <i>Fertility and Sterility</i> , 2013, 99, 979-997.	0.5	224
1734	Quantifying the transcriptional output of single alleles in single living mammalian cells. <i>Nature Protocols</i> , 2013, 8, 393-408.	5.5	27
1735	The neuron-specific chromatin regulatory subunit BAF53b is necessary for synaptic plasticity and memory. <i>Nature Neuroscience</i> , 2013, 16, 552-561.	7.1	213
1736	A NGS approach to the encrusting Mediterranean sponge <i>C. rella elegans</i> (Porifera, Demospongiae). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> along three life cycle stages. <i>Molecular Ecology Resources</i> , 2013, 13, 494-509.	2.2	14
1737	A global view of transcriptome dynamics during flower development in chickpea by deep sequencing. <i>Plant Biotechnology Journal</i> , 2013, 11, 691-701.	4.1	104
1738	Panning for Long Noncoding RNAs. <i>Biomolecules</i> , 2013, 3, 226-241.	1.8	13
1739	Merging Multiple Omics Datasets In Silico: Statistical Analyses and Data Interpretation. <i>Methods in Molecular Biology</i> , 2013, 985, 459-470.	0.4	19
1740	Next-generation sequencing-based transcriptome profiling analysis of <i>Pohlia nutans</i> reveals insight into the stress-relevant genes in Antarctic moss. <i>Extremophiles</i> , 2013, 17, 391-403.	0.9	30
1741	Genome-wide mapping of RNA structure using nuclease digestion and high-throughput sequencing. <i>Nature Protocols</i> , 2013, 8, 849-869.	5.5	85
1742	Next-Generation Sequencing Platforms. <i>Annual Review of Analytical Chemistry</i> , 2013, 6, 287-303.	2.8	519



#	ARTICLE	IF	CITATIONS
1743	Next-generation sequencing: a powerful tool for the discovery of molecular markers in breast ductal carcinoma <i>in situ</i> . <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 151-165.	1.5	40
1744	Whole-transcriptome, high-throughput RNA sequence analysis of the bovine macrophage response to <i>Mycobacterium bovis</i> infection <i>in vitro</i> . <i>BMC Genomics</i> , 2013, 14, 230.	1.2	49
1745	Computational solutions for omics data. <i>Nature Reviews Genetics</i> , 2013, 14, 333-346.	7.7	288
1746	Molecular advances in QTL discovery and application in pig breeding. <i>Trends in Genetics</i> , 2013, 29, 215-224.	2.9	52
1747	Cancer genome-sequencing study design. <i>Nature Reviews Genetics</i> , 2013, 14, 321-332.	7.7	100
1748	Role of miRNAs in CD4 T cell plasticity during inflammation and tolerance. <i>Frontiers in Genetics</i> , 2013, 4, 8.	1.1	56
1749	Genome-wide profiles of CtBP link metabolism with genome stability and epithelial reprogramming in breast cancer. <i>Nature Communications</i> , 2013, 4, 1449.	5.8	111
1750	Transcriptome sequencing, annotation and expression analysis of <i>Nannochloropsis</i> sp. at different growth phases. <i>Gene</i> , 2013, 523, 117-121.	1.0	39
1751	The Parkinson's Disease-Associated LRRK2 Mutation R1441G Inhibits Neuronal Differentiation of Neural Stem Cells. <i>Stem Cells and Development</i> , 2013, 22, 2487-2496.	1.1	37
1752	Analyzing the Meiotic Transcriptome Using Isolated Meocytes of <i>Arabidopsis thaliana</i> . <i>Methods in Molecular Biology</i> , 2013, 990, 203-213.	0.4	25
1753	Effects of Exposure to 17 $\beta$ -Ethinylestradiol during Sexual Differentiation on the Transcriptome of the African Clawed Frog ( <i>Xenopus laevis</i> ). <i>Environmental Science &amp; Technology</i> , 2013, 47, 4822-4828.	4.6	11
1754	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. <i>Journal of Pathology</i> , 2013, 230, 249-260.	2.1	57
1755	Ectopic Overexpression of SlHsfA3, a Heat Stress Transcription Factor from Tomato, Confers Increased Thermotolerance and Salt Hypersensitivity in Germination in Transgenic <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2013, 8, e54880.	1.1	78
1756	Systematic study of human long intergenic non-coding RNAs and their impact on cancer. <i>Science China Life Sciences</i> , 2013, 56, 324-334.	2.3	36
1757	Identifying host pathogenic pathways in bovine digital dermatitis by RNA-Seq analysis. <i>Veterinary Journal</i> , 2013, 197, 699-706.	0.6	22
1758	Exploring the sampling universe of RNA-seq. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 175-88.	0.2	5
1759	Comparative Study of Transcriptome Profiles of Mechanical- and Skin-Transformed <i>Schistosoma mansoni</i> Schistosomula. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2091.	1.3	62
1760	The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. <i>Nature Genetics</i> , 2013, 45, 701-706.	9.4	409

#	ARTICLE	IF	CITATIONS
1761	Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. <i>Molecular Ecology Resources</i> , 2013, 13, 559-572.	2.2	167
1762	An update on recent methods applied for deciphering the diversity of the noncoding RNA genome structure and function. <i>Methods</i> , 2013, 63, 3-17.	1.9	11
1763	De novo characterization of <i>Lentinula edodes</i> C91-3 transcriptome by deep Solexa sequencing. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 111-115.	1.0	26
1764	Genome Wide Proteomics of ERBB2 and EGFR and Other Oncogenic Pathways in Inflammatory Breast Cancer. <i>Journal of Proteome Research</i> , 2013, 12, 2805-2817.	1.8	38
1765	Metatranscriptomic analysis of lactic acid bacterial gene expression during kimchi fermentation. <i>International Journal of Food Microbiology</i> , 2013, 163, 171-179.	2.1	133
1766	Comparison of transcriptome under red and blue light culture of <i>Saccharina japonica</i> (Phaeophyceae). <i>Planta</i> , 2013, 237, 1123-1133.	1.6	58
1767	The Vast, Conserved Mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013, 9, e1002917.	1.5	62
1768	Human Corneal Epithelial Subpopulations: Oxygen Dependent <i>Ex Vivo</i> Expansion and Transcriptional Profiling. <i>Acta Ophthalmologica</i> , 2013, 91, 1-34.	0.6	7
1769	Identification and characterization of genes regulated by AqsR, a LuxR-type regulator in <i>Acinetobacter oleivorans</i> DR1. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 6967-6978.	1.7	14
1770	The draft genome of the fast-growing non-timber forest species moso bamboo ( <i>Phyllostachys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1079.45 483		
1771	Construction of ethylene regulatory network based on the phytohormones related gene transcriptome profiling and prediction of transcription factor activities in soybean. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 1303-1317.	1.0	16
1772	Systems-integration of plant metabolism: means, motive and opportunity. <i>Current Opinion in Plant Biology</i> , 2013, 16, 381-388.	3.5	35
1773	Identification of somatic mutations in human prostate cancer by RNA-Seq. <i>Gene</i> , 2013, 519, 343-347.	1.0	24
1774	High-Throughput RNA Sequencing in B-Cell Lymphomas. <i>Methods in Molecular Biology</i> , 2013, 971, 295-312.	0.4	5
1775	Global identification of miRNAs and targets in <i>Populus euphratica</i> under salt stress. <i>Plant Molecular Biology</i> , 2013, 81, 525-539.	2.0	138
1776	De novo transcriptome sequencing and comparative analysis of differentially expressed genes in <i>Gossypium aridum</i> under salt stress. <i>Gene</i> , 2013, 525, 26-34.	1.0	70
1777	Transcriptional analysis of genes involved in nodulation in soybean roots inoculated with <i>Bradyrhizobium japonicum</i> strain CPAC 15. <i>BMC Genomics</i> , 2013, 14, 153.	1.2	23
1778	Synthesis and degradation jointly determine the responsiveness of the cellular proteome. <i>BioEssays</i> , 2013, 35, 597-601.	1.2	34

#	ARTICLE	IF	CITATIONS
1779	Ribosome profiling: a Hi-C monitor for protein synthesis at the genome-wide scale. Wiley Interdisciplinary Reviews RNA, 2013, 4, 473-490.	3.2	72
1780	Malt1-Induced Cleavage of Regnase-1 in CD4+ Helper T Cells Regulates Immune Activation. Cell, 2013, 153, 1036-1049.	13.5	296
1781	Emerging Tools for Synthetic Genome Design. Molecules and Cells, 2013, 35, 359-370.	1.0	17
1783	RNA-Seq reveals differentially expressed isoforms and novel splice variants in buccal mucosal cancer. Gene, 2013, 516, 24-32.	1.0	11
1784	New insight into transcription of human endogenous retroviral elements. New Biotechnology, 2013, 30, 314-318.	2.4	15
1785	RNA Protein Interaction in Neurons. Annual Review of Neuroscience, 2013, 36, 243-270.	5.0	155
1786	Transcriptome analysis of the parasite Encephalitozoon cuniculi: an in-depth examination of pre-mRNA splicing in a reduced eukaryote. BMC Genomics, 2013, 14, 207.	1.2	43
1787	Statistical methods in experimentation recommendation models for discovering gene regulation pathways. Wiley Interdisciplinary Reviews: Computational Statistics, 2013, 5, 121-134.	2.1	0
1788	Genome-Wide Quantitative Enhancer Activity Maps Identified by STARR-seq. Science, 2013, 339, 1074-1077.	6.0	897
1789	Helper T cell identity and evolution of differential transcriptomes and epigenomes. Immunological Reviews, 2013, 252, 24-40.	2.8	90
1790	Single-cell transcriptomics for drug target discovery. Current Opinion in Pharmacology, 2013, 13, 786-790.	1.7	13
1791	Differential gene expression in <i>Acromyrmex</i> leaf-cutting ants after challenges with two fungal pathogen <i>S.</i> Molecular Ecology, 2013, 22, 2173-2187.	2.0	28
1792	Identification of new protein coding sequences and signal peptidase cleavage sites of Helicobacter pylori strain 26695 by proteogenomics. Journal of Proteomics, 2013, 86, 27-42.	1.2	37
1793	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	9.4	990
1794	Deep RNA-Seq uncovers the peach transcriptome landscape. Plant Molecular Biology, 2013, 83, 365-377.	2.0	103
1795	RNA sequencing and transcriptomal analysis of human monocyte to macrophage differentiation. Gene, 2013, 519, 279-287.	1.0	37
1796	AID stabilizes stem-cell phenotype by removing epigenetic memory of pluripotency genes. Nature, 2013, 500, 89-92.	13.7	78
1797	Pediatric systems medicine: evaluating needs and opportunities using congenital heart block as a case study. Pediatric Research, 2013, 73, 508-513.	1.1	8

#	ARTICLE	IF	CITATIONS
1798	Identification of novel exons and transcripts by comprehensive RNA-Seq of horn cancer transcriptome in <i>Bos indicus</i> . <i>Journal of Biotechnology</i> , 2013, 165, 37-44.	1.9	13
1799	Vitamin C induces Tet-dependent DNA demethylation and a blastocyst-like state in ES cells. <i>Nature</i> , 2013, 500, 222-226.	13.7	715
1800	Genome-Wide Annotation and Quantitation of Translation by Ribosome Profiling. <i>Current Protocols in Molecular Biology</i> , 2013, 103, Unit 4.18.	2.9	55
1801	The Evolution of Lineage-Specific Regulatory Activities in the Human Embryonic Limb. <i>Cell</i> , 2013, 154, 185-196.	13.5	202
1802	Systems Metabolic Engineering. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	3
1803	Characterizing the Genetic Basis for Nicotine Induced Cancer Development: A Transcriptome Sequencing Study. <i>PLoS ONE</i> , 2013, 8, e67252.	1.1	22
1804	Analysis of RNA-Seq Data with TopHat and Cufflinks for Genome-Wide Expression Analysis of Jasmonate-Treated Plants and Plant Cultures. <i>Methods in Molecular Biology</i> , 2013, 1011, 305-315.	0.4	68
1805	Apolipoprotein A5 deficiency aggravates high-fat diet-induced obesity due to impaired central regulation of food intake. <i>FASEB Journal</i> , 2013, 27, 3354-3362.	0.2	11
1806	EZH2 Is Required for Germinal Center Formation and Somatic EZH2 Mutations Promote Lymphoid Transformation. <i>Cancer Cell</i> , 2013, 23, 677-692.	7.7	706
1807	Divergent low water potential response in <i>Arabidopsis thaliana</i> accessions Landsberg <i>erecta</i> and Shahdara. <i>Plant, Cell and Environment</i> , 2013, 36, 994-1008.	2.8	29
1808	Transcriptomics in the Age of Ultra High-Throughput Sequencing. , 2013, , 145-154.		0
1809	Non-coding transcription at cis-regulatory elements: Computational and experimental approaches. <i>Methods</i> , 2013, 63, 66-75.	1.9	6
1810	Genome-wide characterization and expression analysis of genetic variants in sweet orange. <i>Plant Journal</i> , 2013, 75, 954-964.	2.8	22
1811	Contribution of Antibody-based Protein Profiling to the Human Chromosome-centric Proteome Project (C-HPP). <i>Journal of Proteome Research</i> , 2013, 12, 2439-2448.	1.8	48
1812	Characterization of the defense transcriptome responsive to <i>Fusarium oxysporum</i> -infection in <i>Arabidopsis</i> using RNA-seq. <i>Gene</i> , 2013, 512, 259-266.	1.0	120
1813	Targeting the endothelial progenitor cell surface proteome to identify novel mechanisms that mediate angiogenic efficacy in a rodent model of vascular disease. <i>Physiological Genomics</i> , 2013, 45, 999-1011.	1.0	22
1814	Genome sequence of the date palm <i>Phoenix dactylifera</i> L. <i>Nature Communications</i> , 2013, 4, 2274.	5.8	248
1815	Peak Finder Metaserver - a novel application for finding peaks in ChIP-seq data. <i>BMC Bioinformatics</i> , 2013, 14, 280.	1.2	13

#	ARTICLE	IF	CITATIONS
1816	Modeling the next generation sequencing sample processing pipeline for the purposes of classification. <i>BMC Bioinformatics</i> , 2013, 14, 307.	1.2	27
1817	RNA-Seq of <i>Bacillus licheniformis</i> : active regulatory RNA features expressed within a productive fermentation. <i>BMC Genomics</i> , 2013, 14, 667.	1.2	40
1818	Quantitative high-throughput profiling of snake venom gland transcriptomes and proteomes ( <i>Ovophis okinavensis</i> and <i>Protobothrops flavoviridis</i> ). <i>BMC Genomics</i> , 2013, 14, 790.	1.2	130
1819	Characterizing developmental and inducible differentiation between juvenile and adult plants of <i>Aechmea fasciata</i> treated with ethylene by transcriptomic analysis. <i>Plant Growth Regulation</i> , 2013, 69, 247-257.	1.8	13
1820	SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. <i>Bioinformatics</i> , 2013, 29, 2971-2978.	1.8	23
1821	A Cancer Stem Cell Model for Studying Brain Metastases From Primary Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2013, 105, 551-562.	3.0	50
1822	Comprehensive genomic profiling in diabetic nephropathy reveals the predominance of proinflammatory pathways. <i>Physiological Genomics</i> , 2013, 45, 710-719.	1.0	21
1823	A Cost-Effective Method for High-Throughput Construction of Illumina Sequencing Libraries. <i>Cold Spring Harbor Protocols</i> , 2013, 2013, pdb.prot074187.	0.2	23
1824	A Fast Workflow for Identification and Quantification of Proteomes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2370-2380.	2.5	94
1825	Application of <sup>TM</sup> omics technologies to biomarker discovery in inflammatory lung diseases. <i>European Respiratory Journal</i> , 2013, 42, 802-825.	3.1	234
1826	Comprehensive evaluation of differential gene expression analysis methods for RNA-seq data. <i>Genome Biology</i> , 2013, 14, R95.	13.9	588
1827	Transcriptome Analysis of Japanese Pear ( <i>Pyrus pyrifolia</i> Nakai) Flower Buds Transitioning Through Endodormancy. <i>Plant and Cell Physiology</i> , 2013, 54, 1132-1151.	1.5	147
1828	Two Major Facilitator Superfamily Sugar Transporters from <i>Trichoderma reesei</i> and Their Roles in Induction of Cellulase Biosynthesis. <i>Journal of Biological Chemistry</i> , 2013, 288, 32861-32872.	1.6	153
1829	Exome RNA sequencing reveals rare and novel alternative transcripts. <i>Nucleic Acids Research</i> , 2013, 41, e6-e6.	6.5	43
1830	COPPER RESPONSE REGULATOR1-Dependent and -Independent Responses of the <i>Chlamydomonas reinhardtii</i> Transcriptome to Dark Anoxia. <i>Plant Cell</i> , 2013, 25, 3186-3211.	3.1	77
1831	Next-Generation Sequencing-Based Transcriptional Profiling of Sacred Lotus <i>“China Antique”</i> . <i>Tropical Plant Biology</i> , 2013, 6, 161-179.	1.0	13
1832	Transcriptomic and Genetic Analysis of Direct Interspecies Electron Transfer. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2397-2404.	1.4	168
1833	RNA sequencing reveals the complex regulatory network in the maize kernel. <i>Nature Communications</i> , 2013, 4, 2832.	5.8	252

#	ARTICLE	IF	CITATIONS
1834	Analysis of Stress-Responsive Transcriptome in the Intestine of Asian Seabass ( <i>Lates calcarifer</i> ) using RNA-Seq. DNA Research, 2013, 20, 449-460.	1.5	97
1835	Spatiotemporal clustering of the epigenome reveals rules of dynamic gene regulation. Genome Research, 2013, 23, 352-364.	2.4	58
1836	Simultaneous Isoform Discovery and Quantification from RNA-Seq. Statistics in Biosciences, 2013, 5, 100-118.	0.6	18
1837	Standard methods for molecular research in <i>Apis mellifera</i> . Journal of Apicultural Research, 2013, 52, 1-54.	0.7	150
1838	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. BMC Genomics, 2013, 14, 486.	1.2	151
1839	Sample size calculation for differential expression analysis of RNA-seq data under Poisson distribution. International Journal of Computational Biology and Drug Design, 2013, 6, 358.	0.3	18
1840	A quantitative model of transcriptional differentiation driving host-pathogen interactions. Briefings in Bioinformatics, 2013, 14, 713-723.	3.2	6
1841	Simultaneous Profiling of 194 Distinct Receptor Transcripts in Human Cells. Science Signaling, 2013, 6, rs13.	1.6	30
1842	Mapping Yeast Transcriptional Networks. Genetics, 2013, 195, 9-36.	1.2	72
1843	Research Resource: Global Identification of Estrogen Receptor $\hat{1}^2$ Target Genes in Triple Negative Breast Cancer Cells. Molecular Endocrinology, 2013, 27, 1762-1775.	3.7	52
1844	Hyper conserved elements in vertebrate mRNA 3' UTRs reveal a translational network of RNA-binding proteins controlled by HuR. Nucleic Acids Research, 2013, 41, 3201-3216.	6.5	38
1845	ABCs of genomics. Hematology American Society of Hematology Education Program, 2013, 2013, 316-323.	0.9	7
1846	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	2.4	51
1847	Multiplatform single-sample estimates of transcriptional activation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17778-17783.	3.3	86
1848	The genomic landscape of cohesin-associated chromatin interactions. Genome Research, 2013, 23, 1224-1234.	2.4	103
1849	Divergence of Iron Metabolism in Wild Malaysian Yeast. G3: Genes, Genomes, Genetics, 2013, 3, 2187-2194.	0.8	11
1850	Characterization of the rat developmental liver transcriptome. Physiological Genomics, 2013, 45, 301-311.	1.0	21
1851	Gene expression rate comparison for multiple high-throughput datasets. IET Systems Biology, 2013, 7, 135-142.	0.8	3

#	ARTICLE	IF	CITATIONS
1852	Functional transcriptomics in the post-ENCODE era. <i>Genome Research</i> , 2013, 23, 1961-1973.	2.4	58
1853	Transgressive physiological and transcriptomic responses to light stress in allopolyploid <i>Glycine dolichocarpa</i> (Leguminosae). <i>Heredity</i> , 2013, 110, 160-170.	1.2	48
1854	Statistical Methods for Ambiguous Sequence Mappings. , 2013, , .		0
1855	An Island-Based Approach for Differential Expression Analysis. , 2013, 2013, 419-429.		1
1856	Genome-Wide Analysis of Gene Expression. , 2013, , 369-374.		3
1857	BamView: visualizing and interpretation of next-generation sequencing read alignments. <i>Briefings in Bioinformatics</i> , 2013, 14, 203-212.	3.2	60
1858	Computational analysis of bacterial RNA-Seq data. <i>Nucleic Acids Research</i> , 2013, 41, e140-e140.	6.5	573
1859	The splicing landscape is globally reprogrammed during male meiosis. <i>Nucleic Acids Research</i> , 2013, 41, 10170-10184.	6.5	71
1860	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. <i>Genome Research</i> , 2013, 23, 1916-1927.	2.4	91
1861	Practical Guidelines for the Comprehensive Analysis of ChIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003326.	1.5	221
1862	<i>Neisseria</i> Prophage Repressor Implicated in Gonococcal Pathogenesis. <i>Infection and Immunity</i> , 2013, 81, 3652-3661.	1.0	14
1863	A contribution to the study of plant development evolution based on gene co-expression networks. <i>Frontiers in Plant Science</i> , 2013, 4, 291.	1.7	22
1864	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	1.5	25
1865	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas059.	1.4	23
1866	Secretion of Protective Antigens by Tissue-Stage Nematode Larvae Revealed by Proteomic Analysis and Vaccination-Induced Sterile Immunity. <i>PLoS Pathogens</i> , 2013, 9, e1003492.	2.1	49
1867	Pervasive Transcription of the Human Genome Produces Thousands of Previously Unidentified Long Intergenic Noncoding RNAs. <i>PLoS Genetics</i> , 2013, 9, e1003569.	1.5	655
1868	Ras-Induced Changes in H3K27me3 Occur after Those in Transcriptional Activity. <i>PLoS Genetics</i> , 2013, 9, e1003698.	1.5	41
1869	The transcriptional response of <i>Arabidopsis</i> leaves to Fe deficiency. <i>Frontiers in Plant Science</i> , 2013, 4, 276.	1.7	152

#	ARTICLE	IF	CITATIONS
1870	Data-based filtering for replicated high-throughput transcriptome sequencing experiments. <i>Bioinformatics</i> , 2013, 29, 2146-2152.	1.8	193
1871	PolyCat: A Resource for Genome Categorization of Sequencing Reads From Allopolyploid Organisms. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 517-525.	0.8	78
1872	De Novo Transcriptome Sequencing Reveals Important Molecular Networks and Metabolic Pathways of the Plant, <i>Chlorophytum borivillianum</i> . <i>PLoS ONE</i> , 2013, 8, e83336.	1.1	65
1873	Systems biology of cancer biomarker detection. <i>Cancer Biomarkers</i> , 2013, 13, 201-213.	0.8	15
1874	Evolutionarily conserved long intergenic non-coding RNAs in the eye. <i>Human Molecular Genetics</i> , 2013, 22, 2992-3002.	1.4	41
1875	The Genome of <i>Tolypocladium inflatum</i> : Evolution, Organization, and Expression of the Cyclosporin Biosynthetic Gene Cluster. <i>PLoS Genetics</i> , 2013, 9, e1003496.	1.5	144
1876	Dynamic Evolution of Endogenous Retrovirus-Derived Genes Expressed in Bovine Conceptuses during the Period of Placentation. <i>Genome Biology and Evolution</i> , 2013, 5, 296-306.	1.1	30
1877	State-of-the-Art Fusion-Finder Algorithms Sensitivity and Specificity. <i>BioMed Research International</i> , 2013, 2013, 1-6.	0.9	79
1878	Novel Circulating Isoforms of Hepcidin. <i>Clinical Chemistry</i> , 2013, 59, 1412-1414.	1.5	8
1879	Functional genomics of tomato in a post-genome-sequencing phase. <i>Breeding Science</i> , 2013, 63, 14-20.	0.9	14
1880	Methylation of Histone H3 on Lysine 79 Associates with a Group of Replication Origins and Helps Limit DNA Replication Once per Cell Cycle. <i>PLoS Genetics</i> , 2013, 9, e1003542.	1.5	88
1881	A Viral Genome Landscape of RNA Polyadenylation from KSHV Latent to Lytic Infection. <i>PLoS Pathogens</i> , 2013, 9, e1003749.	2.1	49
1882	The Developmental Transcriptome of the Mosquito <i>Aedes aegypti</i> , an Invasive Species and Major Arbovirus Vector. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1493-1509.	0.8	189
1883	Advances in functional genomics for investigating salinity stress tolerance mechanisms in cereals. <i>Frontiers in Plant Science</i> , 2013, 4, 123.	1.7	62
1884	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.	1.8	22
1885	Human Genome Replication Proceeds through Four Chromatin States. <i>PLoS Computational Biology</i> , 2013, 9, e1003233.	1.5	54
1886	Identification of Rtl1, a Retrotransposon-Derived Imprinted Gene, as a Novel Driver of Hepatocarcinogenesis. <i>PLoS Genetics</i> , 2013, 9, e1003441.	1.5	76
1887	Masculinization of Gene Expression Is Associated with Exaggeration of Male Sexual Dimorphism. <i>PLoS Genetics</i> , 2013, 9, e1003697.	1.5	105



#	ARTICLE	IF	CITATIONS
1888	The MAPKKK Gene Family in <i>Gossypium raimondii</i> : Genome-Wide Identification, Classification and Expression Analysis. <i>International Journal of Molecular Sciences</i> , 2013, 14, 18740-18757.	1.8	40
1889	Massive Mitochondrial Gene Transfer in a Parasitic Flowering Plant Clade. <i>PLoS Genetics</i> , 2013, 9, e1003265.	1.5	115
1890	Discovery of a Splicing Regulator Required for Cell Cycle Progression. <i>PLoS Genetics</i> , 2013, 9, e1003305.	1.5	40
1891	Grape RNA-Seq analysis pipeline environment. <i>Bioinformatics</i> , 2013, 29, 614-621.	1.8	30
1892	Dissection of Regulatory Networks that Are Altered in Disease via Differential Co-expression. <i>PLoS Computational Biology</i> , 2013, 9, e1002955.	1.5	164
1893	Proteomic Analysis of the Excretory-Secretory Products from Larval Stages of <i>Ascaris suum</i> Reveals High Abundance of Glycosyl Hydrolases. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2467.	1.3	63
1894	Expanding roles in a library-based bioinformatics service program: a case study. <i>Journal of the Medical Library Association: JMLA</i> , 2013, 101, 303-309.	0.6	19
1895	FishingCNV: a graphical software package for detecting rare copy number variations in exome-sequencing data. <i>Bioinformatics</i> , 2013, 29, 1461-1462.	1.8	42
1896	Systematically Differentiating Functions for Alternatively Spliced Isoforms through Integrating RNA-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003314.	1.5	78
1897	Differential Gene Expression in <i>Pycnoporus coccineus</i> during Interspecific Mycelial Interactions with Different Competitors. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6626-6636.	1.4	33
1898	TIGAR: transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference. <i>Bioinformatics</i> , 2013, 29, 2292-2299.	1.8	36
1899	Genome-wide transcriptome analysis between Small-tail Han sheep and the Surabaya fur sheep using high-throughput RNA sequencing. <i>Reproduction</i> , 2013, 145, 587-596.	1.1	72
1900	Mutually Exclusive Alterations in Secondary Metabolism Are Critical for the Uptake of Insoluble Iron Compounds by <i>Arabidopsis</i> and <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2013, 162, 1473-1485.	2.3	212
1901	Accurate detection of differential RNA processing. <i>Nucleic Acids Research</i> , 2013, 41, 5189-5198.	6.5	39
1902	Phylogenomic Distance Method for Analyzing Transcriptome Evolution Based on RNA-seq Data. <i>Genome Biology and Evolution</i> , 2013, 5, 1746-1753.	1.1	16
1903	Conserved Gene Regulatory Function of the Carboxy-Terminal Domain of Dictyostelid C-Module-Binding Factor. <i>Eukaryotic Cell</i> , 2013, 12, 460-468.	3.4	5
1904	Genome-Wide Detection of Condition-Sensitive Alternative Splicing in <i>Arabidopsis</i> Roots. <i>Plant Physiology</i> , 2013, 162, 1750-1763.	2.3	113
1905	Coordinated regulation of synthesis and stability of RNA during the acute TNF-induced proinflammatory response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2240-2245.	3.3	112

#	ARTICLE	IF	CITATIONS
1906	EBARDenovo: highly accurate <i>de novo</i> assembly of RNA-Seq with efficient chimera-detection. <i>Bioinformatics</i> , 2013, 29, 1004-1010.	1.8	33
1907	Early <i>de novo</i> DNA methylation and prolonged demethylation in the muscle lineage. <i>Epigenetics</i> , 2013, 8, 317-332.	1.3	85
1908	Arpeggio: harmonic compression of ChIP-seq data reveals protein-chromatin interaction signatures. <i>Nucleic Acids Research</i> , 2013, 41, e161-e161.	6.5	7
1909	CoLlde. <i>RNA Biology</i> , 2013, 10, 1221-1230.	1.5	28
1910	Characterization of the human ESC transcriptome by hybrid sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4821-30.	3.3	316
1911	Novel Proteins Required for Meiotic Silencing by Unpaired DNA and siRNA Generation in <i>Neurospora crassa</i> . <i>Genetics</i> , 2013, 194, 91-100.	1.2	34
1912	The peptide-encoding CEP1 gene modulates lateral root and nodule numbers in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 5395-5409.	2.4	182
1913	OLego: fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. <i>Nucleic Acids Research</i> , 2013, 41, 5149-5163.	6.5	116
1914	The Transcriptome of the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus in <i>Trichoplusia ni</i> Cells. <i>Journal of Virology</i> , 2013, 87, 6391-6405.	1.5	152
1915	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 387-397.	0.8	59
1916	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. <i>Bioinformatics</i> , 2013, 29, 2529-2538.	1.8	57
1917	Sequential activation of genetic programs in mouse mammary epithelium during pregnancy depends on STAT5A/B concentration. <i>Nucleic Acids Research</i> , 2013, 41, 1622-1636.	6.5	72
1918	TIARA genome database: update 2013. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, bat003-bat003.	1.4	6
1919	NGSUtils: a software suite for analyzing and manipulating next-generation sequencing datasets. <i>Bioinformatics</i> , 2013, 29, 494-496.	1.8	219
1920	Genetic Variants Contribute to Gene Expression Variability in Humans. <i>Genetics</i> , 2013, 193, 95-108.	1.2	98
1921	Human TREX component Thoc5 affects alternative polyadenylation site choice by recruiting mammalian cleavage factor I. <i>Nucleic Acids Research</i> , 2013, 41, 7060-7072.	6.5	57
1922	The Differential Transcription Network between Embryo and Endosperm in the Early Developing Maize Seed. <i>Plant Physiology</i> , 2013, 162, 440-455.	2.3	76
1923	Deep RNA Sequencing Reveals Complex Transcriptional Landscape of a Bat Adenovirus. <i>Journal of Virology</i> , 2013, 87, 503-511.	1.5	15

#	ARTICLE	IF	CITATIONS
1924	Flagellated Algae Protein Evolution Suggests the Prevalence of Lineage-Specific Rules Governing Evolutionary Rates of Eukaryotic Proteins. <i>Genome Biology and Evolution</i> , 2013, 5, 913-922.	1.1	6
1925	TrueSight: a new algorithm for splice junction detection using RNA-seq. <i>Nucleic Acids Research</i> , 2013, 41, e51-e51.	6.5	31
1926	Transcriptomic Analysis of Cadmium Stress Response in the Heavy Metal Hyperaccumulator <i>Sedum alfredii</i> Hance. <i>PLoS ONE</i> , 2013, 8, e64643.	1.1	100
1927	Higher order asymptotics for negative binomial regression inferences from RNA-sequencing data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 49-70.	0.2	9
1928	Evolution of the Eye Transcriptome under Constant Darkness in <i>Sinocyclocheilus</i> Cavefish. <i>Molecular Biology and Evolution</i> , 2013, 30, 1527-1543.	3.5	83
1929	Basics of Molecular Biology. <i>Advanced Topics in Science and Technology in China</i> , 2013, , 541-601.	0.0	1
1930	RNA-Seq Reveals Dynamic Changes of Gene Expression in Key Stages of Intestine Regeneration in the Sea Cucumber <i>Apostichopus japonicus</i> . <i>PLoS ONE</i> , 2013, 8, e69441.	1.1	53
1931	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. <i>Rna</i> , 2013, 19, 479-489.	1.6	29
1932	Outlier Kinase Expression by RNA Sequencing as Targets for Precision Therapy. <i>Cancer Discovery</i> , 2013, 3, 280-293.	7.7	40
1933	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <i>Genome Research</i> , 2013, 23, 1651-1662.	2.4	260
1934	Translating mRNAs strongly correlate to proteins in a multivariate manner and their translation ratios are phenotype specific. <i>Nucleic Acids Research</i> , 2013, 41, 4743-4754.	6.5	157
1935	DEXUS: identifying differential expression in RNA-Seq studies with unknown conditions. <i>Nucleic Acids Research</i> , 2013, 41, e198-e198.	6.5	26
1936	Horizontal Transfer of DNA from the Mitochondrial to the Plastid Genome and Its Subsequent Evolution in Milkweeds ( <i>Apocynaceae</i> ). <i>Genome Biology and Evolution</i> , 2013, 5, 1872-1885.	1.1	129
1937	Transcriptional Changes in the Transition from Vegetative Cells to Asexual Development in the Model Fungus <i>Aspergillus nidulans</i> . <i>Eukaryotic Cell</i> , 2013, 12, 311-321.	3.4	40
1938	IQdb: an intelligence quotient score-associated gene resource for human intelligence. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat063.	1.4	15
1939	Genome-wide analysis of light-regulated alternative splicing mediated by photoreceptors in <i>Physcomitrella patens</i> . <i>Genome Biology</i> , 2013, 15, R10.	13.9	89
1940	High Levels of Gene Expression Explain the Strong Evolutionary Constraint of Mitochondrial Protein-Coding Genes. <i>Molecular Biology and Evolution</i> , 2013, 30, 272-284.	3.5	67
1941	RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. <i>Nucleic Acids Research</i> , 2013, 41, e94-e94.	6.5	41

#	ARTICLE	IF	CITATIONS
1942	Sweating the Small Stuff. <i>Pancreas</i> , 2013, 42, 740-759.	0.5	28
1943	Comparative Genomic and Transcriptomic Analyses Reveal Habitat Differentiation and Different Transcriptional Responses during Pectin Metabolism in <i>Alishewanella</i> Species. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6351-6361.	1.4	11
1944	Phosphotyrosine Signaling Proteins that Drive Oncogenesis Tend to be Highly Interconnected. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1204-1213.	2.5	31
1945	EDGE-pro: Estimated Degree of Gene Expression in Prokaryotic Genomes. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11250.	0.6	141
1946	De Novo Transcriptome Assembly and Differential Gene Expression Profiling of Three <i>Capra hircus</i> Skin Types during Anagen of the Hair Growth Cycle. <i>International Journal of Genomics</i> , 2013, 2013, 1-9.	0.8	11
1947	Whole-Transcriptome Shotgun Sequencing (RNA-seq) Screen Reveals Upregulation of Cellobiose and Motility Operons of <i>Lactobacillus ruminis</i> L5 during Growth on Tetrasaccharides Derived from Barley $\beta$ -Glucan. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5661-5669.	1.4	27
1948	Global Analysis of Differentially Expressed Genes and Proteins in the Wheat Callus Infected by <i>Agrobacterium tumefaciens</i> . <i>PLoS ONE</i> , 2013, 8, e79390.	1.1	29
1949	Probabilistic error correction for RNA sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e109-e109.	6.5	68
1950	Gibberellin metabolism in <i>Vitis vinifera</i> L. during bloom and fruit-set: functional characterization and evolution of grapevine gibberellin oxidases. <i>Journal of Experimental Botany</i> , 2013, 64, 4403-4419.	2.4	102
1951	RNA-Seq of Arabidopsis Pollen Uncovers Novel Transcription and Alternative Splicing. <i>Plant Physiology</i> , 2013, 162, 1092-1109.	2.3	195
1952	<i>Cecropia peltata</i> Accumulates Starch or Soluble Glycogen by Differentially Regulating Starch Biosynthetic Genes. <i>Plant Cell</i> , 2013, 25, 1400-1415.	3.1	23
1953	An RNA-Seq Transcriptome Analysis of Orthophosphate-Deficient White Lupin Reveals Novel Insights into Phosphorus Acclimation in Plants. <i>Plant Physiology</i> , 2013, 161, 705-724.	2.3	184
1954	DROMPA: easy-to-handle peak calling and visualization software for the computational analysis and validation of ChIP-seq data. <i>Genes To Cells</i> , 2013, 18, 589-601.	0.5	67
1955	Quantification of tomato and <i>Arabidopsis</i> mobile RNA's trafficking into the parasitic plant <i>Cuscuta pentagona</i> . <i>New Phytologist</i> , 2013, 200, 1225-1233.	3.5	40
1956	<i>Lmo2</i> Induces Hematopoietic Stem Cell-Like Features in T-Cell Progenitor Cells Prior to Leukemia. <i>Stem Cells</i> , 2013, 31, 882-894.	1.4	47
1957	Therapeutic Activities of Engrafted Neural Stem/Precursor Cells Are Not Dormant in the Chronically Injured Spinal Cord. <i>Stem Cells</i> , 2013, 31, 1535-1547.	1.4	57
1958	Identification of novel point mutations in splicing sites integrating whole-exome and RNA-seq data in myeloproliferative diseases. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2013, 1, 246-259.	0.6	17
1959	Transcriptome Profiling Reveals Auxin and Cytokinin Regulating Somatic Embryogenesis in Different Sister Lines of Cotton Cultivar CCR124. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 631-642.	4.1	56

#	ARTICLE	IF	CITATIONS
1960	Age-associated changes in gene expression and developmental competence of bovine oocytes, and a possible countermeasure against age-associated events. <i>Molecular Reproduction and Development</i> , 2013, 80, 508-521.	1.0	58
1961	Structure, Transcription, and Variability of Metazoan Mitochondrial Genome: Perspectives from an Unusual Mitochondrial Inheritance System. <i>Genome Biology and Evolution</i> , 2013, 5, 1535-1554.	1.1	67
1962	PtH7, a class III HD-Zip Gene, Plays a Critical Role in Regulation of Vascular Cambium Differentiation in <i>Populus</i> . <i>Molecular Plant</i> , 2013, 6, 1331-1343.	3.9	108
1963	Transcriptome sequencing of neonatal thymic epithelial cells. <i>Scientific Reports</i> , 2013, 3, 1860.	1.6	72
1964	Chronic Ethanol Exposure Increases Cytochrome P450 and Decreases Activated in Blocked Unfolded Protein Response Gene Family Transcripts in <i>Caenorhabditis elegans</i> . <i>Journal of Biochemical and Molecular Toxicology</i> , 2013, 27, 219-228.	1.4	14
1965	An RNA-seq protocol to identify mRNA expression changes in mouse diaphyseal bone: Applications in mice with bone property altering <i>Lrp5</i> mutations. <i>Journal of Bone and Mineral Research</i> , 2013, 28, 2081-2093.	3.1	76
1966	Nucleosome Distribution near the 3' Ends of Genes in the Human Genome. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2051-2055.	0.6	9
1967	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. , 2013, , .		0
1968	Modeling exome sequencing data with generalized Gaussian distribution with application to copy number variation detection. , 2013, , .		0
1969	Hypoxic survival requires a 2-on-2 hemoglobin in a process involving nitric oxide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10854-10859.	3.3	63
1970	In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. <i>Journal of Experimental Medicine</i> , 2013, 210, 951-968.	4.2	121
1971	Glucocorticoid receptor represses proinflammatory genes at distinct steps of the transcription cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14616-14621.	3.3	55
1972	Identification of Complete Hydatidiform Mole Pregnancy-Associated MicroRNAs in Plasma. <i>Clinical Chemistry</i> , 2013, 59, 1410-1412.	1.5	20
1973	Identification of T6SS-dependent effector and immunity proteins by Tn-seq in <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2623-2628.	3.3	260
1974	Characterization and comparison of human nuclear and cytosolic editomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2741-7.	3.3	63
1975	Loss of T Cell Progenitor Checkpoint Control Underlies Leukemia Initiation in Rag1-Deficient Nonobese Diabetic Mice. <i>Journal of Immunology</i> , 2013, 190, 3276-3288.	0.4	5
1976	Translational Redefinition of UGA Codons Is Regulated by Selenium Availability. <i>Journal of Biological Chemistry</i> , 2013, 288, 19401-19413.	1.6	90
1977	Impact of Bioinformatic Procedures in the Development and Translation of High-Throughput Molecular Classifiers in Oncology. <i>Clinical Cancer Research</i> , 2013, 19, 4315-4325.	3.2	32

#	ARTICLE	IF	CITATIONS
1978	Loss of Arp2/3 induces an NF- $\kappa$ B-dependent, nonautonomous effect on chemotactic signaling. <i>Journal of Cell Biology</i> , 2013, 203, 907-916.	2.3	37
1979	Stability, delivery and functions of human sperm RNAs at fertilization. <i>Nucleic Acids Research</i> , 2013, 41, 4104-4117.	6.5	288
1980	Concise Review: New Paradigms for Down Syndrome Research Using Induced Pluripotent Stem Cells: Tackling Complex Human Genetic Disease. <i>Stem Cells Translational Medicine</i> , 2013, 2, 175-184.	1.6	13
1981	Identification of Cytokinin-Responsive Genes Using Microarray Meta-Analysis and RNA-Seq in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 162, 272-294.	2.3	230
1982	Photoreceptor phagocytosis is mediated by phosphoinositide signaling. <i>FASEB Journal</i> , 2013, 27, 4585-4595.	0.2	40
1985	Embedding siRNA sequences targeting Apolipoprotein B100 in shRNA and miRNA scaffolds results in differential processing and in vivo efficacy. <i>Molecular Therapy</i> , 2013, 21, 217-227.	3.7	22
1986	HDAC inhibitors induce transcriptional repression of high copy number genes in breast cancer through elongation blockade. <i>Oncogene</i> , 2013, 32, 2828-2835.	2.6	77
1987	BSRD: a repository for bacterial small regulatory RNA. <i>Nucleic Acids Research</i> , 2013, 41, D233-D238.	6.5	104
1988	Comparison of normalization methods for differential gene expression analysis in RNA-Seq experiments. <i>Communicative and Integrative Biology</i> , 2013, 6, e25849.	0.6	105
1989	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2013, 7, 44-62.	1.1	8
1990	Structural and Functional Characterization of the N Terminus of <i>Schizosaccharomyces pombe</i> Cwf10. <i>Eukaryotic Cell</i> , 2013, 12, 1472-1489.	3.4	12
1991	Cleavage of Fibrinogen by Proteinases Elicits Allergic Responses Through Toll-Like Receptor 4. <i>Science</i> , 2013, 341, 792-796.	6.0	194
1992	CNCTDISCRIMINATOR: CODING AND NONCODING TRANSCRIPT DISCRIMINATOR – AN EXCURSION THROUGH HYPOTHESIS LEARNING AND ENSEMBLE LEARNING APPROACHES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1342002.	0.3	6
1993	The Metabolic Regulation of Sporulation and Parasporal Crystal Formation in <i>Bacillus thuringiensis</i> Revealed by Transcriptomics and Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1363-1376.	2.5	109
1994	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2169-2174.	0.6	33
1995	Turning single cells into microarrays by super-resolution barcoding. <i>Briefings in Functional Genomics</i> , 2013, 12, 75-80.	1.3	10
1996	Effect of Intracellular Expression of Antimicrobial Peptide LL-37 on Growth of <i>Escherichia coli</i> Strain TOP10 under Aerobic and Anaerobic Conditions. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 4707-4716.	1.4	21
1997	Coevolution and Life Cycle Specialization of Plant Cell Wall Degrading Enzymes in a Hemibiotrophic Pathogen. <i>Molecular Biology and Evolution</i> , 2013, 30, 1337-1347.	3.5	77

#	ARTICLE	IF	CITATIONS
1998	Transcriptome Sequencing Reveals the Character of Incomplete Dosage Compensation across Multiple Tissues in Flycatchers. <i>Genome Biology and Evolution</i> , 2013, 5, 1555-1566.	1.1	59
1999	Phosphorylation of an ERF Transcription Factor by <i>Arabidopsis</i> MPK3/MPK6 Regulates Plant Defense Gene Induction and Fungal Resistance. <i>Plant Cell</i> , 2013, 25, 1126-1142.	3.1	362
2000	Recent advances in biocatalyst development in the pharmaceutical industry. <i>Pharmaceutical Bioprocessing</i> , 2013, 1, 179-196.	0.8	11
2001	Distinct global shifts in genomic binding profiles of limb malformation-associated <i>HOXD13</i> mutations. <i>Genome Research</i> , 2013, 23, 2091-2102.	2.4	31
2002	Genomic Heterogeneity of Translocation Renal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2013, 19, 4673-4684.	3.2	77
2003	The Draft Genome and Transcriptome of <i>Panagrellus redivivus</i> Are Shaped by the Harsh Demands of a Free-Living Lifestyle. <i>Genetics</i> , 2013, 193, 1279-1295.	1.2	57
2004	Zinc Deficiency Impacts CO <sub>2</sub> Assimilation and Disrupts Copper Homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 10672-10683.	1.6	72
2005	Tips for Preparing mRNA-Seq Libraries from Poly(A) <sup>+</sup> mRNA for Illumina Transcriptome High-Throughput Sequencing. <i>Cold Spring Harbor Protocols</i> , 2013, 2013, pdb.ip073908.	0.2	1
2007	Pro-inflammatory cytokines can act as intracellular modulators of commensal bacterial virulence. <i>Open Biology</i> , 2013, 3, 130048.	1.5	28
2008	Functional Diversification of Cerato-Platanins in <i>Moniliophthora perniciosa</i> as Seen by Differential Expression and Protein Function Specialization. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1281-1293.	1.4	58
2009	Identification of a novel gene fusion RNF213-SLC26A11 in chronic myeloid leukemia by RNA-Seq. <i>Molecular Medicine Reports</i> , 2013, 7, 591-597.	1.1	15
2010	Massively parallel sequencing: the new frontier of hematologic genomics. <i>Blood</i> , 2013, 122, 3268-3275.	0.6	23
2011	BREEDING AND GENETICS SYMPOSIUM: Networks and pathways to guide genomic selection. <i>Journal of Animal Science</i> , 2013, 91, 537-552.	0.2	57
2012	Grouped False-Discovery Rate for Removing the Gene-set-Level Bias of RNA-seq. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S13099.	0.6	3
2013	Transcriptomic signatures in cartilage ageing. <i>Arthritis Research and Therapy</i> , 2013, 15, R98.	1.6	61
2014	Transcriptome and proteome quantification of a tumor model provides novel insights into post-transcriptional gene regulation. <i>Genome Biology</i> , 2013, 14, r133.	13.9	40
2015	De Novo Transcriptome Sequencing in <i>Trigonella foenum-graecum</i> L. to Identify Genes Involved in the Biosynthesis of Diosgenin. <i>Plant Genome</i> , 2013, 6, plantgenome2012.08.0021.	1.6	39
2016	Transcriptome analysis of the bloodstream stage from the parasite <i>Trypanosoma vivax</i> . <i>BMC Genomics</i> , 2013, 14, 149.	1.2	36

#	ARTICLE	IF	CITATIONS
2017	NEXT-peak: a normal-exponential two-peak model for peak-calling in ChIP-seq data. BMC Genomics, 2013, 14, 349.	1.2	4
2018	Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in Arabidopsis thaliana roots. BMC Genomics, 2013, 14, 701.	1.2	76
2019	Probing functional polymorphisms in the dengue vector, Aedes aegypti. BMC Genomics, 2013, 14, 739.	1.2	12
2020	A genome-wide survey of maternal and embryonic transcripts during Xenopus tropicalis development. BMC Genomics, 2013, 14, 762.	1.2	50
2021	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in Anopheles gambiae. BMC Genomics, 2013, 14, 749.	1.2	94
2022	Epigenetic Repression of Male Gametophyte-Specific Genes in the Arabidopsis Sporophyte. Molecular Plant, 2013, 6, 1176-1186.	3.9	13
2023	De Novo Biosynthesis of Sexual Pheromone in the Labial Gland of Bumblebee Males. ChemBioChem, 2013, 14, 361-371.	1.3	29
2024	Sequencing and De Novo Analysis of the Hemocytes Transcriptome in Litopenaeus vannamei Response to White Spot Syndrome Virus Infection. PLoS ONE, 2013, 8, e76718.	1.1	79
2025	Gene Expression Profiles Deciphering Leaf Senescence Variation between Early- and Late-Senescence Cotton Lines. PLoS ONE, 2013, 8, e69847.	1.1	44
2026	Quantitative Transcriptomics using Designed Primer-based Amplification. Scientific Reports, 2013, 3, 1740.	1.6	38
2027	Metastatic Cancer. , 2013, , 776-788.		2
2028	Integrated Analysis of Transcriptomic and Proteomic Data. Current Genomics, 2013, 14, 91-110.	0.7	387
2030	De Novo Transcriptome Assembly in Chili Pepper (Capsicum frutescens) to Identify Genes Involved in the Biosynthesis of Capsaicinoids. PLoS ONE, 2013, 8, e48156.	1.1	114
2031	Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. PLoS ONE, 2013, 8, e53171.	1.1	62
2032	Transcript Profile Analyses of Maize Silks Reveal Effective Activation of Genes Involved in Microtubule-Based Movement, Ubiquitin-Dependent Protein Degradation, and Transport in the Pollination Process. PLoS ONE, 2013, 8, e53545.	1.1	16
2033	Comparative Analysis of the Transcriptome in Tissues Secreting Purple and White Nacre in the Pearl Mussel Hyriopsis cumingii. PLoS ONE, 2013, 8, e53617.	1.1	83
2034	Efficient and Comprehensive Representation of Uniqueness for Next-Generation Sequencing by Minimum Unique Length Analyses. PLoS ONE, 2013, 8, e53822.	1.1	29
2035	Identification of Human HK Genes and Gene Expression Regulation Study in Cancer from Transcriptomics Data Analysis. PLoS ONE, 2013, 8, e54082.	1.1	22



#	ARTICLE	IF	CITATIONS
2036	Transcriptomic Immune Response of <i>Tenebrio molitor</i> Pupae to Parasitization by <i>Scleroderma guani</i> . PLoS ONE, 2013, 8, e54411.	1.1	54
2037	mRNA-seq Analysis of the <i>Gossypium arboreum</i> transcriptome Reveals Tissue Selective Signaling in Response to Water Stress during Seedling Stage. PLoS ONE, 2013, 8, e54762.	1.1	45
2038	Association of RNAs with <i>Bacillus subtilis</i> Hfq. PLoS ONE, 2013, 8, e55156.	1.1	60
2039	Expression Profile of Ectopic Olfactory Receptors Determined by Deep Sequencing. PLoS ONE, 2013, 8, e55368.	1.1	240
2040	An Integrated Transcriptome-Wide Analysis of Cave and Surface Dwelling <i>Astyanax mexicanus</i> . PLoS ONE, 2013, 8, e55659.	1.1	69
2041	Stallion Sperm Transcriptome Comprises Functionally Coherent Coding and Regulatory RNAs as Revealed by Microarray Analysis and RNA-seq. PLoS ONE, 2013, 8, e56535.	1.1	88
2042	Transcriptional Profiling of Mouse Uterus at Pre-Implantation Stage under VEGF Repression. PLoS ONE, 2013, 8, e57287.	1.1	6
2043	Comparative Transcriptional Profiling Provides Insights into the Evolution and Development of the Zygomorphic Flower of <i>Vicia sativa</i> (Papilionoideae). PLoS ONE, 2013, 8, e57338.	1.1	29
2044	Integrative Genome-Wide Gene Expression Profiling of Clear Cell Renal Cell Carcinoma in Czech Republic and in the United States. PLoS ONE, 2013, 8, e57886.	1.1	99
2045	Using RNA-Seq to Profile Soybean Seed Development from Fertilization to Maturity. PLoS ONE, 2013, 8, e59270.	1.1	122
2046	De Novo Transcriptome Sequence Assembly and Analysis of RNA Silencing Genes of <i>Nicotiana benthamiana</i> . PLoS ONE, 2013, 8, e59534.	1.1	152
2047	RNA-Seq Analysis of <i>Cocos nucifera</i> : Transcriptome Sequencing and De Novo Assembly for Subsequent Functional Genomics Approaches. PLoS ONE, 2013, 8, e59997.	1.1	71
2048	Development and Characterization of 1,827 Expressed Sequence Tag-Derived Simple Sequence Repeat Markers for Ramie ( <i>Boehmeria nivea</i> L. Gaud). PLoS ONE, 2013, 8, e60346.	1.1	35
2049	Maize Gene Atlas Developed by RNA Sequencing and Comparative Evaluation of Transcriptomes Based on RNA Sequencing and Microarrays. PLoS ONE, 2013, 8, e61005.	1.1	152
2050	Molecular and Immunological Characterization of Ragweed ( <i>Ambrosia artemisiifolia</i> L.) Pollen after Exposure of the Plants to Elevated Ozone over a Whole Growing Season. PLoS ONE, 2013, 8, e61518.	1.1	58
2051	RNA-Seq Profiling Reveals Novel Hepatic Gene Expression Pattern in Aflatoxin B1 Treated Rats. PLoS ONE, 2013, 8, e61768.	1.1	61
2052	Ectopic Overexpression of SsCBF1, a CRT/DRE-Binding Factor from the Nightshade Plant <i>Solanum lycopersicoides</i> , Confers Freezing and Salt Tolerance in Transgenic <i>Arabidopsis</i> . PLoS ONE, 2013, 8, e61810.	1.1	29
2053	Genome-Wide Expression Analysis of Soybean MADS Genes Showing Potential Function in the Seed Development. PLoS ONE, 2013, 8, e62288.	1.1	40

#	ARTICLE	IF	CITATIONS
2054	Simultaneous Transcriptome Analysis of Sorghum and <i>Bipolaris sorghicola</i> by Using RNA-seq in Combination with De Novo Transcriptome Assembly. PLoS ONE, 2013, 8, e62460.	1.1	79
2055	Characterization of Gonadal Transcriptomes from Nile Tilapia ( <i>Oreochromis niloticus</i> ) Reveals Differentially Expressed Genes. PLoS ONE, 2013, 8, e63604.	1.1	195
2056	Transcriptomic Analysis of a Tertiary Relict Plant, Extreme Xerophyte <i>Reaumuria soongorica</i> to Identify Genes Related to Drought Adaptation. PLoS ONE, 2013, 8, e63993.	1.1	55
2057	Transcriptional Dissection of Human Limbal Niche Compartments by Massive Parallel Sequencing. PLoS ONE, 2013, 8, e64244.	1.1	25
2058	Comparative Transcriptome Profiling Reveals Different Expression Patterns in <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Strains with Putative Virulence-Relevant Genes. PLoS ONE, 2013, 8, e64267.	1.1	18
2059	Transcriptome Analysis of <i>Barbarea vulgaris</i> Infested with Diamondback Moth ( <i>Plutella xylostella</i> ) Larvae. PLoS ONE, 2013, 8, e64481.	1.1	28
2060	De Novo Characterization of Japanese Scallop <i>Mizuhopecten yessoensis</i> Transcriptome and Analysis of Its Gene Expression following Cadmium Exposure. PLoS ONE, 2013, 8, e64485.	1.1	42
2061	Genome-Wide Analysis of the <i>Salmonella</i> Fis Regulon and Its Regulatory Mechanism on Pathogenicity Islands. PLoS ONE, 2013, 8, e64688.	1.1	29
2062	Digital Gene Expression Analysis of Corky Split Vein Caused by Boron Deficiency in "Newhall" Navel Orange ( <i>Citrus sinensis</i> Osbeck) for Selecting Differentially Expressed Genes Related to Vascular Hypertrophy. PLoS ONE, 2013, 8, e65737.	1.1	27
2063	Global Transcriptome Profiling of <i>Salicornia europaea</i> L. Shoots under NaCl Treatment. PLoS ONE, 2013, 8, e65877.	1.1	38
2064	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. PLoS ONE, 2013, 8, e66129.	1.1	62
2065	Rapidly Evolving Genes and Stress Adaptation of Two Desert Poplars, <i>Populus euphratica</i> and <i>P. pruinosa</i> . PLoS ONE, 2013, 8, e66370.	1.1	52
2066	MicroRNA and piRNA Profiles in Normal Human Testis Detected by Next Generation Sequencing. PLoS ONE, 2013, 8, e66809.	1.1	98
2067	Evaluating the Impact of Sequencing Depth on Transcriptome Profiling in Human Adipose. PLoS ONE, 2013, 8, e66883.	1.1	60
2068	Gene Expression Analysis of Zebrafish Melanocytes, Iridophores, and Retinal Pigmented Epithelium Reveals Indicators of Biological Function and Developmental Origin. PLoS ONE, 2013, 8, e67801.	1.1	90
2069	Transcriptome Analysis in Sheepgrass ( <i>Leymus chinensis</i> ): A Dominant Perennial Grass of the Eurasian Steppe. PLoS ONE, 2013, 8, e67974.	1.1	68
2070	Normalizing RNA-Sequencing Data by Modeling Hidden Covariates with Prior Knowledge. PLoS ONE, 2013, 8, e68141.	1.1	68
2071	Detecting Splicing Variants in Idiopathic Pulmonary Fibrosis from Non-Differentially Expressed Genes. PLoS ONE, 2013, 8, e68352.	1.1	26

#	ARTICLE	IF	CITATIONS
2072	Genome-Wide Identification of Molecular Pathways and Biomarkers in Response to Arsenic Exposure in Zebrafish Liver. PLoS ONE, 2013, 8, e68737.	1.1	49
2073	TCW: Transcriptome Computational Workbench. PLoS ONE, 2013, 8, e69401.	1.1	17
2074	Differential Expression Patterns in Chemosensory and Non-Chemosensory Tissues of Putative Chemosensory Genes Identified by Transcriptome Analysis of Insect Pest the Purple Stem Borer <i>Sesamia inferens</i> (Walker). PLoS ONE, 2013, 8, e69715.	1.1	120
2075	High-Resolution Transcriptomic Analyses of <i>Sinorhizobium</i> sp. NGR234 Bacteroids in Determinate Nodules of <i>Vigna unguiculata</i> and Indeterminate Nodules of <i>Leucaena leucocephala</i> . PLoS ONE, 2013, 8, e70531.	1.1	67
2076	Identification and Characterization of Long Non-Coding RNAs Related to Mouse Embryonic Brain Development from Available Transcriptomic Data. PLoS ONE, 2013, 8, e71152.	1.1	55
2077	Global Transcriptome Analysis of Orange Wheat Blossom Midge, <i>Sitodiplosis mosellana</i> (Gehin) (Diptera: Cecidomyiidae) to Identify Candidate Transcripts Regulating Diapause. PLoS ONE, 2013, 8, e71564.	1.1	22
2078	De novo Assembly of the Indo-Pacific Humpback Dolphin Leucocyte Transcriptome to Identify Putative Genes Involved in the Aquatic Adaptation and Immune Response. PLoS ONE, 2013, 8, e72417.	1.1	29
2079	Characterization and Comparative Analyses of Muscle Transcriptomes in Dorper and Small-Tailed Han Sheep Using RNA-Seq Technique. PLoS ONE, 2013, 8, e72686.	1.1	53
2080	RNA-Seq Reveals Spliceosome and Proteasome Genes as Most Consistent Transcripts in Human Cancer Cells. PLoS ONE, 2013, 8, e72884.	1.1	46
2081	AbaA Regulates Conidiogenesis in the Ascomycete Fungus <i>Fusarium graminearum</i> . PLoS ONE, 2013, 8, e72915.	1.1	75
2082	Transcriptome Sequence and Plasmid Copy Number Analysis of the Brewery Isolate <i>Pediococcus clausenii</i> ATCC BAA-344T during Growth in Beer. PLoS ONE, 2013, 8, e73627.	1.1	20
2083	Development of Genomic Resources for a thraustochytrid Pathogen and Investigation of Temperature Influences on Gene Expression. PLoS ONE, 2013, 8, e74196.	1.1	20
2084	Parasitization by <i>Cotesia chilonis</i> Influences Gene Expression in Fatbody and Hemocytes of <i>Chilo suppressalis</i> . PLoS ONE, 2013, 8, e74309.	1.1	29
2085	Next-Generation Sequence Analysis of Cancer Xenograft Models. PLoS ONE, 2013, 8, e74432.	1.1	30
2086	RNA-Seq Reveals Infection-Related Gene Expression Changes in <i>Phytophthora capsici</i> . PLoS ONE, 2013, 8, e74588.	1.1	49
2087	Gaucher Disease: Transcriptome Analyses Using Microarray or mRNA Sequencing in a <i>Gba1</i> Mutant Mouse Model Treated with Velaglycerase alfa or Imiglycerase. PLoS ONE, 2013, 8, e74912.	1.1	18
2088	Identification of Proteins Associated with Polyhydroxybutyrate Granules from <i>Herbaspirillum seropedicae</i> SmR1 - Old Partners, New Players. PLoS ONE, 2013, 8, e75066.	1.1	31
2089	Transcriptome Sequencing and Differential Gene Expression Analysis of Delayed Gland Morphogenesis in <i>Gossypium australe</i> during Seed Germination. PLoS ONE, 2013, 8, e75323.	1.1	26

#	ARTICLE	IF	CITATIONS
2090	Alterations of the Transcriptome of <i>Sulfolobus acidocaldarius</i> by Exoribonuclease aCPSF2. PLoS ONE, 2013, 8, e76569.	1.1	21
2091	Novel CIC Point Mutations and an Exon-Spanning, Homozygous Deletion Identified in Oligodendroglial Tumors by a Comprehensive Genomic Approach Including Transcriptome Sequencing. PLoS ONE, 2013, 8, e76623.	1.1	16
2092	Transcriptome Sequencing and Expression Analysis of Terpenoid Biosynthesis Genes in <i>Litsea cubeba</i> . PLoS ONE, 2013, 8, e76890.	1.1	80
2093	Transcriptome Comparison between Porcine Subcutaneous and Intramuscular Stromal Vascular Cells during Adipogenic Differentiation. PLoS ONE, 2013, 8, e77094.	1.1	43
2094	Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885.	1.1	44
2095	RNA-Seq Analysis Reveals Candidate Genes for Ontogenic Resistance in <i>Malus-Venturia</i> Pathosystem. PLoS ONE, 2013, 8, e78457.	1.1	57
2096	Inferring Polymorphism-Induced Regulatory Gene Networks Active in Human Lymphocyte Cell Lines by Weighted Linear Mixed Model Analysis of Multiple RNA-Seq Datasets. PLoS ONE, 2013, 8, e78868.	1.1	4
2097	Echidna Venom Gland Transcriptome Provides Insights into the Evolution of Monotreme Venom. PLoS ONE, 2013, 8, e79092.	1.1	18
2098	MicroRNA Transcriptome in Swine Small Intestine during Weaning Stress. PLoS ONE, 2013, 8, e79343.	1.1	26
2099	rSeqDiff: Detecting Differential Isoform Expression from RNA-Seq Data Using Hierarchical Likelihood Ratio Test. PLoS ONE, 2013, 8, e79448.	1.1	29
2100	Transcriptome Comparison Reveals Key Candidate Genes Responsible for the Unusual Reblooming Trait in Tree Peonies. PLoS ONE, 2013, 8, e79996.	1.1	25
2101	Next-Generation Sequencing-Based Transcriptome Analysis of <i>Helicoverpa armigera</i> Larvae Immune-Primed with <i>Photorhabdus luminescens</i> TT01. PLoS ONE, 2013, 8, e80146.	1.1	32
2102	Discovery of Genes Related to Witches Broom Disease in <i>Paulownia tomentosa</i> ã— <i>Paulownia fortunei</i> by a De Novo Assembled Transcriptome. PLoS ONE, 2013, 8, e80238.	1.1	36
2103	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. PLoS ONE, 2013, 8, e80306.	1.1	90
2104	Simultaneous Transcriptional Profiling of Bacteria and Their Host Cells. PLoS ONE, 2013, 8, e80597.	1.1	125
2105	Prediction and Characterization of Small Non-Coding RNAs Related to Secondary Metabolites in <i>Saccharopolyspora erythraea</i> . PLoS ONE, 2013, 8, e80676.	1.1	5
2106	Transcriptome Sequencing Analysis Reveals the Regulation of the Hypopharyngeal Glands in the Honey Bee, <i>Apis mellifera carnica</i> Pollmann. PLoS ONE, 2013, 8, e81001.	1.1	24
2107	Transcriptional Reprogramming of Wheat and the Hemibiotrophic Pathogen <i>Septoria tritici</i> during Two Phases of the Compatible Interaction. PLoS ONE, 2013, 8, e81606.	1.1	102

#	ARTICLE	IF	CITATIONS
2108	Floral Transcriptome Sequencing for SSR Marker Development and Linkage Map Construction in the Tea Plant ( <i>Camellia sinensis</i> ). PLoS ONE, 2013, 8, e81611.	1.1	80
2109	Comparative Transcriptome Analysis of Two Rice Varieties in Response to Rice Stripe Virus and Small Brown Planthoppers during Early Interaction. PLoS ONE, 2013, 8, e82126.	1.1	94
2110	De novo Sequencing, Characterization, and Comparison of Inflorescence Transcriptomes of <i>Cornus canadensis</i> and <i>C. florida</i> (Cornaceae). PLoS ONE, 2013, 8, e82674.	1.1	12
2111	Ecological Adaption Analysis of the Cotton Aphid ( <i>Aphis gossypii</i> ) in Different Phenotypes by Transcriptome Comparison. PLoS ONE, 2013, 8, e83180.	1.1	30
2112	Small RNA Analysis in Sindbis Virus Infected Human HEK293 Cells. PLoS ONE, 2013, 8, e84070.	1.1	11
2113	Genome-Wide Analyses of Radioresistance-Associated miRNA Expression Profile in Nasopharyngeal Carcinoma Using Next Generation Deep Sequencing. PLoS ONE, 2013, 8, e84486.	1.1	60
2114	RNA-Seq Differentiates Tumour and Host mRNA Expression Changes Induced by Treatment of Human Tumour Xenografts with the VEGFR Tyrosine Kinase Inhibitor Cediranib. PLoS ONE, 2013, 8, e66003.	1.1	29
2115	RNA-Seq Analysis of <i>Mycobacterium avium</i> Non-Coding Transcriptome. PLoS ONE, 2013, 8, e74209.	1.1	23
2116	The Dynamics of Soybean Leaf and Shoot Apical Meristem Transcriptome Undergoing Floral Initiation Process. PLoS ONE, 2013, 8, e65319.	1.1	40
2117	Identification of Differentially Expressed Genes in Shoot Apex of Garlic ( <i>Allium sativum</i> L.) Using Illumina Sequencing. Journal of Plant Studies, 2013, 2, .	0.3	5
2118	Detection and Impact of Rare Regulatory Variants in Human Disease. Frontiers in Genetics, 2013, 4, 67.	1.1	18
2119	MicroRNA expression profiles in avian haemopoietic cells. Frontiers in Genetics, 2013, 4, 153.	1.1	14
2120	Global Molecular Analyses of Methane Metabolism in Methanotrophic Alphaproteobacterium, <i>Methylosinus trichosporium</i> OB3b. Part I: Transcriptomic Study. Frontiers in Microbiology, 2013, 4, 40.	1.5	73
2121	Bridging the gap between systems biology and synthetic biology. Frontiers in Microbiology, 2013, 4, 211.	1.5	19
2122	A Comparison of Methods for RNA-Seq Differential Expression Analysis and a New Empirical Bayes Approach. Biosensors, 2013, 3, 238-258.	2.3	22
2123	Biosynthesis of Polyunsaturated Fatty Acids in the Oleaginous Marine Diatom <i>Fistulifera</i> sp. Strain JPCC DA0580. Marine Drugs, 2013, 11, 5008-5023.	2.2	27
2124	Minor introns are embedded molecular switches regulated by highly unstable U6atac snRNA. ELife, 2013, 2, e00780.	2.8	91
2125	Multiple Suboptimal Solutions for Prediction Rules in Gene Expression Data. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-14.	0.7	1

#	ARTICLE	IF	CITATIONS
2126	An Overview of the Statistical Methods Used for Inferring Gene Regulatory Networks and Protein-Protein Interaction Networks. <i>Advances in Bioinformatics</i> , 2013, 2013, 1-12.	5.7	16
2127	Molecular Signatures of Recurrent Hepatocellular Carcinoma Secondary to Hepatitis C Virus following Liver Transplantation. <i>Journal of Transplantation</i> , 2013, 2013, 1-14.	0.3	9
2128	Statistical Analysis of Mapped Reads from mRNA-Seq Data. , 0, , 77-104.		0
2129	Model-Based Methods for Transcript Expression-Level Quantification in RNA-Seq. , 2013, , 105-125.		1
2130	RNA Sequencing. <i>Seibutsu Butsuri</i> , 2013, 53, 290-294.	0.0	0
2131	A Brief Overview of Multivariate Data Analysis in Biological Sciences. <i>Journal of Biology and Life Science</i> , 2013, 5, 72.	0.2	0
2132	High-throughput sequencing identification of genes involved with <i>Varroa destructor</i> resistance in the eastern honeybee, <i>Apis cerana</i> . <i>Genetics and Molecular Research</i> , 2014, 13, 9086-9096.	0.3	6
2133	Transcriptional responses in eastern honeybees ( <i>Apis cerana</i> ) infected with mites, <i>Varroa destructor</i> . <i>Genetics and Molecular Research</i> , 2014, 13, 8888-8900.	0.3	8
2134	Molecular Evolution of Glycoside Hydrolase Genes in the Western Corn Rootworm ( <i>Diabrotica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42.	1.1	57
2135	Comparison of RNA-Seq and Microarray in Transcriptome Profiling of Activated T Cells. <i>PLoS ONE</i> , 2014, 9, e78644.	1.1	770
2136	Multi-Tissue Omics Analyses Reveal Molecular Regulatory Networks for Puberty in Composite Beef Cattle. <i>PLoS ONE</i> , 2014, 9, e102551.	1.1	125
2137	Selection of Reference Genes for Quantitative Real-Time PCR Normalization in <i>Panax ginseng</i> at Different Stages of Growth and in Different Organs. <i>PLoS ONE</i> , 2014, 9, e112177.	1.1	49
2138	RNA-Seq Profiling of a Defective Seed Coat Mutation in <i>Glycine max</i> Reveals Differential Expression of Proline-Rich and Other Cell Wall Protein Transcripts. <i>PLoS ONE</i> , 2014, 9, e96342.	1.1	16
2139	Genome-Wide Transcriptome Analysis Reveals that Cadmium Stress Signaling Controls the Expression of Genes in Drought Stress Signal Pathways in Rice. <i>PLoS ONE</i> , 2014, 9, e96946.	1.1	102
2140	Infection of Apple by Apple Stem Grooving Virus Leads to Extensive Alterations in Gene Expression Patterns but No Disease Symptoms. <i>PLoS ONE</i> , 2014, 9, e95239.	1.1	22
2141	Comprehensive Analysis of Alternative Splicing in <i>Digitalis purpurea</i> by Strand-Specific RNA-Seq. <i>PLoS ONE</i> , 2014, 9, e106001.	1.1	12
2142	Comparative Transcriptomic Characterization of the Early Development in Pacific White Shrimp <i>Litopenaeus vannamei</i> . <i>PLoS ONE</i> , 2014, 9, e106201.	1.1	114
2143	De Novo Transcriptome Assembly from Fat Body and Flight Muscles Transcripts to Identify Morph-Specific Gene Expression Profiles in <i>Gryllus firmus</i> . <i>PLoS ONE</i> , 2014, 9, e82129.	1.1	37

#	ARTICLE	IF	CITATIONS
2144	Insights into Hepatopancreatic Functions for Nutrition Metabolism and Ovarian Development in the Crab <i>Portunus trituberculatus</i> : Gene Discovery in the Comparative Transcriptome of Different Hepatopancreas Stages. PLoS ONE, 2014, 9, e84921.	1.1	106
2145	Functional and Evolutionary Characterization of the CONSTANS Gene Family in Short-Day Photoperiodic Flowering in Soybean. PLoS ONE, 2014, 9, e85754.	1.1	84
2146	RNA-Seq Analysis Provides Insights for Understanding Photoautotrophic Polyhydroxyalkanoate Production in Recombinant <i>Synechocystis</i> Sp.. PLoS ONE, 2014, 9, e86368.	1.1	32
2147	Comprehensive Transcriptome Analysis of Developing Xylem Responding to Artificial Bending and Gravitational Stimuli in <i>Betula platyphylla</i> . PLoS ONE, 2014, 9, e87566.	1.1	20
2148	De Novo Assembly and Annotation of <i>Salvia splendens</i> Transcriptome Using the Illumina Platform. PLoS ONE, 2014, 9, e87693.	1.1	36
2149	Transcriptomics and Identification of the Chemoreceptor Superfamily of the Pupal Parasitoid of the Oriental Fruit Fly, <i>Spalangia endius</i> Walker (Hymenoptera: Pteromalidae). PLoS ONE, 2014, 9, e87800.	1.1	14
2150	Extensive Expression Differences along Porcine Small Intestine Evidenced by Transcriptome Sequencing. PLoS ONE, 2014, 9, e88515.	1.1	44
2151	RNA-Seq Analysis of Transcriptome and Glucosinolate Metabolism in Seeds and Sprouts of Broccoli ( <i>Brassica oleracea</i> var. <i>italica</i> ). PLoS ONE, 2014, 9, e88804.	1.1	63
2152	A Vanillin Derivative Causes Mitochondrial Dysfunction and Triggers Oxidative Stress in <i>Cryptococcus neoformans</i> . PLoS ONE, 2014, 9, e89122.	1.1	42
2153	Normalization of RNA-Sequencing Data from Samples with Varying mRNA Levels. PLoS ONE, 2014, 9, e89158.	1.1	44
2154	Meta-Analysis of Pathway Enrichment: Combining Independent and Dependent Omics Data Sets. PLoS ONE, 2014, 9, e89297.	1.1	44
2155	Transcriptome Analysis Reveals Common and Distinct Mechanisms for Sheepgrass ( <i>Leymus chinensis</i> ) Responses to Defoliation Compared to Mechanical Wounding. PLoS ONE, 2014, 9, e89495.	1.1	29
2156	Transcriptome Sequencing and De Novo Analysis of <i>Youngia japonica</i> Using the Illumina Platform. PLoS ONE, 2014, 9, e90636.	1.1	24
2157	Transcriptome Profiling of a Multiple Recurrent Muscle-Invasive Urothelial Carcinoma of the Bladder by Deep Sequencing. PLoS ONE, 2014, 9, e91466.	1.1	32
2158	Transcriptomic Analysis of the Rice White Tip Nematode, <i>Aphelenchoides besseyi</i> (Nematoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	1.1	33
2159	De Novo Assembly of <i>Auricularia polytricha</i> Transcriptome Using Illumina Sequencing for Gene Discovery and SSR Marker Identification. PLoS ONE, 2014, 9, e91740.	1.1	45
2160	Sequencing Degraded RNA Addressed by 3' Tag Counting. PLoS ONE, 2014, 9, e91851.	1.1	110
2161	RNA-Sequence Analysis of Primary Alveolar Macrophages after In Vitro Infection with Porcine Reproductive and Respiratory Syndrome Virus Strains of Differing Virulence. PLoS ONE, 2014, 9, e91918.	1.1	37

#	ARTICLE	IF	CITATIONS
2162	RNA-Seq Analysis Using De Novo Transcriptome Assembly as a Reference for the Salmon Louse <i>Caligus rogercresseyi</i> . PLoS ONE, 2014, 9, e92239.	1.1	67
2163	Temporal Profile of the Renal Transcriptome of HIV-1 Transgenic Mice during Disease Progression. PLoS ONE, 2014, 9, e93019.	1.1	10
2164	Transcriptome Analysis of Integument Differentially Expressed Genes in the Pigment Mutant (quail) during Molting of Silkworm, <i>Bombyx mori</i> . PLoS ONE, 2014, 9, e94185.	1.1	22
2165	FANSe2: A Robust and Cost-Efficient Alignment Tool for Quantitative Next-Generation Sequencing Applications. PLoS ONE, 2014, 9, e94250.	1.1	42
2166	De Novo Transcriptome and Small RNA Analyses of Two <i>Amorphophallus</i> Species. PLoS ONE, 2014, 9, e95428.	1.1	14
2167	Changes in the Organics Metabolism in the Hepatopancreas Induced by Eyestalk Ablation of the Chinese Mitten Crab <i>Eriocheir sinensis</i> Determined via Transcriptome and DGE Analysis. PLoS ONE, 2014, 9, e95827.	1.1	27
2168	The DNA Methylome and Transcriptome of Different Brain Regions in Schizophrenia and Bipolar Disorder. PLoS ONE, 2014, 9, e95875.	1.1	75
2169	Massively Parallel Sequencing of Human Urinary Exosome/Microvesicle RNA Reveals a Predominance of Non-Coding RNA. PLoS ONE, 2014, 9, e96094.	1.1	107
2170	Transcriptional Response of Virus-Infected Cassava and Identification of Putative Sources of Resistance for Cassava Brown Streak Disease. PLoS ONE, 2014, 9, e96642.	1.1	75
2171	Transcriptome Assembly and Analysis of Tibetan Hulless Barley ( <i>Hordeum vulgare</i> L. var. <i>nudum</i> ) Developing Grains, with Emphasis on Quality Properties. PLoS ONE, 2014, 9, e98144.	1.1	25
2172	Transcriptome Analysis of Shade-Induced Inhibition on Leaf Size in Relay Intercropped Soybean. PLoS ONE, 2014, 9, e98465.	1.1	44
2173	Impact of Hfq on the <i>Bacillus subtilis</i> Transcriptome. PLoS ONE, 2014, 9, e98661.	1.1	40
2174	Exploring the Polyadenylated RNA Virome of Sweet Potato through High-Throughput Sequencing. PLoS ONE, 2014, 9, e98884.	1.1	20
2175	Comparative Transcriptional Analysis of Asexual and Sexual Morphs Reveals Possible Mechanisms in Reproductive Polyphenism of the Cotton Aphid. PLoS ONE, 2014, 9, e99506.	1.1	19
2176	RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells. PLoS ONE, 2014, 9, e99625.	1.1	139
2177	Comparative Transcriptome Profiling of Two Tibetan Wild Barley Genotypes in Responses to Low Potassium. PLoS ONE, 2014, 9, e100567.	1.1	76
2178	Transcriptome Analysis of <i>Dastarcus helophoroides</i> (Coleoptera: Bothrideridae) Using Illumina HiSeq Sequencing. PLoS ONE, 2014, 9, e100673.	1.1	17
2179	Transcriptome Analysis by Illumina High-Throughput Paired-End Sequencing Reveals the Complexity of Differential Gene Expression during In Vitro Plantlet Growth and Flowering in <i>Amaranthus tricolor</i> L.. PLoS ONE, 2014, 9, e100919.	1.1	20



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2180	De Novo Sequencing-Based Transcriptome and Digital Gene Expression Analysis Reveals Insecticide Resistance-Relevant Genes in <i>Propylaea japonica</i> (Thunberg) (Coleoptea: Coccinellidae). PLoS ONE, 2014, 9, e100946.	1.1	27
2181	Transcriptome Analysis of a Petal Anthocyanin Polymorphism in the Arctic Mustard, <i>Parrya nudicaulis</i> . PLoS ONE, 2014, 9, e101338.	1.1	18
2182	Assessment of the Impact of Using a Reference Transcriptome in Mapping Short RNA-Seq Reads. PLoS ONE, 2014, 9, e101374.	1.1	21
2183	Four Methods of Preparing mRNA 5' End Libraries Using the Illumina Sequencing Platform. PLoS ONE, 2014, 9, e101812.	1.1	19
2184	De Novo Transcriptome Assembly from Inflorescence of <i>Orchis italica</i> : Analysis of Coding and Non-Coding Transcripts. PLoS ONE, 2014, 9, e102155.	1.1	30
2185	Discovery and Comparative Profiling of microRNAs in Representative Monopodial Bamboo ( <i>Phyllostachys edulis</i> ) and Sympodial Bamboo ( <i>Dendrocalamus latiflorus</i> ). PLoS ONE, 2014, 9, e102375.	1.1	11
2186	Transcriptome Wide Identification and Validation of Calcium Sensor Gene Family in the Developing Spikes of Finger Millet Genotypes for Elucidating Its Role in Grain Calcium Accumulation. PLoS ONE, 2014, 9, e103963.	1.1	55
2187	Extensive Transcription Analysis of the <i>Hyposoter didymator</i> Ichnovirus Genome in Permissive and Non-Permissive Lepidopteran Host Species. PLoS ONE, 2014, 9, e104072.	1.1	35
2188	SNP Identification by Transcriptome Sequencing and Candidate Gene-Based Association Analysis for Heat Tolerance in the Bay Scallop <i>Argopecten irradians</i> . PLoS ONE, 2014, 9, e104960.	1.1	20
2189	Transcriptome of American Oysters, <i>Crassostrea virginica</i> , in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. PLoS ONE, 2014, 9, e105097.	1.1	74
2190	RNA-Seq Gene Profiling - A Systematic Empirical Comparison. PLoS ONE, 2014, 9, e107026.	1.1	72
2191	Identification of Differentially Expressed Genes in Breast Muscle and Skin Fat of Postnatal Pekin Duck. PLoS ONE, 2014, 9, e107574.	1.1	21
2192	Plasmid-Encoded Tetracycline Efflux Pump Protein Alters Bacterial Stress Responses and Ecological Fitness of <i>Acinetobacter oleivorans</i> . PLoS ONE, 2014, 9, e107716.	1.1	22
2193	Specific Gene Expression Responses to Parasite Genotypes Reveal Redundancy of Innate Immunity in Vertebrates. PLoS ONE, 2014, 9, e108001.	1.1	23
2194	Transcriptional Responses of Olive Flounder ( <i>Paralichthys olivaceus</i> ) to Low Temperature. PLoS ONE, 2014, 9, e108582.	1.1	57
2195	Carrot yellow leaf virus Is Associated with Carrot Internal Necrosis. PLoS ONE, 2014, 9, e109125.	1.1	75
2196	De Novo Transcriptome Sequencing Analysis and Comparison of Differentially Expressed Genes (DEGs) in <i>Macrobrachium rosenbergii</i> in China. PLoS ONE, 2014, 9, e109656.	1.1	15
2197	A Snapshot of the Hepatic Transcriptome: Ad Libitum Alcohol Intake Suppresses Expression of Cholesterol Synthesis Genes in Alcohol-Preferring (P) Rats. PLoS ONE, 2014, 9, e110501.	1.1	10

#	ARTICLE	IF	CITATIONS
2198	Genome-Scale Transcriptome Analysis of the Alpine "Glasshouse" Plant <i>Rheum nobile</i> (Polygonaceae) with Special Translucent Bracts. PLoS ONE, 2014, 9, e110712.	1.1	8
2199	A Transcriptome Analysis Suggests Apoptosis-Related Signaling Pathways in Hemocytes of <i>Spodoptera litura</i> After Parasitization by <i>Microplitis bicoloratus</i> . PLoS ONE, 2014, 9, e110967.	1.1	23
2200	Comparative Analysis and Modeling of the Severity of Steatohepatitis in DDC-Treated Mouse Strains. PLoS ONE, 2014, 9, e111006.	1.1	11
2201	Distinct Strains of <i>Toxoplasma gondii</i> Feature Divergent Transcriptomes Regardless of Developmental Stage. PLoS ONE, 2014, 9, e111297.	1.1	37
2202	Genome-Wide Classification and Evolutionary and Expression Analyses of Citrus MYB Transcription Factor Families in Sweet Orange. PLoS ONE, 2014, 9, e112375.	1.1	50
2203	De novo Assembly of the Grass Carp <i>Ctenopharyngodon idella</i> Transcriptome to Identify miRNA Targets Associated with Motile Aeromonad Septicemia. PLoS ONE, 2014, 9, e112722.	1.1	24
2204	RNA-Seq Reveals Leaf Cuticular Wax-Related Genes in Welsh Onion. PLoS ONE, 2014, 9, e113290.	1.1	24
2205	Comparison of Whole Blood RNA Preservation Tubes and Novel Generation RNA Extraction Kits for Analysis of mRNA and miRNA Profiles. PLoS ONE, 2014, 9, e113298.	1.1	58
2206	Transcriptome-Wide Profiling and Expression Analysis of Diploid and Autotetraploid <i>Paulownia tomentosa</i> – <i>Paulownia fortunei</i> under Drought Stress. PLoS ONE, 2014, 9, e113313.	1.1	23
2207	Transcriptome Analysis on the Inflammatory Cell Infiltration of Nonalcoholic Steatohepatitis in Bama Minipigs Induced by a Long-Term High-Fat, High-Sucrose Diet. PLoS ONE, 2014, 9, e113724.	1.1	27
2208	Transcriptome Changes in <i>Eriocheir sinensis</i> Megalopae after Desalination Provide Insights into Osmoregulation and Stress Adaption in Larvae. PLoS ONE, 2014, 9, e114187.	1.1	51
2209	De novo Sequencing, Assembly and Characterization of Antennal Transcriptome of <i>Anomala corpulenta</i> Motschulsky (Coleoptera: Rutelidae). PLoS ONE, 2014, 9, e114238.	1.1	22
2210	Integrated Analysis of Whole Genome and Transcriptome Sequencing Reveals Diverse Transcriptomic Aberrations Driven by Somatic Genomic Changes in Liver Cancers. PLoS ONE, 2014, 9, e114263.	1.1	79
2211	RNA-Seq Analysis of Oil Palm under Cold Stress Reveals a Different C-Repeat Binding Factor (CBF) Mediated Gene Expression Pattern in <i>Elaeis guineensis</i> Compared to Other Species. PLoS ONE, 2014, 9, e114482.	1.1	31
2212	Drought Tolerance Conferred to Sugarcane by Association with <i>Gluconacetobacter diazotrophicus</i> : A Transcriptomic View of Hormone Pathways. PLoS ONE, 2014, 9, e114744.	1.1	187
2213	Developmental Programming of Long Non-Coding RNAs during Postnatal Liver Maturation in Mice. PLoS ONE, 2014, 9, e114917.	1.1	25
2214	Subgroup-Elimination Transcriptomics Identifies Signaling Proteins that Define Subclasses of TRPV1-Positive Neurons and a Novel Paracrine Circuit. PLoS ONE, 2014, 9, e115731.	1.1	37
2215	Genome-Scale Transcriptome Analysis in Response to Nitric Oxide in Birch Cells: Implications of the Triterpene Biosynthetic Pathway. PLoS ONE, 2014, 9, e116157.	1.1	19

#	ARTICLE	IF	CITATIONS
2216	De Novo Assembly and Characterization of <i>Sophora japonica</i> Transcriptome Using RNA-seq. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	15
2217	Melatonin Therapy Prevents Programmed Hypertension and Nitric Oxide Deficiency in Offspring Exposed to Maternal Caloric Restriction. <i>Oxidative Medicine and Cellular Longevity</i> , 2014, 2014, 1-21.	1.9	59
2218	Transcriptome Sequencing in a Tibetan Barley Landrace with High Resistance to Powdery Mildew. <i>Scientific World Journal, The</i> , 2014, 2014, 1-9.	0.8	28
2219	Utility of network integrity methods in therapeutic target identification. <i>Frontiers in Genetics</i> , 2014, 5, 12.	1.1	48
2220	Transcriptome analysis of <i>Listeria monocytogenes</i> exposed to biocide stress reveals a multi-system response involving cell wall synthesis, sugar uptake, and motility. <i>Frontiers in Microbiology</i> , 2014, 5, 68.	1.5	75
2221	Comparison of transcriptional profiles of <i>Clostridium thermocellum</i> grown on cellobiose and pretreated yellow poplar using RNA-Seq. <i>Frontiers in Microbiology</i> , 2014, 5, 142.	1.5	48
2222	Experimental heart failure causes depression-like behavior together with differential regulation of inflammatory and structural genes in the brain. <i>Frontiers in Behavioral Neuroscience</i> , 2014, 8, 376.	1.0	44
2223	Dissecting gene expression at the blood-brain barrier. <i>Frontiers in Neuroscience</i> , 2014, 8, 355.	1.4	30
2224	Functional genomic analysis and neuroanatomical localization of miR-2954, a song-responsive sex-linked microRNA in the zebra finch. <i>Frontiers in Neuroscience</i> , 2014, 8, 409.	1.4	14
2225	Dynamic Transcriptional Events in Distal Sural Nerve Revealed by Transcriptome Analysis. <i>Experimental Neurobiology</i> , 2014, 23, 169-172.	0.7	2
2226	Methylation Affects Transposition and Splicing of a Large CACTA Transposon from a MYB Transcription Factor Regulating Anthocyanin Synthase Genes in Soybean Seed Coats. <i>PLoS ONE</i> , 2014, 9, e111959.	1.1	48
2227	Transcriptome Sequencing and Analysis of Leaf Tissue of <i>Avicennia marina</i> Using the Illumina Platform. <i>PLoS ONE</i> , 2014, 9, e108785.	1.1	18
2228	Gene expression characteristics of growth-inhibited rice seedlings induced by low-energy N <sup>+</sup> -beam implantation. <i>Genetics and Molecular Research</i> , 2014, 13, 6259-6271.	0.3	7
2229	Histological and Biochemical Comparisons between Right Atrium and Left Atrium in Patients with Mitral Valvular Atrial Fibrillation. <i>Korean Circulation Journal</i> , 2014, 44, 233.	0.7	18
2230	Generation and Characterization of a Sugarbeet Transcriptome and Transcriptome-Based SSR Markers. <i>Plant Genome</i> , 2014, 7, plantgenome2013.11.0038.	1.6	24
2232	Notch signaling genes. <i>Epigenetics</i> , 2014, 9, 842-850.	1.3	49
2233	Defects in a New Class of Sulfate/Anion Transporter Link Sulfur Acclimation Responses to Intracellular Glutathione Levels and Cell Cycle Control. <i>Plant Physiology</i> , 2014, 166, 1852-1868.	2.3	9
2234	The Arabidopsis ZINC FINGER PROTEIN3 Interferes with Abscisic Acid and Light Signaling in Seed Germination and Plant Development. <i>Plant Physiology</i> , 2014, 165, 1203-1220.	2.3	89

#	ARTICLE	IF	CITATIONS
2235	Transcriptomics in Health and Disease. , 2014, , .		3
2236	Isoform Expression Analysis Based on RNA-seq Data. , 2014, , 247-259.		0
2237	Identification of Biomarkers and Expression Signatures. , 2014, , 69-78.		0
2238	Origin and Development of the Root Cap in Rice. <i>Plant Physiology</i> , 2014, 166, 603-613.	2.3	39
2239	<i>MIR125B1</i> represses the degradation of the PML-RARA oncoprotein by an autophagy-lysosomal pathway in acute promyelocytic leukemia. <i>Autophagy</i> , 2014, 10, 1726-1737.	4.3	44
2240	Exploring the Transcriptome of Mycorrhizal Interactions. <i>Advances in Botanical Research</i> , 2014, 70, 53-78.	0.5	8
2241	Isolation and expression profiles of gibberellin metabolism genes in developing male and female cones of <i>Pinus tabuliformis</i> . <i>Functional and Integrative Genomics</i> , 2014, 14, 697-705.	1.4	25
2242	Investigation of factors affecting RNA-seq gene expression calls. , 2014, 2014, 5232-5.		7
2243	Vascular endothelial growth factor coordinates islet innervation via vascular scaffolding. <i>Development (Cambridge)</i> , 2014, 141, 1480-1491.	1.2	77
2244	Deep sequencing analyses expands the <i>Pseudomonas aeruginosa</i> AmpR regulon to include small RNA-mediated regulation of iron acquisition, heat shock and oxidative stress response. <i>Nucleic Acids Research</i> , 2014, 42, 979-998.	6.5	62
2245	Translational pain research: Lessons from genetics and genomics. <i>Science Translational Medicine</i> , 2014, 6, 249sr4.	5.8	45
2246	Breed-specific transcriptome response of spleen from six to eight week old piglet after infection with <i>Streptococcus suis</i> type 2. <i>Molecular Biology Reports</i> , 2014, 41, 7865-7873.	1.0	13
2247	Transcriptional response of soybean to thiamethoxam seed treatment in the presence and absence of drought stress. <i>BMC Genomics</i> , 2014, 15, 1055.	1.2	20
2248	Comparative evaluation of gene set analysis approaches for RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 397.	1.2	25
2249	Comprehensive analysis of differentially expressed genes and transcriptional regulation induced by salt stress in two contrasting cotton genotypes. <i>BMC Genomics</i> , 2014, 15, 760.	1.2	166
2250	Deep sequencing-based comparative transcriptional profiles of <i>Cymbidium hybridum</i> roots in response to mycorrhizal and non-mycorrhizal beneficial fungi. <i>BMC Genomics</i> , 2014, 15, 747.	1.2	44
2251	New gene models and alternative splicing in the maize pathogen <i>Colletotrichum graminicola</i> revealed by RNA-Seq analysis. <i>BMC Genomics</i> , 2014, 15, 842.	1.2	59
2252	The diversity of small non-coding RNAs in the diatom <i>Phaeodactylum tricornutum</i> . <i>BMC Genomics</i> , 2014, 15, 698.	1.2	40

#	ARTICLE	IF	CITATIONS
2253	PD_NGSAtlas: a reference database combining next-generation sequencing epigenomic and transcriptomic data for psychiatric disorders. <i>BMC Medical Genomics</i> , 2014, 7, 71.	0.7	9
2254	Flavonoid supplementation affects the expression of genes involved in cell wall formation and lignification metabolism and increases sugar content and saccharification in the fast-growing eucalyptus hybrid <i>E. urophylla</i> x <i>E. grandis</i> . <i>BMC Plant Biology</i> , 2014, 14, 301.	1.6	8
2255	De novo assembly and characterization of the transcriptome of the toxic dinoflagellate <i>Karenia brevis</i> . <i>BMC Genomics</i> , 2014, 15, 888.	1.2	40
2256	Role of oxygen and the OxyR protein in the response to iron limitation in <i>Rhodobacter sphaeroides</i> . <i>BMC Genomics</i> , 2014, 15, 794.	1.2	40
2257	Allelic mapping bias in RNA-sequencing is not a major confounder in eQTL studies. <i>Genome Biology</i> , 2014, 15, 467.	3.8	67
2258	Dysregulation of genome-wide gene expression and DNA methylation in abnormal cloned piglets. <i>BMC Genomics</i> , 2014, 15, 811.	1.2	45
2259	Transcriptome analysis of epithelioma papulosum cyprini cells after SVCV infection. <i>BMC Genomics</i> , 2014, 15, 935.	1.2	49
2260	Global transcriptome analysis of hexavalent chromium stress responses in <i>Staphylococcus aureus</i> LZ-01. <i>Ecotoxicology</i> , 2014, 23, 1534-1545.	1.1	27
2261	Global transcriptome analysis of <i>Mesorhizobium alhagi</i> CCNWXJ12-2 under salt stress. <i>BMC Microbiology</i> , 2014, 14, 1.	1.3	25
2262	RNA-Seq reveals a xenobiotic stress response in the soybean aphid, <i>Aphis glycines</i> , when fed aphid-resistant soybean. <i>BMC Genomics</i> , 2014, 15, 972.	1.2	75
2263	Evolutionary history of Methyltransferase 1 genes in hexaploid wheat. <i>BMC Genomics</i> , 2014, 15, 922.	1.2	12
2264	Transcriptome profiling shows gene regulation patterns in a flavonoid pathway in response to exogenous phenylalanine in <i>Boesenbergia rotunda</i> cell culture. <i>BMC Genomics</i> , 2014, 15, 984.	1.2	21
2265	Kinetic transcriptome analysis reveals an essentially intact induction system in a cellulase hyper-producer <i>Trichoderma reesei</i> strain. <i>Biotechnology for Biofuels</i> , 2014, 7, 173.	6.2	7
2266	Small RNAs as important regulators for the hybrid vigour of super-hybrid rice. <i>Journal of Experimental Botany</i> , 2014, 65, 5989-6002.	2.4	30
2267	ExpressionData - A public resource of high quality curated datasets representing gene expression across anatomy, development and experimental conditions. <i>BioData Mining</i> , 2014, 7, 18.	2.2	22
2268	A transcriptomic analysis of <i>Chrysanthemum nankingense</i> provides insights into the basis of low temperature tolerance. <i>BMC Genomics</i> , 2014, 15, 844.	1.2	79
2269	Contrasting nitrogen fertilization treatments impact xylem gene expression and secondary cell wall lignification in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2014, 14, 256.	1.6	41
2270	Exploring features and function of <i>Ss-riok-3</i> , an enigmatic kinase gene from <i>Strongyloides stercoralis</i> . <i>Parasites and Vectors</i> , 2014, 7, 561.	1.0	6

#	ARTICLE	IF	CITATIONS
2271	Identification and molecular characterization of tissue-preferred rice genes and their upstream regularly sequences on a genome-wide level. <i>BMC Plant Biology</i> , 2014, 14, 331.	1.6	4
2272	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. <i>Genome Biology</i> , 2014, 15, 523.	3.8	147
2273	Profiling and comparison of color body wall transcriptome of normal juvenile sea cucumber ( <i>Apostichopus japonicus</i> ) and those produced by crossing albino. <i>Journal of Ocean University of China</i> , 2014, 13, 1033-1042.	0.6	8
2274	The importance of study design for detecting differentially abundant features in high-throughput experiments. <i>Genome Biology</i> , 2014, 15, 527.	3.8	13
2275	De novo characterization of the <i>Rehmannia glutinosa</i> leaf transcriptome and analysis of gene expression associated with replanting disease. <i>Molecular Breeding</i> , 2014, 34, 905-915.	1.0	21
2276	<i>Cryptococcus inositol</i> utilization modulates the host protective immune response during brain infection. <i>Cell Communication and Signaling</i> , 2014, 12, 51.	2.7	23
2277	BADGE: A novel Bayesian model for accurate abundance quantification and differential analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, S6.	1.2	11
2278	Expression profile of <i>Caenorhabditis elegans</i> mutant for the Werner syndrome gene ortholog reveals the impact of vitamin C on development to increase life span. <i>BMC Genomics</i> , 2014, 15, 940.	1.2	15
2279	DNA copy number evolution in <i>Drosophila</i> cell lines. <i>Genome Biology</i> , 2014, 15, R70.	3.8	96
2280	Transcriptomic analysis of developmental features of <i>Bombyx mori</i> wing disc during metamorphosis. <i>BMC Genomics</i> , 2014, 15, 820.	1.2	69
2281	Transcriptomic complexity in young maize primary roots in response to low water potentials. <i>BMC Genomics</i> , 2014, 15, 741.	1.2	69
2282	Comparative transcriptome sequencing of tolerant rice introgression line and its parents in response to drought stress. <i>BMC Genomics</i> , 2014, 15, 1026.	1.2	115
2284	Genomic Organization, Transcriptomic Analysis, and Functional Characterization of Avian $\beta$ - and $\beta$ 2-Keratins in Diverse Feather Forms. <i>Genome Biology and Evolution</i> , 2014, 6, 2258-2273.	1.1	67
2285	FineSplice, enhanced splice junction detection and quantification: a novel pipeline based on the assessment of diverse RNA-Seq alignment solutions. <i>Nucleic Acids Research</i> , 2014, 42, e71-e71.	6.5	30
2286	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	3.3	635
2287	Using normalization to resolve RNA-Seq biases caused by amplification from minimal input. <i>Physiological Genomics</i> , 2014, 46, 808-820.	1.0	13
2288	Overexpression of Molecular Chaperone Genes in Nucleomorph Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1437-1443.	3.5	12
2289	Transcriptome profiling of human hippocampus dentate gyrus granule cells in mental illness. <i>Translational Psychiatry</i> , 2014, 4, e366-e366.	2.4	64

#	ARTICLE	IF	CITATIONS
2290	ADAR1 deaminase contributes to scheduled skeletal myogenesis progression via stage-specific functions. <i>Cell Death and Differentiation</i> , 2014, 21, 707-719.	5.0	28
2291	Haploinsufficiency of <i>Sf3b1</i> leads to compromised stem cell function but not to myelodysplasia. <i>Leukemia</i> , 2014, 28, 1844-1850.	3.3	42
2292	Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle. <i>Nature Genetics</i> , 2014, 46, 253-260.	9.4	685
2293	Methods to Study Splicing from High-Throughput RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2014, 1126, 357-397.	0.4	68
2294	Nitric oxide production and scavenging in waterlogged roots of rape seedlings. <i>Genes and Genomics</i> , 2014, 36, 691-699.	0.5	11
2295	Genome-wide comparative analysis of flowering genes between <i>Arabidopsis</i> and mungbean. <i>Genes and Genomics</i> , 2014, 36, 799-808.	0.5	14
2296	Functions of noncoding sequences in mammalian genomes. <i>Biochemistry (Moscow)</i> , 2014, 79, 1442-1469.	0.7	63
2297	An Avian Retrovirus Uses Canonical Expression and Processing Mechanisms To Generate Viral MicroRNA. <i>Journal of Virology</i> , 2014, 88, 2-9.	1.5	40
2298	Methodologies in the Era of Cardiovascular Omics, 2014, , 15-55.		0
2299	Defining a personal, allele-specific, and single-molecule long-read transcriptome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9869-9874.	3.3	259
2301	Transcriptome analysis of the salivary glands of <i>Nephotettix cincticeps</i> (Uhler). <i>Journal of Insect Physiology</i> , 2014, 71, 170-176.	0.9	44
2302	Overexpression of the maize <i>GRF10</i> , an endogenous truncated growth-regulating factor protein, leads to reduction in leaf size and plant height. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 1053-1063.	4.1	80
2303	Genome-wide profiling of Hfq-binding RNAs uncovers extensive post-transcriptional rewiring of major stress response and symbiotic regulons in <i>Sinorhizobium meliloti</i> . <i>RNA Biology</i> , 2014, 11, 563-579.	1.5	65
2304	Transcriptome Expression Profiling in Response to Drought Stress in <i>Paulownia australis</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 4583-4607.	1.8	21
2305	Odorant and Gustatory Receptors in the Tsetse Fly <i>Glossina morsitans morsitans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2663.	1.3	51
2306	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. <i>PLoS Computational Biology</i> , 2014, 10, e1003531.	1.5	2,343
2307	The Coding and Noncoding Architecture of the <i>Caulobacter crescentus</i> Genome. <i>PLoS Genetics</i> , 2014, 10, e1004463.	1.5	136
2308	The Olfactory Transcriptomes of Mice. <i>PLoS Genetics</i> , 2014, 10, e1004593.	1.5	134

#	ARTICLE	IF	CITATIONS
2309	A Systems Genetics Approach Identifies CXCL14, ITGAX, and LPCAT2 as Novel Aggressive Prostate Cancer Susceptibility Genes. <i>PLoS Genetics</i> , 2014, 10, e1004809.	1.5	68
2310	Specific gene-regulation networks during the pre-implantation development of the pig embryo as revealed by deep sequencing. <i>BMC Genomics</i> , 2014, 15, 4.	1.2	130
2311	cGMP and NHR Signaling Co-regulate Expression of Insulin-Like Peptides and Developmental Activation of Infective Larvae in <i>Strongyloides stercoralis</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004235.	2.1	41
2312	Perturbations in small molecule synthesis uncovers an iron-responsive secondary metabolite network in <i>Aspergillus fumigatus</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 530.	1.5	59
2313	A Cohesin-Independent Role for NIPBL at Promoters Provides Insights in CdLS. <i>PLoS Genetics</i> , 2014, 10, e1004153.	1.5	123
2314	Transcriptional and Proteomic Responses to Carbon Starvation in <i>Paracoccidioides</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2855.	1.3	65
2315	Quality control on the frontier. <i>Frontiers in Genetics</i> , 2014, 5, 157.	1.1	21
2316	Non-coding RNAs in pluripotency and neural differentiation of human pluripotent stem cells. <i>Frontiers in Genetics</i> , 2014, 5, 132.	1.1	22
2317	Genome-wide profiling of DNA methylation and gene expression in <i>Crassostrea gigas</i> male gametes. <i>Frontiers in Physiology</i> , 2014, 5, 224.	1.3	92
2318	Global transcriptome analysis of developing chickpea ( <i>Cicer arietinum</i> L.) seeds. <i>Frontiers in Plant Science</i> , 2014, 5, 698.	1.7	50
2319	Next-generation sequencing and bioinformatic approaches to detect and analyze influenza virus in ferrets. <i>Journal of Infection in Developing Countries</i> , 2014, 8, 498-509.	0.5	19
2320	Discovery of a "White-Gray-Opaque" Tristable Phenotypic Switching System in <i>Candida albicans</i> : Roles of Non-genetic Diversity in Host Adaptation. <i>PLoS Biology</i> , 2014, 12, e1001830.	2.6	122
2321	Juvenile Hormone-Receptor Complex Acts on Mcm4 and Mcm7 to Promote Polyploidy and Vitellogenesis in the Migratory Locust. <i>PLoS Genetics</i> , 2014, 10, e1004702.	1.5	83
2322	Toward Understanding the Functional Role of Ss-riok-1, a RIO Protein Kinase-Encoding Gene of <i>Strongyloides stercoralis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3062.	1.3	13
2323	RNA-Seq Reveals Infection-Induced Gene Expression Changes in the Snail Intermediate Host of the Carcinogenic Liver Fluke, <i>Opisthorchis viverrini</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2765.	1.3	14
2324	Metabolic Reprogramming during Purine Stress in the Protozoan Pathogen <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003938.	2.1	74
2325	The Homeodomain Protein Ladybird Late Regulates Synthesis of Milk Proteins during Pregnancy in the Tsetse Fly ( <i>Glossina morsitans</i> ). <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2645.	1.3	27
2326	Effects of specific organs on seed oil accumulation in <i>Brassica napus</i> L. <i>Plant Science</i> , 2014, 227, 60-68.	1.7	20



#	ARTICLE	IF	CITATIONS
2327	Emerging RNA-Seq Applications in Food Science. <i>Comprehensive Analytical Chemistry</i> , 2014, , 107-128.	0.7	2
2328	RNA-Seq Analysis of Enteroendocrine Cells Reveals a Role for FABP5 in the Control of GIP Secretion. <i>Molecular Endocrinology</i> , 2014, 28, 1855-1865.	3.7	21
2329	Analysis of Deep Sequencing Data. <i>Comprehensive Analytical Chemistry</i> , 2014, , 325-354.	0.7	0
2330	MultiRankSeq: Multiperspective Approach for RNAseq Differential Expression Analysis and Quality Control. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	50
2331	Renal Gene Expression Database (RGED): a relational database of gene expression profiles in kidney disease. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau092-bau092.	1.4	21
2332	Transcript profiles of maize embryo sacs and preliminary identification of genes involved in the embryo sac-pollen tube interaction. <i>Frontiers in Plant Science</i> , 2014, 5, 702.	1.7	20
2333	Transcriptome Profiles of the Protoscolecetes of <i>Echinococcus granulosus</i> Reveal that Excretory-Secretory Products Are Essential to Metabolic Adaptation. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3392.	1.3	28
2334	Sire evaluation and selection of Indian dromedary females for milk production: issues and strategies. <i>Journal of Camel Practice and Research</i> , 2014, 21, 93.	0.0	2
2335	Genome-Wide Analysis of the RNA Helicase Gene Family in <i>Gossypium raimondii</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 4635-4656.	1.8	24
2336	Expression Analysis of Immune Related Genes Identified from the Coelomocytes of Sea Cucumber ( <i>Apostichopus japonicus</i> ) in Response to LPS Challenge. <i>International Journal of Molecular Sciences</i> , 2014, 15, 19472-19486.	1.8	25
2337	Insights into the Trypanosome-Host Interactions Revealed through Transcriptomic Analysis of Parasitized Tsetse Fly Salivary Glands. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2649.	1.3	67
2338	Methods to Determine the Transcriptomes of Trypanosomes in Mixtures with Mammalian Cells: The Effects of Parasite Purification and Selective cDNA Amplification. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2806.	1.3	10
2339	The Case for Junk DNA. <i>PLoS Genetics</i> , 2014, 10, e1004351.	1.5	202
2340	Three Groups of Transposable Elements with Contrasting Copy Number Dynamics and Host Responses in the Maize ( <i>Zea mays ssp. mays</i> ) Genome. <i>PLoS Genetics</i> , 2014, 10, e1004298.	1.5	52
2341	Wolbachia is not all about sex: male-feminizing Wolbachia alters the leafhopper <i>Zyginidia pullula</i> transcriptome in a mainly sex-independent manner. <i>Frontiers in Microbiology</i> , 2014, 5, 430.	1.5	15
2342	Transcriptional and biochemical responses of monoacylglycerol acyltransferase-mediated oil synthesis and associated senescence-like responses in <i>Nicotiana benthamiana</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 204.	1.7	7
2343	Predicting the Function of 4-Coumarate:CoA Ligase (LJ4CL1) in <i>Lonicera japonica</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 2386-2399.	1.8	10
2344	Triterpenoid Saponin Biosynthetic Pathway Profiling and Candidate Gene Mining of the <i>Ilex asprella</i> Root Using RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2014, 15, 5970-5987.	1.8	41

#	ARTICLE	IF	CITATIONS
2345	Plant-Pathogen Interaction, Circadian Rhythm, and Hormone-Related Gene Expression Provide Indicators of Phytoplasma Infection in <i>Paulownia fortunei</i> . <i>International Journal of Molecular Sciences</i> , 2014, 15, 23141-23162.	1.8	41
2346	A Novel Highly Divergent Protein Family Identified from a Viviparous Insect by RNA-seq Analysis: A Potential Target for Tsetse Fly-Specific Abortifacients. <i>PLoS Genetics</i> , 2014, 10, e1003874.	1.5	46
2347	Non-coding roX RNAs Prevent the Binding of the MSL-complex to Heterochromatic Regions. <i>PLoS Genetics</i> , 2014, 10, e1004865.	1.5	27
2348	LANA Binds to Multiple Active Viral and Cellular Promoters and Associates with the H3K4Methyltransferase hSET1 Complex. <i>PLoS Pathogens</i> , 2014, 10, e1004240.	2.1	68
2349	Proteomic Approaches and Identification of Novel Therapeutic Targets for Alcoholism. <i>Neuropsychopharmacology</i> , 2014, 39, 104-130.	2.8	40
2350	Evolutionary Interrogation of Human Biology in Well-Annotated Genomic Framework of Rhesus Macaque. <i>Molecular Biology and Evolution</i> , 2014, 31, 1309-1324.	3.5	35
2351	Next Generation Sequencing. , 2014, , 4131-4139.		2
2352	The <i>Opisthorchis viverrini</i> genome provides insights into life in the bile duct. <i>Nature Communications</i> , 2014, 5, 4378.	5.8	144
2353	Efficient RNA isoform identification and quantification from RNA-Seq data with network flows. <i>Bioinformatics</i> , 2014, 30, 2447-2455.	1.8	65
2354	De Novo Transcriptome Sequence Assembly and Identification of AP2/ERF Transcription Factor Related to Abiotic Stress in Parsley ( <i>Petroselinum crispum</i> ). <i>PLoS ONE</i> , 2014, 9, e108977.	1.1	21
2355	Gonadal Transcriptome Analysis of Male and Female Olive Flounder ( <i>Paralichthys olivaceus</i> ). <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	68
2356	The meiotic transcriptome architecture of plants. <i>Frontiers in Plant Science</i> , 2014, 5, 220.	1.7	27
2357	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140021.	2.4	30
2358	RNA Sequencing Reveals Upregulation of RUNX1-RUNX1T1 Gene Signatures in Clear Cell Renal Cell Carcinoma. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	15
2359	SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. <i>Nucleic Acids Research</i> , 2014, 42, e113-e113.	6.5	17
2360	SEEDSTICK is a Master Regulator of Development and Metabolism in the Arabidopsis Seed Coat. <i>PLoS Genetics</i> , 2014, 10, e1004856.	1.5	86
2361	Recent advances in the involvement of long non-coding RNAs in neural stem cell biology and brain pathophysiology. <i>Frontiers in Physiology</i> , 2014, 5, 155.	1.3	27
2362	Widespread Genome Reorganization of an Obligate Virus Mutualist. <i>PLoS Genetics</i> , 2014, 10, e1004660.	1.5	83

#	ARTICLE	IF	CITATIONS
2363	Signature Gene Expression Reveals Novel Clues to the Molecular Mechanisms of Dimorphic Transition in <i>Penicillium marneffe</i> . <i>PLoS Genetics</i> , 2014, 10, e1004662.	1.5	38
2364	Reduction in Fecundity and Shifts in Cellular Processes by a Native Virus on an Invasive Insect. <i>Genome Biology and Evolution</i> , 2014, 6, 873-885.	1.1	20
2365	Analysis options for high-throughput sequencing in miRNA expression profiling. <i>BMC Research Notes</i> , 2014, 7, 144.	0.6	75
2366	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	1.2	82
2367	Genome-wide identification and functional analysis of Apobec-1-mediated C-to-U RNA editing in mouse small intestine and liver. <i>Genome Biology</i> , 2014, 15, R79.	13.9	87
2368	CAMDA 2014: Making sense of RNA-Seq data: From low-level processing to functional analysis. <i>Systems Biomedicine (Austin, Tex)</i> , 2014, 2, 31-40.	0.7	6
2369	Transcriptome analysis of blood orange ( <i>Citrus sinensis</i> ) following fruit bagging treatment by digital gene expression profiling. <i>Journal of Horticultural Science and Biotechnology</i> , 2014, 89, 397-407.	0.9	8
2370	Tissue- and Stage-Dependent Dosage Compensation on the Neo-X Chromosome in <i>Drosophila pseudoobscura</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 614-624.	3.5	36
2371	Improved variational Bayes inference for transcript expression estimation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 203-16.	0.2	10
2372	Transcriptomic analysis of a psammophyte food crop, sand rice ( <i>Agriophyllum squarrosum</i> ) and identification of candidate genes essential for sand dune adaptation. <i>BMC Genomics</i> , 2014, 15, 872.	1.2	27
2373	Transcriptome dynamics-based operon prediction in prokaryotes. <i>BMC Bioinformatics</i> , 2014, 15, 145.	1.2	24
2374	Genome-wide analysis of regulation of gene expression and H3K9me2 distribution by JIL-1 kinase mediated histone H3S10 phosphorylation in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2014, 42, 5456-5467.	6.5	21
2375	Strand-specific RNA-Seq reveals widespread and developmentally regulated transcription of natural antisense transcripts in <i>Plasmodium falciparum</i> . <i>BMC Genomics</i> , 2014, 15, 150.	1.2	93
2376	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. <i>Physiological Genomics</i> , 2014, 46, 195-206.	1.0	56
2377	<i>Drosophila</i> Syncip modulates the expression of mRNAs encoding key synaptic proteins required for morphology at the neuromuscular junction. <i>Rna</i> , 2014, 20, 1593-1606.	1.6	46
2378	Dynamic shifts in occupancy by TAL1 are guided by GATA factors and drive large-scale reprogramming of gene expression during hematopoiesis. <i>Genome Research</i> , 2014, 24, 1945-1962.	2.4	71
2379	Population and single-cell genomics reveal the <i>Aire</i> dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. <i>Genome Research</i> , 2014, 24, 1918-1931.	2.4	308
2380	Relaxed Selection Drives a Noisy Noncoding Transcriptome in Members of the Mycobacterium tuberculosis Complex. <i>MBio</i> , 2014, 5, e01169-14.	1.8	20

#	ARTICLE	IF	CITATIONS
2381	High-Resolution Transcriptomic Analysis of the Adaptive Response of <i>Staphylococcus aureus</i> during Acute and Chronic Phases of Osteomyelitis. <i>MBio</i> , 2014, 5, .	1.8	65
2382	ORMAN: Optimal resolution of ambiguous RNA-Seq multimappings in the presence of novel isoforms. <i>Bioinformatics</i> , 2014, 30, 644-651.	1.8	17
2383	Small RNA profiling of <i>Xenopus</i> embryos reveals novel miRNAs and a new class of small RNAs derived from intronic transposable elements. <i>Genome Research</i> , 2014, 24, 96-106.	2.4	18
2384	PseudoLasso. , 2014, , .		0
2385	Transdifferentiation of Differentiated Ovary into Functional Testis by Long-Term Treatment of Aromatase Inhibitor in Nile Tilapia. <i>Endocrinology</i> , 2014, 155, 1476-1488.	1.4	106
2386	Identification and characterization of genes involved in the jasmonate biosynthetic and signaling pathways in mulberry ( <i>Morus notabilis</i> ). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 663-672.	4.1	6
2387	Transcriptome responses to phosphate deficiency in <i>Poncirus trifoliata</i> (L.) Raf. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 3207-3215.	1.0	7
2388	Differential Expression Analysis on RNA-Seq Count Data Based on Penalized Matrix Decomposition. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 12-18.	2.2	12
2389	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014, 15, 519.	3.8	129
2390	Transcriptome sequencing and metabolite analysis reveals the role of delphinidin metabolism in flower colour in grape hyacinth. <i>Journal of Experimental Botany</i> , 2014, 65, 3157-3164.	2.4	185
2391	De novo assembly and analysis of <i>Cassia obtusifolia</i> seed transcriptome to identify genes involved in the biosynthesis of active metabolites. <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 791-799.	0.6	14
2392	Cell motility and biofilm formation in <i>Bacillus subtilis</i> are affected by the ribosomal proteins, S11 and S21. <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 898-907.	0.6	22
2393	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. <i>Genome Research</i> , 2014, 24, 1169-1179.	2.4	64
2394	Transcription factors and glyoxylate cycle genes prominent in the transition of soybean cotyledons to the first functional leaves of the seedling. <i>Functional and Integrative Genomics</i> , 2014, 14, 683-696.	1.4	9
2395	Context-Selective Death of Acute Myeloid Leukemia Cells Triggered by the Novel Hybrid Retinoid-HDAC Inhibitor MC2392. <i>Cancer Research</i> , 2014, 74, 2328-2339.	0.4	33
2396	A recent L1 insertion within <i>SPEF2</i> gene is associated with changes in <i>PRLR</i> expression in sow reproductive organs. <i>Animal Genetics</i> , 2014, 45, 500-507.	0.6	4
2397	Long noncoding RNA's responsive to <i>Fusarium oxysporum</i> infection in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2014, 201, 574-584.	3.5	188
2398	Global Dissection of Alternative Splicing in Paleopolyploid Soybean. <i>Plant Cell</i> , 2014, 26, 996-1008.	3.1	273

#	ARTICLE	IF	CITATIONS
2399	Transcriptome analyses suggest a disturbance of iron homeostasis in soybean leaves during white mould disease establishment. <i>Molecular Plant Pathology</i> , 2014, 15, 576-588.	2.0	11
2400	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. <i>Cell Metabolism</i> , 2014, 20, 1076-1087.	7.2	143
2401	mRNA and Small RNA Transcriptomes Reveal Insights into Dynamic Homoeolog Regulation of Allopolyploid Heterosis in Nascent Hexaploid Wheat. <i>Plant Cell</i> , 2014, 26, 1878-1900.	3.1	308
2402	Molecular Signatures of Mouse TRPV1-Lineage Neurons Revealed by RNA-Seq Transcriptome Analysis. <i>Journal of Pain</i> , 2014, 15, 1338-1359.	0.7	104
2403	Transcriptomic response to estrogen exposure in the male Zhikong scallop, <i>Chlamys farreri</i> . <i>Marine Pollution Bulletin</i> , 2014, 89, 59-66.	2.3	7
2404	Methods for integration of transcriptomic data in genome-scale metabolic models. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 59-65.	1.9	75
2405	Retinoic acid signalling regulates the development of tonotopically patterned hair cells in the chicken cochlea. <i>Nature Communications</i> , 2014, 5, 3840.	5.8	43
2406	Genome-wide identification and expression analyses of cytochrome <i>P450</i> genes in mulberry ( <i>Morus notabilis</i> ). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 887-901.	4.1	53
2407	Ammonium induces differential expression of methane and nitrogen metabolism-related genes in <i>Methylocystis</i> sp. strain SC2. <i>Environmental Microbiology</i> , 2014, 16, 3115-3127.	1.8	40
2408	The Heat Shock Factor A4A Confers Salt Tolerance and Is Regulated by Oxidative Stress and the Mitogen-Activated Protein Kinases MPK3 and MPK6. <i>Plant Physiology</i> , 2014, 165, 319-334.	2.3	186
2409	An RNA-seq transcriptome analysis of floral buds of an interspecific Brassica hybrid between <i>B. carinata</i> and <i>B. napus</i> . <i>Plant Reproduction</i> , 2014, 27, 225-237.	1.3	8
2410	The <i>Streptococcus suis</i> transcriptional landscape reveals adaptation mechanisms in pig blood and cerebrospinal fluid. <i>Rna</i> , 2014, 20, 882-898.	1.6	59
2411	Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. <i>Nature Communications</i> , 2014, 5, 5519.	5.8	205
2412	The RNA-seq approach to discriminate gene expression profiles in response to melatonin on cucumber lateral root formation. <i>Journal of Pineal Research</i> , 2014, 56, 39-50.	3.4	263
2413	Transcriptional control of floral anthocyanin pigmentation in monkeyflowers ( <i>Mimulus</i> ). <i>New Phytologist</i> , 2014, 204, 1013-1027.	3.5	112
2414	Evidence of nickel (Ni) efflux in Ni-tolerant ectomycorrhizal <i>Pisolithus isolithus albus</i> isolated from ultramafic soil. <i>Environmental Microbiology Reports</i> , 2014, 6, 510-518.	1.0	22
2415	Should pharmacologists care about alternative splicing? IUPHAR Review 4. <i>British Journal of Pharmacology</i> , 2014, 171, 1231-1240.	2.7	7
2416	Transcriptional activity of transposable elements in coelacanth. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2014, 322, 379-389.	0.6	11

#	ARTICLE	IF	CITATIONS
2417	Genome-guided transcript assembly by integrative analysis of RNA sequence data. <i>Nature Biotechnology</i> , 2014, 32, 341-346.	9.4	51
2418	Comparative transcriptome analysis of RNA-seq data for cold-tolerant and cold-sensitive rice genotypes under cold stress. <i>Journal of Plant Biology</i> , 2014, 57, 337-348.	0.9	74
2419	Melatonin prevents maternal fructose intake-induced programmed hypertension in the offspring: roles of nitric oxide and arachidonic acid metabolites. <i>Journal of Pineal Research</i> , 2014, 57, 80-89.	3.4	80
2420	HBx induces hypomethylation of distal intragenic CpG islands required for active expression of developmental regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9555-9560.	3.3	55
2421	Introduction to RNA-Seq and its Applications to Drug Discovery and Development. <i>Drug Development Research</i> , 2014, 75, 324-330.	1.4	42
2422	Reduction in maternal Polycomb levels contributes to transgenerational inheritance of a response to toxic stress in flies. <i>Journal of Physiology</i> , 2014, 592, 2343-2355.	1.3	19
2423	Advancing next-generation sequencing data analytics with scalable distributed infrastructure. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 894-906.	1.4	4
2424	A piggyBac-based reporter system for scalable in vitro and in vivo analysis of 3' untranslated region-mediated gene regulation. <i>Nucleic Acids Research</i> , 2014, 42, e86-e86.	6.5	11
2425	COV2HTML: A Visualization and Analysis Tool of Bacterial Next Generation Sequencing (NGS) Data for Postgenomics Life Scientists. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 184-195.	1.0	35
2426	Downregulation of the acetyl-CoA metabolic network in adipose tissue of obese diabetic individuals and recovery after weight loss. <i>Diabetologia</i> , 2014, 57, 2384-2392.	2.9	38
2427	In vitro Transcriptome Analysis of Two Chinese Isolates of <i>Streptococcus suis</i> Serotype 2. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 266-275.	3.0	4
2428	DNA methylome in spleen of avian pathogenic <i>Escherichia coli</i> -challenged broilers and integration with mRNA expression. <i>Scientific Reports</i> , 2014, 4, 4299.	1.6	39
2429	A dynamic alternative splicing program regulates gene expression during terminal erythropoiesis. <i>Nucleic Acids Research</i> , 2014, 42, 4031-4042.	6.5	76
2430	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. <i>Bioinformatics</i> , 2014, 30, 2598-2602.	1.8	315
2431	RNA-seq transcriptome profiling reveals that <i>Medicago truncatula</i> nodules acclimate N <sub>2</sub> fixation before emerging P deficiency reaches the nodules. <i>Journal of Experimental Botany</i> , 2014, 65, 6035-6048.	2.4	76
2432	Identification of Immunity-Related Genes in <i>Ostrinia furnacalis</i> against Entomopathogenic Fungi by RNA-Seq Analysis. <i>PLoS ONE</i> , 2014, 9, e86436.	1.1	58
2433	A Comprehensive Transcriptomic Analysis of Infant and Adult Mouse Ovary. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 239-248.	3.0	20
2434	RNA sequencing: current and prospective uses in metabolic research. <i>Journal of Molecular Endocrinology</i> , 2014, 53, R93-R101.	1.1	17

#	ARTICLE	IF	CITATIONS
2435	The de novo Transcriptome and Its Analysis in the Worldwide Vegetable Pest, <i>Delia antiqua</i> (Diptera: Tj ETQq0 0 0 0 rBT /Overlock 10 Tf	0.8	16
2436	Evaluation of TRAP-sequencing technology with a versatile conditional mouse model. <i>Nucleic Acids Research</i> , 2014, 42, e14-e14.	6.5	40
2437	Transcriptional landscape and essential genes of <i>Neisseria gonorrhoeae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10579-10595.	6.5	74
2438	Quantitative Characterization of Defective Virus Emergence by Deep Sequencing. <i>Journal of Virology</i> , 2014, 88, 2623-2632.	1.5	29
2439	Impact of next-generation sequencing error on analysis of barcoded plasmid libraries of known complexity and sequence. <i>Nucleic Acids Research</i> , 2014, 42, e129-e129.	6.5	31
2440	Identification of the mulberry genes involved in ethylene biosynthesis and signaling pathways and the expression of MaERF-B2-1 and MaERF-B2-2 in the response to flooding stress. <i>Functional and Integrative Genomics</i> , 2014, 14, 767-777.	1.4	8
2441	Transcriptome de novo assembly and differentially expressed genes related to cytoplasmic male sterility in kenaf ( <i>Hibiscus cannabinus</i> L.). <i>Molecular Breeding</i> , 2014, 34, 1879-1891.	1.0	33
2442	Statistical calibration of qRT-PCR, microarray and RNA-Seq gene expression data with measurement error models. <i>Annals of Applied Statistics</i> , 2014, 8, .	0.5	4
2443	PLEK: a tool for predicting long non-coding RNAs and messenger RNAs based on an improved k-mer scheme. <i>BMC Bioinformatics</i> , 2014, 15, 311.	1.2	574
2444	trieFinder: an efficient program for annotating Digital Gene Expression (DGE) tags. <i>BMC Bioinformatics</i> , 2014, 15, 329.	1.2	2
2445	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. <i>BMC Genomics</i> , 2014, 15, 1008.	1.2	52
2446	Transcriptome structure variability in <i>Saccharomyces cerevisiae</i> strains determined with a newly developed assembly software. <i>BMC Genomics</i> , 2014, 15, 1045.	1.2	15
2447	Flower development and sex specification in wild grapevine. <i>BMC Genomics</i> , 2014, 15, 1095.	1.2	41
2448	Genome-wide and single-base resolution DNA methylomes of the Pacific oyster <i>Crassostrea gigas</i> provide insight into the evolution of invertebrate CpG methylation. <i>BMC Genomics</i> , 2014, 15, 1119.	1.2	110
2449	Bovine serum albumin in saliva mediates grazing response in <i>Leymus chinensis</i> revealed by RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 1126.	1.2	12
2450	Evaluation and validation of a robust single cell RNA-amplification protocol through transcriptional profiling of enriched lung cancer initiating cells. <i>BMC Genomics</i> , 2014, 15, 1129.	1.2	19
2451	An RNA sequencing transcriptome analysis of the high-temperature stressed tall fescue reveals novel insights into plant thermotolerance. <i>BMC Genomics</i> , 2014, 15, 1147.	1.2	49
2452	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. <i>BMC Genomics</i> , 2014, 15, 1148.	1.2	13

#	ARTICLE	IF	CITATIONS
2453	miRNome traits analysis on endothelial lineage cells discloses biomarker potential circulating microRNAs which affect progenitor activities. BMC Genomics, 2014, 15, 802.	1.2	31
2454	Genes and signaling networks regulated during zebrafish optic vesicle morphogenesis. BMC Genomics, 2014, 15, 825.	1.2	24
2455	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. BMC Genomics, 2014, 15, 846.	1.2	10
2456	IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. BMC Genomics, 2014, 15, 862.	1.2	21
2457	An RNA-Seq based gene expression atlas of the common bean. BMC Genomics, 2014, 15, 866.	1.2	142
2458	Transcriptomic portrait of human Mesenchymal Stromal/Stem cells isolated from bone marrow and placenta. BMC Genomics, 2014, 15, 910.	1.2	59
2459	Transcriptome profiling using pyrosequencing shows genes associated with bast fiber development in ramie ( <i>Boehmeria nivea</i> L.). BMC Genomics, 2014, 15, 919.	1.2	43
2460	Differential transcriptomic analyses revealed genes and signaling pathways involved in iono-osmoregulation and cellular remodeling in the gills of euryhaline Mozambique tilapia, <i>Oreochromis mossambicus</i> . BMC Genomics, 2014, 15, 921.	1.2	66
2461	Characterizing the developmental transcriptome of the oriental fruit fly, <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) through comparative genomic analysis with <i>Drosophila melanogaster</i> utilizing modENCODE datasets. BMC Genomics, 2014, 15, 942.	1.2	37
2462	Interspecific and host-related gene expression patterns in nematode-trapping fungi. BMC Genomics, 2014, 15, 968.	1.2	30
2463	Transcriptome of the inflorescence meristems of the biofuel plant <i>Jatropha curcas</i> treated with cytokinin. BMC Genomics, 2014, 15, 974.	1.2	49
2464	Transcriptomic analysis of the phytopathogenic oomycete <i>Phytophthora cactorum</i> provides insights into infection-related effectors. BMC Genomics, 2014, 15, 980.	1.2	33
2465	Omics profiles used to evaluate the gene expression of <i>Exiguobacterium antarcticum</i> B7 during cold adaptation. BMC Genomics, 2014, 15, 986.	1.2	21
2466	The temporal foliar transcriptome of the perennial C3 desert plant <i>Rhazya stricta</i> in its natural environment. BMC Plant Biology, 2014, 14, 2.	1.6	27
2467	Genome-wide expression analysis of reactive oxygen species gene network in Mizuna plants grown in long-term spaceflight. BMC Plant Biology, 2014, 14, 4.	1.6	85
2468	RNA-seq: impact of RNA degradation on transcript quantification. BMC Biology, 2014, 12, 42.	1.7	366
2469	A Comparison of RNA-Seq and Exon Arrays for Whole Genome Transcription Profiling of the L5 Spinal Nerve Transection Model of Neuropathic Pain in the Rat. Molecular Pain, 2014, 10, 1744-8069-10-7.	1.0	75
2470	Next generation sequencing and de novo transcriptomics to study gene evolution. Plant Methods, 2014, 10, 34.	1.9	23



#	ARTICLE	IF	CITATIONS
2471	Expression level of a flavonoid 3- $\beta$ -hydroxylase gene determines pathogen-induced color variation in sorghum. <i>BMC Research Notes</i> , 2014, 7, 761.	0.6	22
2472	Comparative transcriptome analysis of the Asteraceae halophyte <i>Karelinia caspica</i> under salt stress. <i>BMC Research Notes</i> , 2014, 7, 927.	0.6	21
2473	Predicting expression: the complementary power of histone modification and transcription factor binding data. <i>Epigenetics and Chromatin</i> , 2014, 7, 36.	1.8	32
2474	OrthoClust: an orthology-based network framework for clustering data across multiple species. <i>Genome Biology</i> , 2014, 15, R100.	13.9	46
2475	Mechanisms of action for 2-phenylethanol isolated from <i>Kloeckera apiculata</i> in control of <i>Penicillium</i> molds of citrus fruits. <i>BMC Microbiology</i> , 2014, 14, 242.	1.3	98
2476	Genome-wide annotation of the soybean WRKY family and functional characterization of genes involved in response to <i>Phakopsora pachyrhizi</i> infection. <i>BMC Plant Biology</i> , 2014, 14, 236.	1.6	79
2477	Exploiting transcriptome data for the development and characterization of gene-based SSR markers related to cold tolerance in oil palm ( <i>Elaeis guineensis</i> ). <i>BMC Plant Biology</i> , 2014, 14, 384.	1.6	21
2478	The <i>Lingulodinium</i> circadian system lacks rhythmic changes in transcript abundance. <i>BMC Biology</i> , 2014, 12, 107.	1.7	38
2479	Molecular profile of cochlear immunity in the resident cells of the organ of Corti. <i>Journal of Neuroinflammation</i> , 2014, 11, 173.	3.1	62
2480	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. <i>Genome Medicine</i> , 2014, 6, 88.	3.6	95
2481	RNA-sequencing reveals the complexities of the transcriptional response to lignocellulosic biofuel substrates in <i>Aspergillus niger</i> . <i>Fungal Biology and Biotechnology</i> , 2014, 1, 3.	2.5	41
2482	Was low CO <sub>2</sub> a driving force of C4 evolution: <i>Arabidopsis</i> responses to long-term low CO <sub>2</sub> stress. <i>Journal of Experimental Botany</i> , 2014, 65, 3657-3667.	2.4	51
2483	Expression and Regulation of MMP1, MMP3, and MMP9 in the Chicken Ovary in Response to Gonadotropins, Sex Hormones, and TGF $\beta$ 11. <i>Biology of Reproduction</i> , 2014, 90, 57.	1.2	57
2484	Transcription Factor RFX1 Is Crucial for Maintenance of Genome Integrity in <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2014, 13, 427-436.	3.4	39
2485	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2014, 13, 154-169.	3.4	66
2486	Construction of mate pair full-length cDNAs libraries and characterization of transcriptional start sites and termination sites. <i>Nucleic Acids Research</i> , 2014, 42, e125-e125.	6.5	12
2487	Aberrant transcriptional regulations in cancers: genome, transcriptome and epigenome analysis of lung adenocarcinoma cell lines. <i>Nucleic Acids Research</i> , 2014, 42, 13557-13572.	6.5	102
2488	Prognostic Impact of Bcl-2 Depends on Tumor Histology and Expression of MALAT-1 lncRNA in Non-Small-Cell Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2014, 9, 1294-1304.	0.5	59

#	ARTICLE	IF	CITATIONS
2489	Discrete Gene Network Models for Understanding Multicellularity and Cell Reprogramming: From Network Structure to Attractor Landscapes Landscape. , 2014, , 241-276.		5
2490	ARH-seq: identification of differential splicing in RNA-seq data. Nucleic Acids Research, 2014, 42, e110-e110.	6.5	10
2491	Oqtans: the RNA-seq workbench in the cloud for complete and reproducible quantitative transcriptome analysis. Bioinformatics, 2014, 30, 1300-1301.	1.8	12
2492	Gene Family Level Comparative Analysis of Gene Expression in Mammals Validates the Ortholog Conjecture. Genome Biology and Evolution, 2014, 6, 754-762.	1.1	51
2493	Modeling Gene Expression Evolution with an Extended Ornstein-Uhlenbeck Process Accounting for Within-Species Variation. Molecular Biology and Evolution, 2014, 31, 201-211.	3.5	110
2494	The Macrophage Transcriptome. , 2014, , 559-585.		1
2495	Divergent and Conserved Elements Comprise the Chemoreceptive Repertoire of the Nonblood-Feeding Mosquito <i>Toxorhynchites amboinensis</i> . Genome Biology and Evolution, 2014, 6, 2883-2896.	1.1	31
2496	Correlating Histone Modification Patterns with Gene Expression Data During Hematopoiesis. Methods in Molecular Biology, 2014, 1150, 175-187.	0.4	6
2497	A catalog of HLA type, HLA expression, and neo-epitope candidates in human cancer cell lines. Oncoimmunology, 2014, 3, e954893.	2.1	92
2498	Comparative Transcriptome Analyses between a Spontaneous Late-Ripening Sweet Orange Mutant and Its Wild Type Suggest the Functions of ABA, Sucrose and JA during Citrus Fruit Ripening. PLoS ONE, 2014, 9, e116056.	1.1	53
2499	Gene Co-expression Modules Underlying Polymorphic and Monomorphic Zooids in the Colonial Hydrozoan, <i>Hydractinia symbiolongicarpus</i> . Integrative and Comparative Biology, 2014, 54, 276-283.	0.9	11
2500	Transcript Profiling Reveals Auxin and Cytokinin Signaling Pathways and Transcription Regulation during In Vitro Organogenesis of Ramie ( <i>Boehmeria nivea</i> L. Gaud). PLoS ONE, 2014, 9, e113768.	1.1	29
2501	ReadXplorer visualization and analysis of mapped sequences. Bioinformatics, 2014, 30, 2247-2254.	1.8	127
2502	RNA-Seq Data: A Complexity Journey. Computational and Structural Biotechnology Journal, 2014, 11, 123-130.	1.9	17
2503	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR. , 2014, , 51-74.		119
2504	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	7.7	415
2505	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	5.8	75
2506	Analysis of Expressed Genes of the Bacterium <i>Candidatus Phytoplasma Mali</i> ™ Highlights Key Features of Virulence and Metabolism. PLoS ONE, 2014, 9, e94391.	1.1	29

#	ARTICLE	IF	CITATIONS
2507	Transcriptome Profiling Identifies Differentially Expressed Genes in Huoyan Goose Ovaries between the Laying Period and Ceased Period. PLoS ONE, 2014, 9, e113211.	1.1	35
2508	Using RNA-seq Data to Detect Differentially Expressed Genes. , 2014, , 25-49.		10
2509	Statistical Analyses of Next Generation Sequencing Data: An Overview. , 2014, , 1-24.		0
2510	Specific adaptation of <i>Ustilaginoidea virens</i> in occupying host florets revealed by comparative and functional genomics. Nature Communications, 2014, 5, 3849.	5.8	202
2511	Current Challenges in the Bioinformatics of Single Cell Genomics. Frontiers in Oncology, 2014, 4, 7.	1.3	40
2512	Efficient Detection of Unpaired DNA Requires a Member of the Rad54-Like Family of Homologous Recombination Proteins. Genetics, 2014, 198, 895-904.	1.2	35
2513	The active enhancer network operated by liganded RXR supports angiogenic activity in macrophages. Genes and Development, 2014, 28, 1562-1577.	2.7	85
2514	Transcriptional Response of <i>Musca domestica</i> Larvae to Bacterial Infection. PLoS ONE, 2014, 9, e104867.	1.1	25
2515	Noxa1 is a master regulator of alternative splicing in pancreatic beta cells. Nucleic Acids Research, 2014, 42, 11818-11830.	6.5	71
2516	Vespucci: a system for building annotated databases of nascent transcripts. Nucleic Acids Research, 2014, 42, 2433-2447.	6.5	18
2517	The integrated disease network. Integrative Biology (United Kingdom), 2014, 6, 1069-1079.	0.6	28
2518	Gene Expression Profiling in Asthma. Advances in Experimental Medicine and Biology, 2014, 795, 157-181.	0.8	11
2519	The Role of Spike-In Standards in the Normalization of RNA-seq. , 2014, , 169-190.		8
2520	Regulation of transcription termination by glucosylated hydroxymethyluracil, base J, in <i>Leishmania major</i> and <i>Trypanosoma brucei</i> . Nucleic Acids Research, 2014, 42, 9717-9729.	6.5	68
2521	CarrotDB: a genomic and transcriptomic database for carrot. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau096-bau096.	1.4	87
2522	Complexity of Gene Expression Evolution after Duplication: Protein Dosage Rebalancing. Genetics Research International, 2014, 2014, 1-8.	2.0	25
2523	Comparison of Metabolic Network between Muscle and Intramuscular Adipose Tissues in Hanwoo Beef Cattle Using a Systems Biology Approach. International Journal of Genomics, 2014, 2014, 1-6.	0.8	19
2524	The JNK-Like MAPK KGB-1 of <i>Caenorhabditis Elegans</i> Promotes Reproduction, Lifespan, and Gene Expressions for Protein Biosynthesis and Germline Homeostasis but Interferes with Hyperosmotic Stress Tolerance. Cellular Physiology and Biochemistry, 2014, 34, 1951-1973.	1.1	25

#	ARTICLE	IF	CITATIONS
2525	Gene Expression and Gene Ontology Enrichment Analysis for H3K4me3 and H3K4me1 in Mouse Liver and Mouse Embryonic Stem Cell Using ChIP-Seq and RNA-Seq. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S13612.	2.3	3
2526	Improved Variant Calling Accuracy by Merging Replicates in Whole-Exome Sequencing Studies. <i>BioMed Research International</i> , 2014, 2014, 1-7.	0.9	12
2527	Comparative Analysis of Glycogene Expression in Different Mouse Tissues Using RNA-Seq Data. <i>International Journal of Genomics</i> , 2014, 2014, 1-18.	0.8	78
2528	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	3.2	65
2529	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. <i>Nucleic Acids Research</i> , 2014, 42, D677-D684.	6.5	25
2530	WetA Is Required for Conidiogenesis and Conidium Maturation in the Ascomycete Fungus <i>Fusarium graminearum</i> . <i>Eukaryotic Cell</i> , 2014, 13, 87-98.	3.4	78
2531	RNA sequencing shows transcriptomic changes in rectosigmoid mucosa in patients with irritable bowel syndrome-diarrhea: a pilot case-control study. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, G1089-G1098.	1.6	52
2532	P-value calibration for multiple testing problems in genomics. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 659-73.	0.2	2
2533	Transcriptome analysis of the effect of <i>Vibrio alginolyticus</i> infection on the innate immunity-related complement pathway in <i>Epinephelus coioides</i> . <i>BMC Genomics</i> , 2014, 15, 1102.	1.2	47
2534	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419
2535	Transcriptome analysis of carbohydrate metabolism during bulblet formation and development in <i>Lilium davidii</i> var. <i>unicolor</i> . <i>BMC Plant Biology</i> , 2014, 14, 358.	1.6	82
2536	Epigenetic modifications are associated with inter-species gene expression variation in primates. <i>Genome Biology</i> , 2014, 15, 547.	3.8	72
2537	NF- $\kappa$ B signaling mediates homeostatic maturation of new T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E846-55.	3.3	22
2538	MorusDB: a resource for mulberry genomics and genome biology. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau054-bau054.	1.4	40
2539	Genomic connectivity networks based on the BrainSpan atlas of the developing human brain. , 2014, , .		1
2540	Differentiating progressive from nonprogressive T1 bladder cancer by gene expression profiling: Applying RNA-sequencing analysis on archived specimens. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2014, 32, 327-336.	0.8	18
2541	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. , 2014, , .		0
2542	A model of liver carcinogenesis originating from hepatic progenitor cells with accumulation of genetic alterations. <i>International Journal of Cancer</i> , 2014, 134, 1067-1076.	2.3	12

#	ARTICLE	IF	CITATIONS
2543	Identification of differentially expressed genes in hepatopancreas of oriental river prawn, <i>Macrobrachium nipponense</i> exposed to environmental hypoxia. <i>Gene</i> , 2014, 534, 298-306.	1.0	65
2544	Gene Ontology based housekeeping gene selection for RNA-seq normalization. <i>Methods</i> , 2014, 67, 354-363.	1.9	24
2545	Transcriptome de novo assembly sequencing and analysis of the toxic dinoflagellate <i>Alexandrium catenella</i> using the Illumina platform. <i>Gene</i> , 2014, 537, 285-293.	1.0	53
2546	The transcriptomic response to copper exposure by the gill tissue of Japanese scallops ( <i>Mizuhopecten</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	28
2547	Transcriptome profiling to identify genes involved in pathogenicity of <i>Valsa mali</i> on apple tree. <i>Fungal Genetics and Biology</i> , 2014, 68, 31-38.	0.9	87
2548	Transcriptome sequencing of sea cucumber ( <i>Apostichopus japonicus</i> ) and the identification of gene-associated markers. <i>Molecular Ecology Resources</i> , 2014, 14, 127-138.	2.2	69
2549	An efficient method for long-term room temperature storage of RNA. <i>European Journal of Human Genetics</i> , 2014, 22, 379-385.	1.4	98
2550	ncRNA-Protein Interactions in Development and Disease from the Perspective of High-Throughput Studies. , 2014, , 87-115.		0
2551	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	51
2552	Identification and Expression Analysis of D-type Cyclin Genes in Early Developing Fruit of Cucumber ( <i>Cucumis sativus</i> L.). <i>Plant Molecular Biology Reporter</i> , 2014, 32, 209-218.	1.0	13
2553	High-throughput analysis of transcriptome variation during water deficit in a poplar hybrid: a general overview. <i>Tree Genetics and Genomes</i> , 2014, 10, 53-66.	0.6	27
2554	RNA-Seq derived identification of differential transcription in the chrysanthemum leaf following inoculation with <i>Alternaria tenuissima</i> . <i>BMC Genomics</i> , 2014, 15, 9.	1.2	33
2555	RIP-seq analysis of eukaryotic Sm proteins identifies three major categories of Sm-containing ribonucleoproteins. <i>Genome Biology</i> , 2014, 15, R7.	13.9	32
2556	Deep transcriptome sequencing of rhizome and aerial-shoot in <i>Sorghum propinquum</i> . <i>Plant Molecular Biology</i> , 2014, 84, 315-327.	2.0	26
2557	Comprehensive transcriptional profiling of NaHCO <sub>3</sub> -stressed <i>Tamarix hispida</i> roots reveals networks of responsive genes. <i>Plant Molecular Biology</i> , 2014, 84, 145-157.	2.0	44
2558	Coregulation of Genetic Programs by the Transcription Factors NFIB and STAT5. <i>Molecular Endocrinology</i> , 2014, 28, 758-767.	3.7	16
2559	Metabolic profiles of prokaryotic and eukaryotic communities in deep-sea sponge <i>Neamphius huxleyi</i> indicated by metagenomics. <i>Scientific Reports</i> , 2014, 4, 3895.	1.6	69
2560	Differential gene expression identified by RNA-Seq and qPCR in two sizes of pearl oyster ( <i>Pinctada</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.0	62

#	ARTICLE	IF	CITATIONS
2561	Differential Transcriptomic Analysis by RNA-Seq of GSNO-Responsive Genes Between Arabidopsis Roots and Leaves. <i>Plant and Cell Physiology</i> , 2014, 55, 1080-1095.	1.5	124
2562	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. <i>Nature Protocols</i> , 2014, 9, 989-1009.	5.5	171
2563	Selection and evaluation of novel reference genes for quantitative reverse transcription PCR (qRT-PCR) based on genome and transcriptome data in <i>Brassica napus</i> L.. <i>Gene</i> , 2014, 538, 113-122.	1.0	111
2564	From single-cell to cell-pool transcriptomes: Stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014, 24, 496-510.	2.4	470
2565	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	5.8	316
2566	Towards an improved apple reference transcriptome using RNA-seq. <i>Molecular Genetics and Genomics</i> , 2014, 289, 427-438.	1.0	33
2567	RNA-seq in the tetraploid <i>Xenopus laevis</i> enables genome-wide insight in a classic developmental biology model organism. <i>Methods</i> , 2014, 66, 398-409.	1.9	15
2568	Diversity and dynamics of the <i>Drosophila</i> transcriptome. <i>Nature</i> , 2014, 512, 393-399.	13.7	647
2569	Dual RNA-seq of the plant pathogen <i>Phytophthora ramorum</i> and its tanoak host. <i>Tree Genetics and Genomes</i> , 2014, 10, 489-502.	0.6	45
2570	Comparative expression analysis of resistant and susceptible <i>Populus</i> clones inoculated with <i>Septoria musiva</i> . <i>Plant Science</i> , 2014, 223, 69-78.	1.7	21
2571	Molecular Profiling of Premalignant Lesions in Lung Squamous Cell Carcinomas Identifies Mechanisms Involved in Stepwise Carcinogenesis. <i>Cancer Prevention Research</i> , 2014, 7, 487-495.	0.7	74
2572	Transcriptomic analysis reveals key regulators of mammogenesis and the pregnancy-lactation cycle. <i>Science China Life Sciences</i> , 2014, 57, 340-355.	2.3	26
2573	The human platelet: strong transcriptome correlations among individuals associate weakly with the platelet proteome. <i>Biology Direct</i> , 2014, 9, 3.	1.9	77
2574	In vivo genome-wide binding of Id2 to E2F4 target genes as part of a reversible program in mice liver. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 3583-3597.	2.4	7
2575	Dormancy within <i>Staphylococcus epidermidis</i> biofilms: a transcriptomic analysis by RNA-seq. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2585-2596.	1.7	25
2576	RNA-seq analysis of bovine intramuscular, subcutaneous and perirenal adipose tissues. <i>Molecular Biology Reports</i> , 2014, 41, 1631-1637.	1.0	29
2577	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , 2014, 15, R29.	13.9	4,603
2578	Virus-independent and common transcriptome responses of leafhopper vectors feeding on maize infected with semi-persistently and persistent propagatively transmitted viruses. <i>BMC Genomics</i> , 2014, 15, 133.	1.2	33

#	ARTICLE	IF	CITATIONS
2579	Anatomy and transcript profiling of gynoecium development in female sterile <i>Brassica napus</i> mediated by one alien chromosome from <i>Orychophragmus violaceus</i> . <i>BMC Genomics</i> , 2014, 15, 61.	1.2	17
2580	Transcription profiling using RNA-Seq demonstrates expression differences in the body walls of juvenile albino and normal sea cucumbers <i>Apostichopus japonicus</i> . <i>Chinese Journal of Oceanology and Limnology</i> , 2014, 32, 34-46.	0.7	17
2581	Transcriptomic analysis of Asiatic lily in the process of vernalization via RNA-seq. <i>Molecular Biology Reports</i> , 2014, 41, 3839-3852.	1.0	26
2582	Genome-wide survey and analysis of microsatellites in the Pacific oyster genome: abundance, distribution, and potential for marker development. <i>Chinese Journal of Oceanology and Limnology</i> , 2014, 32, 8-21.	0.7	2
2583	<i>Drechlerella stenobrocha</i> genome illustrates the mechanism of constricting rings and the origin of nematode predation in fungi. <i>BMC Genomics</i> , 2014, 15, 114.	1.2	72
2584	Construction and de novo characterization of a transcriptome of <i>Chrysanthemum lavandulifolium</i> : analysis of gene expression patterns in floral bud emergence. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 116, 297-309.	1.2	36
2585	Comparative analysis on transcriptome sequencings of six <i>Sargassum</i> species in China. <i>Acta Oceanologica Sinica</i> , 2014, 33, 37-44.	0.4	11
2586	De novo sequencing and comparative analysis of three red algal species of Family Solieriaceae to discover putative genes associated with carrageenan biosynthesis. <i>Acta Oceanologica Sinica</i> , 2014, 33, 45-53.	0.4	7
2587	Characterization of mango ( <i>Mangifera indica</i> L.) transcriptome and chloroplast genome. <i>Plant Molecular Biology</i> , 2014, 85, 193-208.	2.0	51
2588	The genetics of gene expression in complex mouse crosses as a tool to study the molecular underpinnings of behavior traits. <i>Mammalian Genome</i> , 2014, 25, 12-22.	1.0	10
2589	Integrated transcriptome analysis of mouse spermatogenesis. <i>BMC Genomics</i> , 2014, 15, 39.	1.2	118
2590	The BRANCHING ENZYME1 gene, encoding a glycoside hydrolase family 13 protein, is required for in vitro plant regeneration in <i>Arabidopsis</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 117, 279-291.	1.2	8
2591	Identification of mechanosensitive genes during skeletal development: alteration of genes associated with cytoskeletal rearrangement and cell signalling pathways. <i>BMC Genomics</i> , 2014, 15, 48.	1.2	80
2592	Large scale in-silico identification and characterization of simple sequence repeats (SSRs) from de novo assembled transcriptome of <i>Catharanthus roseus</i> (L.) G. Don. <i>Plant Cell Reports</i> , 2014, 33, 905-918.	2.8	28
2593	Differential transcriptional profile of <i>Corynebacterium pseudotuberculosis</i> in response to abiotic stresses. <i>BMC Genomics</i> , 2014, 15, 14.	1.2	45
2594	The transcriptome landscape of <i>Prochlorococcus</i> MED4 and the factors for stabilizing the core genome. <i>BMC Microbiology</i> , 2014, 14, 11.	1.3	6
2595	Transcriptomic analysis of cut tree peony with glucose supply using the RNA-Seq technique. <i>Plant Cell Reports</i> , 2014, 33, 111-129.	2.8	34
2596	RNA-Seq revealed complex response to heat stress on transcriptomic level in <i>Saccharina japonica</i> (Laminariales, Phaeophyta). <i>Journal of Applied Phycology</i> , 2014, 26, 1585-1596.	1.5	54

#	ARTICLE	IF	CITATIONS
2597	Inferring therapeutic targets from heterogeneous data: HKDC1 is a novel potential therapeutic target for cancer. <i>Bioinformatics</i> , 2014, 30, 748-752.	1.8	35
2598	The Transcription Factor GATA3 Is Critical for the Development of All IL-7R <sup>+</sup> -Expressing Innate Lymphoid Cells. <i>Immunity</i> , 2014, 40, 378-388.	6.6	320
2599	Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines. <i>Journal of Proteome Research</i> , 2014, 13, 200-211.	1.8	14
2600	Sequential transcriptome analysis of human liver cancer indicates late stage acquisition of malignant traits. <i>Journal of Hepatology</i> , 2014, 60, 346-353.	1.8	85
2601	Extensive transcriptional complexity during hypoxia-regulated expression of the myoglobin gene in cancer. <i>Human Molecular Genetics</i> , 2014, 23, 479-490.	1.4	23
2602	Second-Generation Sequencing for Cancer Genome Analysis. , 2014, , 13-30.		2
2603	RNA-Seq Technology and Its Application in Fish Transcriptomics. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 98-110.	1.0	262
2604	Comparative transcriptome analysis between somatic embryos (<sc>SE</sc>s) and zygotic embryos in cotton: evidence for stress response functions in <sc>SE</sc> development. <i>Plant Biotechnology Journal</i> , 2014, 12, 161-173.	4.1	103
2605	Transcriptional data mining of <i>Salvia miltiorrhiza</i> in response to methyl jasmonate to examine the mechanism of bioactive compound biosynthesis and regulation. <i>Physiologia Plantarum</i> , 2014, 152, 241-255.	2.6	86
2606	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014, 32, 462-464.	9.4	594
2607	A change-point model for identifying 3' UTR switching by next-generation RNA sequencing. <i>Bioinformatics</i> , 2014, 30, 2162-2170.	1.8	43
2608	Differential gene expression in laboratory strains of human head and body lice when challenged with <i>Bartonella quintana</i>, a pathogenic bacterium. <i>Insect Molecular Biology</i> , 2014, 23, 244-254.	1.0	23
2609	Multiplexed DNA repair assays for multiple lesions and multiple doses via transcription inhibition and transcriptional mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1823-32.	3.3	114
2610	RNA-seq Analysis of Antibiotic-Producing <i>Bacillus subtilis</i> SC-8 in Response to Signal Peptide PapR of <i>Bacillus cereus</i> . <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 580-594.	1.4	3
2611	Accuracy of allele frequency estimation using pooled <sc>RNA</sc>-Seq. <i>Molecular Ecology Resources</i> , 2014, 14, 381-392.	2.2	54
2612	ChildSeq-RNA. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 361-370.	1.2	26
2613	Transcriptomic and proteomic responses of <i>Serratia marcescens</i> to spaceflight conditions involve large-scale changes in metabolic pathways. <i>Advances in Space Research</i> , 2014, 53, 1108-1117.	1.2	13
2614	Next-Generation Sequencing RNA-Seq Library Construction. <i>Current Protocols in Molecular Biology</i> , 2014, 106, 4.21.1-19.	2.9	48



#	ARTICLE	IF	CITATIONS
2615	Model-based clustering for RNA-seq data. <i>Bioinformatics</i> , 2014, 30, 197-205.	1.8	112
2616	Cancer Transcriptome Sequencing and Analysis. , 2014, , 31-47.		1
2617	The Significance of Transcriptome Sequencing in Personalized Cancer Medicine. , 2014, , 49-64.		2
2618	FlyBase 102â€”advanced approaches to interrogating FlyBase. <i>Nucleic Acids Research</i> , 2014, 42, D780-D788.	6.5	287
2619	Nuclear lncRNAs as epigenetic regulatorsâ€”Beyond skepticism. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 215-222.	0.9	63
2620	Maternal Plasma RNA Sequencing for Genome-Wide Transcriptomic Profiling and Identification of Pregnancy-Associated Transcripts. <i>Clinical Chemistry</i> , 2014, 60, 954-962.	1.5	80
2621	Alterations in the <i>Staphylococcus epidermidis</i> biofilm transcriptome following interaction with whole human blood. <i>Pathogens and Disease</i> , 2014, 70, 444-448.	0.8	23
2622	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014, 24, 708-717.	2.4	99
2623	Transcriptome population genomics reveals severe bottleneck and domestication cost in the African rice ( <i>Oryza glaberrima</i> ). <i>Molecular Ecology</i> , 2014, 23, 2210-2227.	2.0	75
2624	Post-transcriptional regulation of gene expression in innate immunity. <i>Nature Reviews Immunology</i> , 2014, 14, 361-376.	10.6	301
2625	MicroRNA-146a directs the symmetric division of Snail-dominant colorectal cancer stem cells. <i>Nature Cell Biology</i> , 2014, 16, 268-280.	4.6	241
2626	Inhibition of SULT4A1 Expression Induces Up-Regulation of Phototransduction Gene Expression in 72-Hour Postfertilization Zebrafish Larvae. <i>Drug Metabolism and Disposition</i> , 2014, 42, 947-953.	1.7	8
2628	Compatible solute, transporter protein, transcription factor, and hormone-related gene expression provides an indicator of drought stress in <i>Paulownia fortunei</i> . <i>Functional and Integrative Genomics</i> , 2014, 14, 479-491.	1.4	32
2629	Methods for Quantifying Gene Expression in Ecoimmunology: From qPCR to RNA-Seq. <i>Integrative and Comparative Biology</i> , 2014, 54, 396-406.	0.9	33
2630	Parseq: reconstruction of microbial transcription landscape from RNA-Seq read counts using state-space models. <i>Bioinformatics</i> , 2014, 30, 1409-1416.	1.8	14
2631	Nitrite-induced hepatotoxicity in Bluntnout bream ( <i>Megalobrama amblycephala</i> ): The mechanistic insight from transcriptome to physiology analysis. <i>Environmental Toxicology and Pharmacology</i> , 2014, 37, 55-65.	2.0	37
2632	The role of carbon starvation in the induction of enzymes that degrade plant-derived carbohydrates in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2014, 72, 34-47.	0.9	95
2633	An RNA Sequencing Transcriptome Analysis Reveals Novel Insights into Molecular Aspects of the Nitrate Impact on the Nodule Activity of <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2014, 164, 400-411.	2.3	84

#	ARTICLE	IF	CITATIONS
2634	Motif-based analysis of large nucleotide data sets using MEME-ChIP. <i>Nature Protocols</i> , 2014, 9, 1428-1450.	5.5	200
2635	A global non-coding RNA system modulates fission yeast protein levels in response to stress. <i>Nature Communications</i> , 2014, 5, 3947.	5.8	54
2636	Transcriptome Comparison of Global Distinctive Features Between Pollination and Parthenocarpic Fruit Set Reveals Transcriptional Phytohormone Cross-Talk in Cucumber ( <i>Cucumis sativus</i> L.). <i>Plant and Cell Physiology</i> , 2014, 55, 1325-1342.	1.5	54
2637	Genomic changes under rapid evolution: selection for parasitoid resistance. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132303.	1.2	41
2638	Systematic analysis of a wasp parasitism arsenal. <i>Molecular Ecology</i> , 2014, 23, 890-901.	2.0	108
2639	Sugar and Auxin Signaling Pathways Respond to High-Temperature Stress during Anther Development as Revealed by Transcript Profiling Analysis in Cotton. <i>Plant Physiology</i> , 2014, 164, 1293-1308.	2.3	189
2640	Tissue-Specific Alternative Splicing Analysis Reveals the Diversity of Chromosome 18 Transcriptome. <i>Journal of Proteome Research</i> , 2014, 13, 173-182.	1.8	12
2641	Analyzing abundance of mRNA molecules with a near-infrared fluorescence technique. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 537-548.	1.9	3
2642	Vitellogenin is not an appropriate biomarker of feminisation in a Crustacean. <i>Aquatic Toxicology</i> , 2014, 153, 89-97.	1.9	23
2643	De novo transcriptome analysis of <i>Liriodendron chinense</i> petals and leaves by Illumina sequencing. <i>Gene</i> , 2014, 534, 155-162.	1.0	64
2644	Biodegradative Bacteria. , 2014, , .		9
2645	A multifunctional protein EWS regulates the expression of Drosha and microRNAs. <i>Cell Death and Differentiation</i> , 2014, 21, 136-145.	5.0	34
2646	Transcriptional Regulation of Fruit Ripening by Tomato FRUITFULL Homologs and Associated MADS Box Proteins. <i>Plant Cell</i> , 2014, 26, 89-101.	3.1	203
2647	Phenotypic, genomic, transcriptomic and proteomic changes in <i>Bacillus cereus</i> after a short-term space flight. <i>Advances in Space Research</i> , 2014, 53, 18-29.	1.2	30
2648	Effect of separate sampling on classification accuracy. <i>Bioinformatics</i> , 2014, 30, 242-250.	1.8	77
2649	Transcriptome Analysis of Psoriasis in a Large Case-Control Sample: RNA-Seq Provides Insights into Disease Mechanisms. <i>Journal of Investigative Dermatology</i> , 2014, 134, 1828-1838.	0.3	318
2650	Methanotrophic archaea possessing diverging methane-oxidizing and electron-transporting pathways. <i>ISME Journal</i> , 2014, 8, 1069-1078.	4.4	160
2651	Unifying immunology with informatics and multiscale biology. <i>Nature Immunology</i> , 2014, 15, 118-127.	7.0	140

#	ARTICLE	IF	CITATIONS
2652	Comparative transcriptome profiling of potassium starvation responsiveness in two contrasting watermelon genotypes. <i>Planta</i> , 2014, 239, 397-410.	1.6	62
2653	Plant Epigenetics and Epigenomics. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	5
2654	Epigenetic modification and inheritance in sexual reversal of fish. <i>Genome Research</i> , 2014, 24, 604-615.	2.4	356
2655	Global gene expression responses to waterlogging in leaves of rape seedlings. <i>Plant Cell Reports</i> , 2014, 33, 289-299.	2.8	56
2656	Genome-Wide Fractionation and Identification of WRKY Transcription Factors in Chinese Cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ) Reveals Collinearity and Their Expression Patterns Under Abiotic and Biotic Stresses. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 781-795.	1.0	69
2657	Joint estimation of isoform expression and isoform-specific read distribution using multisample RNA-Seq data. <i>Bioinformatics</i> , 2014, 30, 506-513.	1.8	20
2658	Quantitative single-cell RNA-seq with unique molecular identifiers. <i>Nature Methods</i> , 2014, 11, 163-166.	9.0	1,047
2659	Treatment with the reactive oxygen species scavenger EUK-207 reduces lung damage and increases survival during 1918 influenza virus infection in mice. <i>Free Radical Biology and Medicine</i> , 2014, 67, 235-247.	1.3	38
2660	Full-length RNA-seq from single cells using Smart-seq2. <i>Nature Protocols</i> , 2014, 9, 171-181.	5.5	3,308
2661	Quantitative developmental transcriptomes of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Developmental Biology</i> , 2014, 385, 160-167.	0.9	132
2662	Flower Development. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	2
2663	Unveiling the mechanism by which microsporidian parasites prevent locust swarm behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1343-1348.	3.3	60
2664	Development of strategies for integrated breeding, genetics and applied genomics for genetic improvement of aquatic organisms. <i>Aquaculture</i> , 2014, 420-421, S121-S123.	1.7	8
2665	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. <i>Genome Research</i> , 2014, 24, 14-24.	2.4	547
2666	Identification of Novel Long Noncoding RNAs Associated with TGF- $\beta$ /Smad3-Mediated Renal Inflammation and Fibrosis by RNA Sequencing. <i>American Journal of Pathology</i> , 2014, 184, 409-417.	1.9	137
2667	Systematic Analyses of the Transcriptome, Translatome, and Proteome Provide a Global View and Potential Strategy for the C-HPP. <i>Journal of Proteome Research</i> , 2014, 13, 38-49.	1.8	60
2668	Long non-coding RNAs: new players in cell differentiation and development. <i>Nature Reviews Genetics</i> , 2014, 15, 7-21.	7.7	2,616
2669	Identification of genes involved in gonadal sex differentiation and the dimorphic expression pattern in undifferentiated gonads of Russian sturgeon <i>Acipenser gueldenstaedtii</i> Brandt & Ratzeburg, 1833. <i>Journal of Applied Ichthyology</i> , 2014, 30, 1557-1564.	0.3	35

#	ARTICLE	IF	CITATIONS
2670	Biases in small RNA deep sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, 1414-1426.	6.5	175
2671	Comparative Genomics and Transcriptomics Analyses Reveal Divergent Lifestyle Features of Nematode Endoparasitic Fungus <i>Hirsutella minnesotensis</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 3077-3093.	1.1	50
2672	tassel-less1 Encodes a Boron Channel Protein Required for Inflorescence Development in Maize. <i>Plant and Cell Physiology</i> , 2014, 55, 1044-1054.	1.5	46
2673	Single-cell analyses of transcriptional heterogeneity during drug tolerance transition in cancer cells by RNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4726-35.	3.3	164
2674	High-Resolution Transcript Profiling of the Atypical Biotrophic Interaction between <i>Theobroma cacao</i> and the Fungal Pathogen <i>Moniliophthora perniciosa</i> . <i>Plant Cell</i> , 2014, 26, 4245-4269.	3.1	99
2675	Gene expression associated with intersterility in <i>Heterobasidion</i> . <i>Fungal Genetics and Biology</i> , 2014, 73, 104-119.	0.9	5
2676	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014, 24, 212-226.	2.4	175
2677	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	7.1	100
2678	Genotyping by sequencing transcriptomes in an evolutionary pre-breeding durum wheat population. <i>Molecular Breeding</i> , 2014, 34, 1531-1548.	1.0	20
2679	Extensive transcriptional response associated with seasonal plasticity of butterfly wing patterns. <i>Molecular Ecology</i> , 2014, 23, 6123-6134.	2.0	37
2680	A quantitative transcriptome reference map of the normal human brain. <i>Neurogenetics</i> , 2014, 15, 267-287.	0.7	33
2681	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014, 5, 5110.	5.8	230
2682	Methods for Processing High-Throughput RNA Sequencing Data. <i>Cold Spring Harbor Protocols</i> , 2014, 2014, pdb.top083352.	0.2	6
2683	Differential expression analysis of RNA-seq data at single-base resolution. <i>Biostatistics</i> , 2014, 15, 413-426.	0.9	56
2684	RNA-seq profiling the transcriptome of secondary seed dormancy in canola ( <i>Brassica napus</i> L.). <i>Science Bulletin</i> , 2014, 59, 4341-4351.	1.7	5
2685	Copy number variants in a highly inbred Iberian porcine strain. <i>Animal Genetics</i> , 2014, 45, 357-366.	0.6	20
2686	Transcriptome analyses to understand effects of the <i>Fusarium</i> deoxynivalenol and nivalenol mycotoxins on <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , 2014, 192, 231-239.	1.9	8
2687	Macrophages: Biology and Role in the Pathology of Diseases. , 2014, , .		13

#	ARTICLE	IF	CITATIONS
2689	RNA Sequencing Identifies Dysregulation of the Human Pancreatic Islet Transcriptome by the Saturated Fatty Acid Palmitate. <i>Diabetes</i> , 2014, 63, 1978-1993.	0.3	226
2690	De novo transcriptome analysis of mulberry ( <i>Morus L.</i> ) under drought stress using RNA-Seq technology. <i>Russian Journal of Bioorganic Chemistry</i> , 2014, 40, 423-432.	0.3	19
2691	Learning regulatory programs by threshold SVD regression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15675-15680.	3.3	21
2692	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 397-406.	2.5	2,819
2693	Crustacean Intersexuality Is Feminization without Demasculinization: Implications for Environmental Toxicology. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13520-13529.	4.6	22
2694	The human liver-specific proteome defined by transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014, 28, 2901-2914.	0.2	73
2695	LKB1 loss in melanoma disrupts directional migration toward extracellular matrix cues. <i>Journal of Cell Biology</i> , 2014, 207, 299-315.	2.3	41
2696	Single-Cell Sequencing Technologies: Current and Future. <i>Journal of Genetics and Genomics</i> , 2014, 41, 513-528.	1.7	74
2697	Functional characterization of the TERRA transcriptome at damaged telomeres. <i>Nature Communications</i> , 2014, 5, 5379.	5.8	212
2698	Selective Constraint Dominates the Evolution of Genes Expressed in a Novel Reproductive Gland. <i>Molecular Biology and Evolution</i> , 2014, 31, 3266-3281.	3.5	12
2699	Transcriptome characteristics of filamentous fungi deduced using high-throughput analytical technologies. <i>Briefings in Functional Genomics</i> , 2014, 13, 440-450.	1.3	12
2700	Increased risk of obesity related to total energy intake with the APOA5-1131T & C polymorphism in Korean premenopausal women. <i>Nutrition Research</i> , 2014, 34, 827-836.	1.3	19
2701	Proteomics informed by transcriptomics identifies novel secreted proteins in <i>Dermacentor andersoni</i> saliva. <i>International Journal for Parasitology</i> , 2014, 44, 1029-1037.	1.3	75
2702	Identification of genes related to the phenotypic variations of a synthesized <i>Paulownia</i> ( <i>Paulownia</i> ) Tj ETQq1 1 0.784314 rgBJ /Overl	1.0	10
2703	Genetics of Gene Expression in CNS. <i>International Review of Neurobiology</i> , 2014, 116, 195-231.	0.9	26
2704	SeaBase: A Multispecies Transcriptomic Resource and Platform for Gene Network Inference. <i>Integrative and Comparative Biology</i> , 2014, 54, 250-263.	0.9	17
2705	Metatranscriptome of an Anaerobic Benzene-Degrading, Nitrate-Reducing Enrichment Culture Reveals Involvement of Carboxylation in Benzene Ring Activation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4095-4107.	1.4	99
2706	Comparison of distinct transcriptional expression patterns of flavonoid biosynthesis in Cabernet Sauvignon grapes from east and west China. <i>Plant Physiology and Biochemistry</i> , 2014, 84, 45-56.	2.8	26

#	ARTICLE	IF	CITATIONS
2707	Bioinformatics-driven discovery of rational combination for overcoming EGFR-mutant lung cancer resistance to EGFR therapy. <i>Bioinformatics</i> , 2014, 30, 2393-2398.	1.8	22
2708	Digital gene expression analysis of reproductive toxicity of benzo[a]pyrene in male scallop <i>Chlamys farreri</i> . <i>Ecotoxicology and Environmental Safety</i> , 2014, 110, 190-196.	2.9	23
2709	Rational experiment design for sequencing-based RNA structure mapping. <i>Rna</i> , 2014, 20, 1864-1877.	1.6	28
2710	Cardiovascular Transcriptomics and Epigenomics Using Next-Generation Sequencing. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 701-710.	5.1	14
2711	Genes involved in the induction of liver growth by peroxisome proliferators. <i>Toxicology Research</i> , 2014, 3, 315-323.	0.9	1
2712	Camelid genomes reveal evolution and adaptation to desert environments. <i>Nature Communications</i> , 2014, 5, 5188.	5.8	299
2713	High-Throughput Transcriptome Sequencing Identifies Candidate Genetic Modifiers of Vulnerability to Fetal Alcohol Spectrum Disorders. <i>Alcoholism: Clinical and Experimental Research</i> , 2014, 38, 1874-1882.	1.4	49
2714	(Post-)Genomics approaches in fungal research. <i>Briefings in Functional Genomics</i> , 2014, 13, 424-439.	1.3	16
2715	Methods for comprehensive experimental identification of RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 203.	13.9	140
2716	Zinc Oxide Nanoparticles Cause Inhibition of Microbial Denitrification by Affecting Transcriptional Regulation and Enzyme Activity. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13800-13807.	4.6	148
2717	Transcriptome and expression profiling analysis of <i>Leuciscus waleckii</i> : an exploration of the alkali-adapted mechanisms of a freshwater teleost. <i>Molecular BioSystems</i> , 2014, 10, 491-504.	2.9	21
2718	mRNA-Seq and MicroRNA-Seq Whole-Transcriptome Analyses of Rhesus Monkey Embryonic Stem Cell Neural Differentiation Revealed the Potential Regulators of Rosette Neural Stem Cells. <i>DNA Research</i> , 2014, 21, 541-554.	1.5	32
2719	LKB1 and AMPK differentially regulate pancreatic $\beta$ -cell identity. <i>FASEB Journal</i> , 2014, 28, 4972-4985.	0.2	71
2720	Identification of gene expression profiles in the actinomycete <i>Gordonia neofelifaecis</i> grown with different steroids. <i>Genome</i> , 2014, 57, 345-353.	0.9	16
2721	Produced Water Exposure Alters Bacterial Response to Biocides. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13001-13009.	4.6	68
2722	The Transcriptome of Utricle Hair Cell Regeneration in the Avian Inner Ear. <i>Journal of Neuroscience</i> , 2014, 34, 3523-3535.	1.7	98
2723	Utility of RNA-seq and GPMDB Protein Observation Frequency for Improving the Sensitivity of Protein Identification by Tandem MS. <i>Journal of Proteome Research</i> , 2014, 13, 4113-4119.	1.8	25
2724	A Normative Study of the Synovial Fluid Proteome from Healthy Porcine Knee Joints. <i>Journal of Proteome Research</i> , 2014, 13, 4377-4387.	1.8	68

#	ARTICLE	IF	CITATIONS
2725	Developmental Heterogeneity of Cardiac Fibroblasts Does Not Predict Pathological Proliferation and Activation. <i>Circulation Research</i> , 2014, 115, 625-635.	2.0	258
2726	Integrative Identification of Epstein-Barr Virus-Associated Mutations and Epigenetic Alterations in Gastric Cancer. <i>Gastroenterology</i> , 2014, 147, 1350-1362.e4.	0.6	90
2727	Bacterial metatranscriptome analysis of a probiotic yogurt using an RNA-Seq approach. <i>International Dairy Journal</i> , 2014, 39, 284-292.	1.5	20
2728	Analysis of global gene expression profiles to identify differentially expressed genes critical for embryo development in <i>Brassica rapa</i> . <i>Plant Molecular Biology</i> , 2014, 86, 425-442.	2.0	18
2729	Alkaline phosphatases and aminopeptidases are altered in a Cry11Aa resistant strain of <i>Aedes aegypti</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2014, 54, 112-121.	1.2	20
2730	Non-coding RNA: a new frontier in regulatory biology. <i>National Science Review</i> , 2014, 1, 190-204.	4.6	175
2731	Analysis Considerations for Utilizing RNA-Seq to Characterize the Brain Transcriptome. <i>International Review of Neurobiology</i> , 2014, 116, 21-54.	0.9	4
2732	Introduction to Sequencing the Brain Transcriptome. <i>International Review of Neurobiology</i> , 2014, 116, 1-19.	0.9	18
2733	Occupancy of tissue-specific cis-regulatory modules by Otx2 and TLE/Groucho for embryonic head specification. <i>Nature Communications</i> , 2014, 5, 4322.	5.8	45
2734	pENCODE: A Plant Encyclopedia of DNA Elements. <i>Annual Review of Genetics</i> , 2014, 48, 49-70.	3.2	38
2735	T cell transcripts and T cell activities in the gills of the teleost fish sea bass ( <i>Dicentrarchus labrax</i> ). <i>Developmental and Comparative Immunology</i> , 2014, 47, 309-318.	1.0	58
2736	Redox-active quinones induces genome-wide DNA methylation changes by an iron-mediated and Tet-dependent mechanism. <i>Nucleic Acids Research</i> , 2014, 42, 1593-1605.	6.5	106
2737	SeeSite: Characterizing Relationships between Splice Junctions and Splicing Enhancers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 648-656.	1.9	2
2738	Using Pseudogene Database to Identify Lineage-Specific Genes and Pseudogenes in Humans and Chimpanzees. <i>Journal of Heredity</i> , 2014, 105, 436-443.	1.0	4
2739	Host-Bacteria Interactions. <i>Methods in Molecular Biology</i> , 2014, . .	0.4	4
2740	Phenotypic and genomic plasticity of alternative male reproductive tactics in sailfin mollies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132310.	1.2	53
2741	Exonuclease-mediated degradation of nascent RNA silences genes linked to severe malaria. <i>Nature</i> , 2014, 513, 431-435.	13.7	73
2742	Genome-wide identification of housekeeping genes in maize. <i>Plant Molecular Biology</i> , 2014, 86, 543-554.	2.0	68

#	ARTICLE	IF	CITATIONS
2743	Estimated Diversity of Messenger RNAs in Each Murine Spermatozoa and Their Potential Function During Early Zygotic Development. <i>Biology of Reproduction</i> , 2014, 90, 94.	1.2	48
2744	Systematic Analysis of Missing Proteins Provides Clues to Help Define All of the Protein-Coding Genes on Human Chromosome 1. <i>Journal of Proteome Research</i> , 2014, 13, 114-125.	1.8	21
2745	ATTED-II in 2014: Evaluation of Gene Coexpression in Agriculturally Important Plants. <i>Plant and Cell Physiology</i> , 2014, 55, e6-e6.	1.5	98
2746	Genome-wide expression profiling of the transcriptomes of four <i>Paulownia tomentosa</i> accessions in response to drought. <i>Genomics</i> , 2014, 104, 295-305.	1.3	20
2747	TAA1-Regulated Local Auxin Biosynthesis in the Root-Apex Transition Zone Mediates the Aluminum-Induced Inhibition of Root Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2889-2904.	3.1	173
2748	Digital Encoding of Cellular mRNAs Enabling Precise and Absolute Gene Expression Measurement by Single-Molecule Counting. <i>Analytical Chemistry</i> , 2014, 86, 2867-2870.	3.2	32
2749	Identification of differentially expressed genes in <i>Chrysanthemum nankingense</i> (Asteraceae) under heat stress by RNA Seq. <i>Gene</i> , 2014, 552, 59-66.	1.0	20
2750	The role of post-translational modifications in acute and chronic cardiovascular disease. <i>Proteomics - Clinical Applications</i> , 2014, 8, 506-521.	0.8	34
2751	Correction of gene expression data: Performance-dependency on inter-replicate and inter-treatment biases. <i>Journal of Biotechnology</i> , 2014, 188, 100-109.	1.9	4
2752	Exploring differentially expressed genes in the ovaries of uniparous and multiparous goats using the RNA-Seq (Quantification) method. <i>Gene</i> , 2014, 550, 148-153.	1.0	28
2753	RNA sequencing reveals high resolution expression change of major plant hormone pathway genes after young seedless grape berries treated with gibberellin. <i>Plant Science</i> , 2014, 229, 215-224.	1.7	49
2754	The Path to Personalized Cardiovascular Medicine. , 2014, , 837-871.		0
2755	Alternative splicing in the fiddler crab cognate ecdysteroid receptor: Variation in receptor isoform expression and DNA binding properties in response to hormone. <i>General and Comparative Endocrinology</i> , 2014, 206, 80-95.	0.8	11
2756	Gene expression profile change and growth inhibition in <i>Drosophila</i> larvae treated with azadirachtin. <i>Journal of Biotechnology</i> , 2014, 185, 51-56.	1.9	36
2757	Genome-wide binding of transcription factors in inv(16) acute myeloid leukemia. <i>Genomics Data</i> , 2014, 2, 170-172.	1.3	6
2758	Understanding pathogenic <i>Burkholderia glumae</i> metabolic and signaling pathways within rice tissues through in vivo transcriptome analyses. <i>Gene</i> , 2014, 547, 77-85.	1.0	23
2759	Expression pattern of immunoglobulin superfamily members in the silkworm, <i>Bombyx mori</i> . <i>Gene</i> , 2014, 548, 198-209.	1.0	5
2760	An RNA-Sequencing Transcriptome and Splicing Database of Glia, Neurons, and Vascular Cells of the Cerebral Cortex. <i>Journal of Neuroscience</i> , 2014, 34, 11929-11947.	1.7	4,119



#	ARTICLE	IF	CITATIONS
2761	LEVERAGING BIOLOGICAL REPLICATES TO IMPROVE ANALYSIS IN CHIP-SEQ EXPERIMENTS. Computational and Structural Biotechnology Journal, 2014, 9, e201401002.	1.9	57
2762	Transcriptome profile analysis of adipose tissues from fat and short-tailed sheep. Gene, 2014, 549, 252-257.	1.0	71
2763	Genetic deletion of MT1/MT2 melatonin receptors enhances murine cognitive and motor performance. Neuroscience, 2014, 277, 506-521.	1.1	30
2764	Discovering Functional Modules by Topic Modeling RNA-Seq Based Toxicogenomic Data. Chemical Research in Toxicology, 2014, 27, 1528-1536.	1.7	13
2765	Diverse expression pattern of wheat transcription factors against abiotic stresses in wheat species. Gene, 2014, 550, 117-122.	1.0	41
2766	Regulation of the Human Endogenous Retrovirus K (HML-2) Transcriptome by the HIV-1 Tat Protein. Journal of Virology, 2014, 88, 8924-8935.	1.5	56
2767	RNA-seq of 272 gliomas revealed a novel, recurrent <i>PTPRZ1-MET</i> fusion transcript in secondary glioblastomas. Genome Research, 2014, 24, 1765-1773.	2.4	316
2768	Whole transcriptome RNA-seq analysis: tumorigenesis and metastasis of melanoma. Gene, 2014, 548, 234-243.	1.0	25
2769	Transgenerationally inherited piRNAs trigger piRNA biogenesis by changing the chromatin of piRNA clusters and inducing precursor processing. Genes and Development, 2014, 28, 1667-1680.	2.7	204
2770	<i>SMN2</i> splicing modifiers improve motor function and longevity in mice with spinal muscular atrophy. Science, 2014, 345, 688-693.	6.0	420
2771	Mining whole genomes and transcriptomes of Jatropha (Jatropha curcas) and Castor bean (Ricinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Biology Reports, 2014, 41, 7683-7695.	1.0	16
2772	RNA-Sequencing: A tool to explore new frontiers in animal genetics. Livestock Science, 2014, 166, 206-216.	0.6	53
2773	A new approach to determining whole viral genomic sequences including termini using a single deep sequencing run. Journal of Virological Methods, 2014, 208, 1-5.	1.0	16
2774	Identification of differentially expressed genes in flax (Linum usitatissimum L.) under saline&quot;alkaline stress by digital gene expression. Gene, 2014, 549, 113-122.	1.0	83
2775	Cell Contact&quot;Dependent Priming and Fc Interaction with CD32+ Immune Cells Contribute to the TGN1412-Triggered Cytokine Response. Journal of Immunology, 2014, 192, 2091-2098.	0.4	39
2776	READemption&quot;a tool for the computational analysis of deep-sequencing&quot;based transcriptome data. Bioinformatics, 2014, 30, 3421-3423.	1.8	180
2777	Antennal transcriptome analysis and comparison of olfactory genes in two sympatric defoliators, Dendrolimus houi and Dendrolimus kikuchii (Lepidoptera: Lasiocampidae). Insect Biochemistry and Molecular Biology, 2014, 52, 69-81.	1.2	74
2778	CellNet: Network Biology Applied to Stem Cell Engineering. Cell, 2014, 158, 903-915.	13.5	490

#	ARTICLE	IF	CITATIONS
2779	Diabetic nephropathyâ€™ emerging epigenetic mechanisms. <i>Nature Reviews Nephrology</i> , 2014, 10, 517-530.	4.1	277
2780	Lineage-Specific Transcriptional Profiles of <i>Symbiodinium</i> spp. Unaltered by Heat Stress in a Coral Host. <i>Molecular Biology and Evolution</i> , 2014, 31, 1343-1352.	3.5	135
2781	Major alterations in transcript profiles between C3â€™C4 and C4 photosynthesis of an amphibious species <i>Eleocharis baldwinii</i> . <i>Plant Molecular Biology</i> , 2014, 86, 93-110.	2.0	14
2782	Transcriptome Responses of the Host <i>Trichoplusia ni</i> to Infection by the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2014, 88, 13781-13797.	1.5	60
2783	Yeast Genetics. <i>Methods in Molecular Biology</i> , 2014, , .	0.4	14
2784	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies. , 2014, , 93-131.		1
2785	RNA-Seq Analysis Pipeline Based on Oshell Environment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 973-978.	1.9	9
2786	Effects of copper on CHO cells: Insights from gene expression analyses. <i>Biotechnology Progress</i> , 2014, 30, 429-442.	1.3	47
2787	PVT: An Efficient Computational Procedure to Speed up Next-generation Sequence Analysis. <i>BMC Bioinformatics</i> , 2014, 15, 167.	1.2	4
2788	An integrative method to normalize RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 188.	1.2	17
2789	Regression hidden Markov modeling reveals heterogeneous gene expression regulation: a case study in mouse embryonic stem cells. <i>BMC Genomics</i> , 2014, 15, 360.	1.2	4
2790	De novo assembly and transcriptome characterization: novel insights into the natural resistance mechanisms of <i>Microtus fortis</i> against <i>Schistosoma japonicum</i> . <i>BMC Genomics</i> , 2014, 15, 417.	1.2	10
2791	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. <i>BMC Genomics</i> , 2014, 15, 419.	1.2	262
2792	De novo assembly of red clover transcriptome based on RNA-Seq data provides insight into drought response, gene discovery and marker identification. <i>BMC Genomics</i> , 2014, 15, 453.	1.2	117
2793	Next-generation sequencing of small RNAs from inner ear sensory epithelium identifies microRNAs and defines regulatory pathways. <i>BMC Genomics</i> , 2014, 15, 484.	1.2	46
2794	Nucleosome organization in the vicinity of transcription factor binding sites in the human genome. <i>BMC Genomics</i> , 2014, 15, 493.	1.2	17
2795	Transcriptome analysis of callus from <i>Picea balfouriana</i> . <i>BMC Genomics</i> , 2014, 15, 553.	1.2	38
2796	Transcriptome analysis gene expression in the liver of <i>Coilia nasus</i> during the stress response. <i>BMC Genomics</i> , 2014, 15, 558.	1.2	36

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2797	Highly sensitive amplicon-based transcript quantification by semiconductor sequencing. <i>BMC Genomics</i> , 2014, 15, 565.	1.2	43
2798	RNA-Seq for gene identification and transcript profiling of three <i>Stevia rebaudiana</i> genotypes. <i>BMC Genomics</i> , 2014, 15, 571.	1.2	55
2799	Oil accumulation mechanisms of the oleaginous microalga <i>Chlorella protothecoides</i> revealed through its genome, transcriptomes, and proteomes. <i>BMC Genomics</i> , 2014, 15, 582.	1.2	134
2800	De novo sequencing and comparative analysis of holy and sweet basil transcriptomes. <i>BMC Genomics</i> , 2014, 15, 588.	1.2	113
2801	The transcriptional landscape of mouse beta cells compared to human beta cells reveals notable species differences in long non-coding RNA and protein-coding gene expression. <i>BMC Genomics</i> , 2014, 15, 620.	1.2	235
2802	All-Food-Seq (AFS): a quantifiable screen for species in biological samples by deep DNA sequencing. <i>BMC Genomics</i> , 2014, 15, 639.	1.2	62
2803	5-hydroxymethylcytosine represses the activity of enhancers in embryonic stem cells: a new epigenetic signature for gene regulation. <i>BMC Genomics</i> , 2014, 15, 670.	1.2	30
2804	Comparative transcriptome profiling of a desert evergreen shrub, <i>Ammopiptanthus mongolicus</i> , in response to drought and cold stresses. <i>BMC Genomics</i> , 2014, 15, 671.	1.2	79
2805	Influence of RNA extraction methods and library selection schemes on RNA-seq data. <i>BMC Genomics</i> , 2014, 15, 675.	1.2	139
2806	De novo transcriptome sequencing and digital gene expression analysis predict biosynthetic pathway of rhynchophylline and isorhynchophylline from <i>Uncaria rhynchophylla</i> , a non-model plant with potent anti-alzheimer's properties. <i>BMC Genomics</i> , 2014, 15, 676.	1.2	74
2807	Transcriptome sequencing of a chimaera reveals coordinated expression of anthocyanin biosynthetic genes mediating yellow formation in herbaceous peony ( <i>Paeonia lactiflora</i> Pall.). <i>BMC Genomics</i> , 2014, 15, 689.	1.2	80
2808	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014, 15, 703.	1.2	74
2809	Establishment and analysis of a reference transcriptome for <i>Spodoptera frugiperda</i> . <i>BMC Genomics</i> , 2014, 15, 704.	1.2	27
2810	Genome-wide transcriptome analysis shows extensive alternative RNA splicing in the zoonotic parasite <i>Schistosoma japonicum</i> . <i>BMC Genomics</i> , 2014, 15, 715.	1.2	15
2811	A memory-efficient algorithm to obtain splicing graphs and de novo expression estimates from de Bruijn graphs of RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, S6.	1.2	5
2812	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, S7.	1.2	15
2813	RNA-seq analyses of multiple meristems of soybean: novel and alternative transcripts, evolutionary and functional implications. <i>BMC Plant Biology</i> , 2014, 14, 169.	1.6	229
2814	The genetic basis for inactivation of Wnt pathway in human osteosarcoma. <i>BMC Cancer</i> , 2014, 14, 450.	1.1	50

#	ARTICLE	IF	CITATIONS
2815	Identification of rapidly induced genes in the response of peanut ( <i>Arachis hypogaea</i> ) to water deficit and abscisic acid. <i>BMC Biotechnology</i> , 2014, 14, 58.	1.7	38
2816	Conserved recurrent gene mutations correlate with pathway deregulation and clinical outcomes of lung adenocarcinoma in never-smokers. <i>BMC Medical Genomics</i> , 2014, 7, 32.	0.7	49
2817	De novo assembly and characterization of the transcriptome in the desiccation-tolerant moss <i>Syntrichia caninervis</i> . <i>BMC Research Notes</i> , 2014, 7, 490.	0.6	69
2818	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. <i>Parasites and Vectors</i> , 2014, 7, 242.	1.0	37
2819	De novo transcriptome sequencing and sequence analysis of the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Parasites and Vectors</i> , 2014, 7, 314.	1.0	29
2820	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014, 14, 213.	1.6	30
2821	Whole-genome bisulfite sequencing of multiple individuals reveals complementary roles of promoter and gene body methylation in transcriptional regulation. <i>Genome Biology</i> , 2014, 15, 408.	3.8	173
2822	Expanded identification and characterization of mammalian circular RNAs. <i>Genome Biology</i> , 2014, 15, 409.	3.8	1,361
2823	Non-exhaustive DNA methylation-mediated transposon silencing in the black truffle genome, a complex fungal genome with massive repeat element content. <i>Genome Biology</i> , 2014, 15, 411.	3.8	67
2824	SOAPdenovo-Trans: <i>de novo</i> transcriptome assembly with short RNA-Seq reads. <i>Bioinformatics</i> , 2014, 30, 1660-1666.	1.8	826
2825	Digital gene expression analysis in the gills of the swimming crab ( <i>Portunus trituberculatus</i> ) exposed to elevated ambient ammonia-N. <i>Aquaculture</i> , 2014, 434, 108-114.	1.7	48
2827	An Eriophyid Mite-Transmitted Plant Virus Contains Eight Genomic RNA Segments with Unusual Heterogeneity in the Nucleocapsid Protein. <i>Journal of Virology</i> , 2014, 88, 11834-11845.	1.5	90
2828	Identification of differentially expressed genes during development of the zebrafish pineal complex using RNA sequencing. <i>Developmental Biology</i> , 2014, 395, 144-153.	0.9	11
2829	Genome-wide transcriptional changes of ramie ( <i>Boehmeria nivea</i> L. Gaud) in response to root-lesion nematode infection. <i>Gene</i> , 2014, 552, 67-74.	1.0	30
2830	RNA- and Antibody-Based Profiling of the Human Proteome with Focus on Chromosome 19. <i>Journal of Proteome Research</i> , 2014, 13, 2019-2027.	1.8	8
2831	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. <i>Nature Biotechnology</i> , 2014, 32, 915-925.	9.4	217
2832	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	9.4	883
2833	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	9.4	420

#	ARTICLE	IF	CITATIONS
2834	Normalization of RNA-seq data using factor analysis of control genes or samples. <i>Nature Biotechnology</i> , 2014, 32, 896-902.	9.4	1,570
2835	Genome-wide screening and co-expression network analysis identify recurrence-specific biomarkers of esophageal squamous cell carcinoma. <i>Tumor Biology</i> , 2014, 35, 10959-10968.	0.8	8
2836	Comparative transcriptomic analysis to identify differentially expressed genes in fat tissue of adult Berkshire and Jeju Native Pig using RNA-seq. <i>Molecular Biology Reports</i> , 2014, 41, 6305-6315.	1.0	29
2837	Gene expression measurements normalized to cell number reveal large scale differences due to cell size changes, transcriptional amplification and transcriptional repression in CHO cells. <i>Journal of Biotechnology</i> , 2014, 189, 58-69.	1.9	13
2838	First study on gene expression of cement proteins and potential adhesion-related genes of a membranous-based barnacle as revealed from Next-Generation Sequencing technology. <i>Biofouling</i> , 2014, 30, 169-181.	0.8	51
2839	Molecular indexing enables quantitative targeted RNA sequencing and reveals poor efficiencies in standard library preparations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1891-1896.	3.3	90
2840	Single-cell analysis of the transcriptome and its application in the characterization of stem cells and early embryos. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 2707-2715.	2.4	31
2841	RNA sequencing: from tag-based profiling to resolving complete transcript structure. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 3537-3551.	2.4	33
2842	Bbssk1, a response regulator required for conidiation, multi-stress tolerance, and virulence of <i>Beauveria bassiana</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5607-5618.	1.7	13
2843	Oxidative stress response and nitrogen utilization are strongly variable in <i>Saccharomyces cerevisiae</i> wine strains with different fermentation performances. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4119-4135.	1.7	38
2844	Comparative transcriptomic analysis of the heat stress response in the filamentous fungus <i>Metarhizium anisopliae</i> using RNA-Seq. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5589-5597.	1.7	48
2845	Transcriptome dynamics of a desert poplar ( <i>Populus pruinosa</i> ) in response to continuous salinity stress. <i>Plant Cell Reports</i> , 2014, 33, 1565-1579.	2.8	42
2846	Identification of glutathione S-transferase genes responding to pathogen infestation in <i>Populus tomentosa</i> . <i>Functional and Integrative Genomics</i> , 2014, 14, 517-529.	1.4	36
2847	Disruption of hex1 in <i>Trichoderma atroviride</i> leads to loss of Woronin body and decreased tolerance to dichlorvos. <i>Biotechnology Letters</i> , 2014, 36, 751-759.	1.1	6
2848	Age-associated changes in bovine oocytes and granulosa cell complexes collected from early antral follicles. <i>Journal of Assisted Reproduction and Genetics</i> , 2014, 31, 1079-1088.	1.2	13
2849	RNA-seq methods for identifying differentially expressed gene in human pancreatic islet cells treated with pro-inflammatory cytokines. <i>Molecular Biology Reports</i> , 2014, 41, 1917-1925.	1.0	13
2850	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	6.0	542
2851	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318

#	ARTICLE	IF	CITATIONS
2852	Global transcriptional analysis reveals surface remodeling of <i>Anaplasma marginale</i> in the tick vector. <i>Parasites and Vectors</i> , 2014, 7, 193.	1.0	11
2853	Reproducibility and reliability assays of the gene expression-measurements. <i>Journal of Biological Research</i> , 2014, 21, 3.	2.2	6
2854	KDM5B focuses H3K4 methylation near promoters and enhancers during embryonic stem cell self-renewal and differentiation. <i>Genome Biology</i> , 2014, 15, R32.	13.9	120
2855	Alternative splicing regulates vesicular trafficking genes in cardiomyocytes during postnatal heart development. <i>Nature Communications</i> , 2014, 5, 3603.	5.8	133
2856	Controlling for Gene Expression Changes in Transcription Factor Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1510-1522.	2.5	23
2857	Exploring the transcriptome space of a recombinant BHK cell line through next generation sequencing. <i>Biotechnology and Bioengineering</i> , 2014, 111, 770-781.	1.7	11
2858	Direct ChIP-bisulfite sequencing reveals a role of H3K27me3 mediating aberrant hypermethylation of promoter CpG islands in cancer cells. <i>Genomics</i> , 2014, 103, 204-210.	1.3	37
2859	Altered Gamma-Aminobutyric Acid Type B Receptor Subunit 1 Splicing In Alcoholics. <i>Biological Psychiatry</i> , 2014, 75, 765-773.	0.7	30
2860	Profiling post-transcriptionally networked mRNA subsets using RIP-Chip and RIP-Seq. <i>Methods</i> , 2014, 67, 13-19.	1.9	29
2861	Computational Analysis of Conserved RNA Secondary Structure in Transcriptomes and Genomes. <i>Annual Review of Biophysics</i> , 2014, 43, 433-456.	4.5	118
2862	Developmental transcriptome analysis of human erythropoiesis. <i>Human Molecular Genetics</i> , 2014, 23, 4528-4542.	1.4	45
2863	Comparative transcriptomic analysis of the regulation of flowering in temperate and tropical lotus ( <i>Nelumbo nucifera</i> ) by <i>scRNA-seq</i> . <i>Annals of Applied Biology</i> , 2014, 165, 73-95.	1.3	26
2864	The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumour subtypes. <i>Nature Communications</i> , 2014, 5, 3963.	5.8	143
2865	Evolutionary Origin and Human-Specific Expansion of a Cancer/Testis Antigen Gene Family. <i>Molecular Biology and Evolution</i> , 2014, 31, 2365-2375.	3.5	15
2866	Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. <i>Nature</i> , 2014, 511, 488-492.	13.7	411
2867	Identification of reference genes for qRT-PCR in human lung squamous-cell carcinoma by RNA-Seq. <i>Acta Biochimica Et Biophysica Sinica</i> , 2014, 46, 330-337.	0.9	52
2868	Identification and characterization of long intergenic non-coding RNAs related to mouse liver development. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1225-1235.	1.0	28
2869	Transcriptomic analysis demonstrates the early responses of local ethylene and redox signaling to low iron stress in <i>Malus xiaojinensis</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 573-584.	0.6	15

#	ARTICLE	IF	CITATIONS
2870	The Use of Molecular Genetics to Refine Prognosis in Acute Myeloid Leukemia. <i>Current Hematologic Malignancy Reports</i> , 2014, 9, 148-157.	1.2	9
2871	Identification of novel reference genes using sika deer antler transcriptome expression data and their validation for quantitative gene expression analysis. <i>Genes and Genomics</i> , 2014, 36, 573-582.	0.5	9
2872	Computational approaches for isoform detection and estimation: good and bad news. <i>BMC Bioinformatics</i> , 2014, 15, 135.	1.2	26
2873	A multivariate approach to the integration of multi-omics datasets. <i>BMC Bioinformatics</i> , 2014, 15, 162.	1.2	238
2874	DAFS: a data-adaptive flag method for RNA-sequencing data to differentiate genes with low and high expression. <i>BMC Bioinformatics</i> , 2014, 15, 92.	1.2	32
2875	Identification of differentially expressed genes between sorghum genotypes with contrasting nitrogen stress tolerance by genome-wide transcriptional profiling. <i>BMC Genomics</i> , 2014, 15, 179.	1.2	118
2876	Transcriptional profiling of mammary gland in Holstein cows with extremely different milk protein and fat percentage using RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 226.	1.2	138
2877	Transcriptome analysis identifies <i>Bacillus anthracis</i> genes that respond to CO <sub>2</sub> through an AtxA-dependent mechanism. <i>BMC Genomics</i> , 2014, 15, 229.	1.2	20
2878	SFGD: a comprehensive platform for mining functional information from soybean transcriptome data and its use in identifying acyl-lipid metabolism pathways. <i>BMC Genomics</i> , 2014, 15, 271.	1.2	43
2879	A house finch ( <i>Haemorhous mexicanus</i> ) spleen transcriptome reveals intra- and interspecific patterns of gene expression, alternative splicing and genetic diversity in passerines. <i>BMC Genomics</i> , 2014, 15, 305.	1.2	12
2880	Deep mRNA sequencing reveals stage-specific transcriptome alterations during microsclerotia development in the smoke tree vascular wilt pathogen, <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2014, 15, 324.	1.2	68
2881	Deep-sequencing transcriptome analysis of low temperature perception in a desert tree, <i>Populus euphratica</i> . <i>BMC Genomics</i> , 2014, 15, 326.	1.2	54
2882	EXPRSS: an Illumina based high-throughput expression-profiling method to reveal transcriptional dynamics. <i>BMC Genomics</i> , 2014, 15, 341.	1.2	36
2883	XSAAnno: a framework for building ortholog models in cross-species transcriptome comparisons. <i>BMC Genomics</i> , 2014, 15, 343.	1.2	27
2884	Comparison of strand-specific transcriptomes of enterohemorrhagic <i>Escherichia coli</i> O157:H7 EDL933 (EHEC) under eleven different environmental conditions including radish sprouts and cattle feces. <i>BMC Genomics</i> , 2014, 15, 353.	1.2	56
2885	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. <i>BMC Genomics</i> , 2014, 15, 398.	1.2	16
2886	The large-scale investigation of gene expression in <i>Leymus chinensis</i> stigmas provides a valuable resource for understanding the mechanisms of poaceae self-incompatibility. <i>BMC Genomics</i> , 2014, 15, 399.	1.2	22
2887	Characterization of a genetic mouse model of lung cancer: a promise to identify Non-Small Cell Lung Cancer therapeutic targets and biomarkers. <i>BMC Genomics</i> , 2014, 15, S1.	1.2	20

#	ARTICLE	IF	CITATIONS
2888	Differential activation of sporamin expression in response to abiotic mechanical wounding and biotic herbivore attack in the sweet potato. <i>BMC Plant Biology</i> , 2014, 14, 112.	1.6	29
2889	A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype. <i>BMC Plant Biology</i> , 2014, 14, 99.	1.6	254
2890	Transcriptional profiling of the host cell response to feline immunodeficiency virus infection. <i>Virology Journal</i> , 2014, 11, 52.	1.4	28
2891	Software for pre-processing Illumina next-generation sequencing short read sequences. <i>Source Code for Biology and Medicine</i> , 2014, 9, 8.	1.7	196
2892	Network topology-based detection of differential gene regulation and regulatory switches in cell metabolism and signaling. <i>BMC Systems Biology</i> , 2014, 8, 56.	3.0	0
2893	The common ground of genomics and systems biology. <i>BMC Systems Biology</i> , 2014, 8, S1.	3.0	22
2894	The global landscape of intron retentions in lung adenocarcinoma. <i>BMC Medical Genomics</i> , 2014, 7, 15.	0.7	32
2895	The human testis-specific proteome defined by transcriptomics and antibody-based profiling. <i>Molecular Human Reproduction</i> , 2014, 20, 476-488.	1.3	189
2896	Heterogeneity in Asthma. <i>Advances in Experimental Medicine and Biology</i> , 2014, , .	0.8	1
2897	A new model for electron flow during anaerobic digestion: direct interspecies electron transfer to <i>Methanosaeta</i> for the reduction of carbon dioxide to methane. <i>Energy and Environmental Science</i> , 2014, 7, 408-415.	15.6	1,074
2898	Genomics of homoploid hybrid speciation: diversity and transcriptional activity of long terminal repeat retrotransposons in hybrid sunflowers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130345.	1.8	46
2899	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	9.0	31
2900	Exosomes in human semen carry a distinctive repertoire of small non-coding RNAs with potential regulatory functions. <i>Nucleic Acids Research</i> , 2014, 42, 7290-7304.	6.5	486
2901	A New Toolbox for Assessing Single Cells. <i>Annual Review of Chemical and Biomolecular Engineering</i> , 2014, 5, 455-477.	3.3	33
2902	Understanding Complex Transcriptome Dynamics in Schizophrenia and Other Neurological Diseases Using RNA Sequencing. <i>International Review of Neurobiology</i> , 2014, 116, 127-152.	0.9	5
2903	Predicting the Important Enzymes in Human Breast Milk Digestion. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 7225-7232.	2.4	55
2904	An integrative analysis of the transcriptome and proteome of the pulp of a spontaneous late-ripening sweet orange mutant and its wild type improves our understanding of fruit ripening in citrus. <i>Journal of Experimental Botany</i> , 2014, 65, 1651-1671.	2.4	129
2905	Defining the Human Adipose Tissue Proteome To Reveal Metabolic Alterations in Obesity. <i>Journal of Proteome Research</i> , 2014, 13, 5106-5119.	1.8	55



#	ARTICLE	IF	CITATIONS
2906	Transcriptome profiling of <i>Vitis amurens</i> , an extremely cold-tolerant Chinese wild <i>Vitis</i> species, reveals candidate genes and events that potentially connected to cold stress. <i>Plant Molecular Biology</i> , 2014, 86, 527-541.	2.0	84
2907	Transcriptome comparison between inactivated and activated ovaries of the honey bee <i>Apis mellifera</i> . <i>Insect Molecular Biology</i> , 2014, 23, 668-681.	1.0	36
2908	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
2909	Pseudogenes. <i>Methods in Molecular Biology</i> , 2014, 1167, v.	0.4	5
2910	<i>S. taphylococcus aureus</i> competence genes: mapping of the <i>SigH</i> , <i>ComK</i> 1 and <i>ComK</i> 2 regulons by transcriptome sequencing. <i>Molecular Microbiology</i> , 2014, 94, 557-579.	1.2	53
2911	Chromosome-8-Coded Proteome of Chinese Chromosome Proteome Data Set (CCPD) 2.0 with Partial Immunohistochemical Verifications. <i>Journal of Proteome Research</i> , 2014, 13, 126-136.	1.8	11
2912	RNA-Seq Reveals Novel Transcriptional Reorganization in Human Alcoholic Brain. <i>International Review of Neurobiology</i> , 2014, 116, 275-300.	0.9	50
2913	Deep sequencing-based transcriptome profiling analysis of <i>Chlamys farreri</i> exposed to benzo[a]pyrene. <i>Gene</i> , 2014, 551, 261-270.	1.0	28
2914	Data Integration and Reproducibility for High-Throughput Transcriptomics. <i>International Review of Neurobiology</i> , 2014, 116, 55-71.	0.9	3
2915	Functional Annotation of <i>Cotesia congregata</i> Bracovirus: Identification of Viral Genes Expressed in Parasitized Host Immune Tissues. <i>Journal of Virology</i> , 2014, 88, 8795-8812.	1.5	56
2916	The Cysteine Protease CEP1, a Key Executor Involved in Tapetal Programmed Cell Death, Regulates Pollen Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2939-2961.	3.1	187
2917	Classification of RNA-seq Data. , 2014, , 219-246.		11
2918	Transcriptome Profiling Identifies Differentially Expressed Genes in Postnatal Developing Pituitary Gland of Miniature Pig. <i>DNA Research</i> , 2014, 21, 207-216.	1.5	36
2919	Resolving Chromosome-Centric Human Proteome with Translating mRNA Analysis: A Strategic Demonstration. <i>Journal of Proteome Research</i> , 2014, 13, 50-59.	1.8	38
2920	Cluster Analysis of RNA-Sequencing Data. , 2014, , 191-217.		9
2921	RNASeqGUI: a GUI for analysing RNA-Seq data. <i>Bioinformatics</i> , 2014, 30, 2514-2516.	1.8	39
2922	BRIC-seq: A genome-wide approach for determining RNA stability in mammalian cells. <i>Methods</i> , 2014, 67, 55-63.	1.9	64
2923	Gene expression patterns associated with caste and reproductive status in ants: worker-specific genes are more derived than queen-specific ones. <i>Molecular Ecology</i> , 2014, 23, 151-161.	2.0	112

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2924	A Novel Statistical Approach for Jointly Analyzing RNA-Seq Data from F1 Reciprocal Crosses and Inbred Lines. <i>Genetics</i> , 2014, 197, 389-399.	1.2	21
2925	Nucleus accumbens neuronal maturation differences in young rats bred for low <i>versus</i> high voluntary running behaviour. <i>Journal of Physiology</i> , 2014, 592, 2119-2135.	1.3	38
2926	Characterization of the house sparrow ( <i>Passer domesticus</i> ) transcriptome: a resource for molecular ecology and immunogenetics. <i>Molecular Ecology Resources</i> , 2014, 14, 636-646.	2.2	14
2927	Advancing avian behavioral neuroendocrinology through genomics. <i>Frontiers in Neuroendocrinology</i> , 2014, 35, 58-71.	2.5	7
2928	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	1.2	40
2929	Midgut transcriptome response to a Cry toxin in the diamondback moth, <i>Plutella xylostella</i> (Lepidoptera: Plutellidae). <i>Gene</i> , 2014, 533, 180-187.	1.0	82
2930	Identification of endometrioid endometrial carcinoma-associated microRNAs in tissue and plasma. <i>Gynecologic Oncology</i> , 2014, 132, 715-721.	0.6	74
2931	RNA-seq dependent transcriptional analysis unveils gene expression profile in the intestine of sea cucumber <i>Apostichopus japonicus</i> during aestivation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014, 10, 30-43.	0.4	28
2932	Transcriptomic profiles of <i>Aspergillus flavus</i> CA42, a strain that produces small sclerotia, by decanal treatment and after recovery. <i>Fungal Genetics and Biology</i> , 2014, 68, 39-47.	0.9	20
2933	Genome-wide analysis of the GRAS gene family in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Genomics</i> , 2014, 103, 135-146.	1.3	114
2934	Current status and future prospects of toxicogenomics in drug discovery. <i>Drug Discovery Today</i> , 2014, 19, 562-578.	3.2	32
2935	Large-scale imaginal disc sorting: A protocol for genomics approaches. <i>Methods</i> , 2014, 68, 260-264.	1.9	7
2936	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014, 103, 189-203.	1.3	49
2937	Transcriptomic dissection of myogenic differentiation signature in caprine by RNA-Seq. <i>Mechanisms of Development</i> , 2014, 132, 79-92.	1.7	18
2938	Transcriptomic profiling of cartilage ageing. <i>Genomics Data</i> , 2014, 2, 27-28.	1.3	10
2939	Bovine and murine tissue expression of insulin like growth factor-I. <i>Gene</i> , 2014, 535, 101-105.	1.0	5
2940	Genome-Wide Analysis of Heat-Sensitive Alternative Splicing in <i>Physcomitrella patens</i> . <i>Plant Physiology</i> , 2014, 165, 826-840.	2.3	119
2941	The combination of transcriptomics and informatics identifies pathways targeted by miR-204 during neurogenesis and axon guidance. <i>Nucleic Acids Research</i> , 2014, 42, 7793-7806.	6.5	31

#	ARTICLE	IF	CITATIONS
2942	<i>Arabidopsis</i> Phytochrome A Directly Targets Numerous Promoters for Individualized Modulation of Genes in a Wide Range of Pathways. <i>Plant Cell</i> , 2014, 26, 1949-1966.	3.1	73
2943	Quantitative proteome profiling of lymph node-positive vs. -negative colorectal carcinomas pinpoints MX1 as a marker for lymph node metastasis. <i>International Journal of Cancer</i> , 2014, 135, 2878-2886.	2.3	21
2944	RNA-Seq and expression microarray highlight different aspects of the fetal amniotic fluid transcriptome. <i>Prenatal Diagnosis</i> , 2014, 34, 1006-1014.	1.1	17
2945	Identification of the involvement of LOXL4 in generation of keratocystic odontogenic tumors by RNA-Seq analysis. <i>International Journal of Oral Science</i> , 2014, 6, 31-38.	3.6	21
2946	Inference of interactions in cyanobacterial-heterotrophic co-cultures via transcriptome sequencing. <i>ISME Journal</i> , 2014, 8, 2243-2255.	4.4	75
2947	Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogen <i>Rhizoctonia solani</i> AG-3. <i>FEMS Microbiology Letters</i> , 2014, 352, 165-173.	0.7	143
2948	New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology. <i>Journal of Arachnology</i> , 2014, 42, 1-15.	0.3	16
2949	A silent mutation in <i>mabA</i> confers isoniazid resistance on <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2014, 91, 538-547.	1.2	59
2950	Transcriptome characterization and sequencing-based identification of drought-responsive genes in potato. <i>Molecular Biology Reports</i> , 2014, 41, 505-517.	1.0	53
2951	GIIRA-RNA-Seq driven gene finding incorporating ambiguous reads. <i>Bioinformatics</i> , 2014, 30, 606-613.	1.8	10
2952	Nitrogen-Sparing Mechanisms in <i>Chlamydomonas</i> Affect the Transcriptome, the Proteome, and Photosynthetic Metabolism. <i>Plant Cell</i> , 2014, 26, 1410-1435.	3.1	314
2953	Transcriptome analysis of grain-filling caryopses reveals the potential formation mechanism of the rice sugary mutant. <i>Gene</i> , 2014, 546, 318-326.	1.0	9
2954	Deep RNA Sequencing Reveals that MicroRNAs Play a Key Role in Lactation in Rats. <i>Journal of Nutrition</i> , 2014, 144, 1142-1149.	1.3	30
2955	Methyl jasmonate represses growth and affects cell cycle progression in cultured <i>Taxus</i> cells. <i>Plant Cell Reports</i> , 2014, 33, 1479-1492.	2.8	53
2956	MetaRef: a pan-genomic database for comparative and community microbial genomics. <i>Nucleic Acids Research</i> , 2014, 42, D617-D624.	6.5	51
2957	Comparative transcriptomic analysis by RNA-seq to discern differential expression of genes in liver and muscle tissues of adult Berkshire and Jeju Native Pig. <i>Gene</i> , 2014, 546, 233-242.	1.0	26
2958	Transcriptomic Response to <i>Yersinia pestis</i> : RIG-I Like Receptor Signaling Response Is Detrimental to the Host against Plague. <i>Journal of Genetics and Genomics</i> , 2014, 41, 379-396.	1.7	18
2959	Global gene expression analysis following spinal cord injury in non-human primates. <i>Experimental Neurology</i> , 2014, 261, 171-179.	2.0	33

#	ARTICLE	IF	CITATIONS
2960	Gene Expression Change in Human Dental Pulp Cells Exposed to a Low-Level Toxic Concentration of Triethylene Glycol Dimethacrylate: An RNA-seq Analysis. <i>Basic and Clinical Pharmacology and Toxicology</i> , 2014, 115, 282-290.	1.2	18
2961	Nutrients drive transcriptional changes that maintain metabolic homeostasis but alter genome architecture in <i>Microcystis</i> . <i>ISME Journal</i> , 2014, 8, 2080-2092.	4.4	84
2962	AroER Tri-Screen Is a Biologically Relevant Assay for Endocrine Disrupting Chemicals Modulating the Activity of Aromatase and/or the Estrogen Receptor. <i>Toxicological Sciences</i> , 2014, 139, 198-209.	1.4	27
2963	RNA-seq profiles from grass carp tissues after reovirus (GCRV) infection based on singular and modular enrichment analyses. <i>Molecular Immunology</i> , 2014, 61, 44-53.	1.0	65
2964	Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. <i>Journal of Proteomics</i> , 2014, 108, 269-283.	1.2	43
2965	Emergence of tissue sensitivity to Hox protein levels underlies the evolution of an adaptive morphological trait. <i>Developmental Biology</i> , 2014, 392, 441-453.	0.9	41
2966	Filaggrin-stratified transcriptomic analysis of pediatric skin identifies mechanistic pathways in patients with atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 134, 82-91.	1.5	118
2967	Analysis of multiple transcriptomes of the African oil palm ( <i>Elaeis guineensis</i> ) to identify reference genes for RT-qPCR. <i>Journal of Biotechnology</i> , 2014, 184, 63-73.	1.9	42
2968	A role of placental growth factor in hair growth. <i>Journal of Dermatological Science</i> , 2014, 74, 125-134.	1.0	29
2969	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. <i>Briefings in Bioinformatics</i> , 2014, 15, 592-611.	3.2	30
2970	VITIS VINIFERA GENOME ANNOTATION IMPROVEMENT USING NEXT-GENERATION SEQUENCING TECHNOLOGIES AND NCBI PUBLIC DATA. <i>Acta Horticulturae</i> , 2014, , 349-356.	0.1	1
2971	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	2.4	21
2972	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. <i>Scientific Data</i> , 2014, 1, 140013.	2.4	22
2973	Profiling Individual Human Embryonic Stem Cells by Quantitative RT-PCR. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	3
2974	RNA-Seq Analysis of Differential Gene Expression in Electroporated Chick Embryonic Spinal Cord. <i>Journal of Visualized Experiments</i> , 2014, , e51951.	0.2	1
2975	Promoter Analysis Reveals Globally Differential Regulation of Human Long Non-Coding RNA and Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e109443.	1.1	72
2976	Unravelling the Transcriptome Profile of the Swine Respiratory Tract Mycoplasmas. <i>PLoS ONE</i> , 2014, 9, e110327.	1.1	34
2977	An iteration normalization and test method for differential expression analysis of RNA-seq data. <i>BioData Mining</i> , 2014, 7, 15.	2.2	8

#	ARTICLE	IF	CITATIONS
2978	Physiological Recordings and RNA Sequencing of the Gustatory Appendages of the Yellow-fever Mosquito <i>Aedes aegypti</i> . <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	1
2979	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES. , 2014, , .		14
2980	Identification of SSRs and differentially expressed genes in two cultivars of celery ( <i>Apium graveolens</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.9	116
2981	A tour through the transcriptional landscape of platelets. <i>Blood</i> , 2014, 124, 493-502.	0.6	103
2982	Quantifying alternative splicing from paired-end RNA-sequencing data. <i>Annals of Applied Statistics</i> , 2014, 8, 309-330.	0.5	38
2984	RNA-seq analysis of synovial fibroblasts in human rheumatoid arthritis. <i>Molecular Medicine Reports</i> , 2014, 10, 241-247.	1.1	20
2986	Smads as muscle biomarkers in amyotrophic lateral sclerosis. <i>Annals of Clinical and Translational Neurology</i> , 2014, 1, 778-787.	1.7	23
2987	Quality Control for RNA-Seq (QuaCRS): An Integrated Quality Control Pipeline. <i>Cancer Informatics</i> , 2014, 13s3, CIN.S14022.	0.9	33
2988	Bootstrap-based differential gene expression analysis for RNA-Seq data with and without replicates. <i>BMC Genomics</i> , 2014, 15, S2.	1.2	48
2990	On the complexity of Minimum Path Cover with Subpath Constraints for multi-assembly. <i>BMC Bioinformatics</i> , 2014, 15, S5.	1.2	23
2991	Transcriptome sequencing of transgenic poplar ( <i>Populus Æ— euramericana</i> 'Guariento') expressing multiple resistance genes. <i>BMC Genetics</i> , 2014, 15, S7.	2.7	23
2992	TIGAR2: sensitive and accurate estimation of transcript isoform expression with longer RNA-Seq reads. <i>BMC Genomics</i> , 2014, 15, S5.	1.2	36
2993	LFCseq: a nonparametric approach for differential expression analysis of RNA-seq data. <i>BMC Genomics</i> , 2014, 15, S7.	1.2	16
2994	â—¼ Quality Control and Preprocessing. , 2014, , 66-87.		1
2995	A comparison of microRNA sequencing reproducibility and noise reduction using mirVana and TRlzol isolation methods. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 102.	0.3	11
2996	Correcting imbalanced reads coverage in bacterial transcriptome sequencing with extreme deep coverage. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 195.	0.3	0
2997	Alternative Splicing. , 2015, , 545-556.		1
2998	Impact of a short-term exposure to spaceflight on the phenotype, genome, transcriptome and proteome of <i>Escherichia coli</i> . <i>International Journal of Astrobiology</i> , 2015, 14, 435-444.	0.9	10

#	ARTICLE	IF	CITATIONS
2999	Analysis of cutaneous MRGPRD free nerve endings and C-LTMRs transcriptomes by RNA-sequencing. <i>Genomics Data</i> , 2015, 5, 132-135.	1.3	4
3000	Next generation sequencing profiling identifies miR-574-3p and miR-660-5p as potential novel prognostic markers for breast cancer. <i>BMC Genomics</i> , 2015, 16, 735.	1.2	73
3001	The potential of circulating extracellular small RNAs (smexRNA) in veterinary diagnosticsâ€”Identifying biomarker signatures by multivariate data analysis. <i>Biomolecular Detection and Quantification</i> , 2015, 5, 15-22.	7.0	12
3002	RNA sequencing of the nephron transcriptome: a technical note. <i>Kidney Research and Clinical Practice</i> , 2015, 34, 219-227.	0.9	1
3003	Gonadal transcriptomic analysis and differentially expressed genes in the testis and ovary of the Pacific white shrimp ( <i>Litopenaeus vannamei</i> ). <i>BMC Genomics</i> , 2015, 16, 1006.	1.2	72
3004	Dormant non-culturable <i>Mycobacterium tuberculosis</i> retains stable low-abundant mRNA. <i>BMC Genomics</i> , 2015, 16, 954.	1.2	89
3005	Genome-wide expression profiles of <i>Pyropia haitanensis</i> in response to osmotic stress by using deep sequencing technology. <i>BMC Genomics</i> , 2015, 16, 1012.	1.2	26
3006	MicroRNA regulation of p21 and TASK1 cellular restriction-factors enhances HIV-1 infection. <i>Journal of Cell Science</i> , 2015, 128, 1607-16.	1.2	51
3007	Use of RNA sequencing to evaluate rheumatic disease patients. <i>Arthritis Research and Therapy</i> , 2015, 17, 167.	1.6	23
3008	Transcriptome changes in <i>Polygonum multiflorum</i> Thunb. roots induced by methyl jasmonate. <i>Journal of Zhejiang University: Science B</i> , 2015, 16, 1027-1041.	1.3	6
3009	Interpretable deep neural networks for enhancer prediction. , 2015, , .		2
3010	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015, 16, 215.	3.8	41
3011	Renal iron overload in rats with diabetic nephropathy. <i>Physiological Reports</i> , 2015, 3, e12654.	0.7	25
3012	Transcriptome Analysis of Nine Tissues to Discover Genes Involved in the Biosynthesis of Active Ingredients in <i>Sophora flavescens</i> , <i>Biological and Pharmaceutical Bulletin</i> , 2015, 38, 876-883.	0.6	22
3013	Methods for biological data integration: perspectives and challenges. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150571.	1.5	196
3014	Highly informative marker sets consisting of genes with low individual degree of differential expression. <i>Scientific Reports</i> , 2015, 5, 14967.	1.6	24
3015	Verifying the markers of ovarian cancer using RNA-seq data. <i>Molecular Medicine Reports</i> , 2015, 12, 1125-1130.	1.1	6
3016	Central role of Th2/Tc2 lymphocytes in pattern <sc>II</sc> multiple sclerosis lesions. <i>Annals of Clinical and Translational Neurology</i> , 2015, 2, 875-893.	1.7	45

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3017	Bayesian factor models for the detection of coherent patterns in gene expression data. <i>Brazilian Journal of Probability and Statistics</i> , 2015, 29, .	0.1	4
3018	Autophagy limits proliferation and glycolytic metabolism in acute myeloid leukemia. <i>Cell Death Discovery</i> , 2015, 1, .	2.0	125
3020	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	1.6	69
3021	Revealing crosstalk of plant and fungi in the symbiotic roots of sewage-cleaning <i>Eichhornia crassipes</i> using direct de novo metatranscriptomic analysis. <i>Scientific Reports</i> , 2015, 5, 15407.	1.6	15
3022	Complete mitochondrial genome of the medicinal fungus <i>Ophiocordyceps sinensis</i> . <i>Scientific Reports</i> , 2015, 5, 13892.	1.6	78
3023	Microbial metabolic networks in a complex electrogenic biofilm recovered from a stimulus-induced metatranscriptomics approach. <i>Scientific Reports</i> , 2015, 5, 14840.	1.6	44
3024	Transcriptomic Analysis of the Regulation of Rhizome Formation in Temperate and Tropical Lotus ( <i>Nelumbo nucifera</i> ). <i>Scientific Reports</i> , 2015, 5, 13059.	1.6	101
3025	Regulation of transcription factors on sexual dimorphism of fig wasps. <i>Scientific Reports</i> , 2015, 5, 10696.	1.6	2
3026	Wavelet-based genetic association analysis of functional phenotypes arising from high-throughput sequencing assays. <i>Annals of Applied Statistics</i> , 2015, 9, 655-686.	0.5	22
3027	Ribosomal profiling adds new coding sequences to the proteome. <i>Biochemical Society Transactions</i> , 2015, 43, 1271-1276.	1.6	35
3029	Identification and comparative expression analysis of odorant binding protein genes in the tobacco cutworm <i>Spodoptera litura</i> . <i>Scientific Reports</i> , 2015, 5, 13800.	1.6	75
3030	Comparative transcriptomic analysis of silkworm <i>Bmovo-1</i> and wild type silkworm ovary. <i>Scientific Reports</i> , 2015, 5, 17867.	1.6	6
3031	Genome-wide analysis of enhancer RNA in gene regulation across 12 mouse tissues. <i>Scientific Reports</i> , 2015, 5, 12648.	1.6	56
3032	Genome-wide identification and characterization of reference genes with different transcript abundances for <i>Streptomyces coelicolor</i> . <i>Scientific Reports</i> , 2015, 5, 15840.	1.6	27
3033	Transcriptome analysis identifies genes involved in adventitious branches formation of <i>Gracilaria lichenoides</i> in vitro. <i>Scientific Reports</i> , 2015, 5, 17099.	1.6	24
3034	A <i>Phytophthora sojae</i> cytoplasmic effector mediates disease resistance and abiotic stress tolerance in <i>Nicotiana benthamiana</i> . <i>Scientific Reports</i> , 2015, 5, 10837.	1.6	39
3035	VisRseq: R-based visual framework for analysis of sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, S2.	1.2	66
3036	The <i>scp</i> RNA-binding protein Arrest (Bruno) regulates alternative splicing to enable myofibril maturation in <i>Drosophila</i> flight muscle. <i>EMBO Reports</i> , 2015, 16, 178-191.	2.0	57

#	ARTICLE	IF	CITATIONS
3037	Characterization of <i>Adelphocoris suturalis</i> (Hemiptera: Miridae) Transcriptome from Different Developmental Stages. <i>Scientific Reports</i> , 2015, 5, 11042.	1.6	17
3038	High-throughput transcriptome sequencing of the cold seep mussel <i>Bathymodiolus platifrons</i> . <i>Scientific Reports</i> , 2015, 5, 16597.	1.6	78
3039	Characterization of the Transcriptional Complexity of the Receptive and Pre-receptive Endometria of Dairy Goats. <i>Scientific Reports</i> , 2015, 5, 14244.	1.6	28
3040	Identification, characterization and molecular analysis of the viable but nonculturable <i>Rhodococcus biphenylivorans</i> . <i>Scientific Reports</i> , 2015, 5, 18590.	1.6	86
3041	Horizontal functional gene transfer from bacteria to fishes. <i>Scientific Reports</i> , 2015, 5, 18676.	1.6	9
3042	Identification of Genes Associated with Smad3-dependent Renal Injury by RNA-seq-based Transcriptome Analysis. <i>Scientific Reports</i> , 2015, 5, 17901.	1.6	20
3043	mirPro—a novel standalone program for differential expression and variation analysis of miRNAs. <i>Scientific Reports</i> , 2015, 5, 14617.	1.6	36
3044	<i>Gossypium barbadense</i> genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. <i>Scientific Reports</i> , 2015, 5, 14139.	1.6	271
3045	Comparative transcriptome analysis of grapevine in response to copper stress. <i>Scientific Reports</i> , 2015, 5, 17749.	1.6	104
3046	Genome-wide expression analysis offers new insights into the origin and evolution of <i>Physcomitrella patens</i> stress response. <i>Scientific Reports</i> , 2015, 5, 17434.	1.6	54
3047	Probiotic <i>Bifidobacterium longum</i> alters gut luminal metabolism through modification of the gut microbial community. <i>Scientific Reports</i> , 2015, 5, 13548.	1.6	126
3048	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. <i>Scientific Reports</i> , 2015, 5, 13517.	1.6	144
3049	Neuropeptides in the cerebral ganglia of the mud crab, <i>Scylla paramamosain</i> : transcriptomic analysis and expression profiles during vitellogenesis. <i>Scientific Reports</i> , 2015, 5, 17055.	1.6	96
3050	mRNA Levels of Imprinted Genes in Bovine In Vivo Oocytes, Embryos and Cross Species Comparisons with Humans, Mice and Pigs. <i>Scientific Reports</i> , 2015, 5, 17898.	1.6	33
3051	Leveraging a Multi-Omics Strategy for Prioritizing Personalized Candidate Mutation-Driver Genes: A Proof-of-Concept Study. <i>Scientific Reports</i> , 2015, 5, 17564.	1.6	13
3053	Global transcriptional and miRNA insights into bases of heterosis in hybridization of Cyprinidae. <i>Scientific Reports</i> , 2015, 5, 13847.	1.6	25
3054	Feeding conditions and breed affect the level of DNA methylation of the mitochondrial uncoupling protein 3 gene in chicken breast muscle1. <i>Journal of Animal Science</i> , 2015, 93, 1522-1534.	0.2	9
3055	TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S23873.	0.6	37



#	ARTICLE	IF	CITATIONS
3056	Genome-wide Identification of WRKY Genes in the Desert Poplar <i>Populus euphratica</i> and Adaptive Evolution of the Genes in Response to Salt Stress. <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S22067.	0.6	20
3057	Reverse enGENEering of Regulatory Networks from Big Data: A Roadmap for Biologists. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12467.	1.0	38
3058	A balanced method detecting differentially expressed genes for RNA-sequencing data**This work is supported by NSFC grant (No. 61472086) to Fei Wang. <i>IFAC-PapersOnLine</i> , 2015, 48, 27-32.	0.5	0
3059	CADBURE: A generic tool to evaluate the performance of spliced aligners on RNA-Seq data. <i>Scientific Reports</i> , 2015, 5, 13443.	1.6	7
3060	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
3061	An NGS Workflow Blueprint for DNA Sequencing Data and Its Application in Individualized Molecular Oncology. <i>Cancer Informatics</i> , 2015, 14s5, CIN.S30793.	0.9	10
3062	Differential Expression Analysis for RNA-Seq: An Overview of Statistical Methods and Computational Software. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S21631.	0.9	23
3063	RNAi knockdown of acetyl-CoA carboxylase gene eliminates jinggangmycin-enhanced reproduction and population growth in the brown planthopper, <i>Nilaparvata lugens</i> . <i>Scientific Reports</i> , 2015, 5, 15360.	1.6	14
3064	SiNG-PCRseq: Accurate inter-sequence quantification achieved by spiking-in a neighbor genome for competitive PCR amplicon sequencing. <i>Scientific Reports</i> , 2015, 5, 11879.	1.6	5
3065	Genome wide discovery of long intergenic non-coding RNAs in Diamondback moth ( <i>Plutella</i> ) Tj ETQq1 1 0.784314 $\frac{rgBT}{Overlock}$ 10 Tf	1.6	78
3066	A high-throughput RNA-seq approach to profile transcriptional responses. <i>Scientific Reports</i> , 2015, 5, 14976.	1.6	22
3067	Molecular basis of canalization in an ascidian species complex adapted to different thermal conditions. <i>Scientific Reports</i> , 2015, 5, 16717.	1.6	16
3068	Circulating microbial RNA and health. <i>Scientific Reports</i> , 2015, 5, 16814.	1.6	16
3069	Dual transcriptome sequencing reveals resistance of TLR4 ligand-activated bone marrow-derived macrophages to inflammation mediated by the BET inhibitor JQ1. <i>Scientific Reports</i> , 2015, 5, 16932.	1.6	24
3070	Detecting Differentially Expressed Genes with RNA-seq Data Using Backward Selection to Account for the Effects of Relevant Covariates. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 577-597.	0.7	7
3071	Transcriptome analysis of <i>Brassica napus</i> pod using RNA-Seq and identification of lipid-related candidate genes. <i>BMC Genomics</i> , 2015, 16, 858.	1.2	35
3072	Quantitative analysis of chromatin interaction changes upon a 4.3 Mb deletion at mouse 4E2. <i>BMC Genomics</i> , 2015, 16, 982.	1.2	2
3073	De novo transcriptome sequencing and analysis of <i>Coccinella septempunctata</i> L. in non-diapause, diapause and diapause-terminated states to identify diapause-associated genes. <i>BMC Genomics</i> , 2015, 16, 1086.	1.2	43

#	ARTICLE	IF	CITATIONS
3074	Expression profiling of white sponge nevus by RNA sequencing revealed pathological pathways. <i>Orphanet Journal of Rare Diseases</i> , 2015, 10, 72.	1.2	5
3075	Analysis of the agrotis segetum pheromone gland transcriptome in the light of Sex pheromone biosynthesis. <i>BMC Genomics</i> , 2015, 16, 711.	1.2	43
3076	Identification of miRNAs with potential roles in regulation of anther development and male-sterility in 7B-1 male-sterile tomato mutant. <i>BMC Genomics</i> , 2015, 16, 878.	1.2	58
3077	Genomic and transcriptomic analyses of the Chinese Maotai-flavored liquor yeast MT1 revealed its unique multi-carbon co-utilization. <i>BMC Genomics</i> , 2015, 16, 1064.	1.2	25
3078	Integrative DNA methylation and gene expression analysis to assess the universality of the CpG island methylator phenotype. <i>Human Genomics</i> , 2015, 9, 26.	1.4	16
3079	Differential expression analysis of RNA sequencing data by incorporating non-exonic mapped reads. <i>BMC Genomics</i> , 2015, 16, S14.	1.2	12
3080	Genome-wide identification of rubber tree ( <i>Hevea brasiliensis</i> Muell. Arg.) aquaporin genes and their response to ethephon stimulation in the laticifer, a rubber-producing tissue. <i>BMC Genomics</i> , 2015, 16, 1001.	1.2	55
3081	Deep sequencing analysis of transcriptomes in <i>Aspergillus flavus</i> in response to resveratrol. <i>BMC Microbiology</i> , 2015, 15, 182.	1.3	42
3082	Gene expression profiling in necrotizing enterocolitis reveals pathways common to those reported in Crohn's disease. <i>BMC Medical Genomics</i> , 2015, 9, 6.	0.7	35
3083	A polynomial delay algorithm for the enumeration of bubbles with length constraints in directed graphs. <i>Algorithms for Molecular Biology</i> , 2015, 10, 20.	0.3	2
3084	MtiBase: a database for decoding microRNA target sites located within CDS and 5'UTR regions from CLIP-Seq and expression profile datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav102.	1.4	23
3085	BSND and ATP6V1G3. <i>Medicine (United States)</i> , 2015, 94, e989.	0.4	13
3086	<i>Fss1</i> is involved in the regulation of an <i>ENA5</i> homologue for sodium and lithium tolerance in <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2015, 17, 2048-2063.	1.8	13
3087	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015, 17, 3098-3109.	1.8	49
3088	Non-immune-related genes and signalling pathways in spleen of <i>Vibrio parahaemolyticus</i> -infected <i>Epinephelus fuscoguttatus</i> (Forsk.). <i>Journal of Fish Diseases</i> , 2015, 38, 761-764.	0.9	5
3089	Regulation of flowering time by the histone deacetylase <i>HDA5</i> in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 82, 925-936.	2.8	94
3090	Nuclear-localized <i>AtHSPR</i> links abscisic acid-dependent salt tolerance and antioxidant defense in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 1274-1294.	2.8	51
3091	IAOseq: inferring abundance of overlapping genes using RNA-seq data. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	3

#	ARTICLE	IF	CITATIONS
3092	Alternative splicing detection workflow needs a careful combination of sample prep and bioinformatics analysis. BMC Bioinformatics, 2015, 16, S2.	1.2	16
3093	Accurate inference of isoforms from multiple sample RNA-Seq data. BMC Genomics, 2015, 16, S15.	1.2	11
3094	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	1.2	8
3095	Prediction of promoters and enhancers using multiple DNA methylation-associated features. BMC Genomics, 2015, 16, S11.	1.2	15
3096	Discovery and characterization of long intergenic non-coding RNAs (lincRNA) module biomarkers in prostate cancer: an integrative analysis of RNA-Seq data. BMC Genomics, 2015, 16, S3.	1.2	50
3097	PDEGEM: Modeling non-uniform read distribution in RNA-Seq data. BMC Medical Genomics, 2015, 8, S14.	0.7	1
3098	EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. BMC Bioinformatics, 2015, 16, 278.	1.2	18
3099	Seq-ing improved gene expression estimates from microarrays using machine learning. BMC Bioinformatics, 2015, 16, 286.	1.2	5
3100	Improving RNA-Seq expression estimation by modeling isoform- and exon-specific read sequencing rate. BMC Bioinformatics, 2015, 16, 332.	1.2	14
3101	Comparing the normalization methods for the differential analysis of Illumina high-throughput RNA-Seq data. BMC Bioinformatics, 2015, 16, 347.	1.2	151
3102	Evaluation of methods for differential expression analysis on multi-group RNA-seq count data. BMC Bioinformatics, 2015, 16, 361.	1.2	72
3103	Ancient gene duplications have shaped developmental stage-specific expression in <i>Pristionchus pacificus</i> . BMC Evolutionary Biology, 2015, 15, 185.	3.2	36
3104	RNA-Seq in <i>Mytilus galloprovincialis</i> : comparative transcriptomics and expression profiles among different tissues. BMC Genomics, 2015, 16, 728.	1.2	86
3105	Venom-gland transcriptome and venom proteome of the Malaysian king cobra ( <i>Ophiophagus hannah</i> ). BMC Genomics, 2015, 16, 687.	1.2	100
3106	De novo sequencing and analysis of the cranberry fruit transcriptome to identify putative genes involved in flavonoid biosynthesis, transport and regulation. BMC Genomics, 2015, 16, 652.	1.2	50
3107	Genome-wide characterization of long intergenic non-coding RNAs (lincRNAs) provides new insight into viral diseases in honey bees <i>Apis cerana</i> and <i>Apis mellifera</i> . BMC Genomics, 2015, 16, 680.	1.2	73
3108	Comparison of stranded and non-stranded RNA-seq transcriptome profiling and investigation of gene overlap. BMC Genomics, 2015, 16, 675.	1.2	82
3109	Transcriptome analysis of complex I-deficient patients reveals distinct expression programs for subunits and assembly factors of the oxidative phosphorylation system. BMC Genomics, 2015, 16, 691.	1.2	12

#	ARTICLE	IF	CITATIONS
3110	Dynamic association rules for gene expression data analysis. <i>BMC Genomics</i> , 2015, 16, 786.	1.2	18
3111	Changes in correlation between promoter methylation and gene expression in cancer. <i>BMC Genomics</i> , 2015, 16, 873.	1.2	113
3112	High-throughput mRNA and miRNA profiling of epithelial-mesenchymal transition in MDCK cells. <i>BMC Genomics</i> , 2015, 16, 944.	1.2	29
3113	Large-scale identification of wheat genes resistant to cereal cyst nematode <i>Heterodera avenae</i> using comparative transcriptomic analysis. <i>BMC Genomics</i> , 2015, 16, 801.	1.2	39
3114	The transcriptome of <i>Candida albicans</i> mitochondria and the evolution of organellar transcription units in yeasts. <i>BMC Genomics</i> , 2015, 16, 827.	1.2	21
3115	De novo assembly and sex-specific transcriptome profiling in the sand fly <i>Phlebotomus perniciosus</i> (Diptera, Phlebotominae), a major Old World vector of <i>Leishmania infantum</i> . <i>BMC Genomics</i> , 2015, 16, 847.	1.2	23
3116	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. <i>BMC Genomics</i> , 2015, 16, 970.	1.2	22
3117	Genes related to mitochondrial functions are differentially expressed in phosphine-resistant and -susceptible <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2015, 16, 968.	1.2	47
3118	RNA-seq reveals differentially expressed genes of rice ( <i>Oryza sativa</i> ) spikelet in response to temperature interacting with nitrogen at meiosis stage. <i>BMC Genomics</i> , 2015, 16, 959.	1.2	27
3119	Transcriptomics of diapause in an isogenic self-fertilizing vertebrate. <i>BMC Genomics</i> , 2015, 16, 989.	1.2	12
3120	mRNA-seq reveals skeletal muscle atrophy in response to handling stress in a marine teleost, the red cusk-eel ( <i>Genypterus chilensis</i> ). <i>BMC Genomics</i> , 2015, 16, 1024.	1.2	29
3121	De novo transcriptome sequence and identification of major bast-related genes involved in cellulose biosynthesis in jute ( <i>Corchorus capsularis</i> L.). <i>BMC Genomics</i> , 2015, 16, 1062.	1.2	30
3122	Using the combined analysis of transcripts and metabolites to propose key genes for differential terpene accumulation across two regions. <i>BMC Plant Biology</i> , 2015, 15, 240.	1.6	72
3123	Physiological and transcriptional analyses of developmental stages along sugarcane leaf. <i>BMC Plant Biology</i> , 2015, 15, 300.	1.6	64
3124	Prophylactic melatonin significantly reduces Alzheimer's neuropathology and associated cognitive deficits independent of antioxidant pathways in $A\beta$ PPsw/PS1 mice. <i>Molecular Neurodegeneration</i> , 2015, 10, 27.	4.4	64
3125	Genome-wide predictors of NF- $\kappa$ B recruitment and transcriptional activity. <i>BioData Mining</i> , 2015, 8, 37.	2.2	14
3126	Expression profiling of in vivo ductal carcinoma in situ progression models identified B cell lymphoma-9 as a molecular driver of breast cancer invasion. <i>Breast Cancer Research</i> , 2015, 17, 128.	2.2	43
3127	Single-cell analysis of lung adenocarcinoma cell lines reveals diverse expression patterns of individual cells invoked by a molecular target drug treatment. <i>Genome Biology</i> , 2015, 16, 66.	3.8	66

#	ARTICLE	IF	CITATIONS
3128	Comparative genomics of <i>Steinernema</i> reveals deeply conserved gene regulatory networks. <i>Genome Biology</i> , 2015, 16, 200.	3.8	77
3129	Gene expression changes in the salivary glands of <i>Anopheles coluzzii</i> elicited by <i>Plasmodium berghei</i> infection. <i>Parasites and Vectors</i> , 2015, 8, 485.	1.0	17
3130	Differential sialotranscriptomes of unfed and fed <i>Rhipicephalus haemaphysaloides</i> , with particular regard to differentially expressed genes of cysteine proteases. <i>Parasites and Vectors</i> , 2015, 8, 597.	1.0	39
3131	Motif signatures in stretch enhancers are enriched for disease-associated genetic variants. <i>Epigenetics and Chromatin</i> , 2015, 8, 23.	1.8	28
3132	Tissue-specific expression of histone H3 variants diversified after species separation. <i>Epigenetics and Chromatin</i> , 2015, 8, 35.	1.8	51
3133	TCLP: an online cancer cell line catalogue integrating HLA type, predicted neo-epitopes, virus and gene expression. <i>Genome Medicine</i> , 2015, 7, 118.	3.6	78
3134	Global analysis of DNA methylation in hepatocellular carcinoma by a liquid hybridization capture-based bisulfite sequencing approach. <i>Clinical Epigenetics</i> , 2015, 7, 86.	1.8	48
3135	Transcriptomic analysis of the host response to an iridovirus infection in Chinese giant salamander, <i>Andrias davidianus</i> . <i>Veterinary Research</i> , 2015, 46, 136.	1.1	31
3136	Effects of subsampling on characteristics of RNA-seq data from triple-negative breast cancer patients. <i>Chinese Journal of Cancer</i> , 2015, 34, 427-38.	4.9	4
3137	Optimization of combination chemotherapy based on the calculation of network entropy for protein-protein interactions in breast cancer cell lines. <i>EPJ Nonlinear Biomedical Physics</i> , 2015, 3, .	0.8	22
3138	A global RNA-seq-driven analysis of CHO host and production cell lines reveals distinct differential expression patterns of genes contributing to recombinant antibody glycosylation. <i>Biotechnology Journal</i> , 2015, 10, 1412-1423.	1.8	23
3139	Cell type-specific responses to salinity in the epidermal bladder cell transcriptome of <i>Mesembryanthemum crystallinum</i> . <i>New Phytologist</i> , 2015, 207, 627-644.	3.5	102
3140	Nonparametric Tests for Differential Histone Enrichment with CHIP-Seq Data. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S13972.	0.9	2
3141	Cancer Informatics: Profiling Age-Related Epigenetic Markers of Stomach Adenocarcinoma in Young and Old Subjects. <i>Cancer Informatics</i> , 2015, 14, CIN.S16912.	0.9	9
3142	B-Cell and Monocyte Contribution to Systemic Lupus Erythematosus Identified by Cell-Type-Specific Differential Expression Analysis in RNA-Seq Data. <i>Bioinformatics and Biology Insights</i> , 2015, 9s3, BBI.S29470.	1.0	30
3143	An evaluation of public genomic references for mapping RNA-seq data from Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2412-2416.	1.7	9
3144	Character trees from transcriptome data: Origin and individuation of morphological characters and the so-called "species signal". <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 588-604.	0.6	66
3145	Functional interactions among filamentous <i>Escherichia coli</i> and <i>epsilon</i> proteobacteria and <i>Bacteroidetes</i> in a deep-sea hydrothermal vent biofilm. <i>Environmental Microbiology</i> , 2015, 17, 4063-4077.	1.8	78

#	ARTICLE	IF	CITATIONS
3146	RNASeq in <i>C. elegans</i> Following Manganese Exposure. Current Protocols in Toxicology / Editorial Board, Mahin D Maines (editor-in-chief) [et Al ], 2015, 65, 11.20.1-11.20.17.	1.1	4
3147	Alternative Splicing Signatures in RNA-seq Data: Percent Spliced in (PSI). Current Protocols in Human Genetics, 2015, 87, 11.16.1-11.16.14.	3.5	104
3148	Reverse genetics in the tide pool: knock-down of target gene expression via <i>RNAi</i> interference in the copepod <i>Tigriopus californicus</i> . Molecular Ecology Resources, 2015, 15, 868-879.	2.2	31
3149	Global transcriptional profiling of longissimus thoracis muscle tissue in fetal and juvenile domestic goat using <i>RNA-seq</i> sequencing. Animal Genetics, 2015, 46, 655-665.	0.6	14
3150	Full-length <i>de novo</i> assembly of <i>RNA-seq</i> data in pea ( <i>Pisum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. Plant Journal, 2015, 84, 1-19.	2.8	173
3151	Evaluation of body growth and immunity-related differentially expressed genes through deep RNA sequencing in the piglets of Jeju native pig and Berkshire. Animal Genetics, 2015, 46, 255-264.	0.6	19
3152	Transcriptome analysis of adiposity in domestic ducks by transcriptomic comparison with their wild counterparts. Animal Genetics, 2015, 46, 299-307.	0.6	11
3153	<i>De novo</i> transcriptome assembly and identification of genes associated with feed conversion ratio and breast muscle yield in domestic ducks. Animal Genetics, 2015, 46, 636-645.	0.6	20
3154	Rapid Detection and Identification of Infectious Pathogens Based on High-throughput Sequencing. Chinese Medical Journal, 2015, 128, 877-883.	0.9	14
3155	Transcriptome Profiling of Developing Murine Lens Through RNA Sequencing. , 2015, 56, 4919.		44
3156	Evaluation of Commercially Available RNA Amplification Kits for RNA Sequencing Using Very Low Input Amounts of Total RNA. Journal of Biomolecular Techniques, 2015, 26, 4-18.	0.8	46
3157	Identification of genes and pathways related to lipopolysaccharide signaling in duckling spleens. Genetics and Molecular Research, 2015, 14, 17312-17321.	0.3	1
3158	The Heptameric SmAP1 and SmAP2 Proteins of the Crenarchaeon <i>Sulfolobus solfataricus</i> Bind to Common and Distinct RNA Targets. Life, 2015, 5, 1264-1281.	1.1	19
3159	Genome-wide Massive Sequencing in Embryonic Stem Cell Biology:Recent Insights and Challenges. Journal of Stem Cell Research & Therapy, 2015, 05, .	0.3	0
3160	The Impact of Molecular Genetic in Acute Myeloid Leukemias. Journal of Blood Disorders & Transfusion, 2015, 06, .	0.1	0
3161	Genomic-Wide Analysis with Microarrays in Human Oncology. Microarrays (Basel, Switzerland), 2015, 4, 454-473.	1.4	10
3162	Transcriptome Profiling of Louisiana iris Root and Identification of Genes Involved in Lead-Stress Response. International Journal of Molecular Sciences, 2015, 16, 28087-28097.	1.8	24
3163	Identification of genes associated with the increased number of four-seed pods in soybean ( <i>Glycine</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	0.3	6

#	ARTICLE	IF	CITATIONS
3164	Identification and Characterization of 40 Isolated <i>Rehmannia glutinosa</i> MYB Family Genes and Their Expression Profiles in Response to Shading and Continuous Cropping. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15009-15030.	1.8	19
3165	Long noncoding RNAs: from identification to functions and mechanisms. <i>Advances in Genomics and Genetics</i> , 0, , 257.	0.8	7
3166	Analysis of alterations to the transcriptome of Loquat ( <i>Eriobotrya japonica</i> Lindl.) under low temperature stress via de novo sequencing. <i>Genetics and Molecular Research</i> , 2015, 14, 9423-9436.	0.3	11
3167	Gene expression profiles in the pituitary glands of Sichuan White geese during prelaying and laying periods. <i>Genetics and Molecular Research</i> , 2015, 14, 12636-12645.	0.3	9
3168	Identification of miRNAs Responsive to <i>Botrytis cinerea</i> in Herbaceous Peony ( <i>Paeonia lactiflora</i> Pall.) by High-Throughput Sequencing. <i>Genes</i> , 2015, 6, 918-934.	1.0	20
3169	Identification of long non-coding RNA involved in osteogenic differentiation from mesenchymal stem cells using RNA-Seq data. <i>Genetics and Molecular Research</i> , 2015, 14, 18268-18279.	0.3	41
3170	A Transcriptomic Study of Maternal Thyroid Adaptation to Pregnancy in Rats. <i>International Journal of Molecular Sciences</i> , 2015, 16, 27339-27349.	1.8	4
3171	Long Noncoding RNA: its partners and their roles in cancer. <i>Neoplasma</i> , 2015, 62, 846-854.	0.7	12
3172	Expression profiles of differentially expressed genes affecting fecundity in goat ovarian tissues. <i>Genetics and Molecular Research</i> , 2015, 14, 18743-18752.	0.3	7
3173	Transcriptomic Analysis of <i>Clostridium thermocellum</i> in Cellulolytic Consortium after Artificial Reconstruction to Enhance Ethanol Production. <i>BioResources</i> , 2015, 10, .	0.5	0
3174	Estrogen and estrogen receptor alpha promotes malignancy and osteoblastic tumorigenesis in prostate cancer. <i>Oncotarget</i> , 2015, 6, 44388-44402.	0.8	48
3175	Transcriptome Profiling of Rust Resistance in Switchgrass Using RNA-Seq Analysis. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0075.	1.6	20
3176	Suppression of Aflatoxin Biosynthesis in <i>Aspergillus flavus</i> by 2-Phenylethanol Is Associated with Stimulated Growth and Decreased Degradation of Branched-Chain Amino Acids. <i>Toxins</i> , 2015, 7, 3887-3902.	1.5	69
3177	Splicing Regulation of Pro-Inflammatory Cytokines and Chemokines: At the Interface of the Neuroendocrine and Immune Systems. <i>Biomolecules</i> , 2015, 5, 2073-2100.	1.8	23
3178	Identification of 4CL Genes in Desert Poplars and Their Changes in Expression in Response to Salt Stress. <i>Genes</i> , 2015, 6, 901-917.	1.0	40
3179	Identification of Genes Putatively Involved in Chitin Metabolism and Insecticide Detoxification in the Rice Leaf Folder ( <i>Cnaphalocrocis medinalis</i> ) Larvae through Transcriptomic Analysis. <i>International Journal of Molecular Sciences</i> , 2015, 16, 21873-21896.	1.8	16
3180	Identification of Ramie Genes in Response to <i>Pratylenchus coffeae</i> Infection Challenge by Digital Gene Expression Analysis. <i>International Journal of Molecular Sciences</i> , 2015, 16, 21989-22007.	1.8	26
3181	Transcriptome Analysis and Identification of Differentially Expressed Transcripts of Immune-Related Genes in Spleen of Gosling and Adult Goose. <i>International Journal of Molecular Sciences</i> , 2015, 16, 22904-22926.	1.8	19

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3182	Exogenous GA3 Application Enhances Xylem Development and Induces the Expression of Secondary Wall Biosynthesis Related Genes in <i>Betula platyphylla</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 22960-22975.	1.8	34
3183	Morphological Characters and Transcriptome Profiles Associated with Black Skin and Red Skin in Crimson Snapper ( <i>Lutjanus erythropterus</i> ). <i>International Journal of Molecular Sciences</i> , 2015, 16, 26991-27004.	1.8	21
3184	Differentially-Expressed Genes Associated with Faster Growth of the Pacific Abalone, <i>Haliotis discus hannai</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 27520-27534.	1.8	34
3185	Data Integration for Microarrays: Enhanced Inference for Gene Regulatory Networks. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 255-269.	1.4	3
3186	C1-Pathways in <i>Methyloversatilis universalis</i> FAM5: Genome Wide Gene Expression and Mutagenesis Studies. <i>Microorganisms</i> , 2015, 3, 175-197.	1.6	14
3187	Identification of Low-Confidence Regions in the Pig Reference Genome ( <i>Sscrofa10.2</i> ). <i>Frontiers in Genetics</i> , 2015, 6, 338.	1.1	28
3188	Genome-Wide Analysis Reveals Selective Modulation of microRNAs and mRNAs by Histone Deacetylase Inhibitor in B Cells Induced to Undergo Class-Switch DNA Recombination and Plasma Cell Differentiation. <i>Frontiers in Immunology</i> , 2015, 6, 627.	2.2	32
3189	H <sub>2</sub> O <sub>2</sub> production rate in <i>Lactobacillus johnsonii</i> is modulated via the interplay of a heterodimeric flavin oxidoreductase with a soluble 28 Kd PAS domain containing protein. <i>Frontiers in Microbiology</i> , 2015, 6, 716.	1.5	13
3190	The inactivation of RNase G reduces the <i>Stenotrophomonas maltophilia</i> susceptibility to quinolones by triggering the heat shock response. <i>Frontiers in Microbiology</i> , 2015, 6, 1068.	1.5	17
3191	A Metagenomics-Based Metabolic Model of Nitrate-Dependent Anaerobic Oxidation of Methane by <i>Methanoperedens</i> -Like Archaea. <i>Frontiers in Microbiology</i> , 2015, 6, 1423.	1.5	170
3192	Transcriptomic identification of chemoreceptor genes in the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 7469-7480.	0.3	12
3193	Digital Gene Expression Analysis to Screen Disease Resistance-Relevant Genes from Leaves of Herbaceous Peony ( <i>Paeonia lactiflora</i> Pall.) Infected by <i>Botrytis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0133305.	1.1	11
3194	Survey of Programs Used to Detect Alternative Splicing Isoforms from Deep Sequencing Data In Silico. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	6
3195	De Novo Assembly and Discovery of Genes That Are Involved in Drought Tolerance in Tibetan <i>Sophora moorcroftiana</i> . <i>PLoS ONE</i> , 2015, 10, e111054.	1.1	55
3196	A Computational Strategy to Select Optimized Protein Targets for Drug Development toward the Control of Cancer Diseases. <i>PLoS ONE</i> , 2015, 10, e0115054.	1.1	40
3197	Transcriptional Responses to Sucrose Mimic the Plant-Associated Life Style of the Plant Growth Promoting Endophyte <i>Enterobacter</i> sp. 638. <i>PLoS ONE</i> , 2015, 10, e0115455.	1.1	34
3198	De Novo Assembly of Transcriptome Sequencing in <i>Caragana korshinskii</i> Kom. and Characterization of EST-SSR Markers. <i>PLoS ONE</i> , 2015, 10, e0115805.	1.1	20
3199	Comparative Transcriptome Analysis Reveals That Lactose Acts as an Inducer and Provides Proper Carbon Sources for Enhancing Exopolysaccharide Yield in the Deep-Sea Bacterium <i>Zunongwangia profunda</i> SM-A87. <i>PLoS ONE</i> , 2015, 10, e0115998.	1.1	1



#	ARTICLE	IF	CITATIONS
3200	Gene Expression Dosage Regulation in an Allopolyploid Fish. PLoS ONE, 2015, 10, e0116309.	1.1	14
3201	Developmental Genetic Mechanisms of C4 Syndrome Based on Transcriptome Analysis of C3 Cotyledons and C4 Assimilating Shoots in <i>Haloxylon ammodendron</i> . PLoS ONE, 2015, 10, e0117175.	1.1	38
3202	Comparison of the Transcriptomes of Mouse Skin Derived Precursors (SKPs) and SKP-Derived Fibroblasts (SFBs) by RNA-Seq. PLoS ONE, 2015, 10, e0117739.	1.1	11
3203	Differential Gene Expression in Ovaries of Qira Black Sheep and Hetian Sheep Using RNA-Seq Technique. PLoS ONE, 2015, 10, e0120170.	1.1	60
3204	Comparative Transcriptome Profiling of the Early Infection of Wheat Roots by <i>Gaeumannomyces graminis</i> var. <i>tritici</i> . PLoS ONE, 2015, 10, e0120691.	1.1	26
3205	Transcriptomic Analysis of the Primary Roots of <i>Alhagi sparsifolia</i> in Response to Water Stress. PLoS ONE, 2015, 10, e0120791.	1.1	13
3206	Dual RNA Sequencing Reveals the Expression of Unique Transcriptomic Signatures in Lipopolysaccharide-Induced BV-2 Microglial Cells. PLoS ONE, 2015, 10, e0121117.	1.1	39
3207	Transcriptome Analysis and Gene Expression Profiling of Abortive and Developing Ovules during Fruit Development in Hazelnut. PLoS ONE, 2015, 10, e0122072.	1.1	25
3208	De novo Assembly and Transcriptomic Profiling of the Grazing Response in <i>Stipa grandis</i> . PLoS ONE, 2015, 10, e0122641.	1.1	15
3209	Transcriptome Analysis and Its Application in Identifying Genes Associated with Fruiting Body Development in Basidiomycete <i>Hypsizygus marmoreus</i> . PLoS ONE, 2015, 10, e0123025.	1.1	54
3210	In silico Neuropeptidome of Female <i>Macrobrachium rosenbergii</i> Based on Transcriptome and Peptide Mining of Eyestalk, Central Nervous System and Ovary. PLoS ONE, 2015, 10, e0123848.	1.1	113
3211	Solexa-Sequencing Based Transcriptome Study of Plaice Skin Phenotype in Rex Rabbits ( <i>Oryctolagus</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.1	93
3212	From Gigabyte to Kilobyte: A Bioinformatics Protocol for Mining Large RNA-Seq Transcriptomics Data. PLoS ONE, 2015, 10, e0125000.	1.1	7
3213	Identification of a 6-Cytokine Prognostic Signature in Patients with Primary Glioblastoma Harboring M2 Microglia/Macrophage Phenotype Relevance. PLoS ONE, 2015, 10, e0126022.	1.1	59
3214	Transcriptome Analysis Comparison of Lipid Biosynthesis in the Leaves and Developing Seeds of <i>Brassica napus</i> . PLoS ONE, 2015, 10, e0126250.	1.1	23
3215	Transcriptional Dynamics of Immortalized Human Mesenchymal Stem Cells during Transformation. PLoS ONE, 2015, 10, e0126562.	1.1	16
3216	Sequencing and De Novo Assembly of the Gonadal Transcriptome of the Endangered Chinese Sturgeon ( <i>Acipenser sinensis</i> ). PLoS ONE, 2015, 10, e0127332.	1.1	76
3217	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. PLoS Neglected Tropical Diseases, 2015, 9, e0003929.	1.3	62

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3218	Transcriptome Profiling of Tomato Fruit Development Reveals Transcription Factors Associated with Ascorbic Acid, Carotenoid and Flavonoid Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0130885.	1.1	72
3219	Integrative Analysis of mRNA and miRNA Expression Profiles of the Tuberos Root Development at Seedling Stages in Turnips. <i>PLoS ONE</i> , 2015, 10, e0137983.	1.1	21
3220	Transcriptome Sequencing of <i>Codonopsis pilosula</i> and Identification of Candidate Genes Involved in Polysaccharide Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0117342.	1.1	35
3221	The 12p13.33/RAD52 Locus and Genetic Susceptibility to Squamous Cell Cancers of Upper Aerodigestive Tract. <i>PLoS ONE</i> , 2015, 10, e0117639.	1.1	10
3222	One Size Doesn't Fit All - RefEditor: Building Personalized Diploid Reference Genome to Improve Read Mapping and Genotype Calling in Next Generation Sequencing Studies. <i>PLoS Computational Biology</i> , 2015, 11, e1004448.	1.5	11
3223	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004465.	1.5	17
3224	Genome-Wide Reprogramming of Transcript Architecture by Temperature Specifies the Developmental States of the Human Pathogen <i>Histoplasma</i> . <i>PLoS Genetics</i> , 2015, 11, e1005395.	1.5	35
3225	Genome Sequence and Transcriptome Analyses of <i>Chrysochromulina tobin</i> : Metabolic Tools for Enhanced Algal Fitness in the Prominent Order Prymnesiales (Haptophyceae). <i>PLoS Genetics</i> , 2015, 11, e1005469.	1.5	58
3226	The Schistosome Esophagus Is a "Hotspot" for Microexon and Lysosomal Hydrolase Gene Expression: Implications for Blood Processing. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004272.	1.3	56
3227	The Structural Variation Is Associated with the Embryonic Lethality of a Novel Red Egg Mutant Fuyin-lre of Silkworm, <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2015, 10, e0128211.	1.1	2
3228	De novo Transcriptome Analysis of <i>Portunus trituberculatus</i> Ovary and Testis by RNA-Seq: Identification of Genes Involved in Gonadal Development. <i>PLoS ONE</i> , 2015, 10, e0128659.	1.1	70
3229	RNA-Seq Analysis of Human Trigeminal and Dorsal Root Ganglia with a Focus on Chemoreceptors. <i>PLoS ONE</i> , 2015, 10, e0128951.	1.1	167
3230	Combined Targeted DNA Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using UNCseq and NGScopy, and RNA Sequencing Using UNCqer for the Detection of Genetic Aberrations in NSCLC. <i>PLoS ONE</i> , 2015, 10, e0129280.	1.1	36
3231	Discovery of Chemosensory Genes in the Oriental Fruit Fly, <i>Bactrocera dorsalis</i> . <i>PLoS ONE</i> , 2015, 10, e0129794.	1.1	42
3232	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus <i>Phytoplasma aurantifolia</i> . <i>PLoS ONE</i> , 2015, 10, e0130425.	1.1	39
3233	Transcriptome Analysis to Identify Cold-Responsive Genes in Amur Carp ( <i>Cyprinus carpio</i> ) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf 50	1.1	35
3234	Identification of Candidate Adherent-Invasive <i>E. coli</i> Signature Transcripts by Genomic/Transcriptomic Analysis. <i>PLoS ONE</i> , 2015, 10, e0130902.	1.1	40
3235	Abraxane, the Nanoparticle Formulation of Paclitaxel Can Induce Drug Resistance by Up-Regulation of P-gp. <i>PLoS ONE</i> , 2015, 10, e0131429.	1.1	70

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3236	De novo Transcriptome Assembly of Common Wild Rice ( <i>Oryza rufipogon</i> Griff.) and Discovery of Drought-Response Genes in Root Tissue Based on Transcriptomic Data. <i>PLoS ONE</i> , 2015, 10, e0131455.	1.1	26
3237	Comparative Anterior Pituitary miRNA and mRNA Expression Profiles of Bama Minipigs and Landrace Pigs Reveal Potential Molecular Network Involved in Animal Postnatal Growth. <i>PLoS ONE</i> , 2015, 10, e0131987.	1.1	21
3238	Transcriptome Profiling of Peripheral Blood in 22q11.2 Deletion Syndrome Reveals Functional Pathways Related to Psychosis and Autism Spectrum Disorder. <i>PLoS ONE</i> , 2015, 10, e0132542.	1.1	40
3239	De Novo Characterization of the Mung Bean Transcriptome and Transcriptomic Analysis of Adventitious Rooting in Seedlings Using RNA-Seq. <i>PLoS ONE</i> , 2015, 10, e0132969.	1.1	31
3240	Transcriptomic Profiling Reveals Complex Molecular Regulation in Cotton Genic Male Sterile Mutant Yu98-8A. <i>PLoS ONE</i> , 2015, 10, e0133425.	1.1	8
3241	Search Engine for Antimicrobial Resistance: A Cloud Compatible Pipeline and Web Interface for Rapidly Detecting Antimicrobial Resistance Genes Directly from Sequence Data. <i>PLoS ONE</i> , 2015, 10, e0133492.	1.1	62
3242	Vitamin D Modulates Expression of the Airway Smooth Muscle Transcriptome in Fatal Asthma. <i>PLoS ONE</i> , 2015, 10, e0134057.	1.1	35
3243	Transcriptome Profiling of Wild-Type and <i>pga</i> -Knockout Mutant Strains Reveal the Role of Exopolysaccharide in <i>Aggregatibacter actinomycetemcomitans</i> . <i>PLoS ONE</i> , 2015, 10, e0134285.	1.1	7
3244	Distinct Responses of <i>Mycobacterium smegmatis</i> to Exposure to Low and High Levels of Hydrogen Peroxide. <i>PLoS ONE</i> , 2015, 10, e0134595.	1.1	24
3245	Heterogeneous Effects of Direct Hypoxia Pathway Activation in Kidney Cancer. <i>PLoS ONE</i> , 2015, 10, e0134645.	1.1	48
3246	Transcriptomic Analysis of Metabolic Pathways in Milkfish That Respond to Salinity and Temperature Changes. <i>PLoS ONE</i> , 2015, 10, e0134959.	1.1	41
3247	Transcriptomic Profiling and H3K27me3 Distribution Reveal Both Demethylase-Dependent and Independent Regulation of Developmental Gene Transcription in Cell Differentiation. <i>PLoS ONE</i> , 2015, 10, e0135276.	1.1	15
3248	De Novo Transcriptome Assembly and Comparative Analysis Elucidate Complicated Mechanism Regulating <i>Astragalus chrysochlorus</i> Response to Selenium Stimuli. <i>PLoS ONE</i> , 2015, 10, e0135677.	1.1	16
3249	De Novo Transcriptome Analysis of <i>Warburgia ugandensis</i> to Identify Genes Involved in Terpenoids and Unsaturated Fatty Acids Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0135724.	1.1	1
3250	Gene Expression Profiling of Development and Anthocyanin Accumulation in Kiwifruit ( <i>Actinidia</i> ) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 1.	1.1	53
3251	Characterization of the Transcriptome of the Xerophyte <i>Ammopiptanthus mongolicus</i> Leaves under Drought Stress by 454 Pyrosequencing. <i>PLoS ONE</i> , 2015, 10, e0136495.	1.1	8
3252	Time-Course RNA-Seq Analysis Reveals Transcriptional Changes in Rice Plants Triggered by Rice stripe virus Infection. <i>PLoS ONE</i> , 2015, 10, e0136736.	1.1	26
3253	Transcriptome Analysis Reveals the Mechanism Underlying the Production of a High Quantity of Chlorogenic Acid in Young Leaves of <i>Lonicera macranthoides</i> Hand.-Mazz. <i>PLoS ONE</i> , 2015, 10, e0137212.	1.1	26

#	ARTICLE	IF	CITATIONS
3254	Global Identification of Genes Specific for Rice Meiosis. PLoS ONE, 2015, 10, e0137399.	1.1	19
3255	Bioinformatics-Based Identification of MicroRNA-Regulated and Rheumatoid Arthritis-Associated Genes. PLoS ONE, 2015, 10, e0137551.	1.1	22
3256	Genome-Wide Identification of the Invertase Gene Family in Populus. PLoS ONE, 2015, 10, e0138540.	1.1	48
3257	CytR Is a Global Positive Regulator of Competence, Type VI Secretion, and Chitinases in <i>Vibrio cholerae</i> . PLoS ONE, 2015, 10, e0138834.	1.1	64
3258	De Novo Assembly of the Whole Transcriptome of the Wild Embryo, Preleptocephalus, Leptocephalus, and Glass Eel of <i>Anguilla japonica</i> and Deciphering the Digestive and Absorptive Capacities during Early Development. PLoS ONE, 2015, 10, e0139105.	1.1	23
3259	Transcriptomic Analysis of Ovaries from Pigs with High And Low Litter Size. PLoS ONE, 2015, 10, e0139514.	1.1	45
3260	Identification and Expression Profiles of Sex Pheromone Biosynthesis and Transport Related Genes in <i>Spodoptera litura</i> . PLoS ONE, 2015, 10, e0140019.	1.1	46
3261	Modeling Exon-Specific Bias Distribution Improves the Analysis of RNA-Seq Data. PLoS ONE, 2015, 10, e0140032.	1.1	1
3262	A Transcriptomic Analysis of Cave, Surface, and Hybrid Isopod Crustaceans of the Species <i>Asellus aquaticus</i> . PLoS ONE, 2015, 10, e0140484.	1.1	24
3263	RNA-Seq Based Identification of Candidate Parasitism Genes of Cereal Cyst Nematode (Heterodera) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	20
3264	Deciphering the Developmental Dynamics of the Mouse Liver Transcriptome. PLoS ONE, 2015, 10, e0141220.	1.1	35
3265	ALDH1A3: A Marker of Mesenchymal Phenotype in Gliomas Associated with Cell Invasion. PLoS ONE, 2015, 10, e0142856.	1.1	28
3266	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. PLoS ONE, 2015, 10, e0143066.	1.1	87
3267	Reproductive Hormone and Transcriptomic Responses of Pituitary Tissue in Anestrus Gilts Induced by Nutrient Restriction. PLoS ONE, 2015, 10, e0143219.	1.1	14
3268	Transcriptome Analysis Revealed Highly Expressed Genes Encoding Secondary Metabolite Pathways and Small Cysteine-Rich Proteins in the Sclerotium of <i>Lignosus rhinocerotis</i> . PLoS ONE, 2015, 10, e0143549.	1.1	17
3269	Analysis of Pigeon ( <i>Columba</i> ) Ovary Transcriptomes to Identify Genes Involved in Blue Light Regulation. PLoS ONE, 2015, 10, e0143568.	1.1	6
3270	Transcript Quantification by RNA-Seq Reveals Differentially Expressed Genes in the Red and Yellow Fruits of <i>Fragaria vesca</i> . PLoS ONE, 2015, 10, e0144356.	1.1	46
3271	Rapid Alterations in Perirenal Adipose Tissue Transcriptomic Networks with Cessation of Voluntary Running. PLoS ONE, 2015, 10, e0145229.	1.1	11

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3272	Comparative Transcriptome Analysis of the Pacific Oyster <i>Crassostrea gigas</i> Characterized by Shell Colors: Identification of Genetic Bases Potentially Involved in Pigmentation. <i>PLoS ONE</i> , 2015, 10, e0145257.	1.1	84
3273	A Computational Pipeline for Cross-Species Analysis of RNA-seq Data Using R and Bioconductor. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S30884.	1.0	15
3274	Maternal Melatonin Therapy Rescues Prenatal Dexamethasone and Postnatal High-Fat Diet Induced Programmed Hypertension in Male Rat Offspring. <i>Frontiers in Physiology</i> , 2015, 6, 377.	1.3	41
3275	Sequencing, de novo assembly and comparative analysis of <i>Raphanus sativus</i> transcriptome. <i>Frontiers in Plant Science</i> , 2015, 6, 198.	1.7	25
3276	Molecular phenotypes associated with anomalous stamen development in <i>Alternanthera philoxeroides</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 242.	1.7	11
3277	An improved fruit transcriptome and the identification of the candidate genes involved in fruit abscission induced by carbohydrate stress in litchi. <i>Frontiers in Plant Science</i> , 2015, 6, 439.	1.7	42
3278	The quest for tolerant varieties: the importance of integrating "omics" techniques to phenotyping. <i>Frontiers in Plant Science</i> , 2015, 6, 448.	1.7	67
3279	Genome-wide digital transcript analysis of putative fruitlet abscission related genes regulated by ethephon in litchi. <i>Frontiers in Plant Science</i> , 2015, 6, 502.	1.7	54
3280	Identification of heat-responsive genes in carnation ( <i>Dianthus caryophyllus</i> L.) by RNA-seq. <i>Frontiers in Plant Science</i> , 2015, 6, 519.	1.7	36
3281	A nitrogen source-dependent inducible and repressible gene expression system in the red alga <i>Cyanidioschyzon merolae</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 657.	1.7	32
3282	Expression profiling and functional analysis reveals that TOR is a key player in regulating photosynthesis and phytohormone signaling pathways in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 677.	1.7	178
3283	Transcriptomic analysis reveals importance of ROS and phytohormones in response to short-term salinity stress in <i>Populus tomentosa</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 678.	1.7	35
3284	De novo assembly and transcriptome analysis of two contrary tillering mutants to learn the mechanisms of tillers outgrowth in switchgrass ( <i>Panicum virgatum</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 749.	1.7	9
3285	Transcriptomic analysis of fruit stored under cold conditions using controlled atmosphere in <i>Prunus persica</i> cv. "Red Pearl". <i>Frontiers in Plant Science</i> , 2015, 6, 788.	1.7	50
3286	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear ( <i>Pyrus communis</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 795.	1.7	53
3287	Dynamic transcription profiles of "Qinguan" apple ( <i>Malus domestica</i> ) leaves in response to <i>Marssonina coronaria</i> inoculation. <i>Frontiers in Plant Science</i> , 2015, 6, 842.	1.7	16
3288	A method for the further assembly of targeted unigenes in a transcriptome after assembly by Trinity. <i>Frontiers in Plant Science</i> , 2015, 6, 843.	1.7	6
3289	The miRNAs and their regulatory networks responsible for pollen abortion in Ogura-CMS Chinese cabbage revealed by high-throughput sequencing of miRNAs, degradomes, and transcriptomes. <i>Frontiers in Plant Science</i> , 2015, 6, 894.	1.7	32

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3290	Genome-wide survey and comprehensive expression profiling of Aux/IAA gene family in chickpea and soybean. <i>Frontiers in Plant Science</i> , 2015, 6, 918.	1.7	83
3291	Impacts of high ATP supply from chloroplasts and mitochondria on the leaf metabolism of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 922.	1.7	43
3292	Gene Expression Reaction Norms Unravel the Molecular and Cellular Processes Underpinning the Plastic Phenotypes of <i>Alternanthera Philoxeroides</i> in Contrasting Hydrological Conditions. <i>Frontiers in Plant Science</i> , 2015, 6, 991.	1.7	9
3293	Comparative Transcriptomic Analyses of Vegetable and Grain Pea ( <i>Pisum sativum</i> L.) Seed Development. <i>Frontiers in Plant Science</i> , 2015, 6, 1039.	1.7	28
3294	Examination of the Abscission-Associated Transcriptomes for Soybean, Tomato, and <i>Arabidopsis</i> Highlights the Conserved Biosynthesis of an Extensible Extracellular Matrix and Boundary Layer. <i>Frontiers in Plant Science</i> , 2015, 6, 1109.	1.7	38
3295	Comparative Transcriptome Analysis of Resistant and Susceptible Tomato Lines in Response to Infection by <i>Xanthomonas perforans</i> Race T3. <i>Frontiers in Plant Science</i> , 2015, 6, 1173.	1.7	60
3296	De Novo Sequencing and Analysis of the Safflower Transcriptome to Discover Putative Genes Associated with Safflor Yellow in <i>Carthamus tinctorius</i> L.. <i>International Journal of Molecular Sciences</i> , 2015, 16, 25657-25677.	1.8	26
3297	Development and cross-species transferability of unigene-derived microsatellite markers in an edible oil woody plant, <i>Camellia oleifera</i> (Theaceae). <i>Genetics and Molecular Research</i> , 2015, 14, 6906-6916.	0.3	17
3298	The developmental transcriptome landscape of bovine skeletal muscle defined by Ribo-Zero ribonucleic acid sequencing <sup>1</sup> . <i>Journal of Animal Science</i> , 2015, 93, 5648-5658.	0.2	31
3299	Resveratrol-induced mitochondrial synthesis and autophagy in oocytes derived from early antral follicles of aged cows. <i>Journal of Reproduction and Development</i> , 2015, 61, 251-259.	0.5	65
3300	Transcriptome Analysis of Interspecific Hybrid between <i>Brassica napus</i> and <i>B. rapa</i> Reveals Heterosis for Oil Rape Improvement. <i>International Journal of Genomics</i> , 2015, 2015, 1-11.	0.8	20
3301	The Effects of <i>Paracoccidioides brasiliensis</i> Infection on GM-CSF- and M-CSF-Induced Mouse Bone Marrow-Derived Macrophage from Resistant and Susceptible Mice Strains. <i>Mediators of Inflammation</i> , 2015, 2015, 1-14.	1.4	7
3302	Transcriptomes That Confer to Plant Defense against Powdery Mildew Disease in <i>Lagerstroemia indica</i> . <i>International Journal of Genomics</i> , 2015, 2015, 1-12.	0.8	7
3303	Predicting the Functions of Long Noncoding RNAs Using RNA-Seq Based on Bayesian Network. <i>BioMed Research International</i> , 2015, 2015, 1-14.	0.9	22
3304	Pervasive transcription read-through promotes aberrant expression of oncogenes and RNA chimeras in renal carcinoma. <i>ELife</i> , 2015, 4, .	2.8	114
3305	Comprehensive Analysis of Transcriptome Sequencing Data in the Lung Tissues of COPD Subjects. <i>International Journal of Genomics</i> , 2015, 2015, 1-9.	0.8	59
3306	Genome-Wide Expression Profiling of Anoxia/Reoxygenation in Rat Cardiomyocytes Uncovers the Role of MitoKATP in Energy Homeostasis. <i>Oxidative Medicine and Cellular Longevity</i> , 2015, 2015, 1-14.	1.9	11
3307	Predicting Long Noncoding RNA and Protein Interactions Using Heterogeneous Network Model. <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	73

#	ARTICLE	IF	CITATIONS
3308	<i>De Novo</i> Transcriptome Sequencing of the Orange-Fleshed Sweet Potato and Analysis of Differentially Expressed Genes Related to Carotenoid Biosynthesis. <i>International Journal of Genomics</i> , 2015, 2015, 1-10.	0.8	27
3309	Genes associated with ant social behavior show distinct transcriptional and evolutionary patterns. <i>ELife</i> , 2015, 4, e04775.	2.8	78
3310	The Impact of Normalization Methods on RNA-Seq Data Analysis. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	89
3311	Differential Expression Analysis in RNA-Seq by a Naive Bayes Classifier with Local Normalization. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	6
3313	MicroRNA Regulation of Abiotic Stress Response in <i>Male Sterile Tomato Mutant</i> . <i>Plant Genome</i> , 2015, 8, eplantgenome2015.02.0008.	1.6	12
3314	Potential involvement of miR-375 in the premalignant progression of oral squamous cell carcinoma mediated via transcription factor KLF5. <i>Oncotarget</i> , 2015, 6, 40172-40185.	0.8	69
3315	The identification of <i>Cucumis sativus</i> Glabrous 1 (CsGL1) required for the formation of trichomes uncovers a novel function for the homeodomain-leucine zipper I gene. <i>Journal of Experimental Botany</i> , 2015, 66, 2515-2526.	2.4	94
3316	Comparative Transcriptome Analyses Reveal Core Parasitism Genes and Suggest Gene Duplication and Repurposing as Sources of Structural Novelty. <i>Molecular Biology and Evolution</i> , 2015, 32, 767-790.	3.5	137
3317	Genome-Wide Dosage-Dependent and -Independent Regulation Contributes to Gene Expression and Evolutionary Novelty in Plant Polyploids. <i>Molecular Biology and Evolution</i> , 2015, 32, 2351-2366.	3.5	57
3318	Large number of putative chemoreception and pheromone biosynthesis genes revealed by analyzing transcriptome from ovipositor-pheromone glands of <i>Chilo suppressalis</i> . <i>Scientific Reports</i> , 2015, 5, 7888.	1.6	69
3319	Myosin VI regulates gene pairing and transcriptional pause release in T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1587-93.	3.3	26
3320	The Putative Cellodextrin Transporter-like Protein CLP1 Is Involved in Cellulase Induction in <i>Neurospora crassa</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 788-796.	1.6	33
3321	Immune cell profiling to guide therapeutic decisions in rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2015, 11, 541-551.	3.5	62
3322	Biochemical and bioinformatic methods for elucidating the role of RNA-protein interactions in posttranscriptional regulation. <i>Briefings in Functional Genomics</i> , 2015, 14, 102-114.	1.3	10
3323	DNA Structure and Promoter Engineering. , 2015, , 241-254.		10
3324	Transcriptomic analysis of Mandarin fish brain cells infected with infectious spleen and kidney necrosis virus with an emphasis on retinoic acid-inducible gene 1-like receptors and apoptosis pathways. <i>Fish and Shellfish Immunology</i> , 2015, 45, 619-629.	1.6	33
3325	Global mapping transcriptional start sites revealed both transcriptional and post-transcriptional regulation of cold adaptation in the methanogenic archaeon <i>Methanobolus psychrophilus</i> . <i>Scientific Reports</i> , 2015, 5, 9209.	1.6	58
3326	Noncoding RNAs in human saliva as potential disease biomarkers. <i>Frontiers in Genetics</i> , 2015, 6, 175.	1.1	44

#	ARTICLE	IF	CITATIONS
3327	agplus: a rapid and flexible tool for aggregation plots. <i>Bioinformatics</i> , 2015, 31, 3046-3047.	1.8	15
3328	Tree shrew database (TreeshrewDB): a genomic knowledge base for the Chinese tree shrew. <i>Scientific Reports</i> , 2014, 4, 7145.	1.6	34
3329	Recent developments in epigenetics of acute and chronic kidney diseases. <i>Kidney International</i> , 2015, 88, 250-261.	2.6	88
3330	A male-determining factor in the mosquito <i>Aedes aegypti</i> . <i>Science</i> , 2015, 348, 1268-1270.	6.0	266
3331	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	4.5	1,014
3332	Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. <i>PeerJ</i> , 2015, 3, e869.	0.9	24
3333	Endogenic oxidative stress response contributes to glutathione over-accumulation in mutant <i>Saccharomyces cerevisiae</i> Y518. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7069-7078.	1.7	6
3334	Metabolite-enabled mutualistic interaction between <i>Shewanella oneidensis</i> and <i>Escherichia coli</i> in a co-culture using an electrode as electron acceptor. <i>Scientific Reports</i> , 2015, 5, 11222.	1.6	35
3335	Transcriptome profiling of muscle by RNA-Seq reveals significant differences in digital gene expression profiling between Angus and Luxi cattle. <i>Animal Production Science</i> , 2015, 55, 1172.	0.6	9
3336	Identification of cDC1- and cDC2-committed DC progenitors reveals early lineage priming at the common DC progenitor stage in the bone marrow. <i>Nature Immunology</i> , 2015, 16, 718-728.	7.0	475
3337	Genome wide transcriptional profiling of <i>Herbaspirillum seropedicae</i> SmR1 grown in the presence of naringenin. <i>Frontiers in Microbiology</i> , 2015, 6, 491.	1.5	20
3338	RNA-seq Transcriptional Profiling of an Arbuscular Mycorrhiza Provides Insights into Regulated and Coordinated Gene Expression in <i>Lotus japonicus</i> and <i>Rhizophagus irregularis</i> . <i>Plant and Cell Physiology</i> , 2015, 56, 1490-1511.	1.5	140
3339	Differential Features of AIRE-Induced and AIRE-Independent Promiscuous Gene Expression in Thymic Epithelial Cells. <i>Journal of Immunology</i> , 2015, 195, 498-506.	0.4	77
3340	RNA-seq-based transcriptome profiling reveals differential gene expression in the lungs of Sprague-Dawley rats during early-phase acute hypobaric hypoxia. <i>Molecular Genetics and Genomics</i> , 2015, 290, 2225-2240.	1.0	15
3341	Non-coding RNA: what is functional and what is junk?. <i>Frontiers in Genetics</i> , 2015, 6, 2.	1.1	602
3342	Integrating Transcriptome and Genome Re-Sequencing Data to Identify Key Genes and Mutations Affecting Chicken Eggshell Qualities. <i>PLoS ONE</i> , 2015, 10, e0125890.	1.1	20
3343	Coronaviruses. <i>Methods in Molecular Biology</i> , 2015, 1282, v.	0.4	102
3344	Intramolecular circularization increases efficiency of RNA sequencing and enables CLIP-Seq of nuclear RNA from human cells. <i>Nucleic Acids Research</i> , 2015, 43, e75-e75.	6.5	12



#	ARTICLE	IF	CITATIONS
3345	Systematic DNA methylation analysis of multiple cell lines reveals common and specific patterns within and across tissues of origin. <i>Human Molecular Genetics</i> , 2015, 24, 4374-4384.	1.4	39
3346	The Human Genome Project: Where Are We Now and Where Are We Going?. , 2015, , 7-31.		0
3347	Elucidation of Abiotic Stress Signaling in Plants. , 2015, , .		12
3348	Widespread disruption of host transcription termination in HSV-1 infection. <i>Nature Communications</i> , 2015, 6, 7126.	5.8	245
3349	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. <i>Journal of Microbiological Methods</i> , 2015, 115, 121-128.	0.7	2
3350	IL-17 signaling components in bivalves: Comparative sequence analysis and involvement in the immune responses. <i>Developmental and Comparative Immunology</i> , 2015, 52, 255-268.	1.0	41
3351	De novo assembly of transcriptome from the gametophyte of the marine red algae <i>Pyropia seriata</i> and identification of abiotic stress response genes. <i>Journal of Applied Phycology</i> , 2015, 27, 1343-1353.	1.5	32
3352	Detecting differential expression from RNA-seq data with expression measurement uncertainty. <i>Frontiers of Computer Science</i> , 2015, 9, 652-663.	1.6	1
3353	Genome-wide transcriptome analysis of mRNAs and microRNAs in Dorset and Small Tail Han sheep to explore the regulation of fecundity. <i>Molecular and Cellular Endocrinology</i> , 2015, 402, 32-42.	1.6	64
3354	Molecular Typing of Blood Cell Antigens. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
3355	Codon usage and codon context bias in <i>Xanthophyllomyces dendrorhous</i> . <i>BMC Genomics</i> , 2015, 16, 293.	1.2	40
3356	Deep Sequencing in Microdissected Renal Tubules Identifies Nephron Segment-Specific Transcriptomes. <i>Journal of the American Society of Nephrology: JASN</i> , 2015, 26, 2669-2677.	3.0	455
3357	Function of Isolated Pancreatic Islets From Patients at Onset of Type 1 Diabetes: Insulin Secretion Can Be Restored After Some Days in a Nondiabetogenic Environment In Vitro. <i>Diabetes</i> , 2015, 64, 2506-2512.	0.3	76
3358	The central nervous system transcriptome of the weakly electric brown ghost knifefish ( <i>Apteronotus</i> ) Tj ETQq1 1 0.784314 rgsBT /Over	1.2	19
3359	Transcriptome changes in <i>Fusarium verticillioides</i> caused by mutation in the transporter-like gene FST1. <i>BMC Microbiology</i> , 2015, 15, 90.	1.3	10
3360	Analysis of conglutin seed storage proteins across lupin species using transcriptomic, protein and comparative genomic approaches. <i>BMC Plant Biology</i> , 2015, 15, 106.	1.6	49
3361	ACTN4 and the pathways associated with cell motility and adhesion contribute to the process of lung cancer metastasis to the brain. <i>BMC Cancer</i> , 2015, 15, 277.	1.1	32
3362	Local adaptation of <i>Gymnocypris przewalskii</i> (Cyprinidae) on the Tibetan Plateau. <i>Scientific Reports</i> , 2015, 5, 9780.	1.6	48

#	ARTICLE	IF	CITATIONS
3363	Transcriptome outlier analysis implicates schizophrenia susceptibility genes and enriches putatively functional rare genetic variants. <i>Human Molecular Genetics</i> , 2015, 24, 4674-4685.	1.4	9
3364	De novo assembly and characterization of the skeletal muscle transcriptome of sheep using Illumina paired-end sequencing. <i>Biotechnology Letters</i> , 2015, 37, 1747-1756.	1.1	6
3365	The transcriptomic response to copper exposure in the digestive gland of Japanese scallops ( <i>Mizuhopecten yessoensis</i> ). <i>Fish and Shellfish Immunology</i> , 2015, 46, 161-167.	1.6	27
3366	De Novo Assembly and Characterization of the Transcriptome of the Chinese Medicinal Herb, <i>Gentiana rigescens</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 11550-11573.	1.8	47
3367	De novo RNA-Seq Analysis of the Venus Clam, <i>Cyclina sinensis</i> , and the Identification of Immune-Related Genes. <i>PLoS ONE</i> , 2015, 10, e0123296.	1.1	15
3368	Transcriptome analysis of BmN cells following over-expression of BmSTAT. <i>Molecular Genetics and Genomics</i> , 2015, 290, 2137-2146.	1.0	11
3369	An improved protocol for small RNA library construction using High Definition adapters. <i>Methods in Next Generation Sequencing</i> , 2015, 2, .	1.5	14
3370	RNA-Seq: Improving Our Understanding of Retinal Biology and Disease. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a017152.	2.9	23
3371	Detoxification strategies and regulation of oxygen production and flowering of <i>Platanus acerifolia</i> under lead (Pb) stress by transcriptome analysis. <i>Environmental Science and Pollution Research</i> , 2015, 22, 12747-12758.	2.7	19
3372	CyanOmics: an integrated database of omics for the model cyanobacterium <i>Synechococcus</i> sp. PCC 7002. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	18
3373	Analysis of the Bovine Monocyte-Derived Macrophage Response to <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection Using RNA-seq. <i>Frontiers in Immunology</i> , 2015, 6, 23.	2.2	61
3374	RNA-Seq transcriptome analysis of porcine cloned and in vitro fertilized blastocysts. <i>Journal of Integrative Agriculture</i> , 2015, 14, 926-938.	1.7	5
3375	Log-Sum Heuristic Recovery for Automated Isoform Discovery and Abundance Estimation from RNA-Seq data. , 2015, , .		0
3376	GELA: A Software Tool for the Analysis of Gene Expression Data. , 2015, , .		2
3377	Applications of next-generation sequencing to the study of biological invasions. <i>Environmental Epigenetics</i> , 2015, 61, 488-504.	0.9	66
3378	TRANSCRIPTOME ANALYSIS USING NEXT-GENERATION SEQUENCING. , 2015, , 915-936.		1
3379	Transcriptome profiling of a spirodiclofen susceptible and resistant strain of the European red mite <i>Panonychus ulmi</i> using strand-specific RNA-seq. <i>BMC Genomics</i> , 2015, 16, 974.	1.2	54
3380	Sex Chromosome Dosage Compensation in <i>Heliconius</i> Butterflies: Global yet Still Incomplete?. <i>Genome Biology and Evolution</i> , 2015, 7, 2545-2559.	1.1	54

#	ARTICLE	IF	CITATIONS
3381	Removal of redundant contigs from de novo RNA-Seq assemblies via homology search improves accurate detection of differentially expressed genes. <i>BMC Genomics</i> , 2015, 16, 1031.	1.2	30
3382	Explaining a Weighted DAG with Few Paths for Solving Genome-Guided Multi-Assembly. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 1345-1354.	1.9	10
3383	Identification and expression profiles of sRNAs and their biogenesis and action-related genes in male and female cones of <i>Pinus tabulaeformis</i> . <i>BMC Genomics</i> , 2015, 16, 693.	1.2	40
3384	Deep sequencing of the Mexican avocado transcriptome, an ancient angiosperm with a high content of fatty acids. <i>BMC Genomics</i> , 2015, 16, 599.	1.2	69
3385	High-throughput and quantitative genome-wide messenger RNA sequencing for molecular phenotyping. <i>BMC Genomics</i> , 2015, 16, 578.	1.2	19
3386	RNA-seq analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio parahaemolyticus</i> infection. <i>Gut Pathogens</i> , 2015, 7, 6.	1.6	66
3387	Chromatin Signature Identifies Monoallelic Gene Expression Across Mammalian Cell Types. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1713-1720.	0.8	36
3388	Gene Model Annotations for <i>Drosophila melanogaster</i> : Impact of High-Throughput Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1721-1736.	0.8	50
3389	Comparison of the Venom Peptides and Their Expression in Closely Related <i>Conus</i> Species: Insights into Adaptive Post-speciation Evolution of <i>Conus</i> Exogenomes. <i>Genome Biology and Evolution</i> , 2015, 7, 1797-1814.	1.1	37
3390	Identification of regulatory network hubs that control lipid metabolism in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 4551-4566.	2.4	100
3391	Babelomics 5.0: functional interpretation for new generations of genomic data. <i>Nucleic Acids Research</i> , 2015, 43, W117-W121.	6.5	114
3392	RNASeqel: accurate and repeat tolerant realignment of RNA-seq reads. <i>Nucleic Acids Research</i> , 2015, 43, e122-e122.	6.5	7
3393	Count ratio model reveals bias affecting NGS fold changes. <i>Nucleic Acids Research</i> , 2015, 43, gkv696.	6.5	14
3394	Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. <i>Nucleic Acids Research</i> , 2015, 43, gkv711.	6.5	605
3395	Photosynthetic Genes and Genes Associated with the C4 Trait in Maize Are Characterized by a Unique Class of Highly Regulated Histone Acetylation Peaks on Upstream Promoters. <i>Plant Physiology</i> , 2015, 168, 1378-1388.	2.3	19
3396	The application of omics technologies in the functional evaluation of inulin and inulin-containing prebiotics dietary supplementation. <i>Nutrition and Diabetes</i> , 2015, 5, e185-e185.	1.5	14
3397	Comparative transcriptome analysis reveals differential transcription in heat-susceptible and heat-tolerant pepper ( <i>Capsicum annum</i> L.) cultivars under heat stress. <i>Journal of Plant Biology</i> , 2015, 58, 411-424.	0.9	69
3398	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. <i>Journal of the American Statistical Association</i> , 2015, 110, 975-986.	1.8	10

#	ARTICLE	IF	CITATIONS
3399	Detecting differentially expressed genes by smoothing effect of gene length on variance estimation. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1542004.	0.3	1
3400	Transcriptome, microRNA, and degradome analyses of the gene expression of <i>Paulownia</i> with phytoplamsa. <i>BMC Genomics</i> , 2015, 16, 896.	1.2	29
3401	Differential expression profiling of the early response to <i>Ustilagoidea virens</i> between false smut resistant and susceptible rice varieties. <i>BMC Genomics</i> , 2015, 16, 955.	1.2	56
3402	A model selection criterion for model-based clustering of annotated gene expression data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 413-28.	0.2	0
3403	Comprehensive characterization of a time-course transcriptional response induced by autotoxins in <i>Panax ginseng</i> using RNA-Seq. <i>BMC Genomics</i> , 2015, 16, 1010.	1.2	35
3404	Effect of low-expression gene filtering on detection of differentially expressed genes in RNA-seq data. , 2015, 2015, 6461-4.		57
3405	Analysis of the transcriptome of green and mutant golden-yellow leaves of <i>Acer palmatum</i> Thunb. using high-throughput RNA sequencing. <i>Journal of Horticultural Science and Biotechnology</i> , 2015, 90, 388-394.	0.9	7
3406	GPR139, an Orphan Receptor Highly Enriched in the Habenula and Septum, Is Activated by the Essential Amino Acids L-Tryptophan and L-Phenylalanine. <i>Molecular Pharmacology</i> , 2015, 88, 911-925.	1.0	55
3407	Expression Analysis and Genome Annotations with RNA Sequencing. , 2015, , 1-12.		0
3408	High-Throughput Transcriptome Analysis of Plant Stress Responses. , 2015, , 195-209.		0
3409	Novel structural co-expression analysis linking the NPM1-associated ribosomal biogenesis network to chronic myelogenous leukemia. <i>Scientific Reports</i> , 2015, 5, 10973.	1.6	14
3410	Transcriptomic comparison of the self-pollinated and cross-pollinated flowers of <i>Erigeron breviscapus</i> to analyze candidate self-incompatibility-associated genes. <i>BMC Plant Biology</i> , 2015, 15, 248.	1.6	27
3411	Abasic pivot substitution harnesses target specificity of RNA interference. <i>Nature Communications</i> , 2015, 6, 10154.	5.8	39
3412	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
3413	Candidate chemosensory genes identified in <i>Colaphellus bowringi</i> by antennal transcriptome analysis. <i>BMC Genomics</i> , 2015, 16, 1028.	1.2	90
3414	Control for stochastic sampling variation and qualitative sequencing error in next generation sequencing. <i>Biomolecular Detection and Quantification</i> , 2015, 5, 30-37.	7.0	17
3415	Discover hidden splicing variations by mapping personal transcriptomes to personal genomes. <i>Nucleic Acids Research</i> , 2015, 43, 10612-10622.	6.5	13
3416	Transcriptomic analysis of human breast cancer cells reveals differentially expressed genes and related cellular functions and pathways in response to gold nanorods. <i>Biophysics Reports</i> , 2015, 1, 106-114.	0.2	4

#	ARTICLE	IF	CITATIONS
3417	Plant-Influenced Gene Expression in the Rice Endophyte <i>Burkholderia kururiensis</i> M130. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 10-21.	1.4	130
3418	m <sup>6</sup> A mRNA methylation facilitates resolution of naïve pluripotency toward differentiation. <i>Science</i> , 2015, 347, 1002-1006.	6.0	1,288
3419	iRNA-seq: computational method for genome-wide assessment of acute transcriptional regulation from total RNA-seq data. <i>Nucleic Acids Research</i> , 2015, 43, e40-e40.	6.5	62
3420	Detained introns are a novel, widespread class of post-transcriptionally spliced introns. <i>Genes and Development</i> , 2015, 29, 63-80.	2.7	346
3421	Association between changes in reproductive activity and D-glucose metabolism in the tephritid fruit fly, <i>Bactrocera dorsalis</i> (Hendel). <i>Scientific Reports</i> , 2015, 4, 7489.	1.6	9
3422	De novo transcriptome sequencing in <i>Pueraria lobata</i> to identify putative genes involved in isoflavones biosynthesis. <i>Plant Cell Reports</i> , 2015, 34, 733-743.	2.8	51
3423	Extracellular biogenic nanomaterials inhibit pyoverdine production in <i>Pseudomonas aeruginosa</i> : a novel insight into impacts of metal(loid)s on environmental bacteria. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1957-1966.	1.7	10
3424	Temporal transcriptome changes induced by methyl jasmonate in <i>Salvia sclarea</i> . <i>Gene</i> , 2015, 558, 41-53.	1.0	31
3425	Differential gene expression analysis of benzo(a)pyrene toxicity in the clam, <i>Ruditapes philippinarum</i> . <i>Ecotoxicology and Environmental Safety</i> , 2015, 115, 126-136.	2.9	15
3426	DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. <i>Nucleic Acids Research</i> , 2015, 43, D87-D91.	6.5	46
3427	Dynamics of GATA1 binding and expression response in a GATA1-induced erythroid differentiation system. <i>Genomics Data</i> , 2015, 4, 1-7.	1.3	10
3428	Digital gene-expression of alfalfa saponin extract on laying hens. <i>Genomics Data</i> , 2015, 3, 97-99.	1.3	4
3429	Ubiquitous human "master" origins of replication are encoded in the DNA sequence via a local enrichment in nucleosome excluding energy barriers. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 064102.	0.7	11
3430	Vision from next generation sequencing: Multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. <i>Progress in Retinal and Eye Research</i> , 2015, 46, 1-30.	7.3	50
3431	Noncoding sRNAs as epigenetic mediators of skeletal muscle regeneration. <i>FEBS Journal</i> , 2015, 282, 1630-1646.	2.2	22
3432	Next-generation transcriptome sequencing, SNP discovery and validation in four market classes of peanut, <i>Arachis hypogaea</i> L.. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1169-1180.	1.0	38
3433	Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. <i>Scientific Reports</i> , 2015, 5, 8410.	1.6	11
3434	Whole-genome sequencing reveals that mutations in myosin-5 confer resistance to the fungicide phenamacril in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2015, 5, 8248.	1.6	65

#	ARTICLE	IF	CITATIONS
3435	PLNseq: a multivariate Poisson lognormal distribution for high-throughput matched RNA-sequencing read count data. <i>Statistics in Medicine</i> , 2015, 34, 1577-1589.	0.8	18
3436	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. <i>Plant Molecular Biology</i> , 2015, 87, 473-487.	2.0	115
3437	Transcriptome Profile in Response to Frost Tolerance in <i>Eucalyptus globulus</i> . <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1472-1485.	1.0	10
3438	Transcriptome profile analysis reveals specific signatures of pollutants in Atlantic eels. <i>Ecotoxicology</i> , 2015, 24, 71-84.	1.1	35
3439	Data for transcriptome and proteome analysis of <i>Eucalyptus</i> infected with <i>Calonectria pseudoreteaudii</i> . <i>Data in Brief</i> , 2015, 3, 24-28.	0.5	32
3440	Transcriptomic changes during tuber dormancy release process revealed by RNA sequencing in potato. <i>Journal of Biotechnology</i> , 2015, 198, 17-30.	1.9	30
3441	Transcriptomic analysis of Rongchang pig brains and livers. <i>Gene</i> , 2015, 560, 96-106.	1.0	12
3442	PhenomeExpress: A refined network analysis of expression datasets by inclusion of known disease phenotypes. <i>Scientific Reports</i> , 2015, 5, 8117.	1.6	25
3443	Transcriptome analysis and microsatellite discovery in the blunt snout bream ( <i>Megalobrama</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 72-82.	1.6	97
3444	Transcriptome Analysis of Shell Color-Related Genes in the Clam <i>Meretrix meretrix</i> . <i>Marine Biotechnology</i> , 2015, 17, 364-374.	1.1	61
3445	Cross-talk between ER and HER2 regulates c-MYC-mediated glutamine metabolism in aromatase inhibitor resistant breast cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2015, 149, 118-127.	1.2	71
3446	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
3447	Transcriptomic Identification and Expression of Starch and Sucrose Metabolism Genes in the Seeds of Chinese Chestnut ( <i>Castanea mollissima</i> ). <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 929-942.	2.4	41
3448	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015, 16, 133-145.	7.7	1,043
3449	Kinetoplast adaptations in American strains from <i>Trypanosoma vivax</i> . <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 773, 69-82.	0.4	21
3450	Ethylmalonyl Coenzyme A Mutase Operates as a Metabolic Control Point in <i>Methylobacterium extorquens</i> AM1. <i>Journal of Bacteriology</i> , 2015, 197, 727-735.	1.0	15
3451	Comparison of software packages for detecting differential expression in RNA-seq studies. <i>Briefings in Bioinformatics</i> , 2015, 16, 59-70.	3.2	361
3452	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. <i>Nature Communications</i> , 2015, 6, 6120.	5.8	178

#	ARTICLE	IF	CITATIONS
3453	Transcriptome sequencing of Prunus sp. rootstocks roots to identify candidate genes involved in the response to root hypoxia. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	34
3454	Transcriptome sequencing and comparative analysis of diploid and autotetraploid <i>Paulownia australis</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	3
3455	Direct Detection of Transcription Factors in Cotyledons during Seedling Development Using Sensitive Silicon-Substrate Photonic Crystal Protein Arrays. <i>Plant Physiology</i> , 2015, 167, 639-649.	2.3	13
3456	Alternative mRNA transcription, processing, and translation: insights from RNA sequencing. <i>Trends in Genetics</i> , 2015, 31, 128-139.	2.9	283
3457	Transcriptome of the human retina, retinal pigmented epithelium and choroid. <i>Genomics</i> , 2015, 105, 253-264.	1.3	71
3458	Transcriptome analysis of response to drought in poplar interspecific hybrids. <i>Genomics Data</i> , 2015, 3, 143-145.	1.3	19
3459	Transcriptome-wide identification of the genes responding to replanting disease in <i>Rehmannia glutinosa</i> L. roots. <i>Molecular Biology Reports</i> , 2015, 42, 881-892.	1.0	23
3460	Oil Accumulation by the Oleaginous Diatom <i>Fistulifera solaris</i> as Revealed by the Genome and Transcriptome. <i>Plant Cell</i> , 2015, 27, 162-176.	3.1	149
3461	Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. <i>Molecular Psychiatry</i> , 2015, 20, 563-572.	4.1	124
3462	Comparative transcriptomic analysis provides insights into the molecular basis of brachyurization and adaptation to benthic lifestyle in <i>Eriocheir sinensis</i> . <i>Gene</i> , 2015, 558, 88-98.	1.0	19
3463	RNA Bioinformatics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
3464	A co-expression gene network associated with developmental regulation of apple fruit acidity. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1247-1263.	1.0	25
3465	RNA-Sequencing and Methylome Analysis. , 2015, , 77-88.		1
3466	Somatic Diseases (Cancer). , 2015, , 297-319.		2
3467	Clinical Genome Sequencing. , 2015, , 21-35.		2
3468	Single cell sequencing: technique, application, and future development. <i>Science Bulletin</i> , 2015, 60, 33-42.	4.3	19
3469	Gene set by de novo assembly of <i>Perilla</i> species and expression profiling between <i>P. frutescens</i> (L.) var. <i>frutescens</i> and var. <i>crispa</i> . <i>Gene</i> , 2015, 559, 155-163.	1.0	18
3470	The Technology of Analyzing Nucleic Acids in Cancer. , 2015, , 347-356.e1.		0

#	ARTICLE	IF	CITATIONS
3471	Evolution of the Insect Desaturase Gene Family with an Emphasis on Social Hymenoptera. <i>Molecular Biology and Evolution</i> , 2015, 32, 456-471.	3.5	60
3472	An ultra-low-input native ChIP-seq protocol for genome-wide profiling of rare cell populations. <i>Nature Communications</i> , 2015, 6, 6033.	5.8	322
3473	Sequencing of first-strand cDNA library reveals full-length transcriptomes. <i>Nature Communications</i> , 2015, 6, 6002.	5.8	24
3474	Transcriptomic response of <i>Manduca sexta</i> immune tissues to parasitization by the bracovirus associated wasp <i>Cotesia congregata</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2015, 62, 86-99.	1.2	33
3475	<sc>H</sc>b<sc>NIN</sc>2, a cytosolic alkaline/neutralâ€invertase, is responsible for sucrose catabolism in rubberâ€producing laticifers of <i><sc>H</sc>veva brasiliensis</i> (para rubber tree). <i>New Phytologist</i> , 2015, 206, 709-725.	3.5	58
3476	Enriched Environment-induced Maternal Weight Loss Reprograms Metabolic Gene Expression in Mouse Offspring. <i>Journal of Biological Chemistry</i> , 2015, 290, 4604-4619.	1.6	25
3477	Analysis of the crow lung transcriptome in response to infection with highly pathogenic H5N1 avian influenza virus. <i>Gene</i> , 2015, 559, 77-85.	1.0	21
3478	Transcriptome and proteome analysis of <i>Eucalyptus</i> infected with <i>Calonectria pseudoreteaudii</i> . <i>Journal of Proteomics</i> , 2015, 115, 117-131.	1.2	37
3479	Epigenetic and transcriptional determinants of the human breast. <i>Nature Communications</i> , 2015, 6, 6351.	5.8	56
3480	Defining the transcriptomic landscape of <i>Candida glabrata</i> by RNA-Seq. <i>Nucleic Acids Research</i> , 2015, 43, 1392-1406.	6.5	74
3481	Guidance for RNA-seq co-expression network construction and analysis: safety in numbers. <i>Bioinformatics</i> , 2015, 31, 2123-2130.	1.8	203
3482	rSeqNP: a non-parametric approach for detecting differential expression and splicing from RNA-Seq data. <i>Bioinformatics</i> , 2015, 31, 2222-2224.	1.8	13
3483	Salamanders in Regeneration Research. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	4
3484	RNA sequencing analysis identifies the metabolic and developmental genes regulated by BbSNF1 during conidiation of the entomopathogenic fungus <i>Beauveria bassiana</i> . <i>Current Genetics</i> , 2015, 61, 143-152.	0.8	25
3485	Transcriptome analysis reveals the role of BpGH3.5 in root elongation of <i>Betula platyphylla</i> â€pendula. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 121, 605-617.	1.2	5
3486	Transcriptome analysis of thermophilic methylotrophic <i>Bacillus methanolicus</i> MGA3 using RNA-sequencing provides detailed insights into its previously uncharted transcriptional landscape. <i>BMC Genomics</i> , 2015, 16, 73.	1.2	49
3487	A proposed adhesin AoMad1 helps nematode-trapping fungus <i>Arthrobotrys oligospora</i> recognizing host signals for life-style switching. <i>Fungal Genetics and Biology</i> , 2015, 81, 172-181.	0.9	32
3488	Functional analysis of C1 family cysteine peptidases in the larval gut of <i>Drosophila melanogaster</i> and <i>Tribolium castaneum</i> . <i>BMC Genomics</i> , 2015, 16, 75.	1.2	39



#	ARTICLE	IF	CITATIONS
3489	SNARE-RNAi Results in Higher Terpene Emission from Ectopically Expressed Caryophyllene Synthase in <i>Nicotiana benthamiana</i> . <i>Molecular Plant</i> , 2015, 8, 454-466.	3.9	12
3490	Reference gene selection for cross-species and cross-ploidy level comparisons in <i>Chrysanthemum</i> spp.. <i>Scientific Reports</i> , 2015, 5, 8094.	1.6	37
3491	Comparative analysis of active retrotransposons in the transcriptomes of three species of heteromyid rodents. <i>Gene</i> , 2015, 562, 95-106.	1.0	3
3492	Transcriptome Analysis of Individual Stromal Cell Populations Identifies Stroma-Tumor Crosstalk in Mouse Lung Cancer Model. <i>Cell Reports</i> , 2015, 10, 1187-1201.	2.9	137
3493	Transcriptome sequencing and analysis of the entomopathogenic fungus <i>Hirsutella sinensis</i> isolated from <i>Ophiocordyceps sinensis</i> . <i>BMC Genomics</i> , 2015, 16, 106.	1.2	30
3494	The transcriptomic profile of <i>Pseudozyma aphidis</i> during production of mannosylerythritol lipids. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1375-1388.	1.7	30
3495	Homocitrate Synthase Expression and Lysine Content in Fruiting Body of Different Developmental Stages in <i>Flammulina velutipes</i> . <i>Current Microbiology</i> , 2015, 70, 821-828.	1.0	15
3496	RNA Sequencing to Study Gene Expression and SNP Variations Associated with Growth in Zebrafish Fed a Plant Protein-Based Diet. <i>Marine Biotechnology</i> , 2015, 17, 353-363.	1.1	32
3497	Expression of RINT1 predicts seizure occurrence and outcomes in patients with low-grade gliomas. <i>Journal of Cancer Research and Clinical Oncology</i> , 2015, 141, 729-734.	1.2	10
3498	mTORC1 upregulation via ERK-dependent gene expression change confers intrinsic resistance to MEK inhibitors in oncogenic KRas-mutant cancer cells. <i>Oncogene</i> , 2015, 34, 5607-5616.	2.6	35
3499	HISAT: a fast spliced aligner with low memory requirements. <i>Nature Methods</i> , 2015, 12, 357-360.	9.0	16,262
3500	Analysis and Visualization of RNA-Seq Expression Data Using RStudio, Bioconductor, and Integrated Genome Browser. <i>Methods in Molecular Biology</i> , 2015, 1284, 481-501.	0.4	69
3501	Ballgown bridges the gap between transcriptome assembly and expression analysis. <i>Nature Biotechnology</i> , 2015, 33, 243-246.	9.4	716
3502	Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. <i>BMC Genomics</i> , 2015, 16, 60.	1.2	84
3503	De novo assembly of bacterial transcriptomes from RNA-seq data. <i>Genome Biology</i> , 2015, 16, 1.	3.8	1,215
3504	Transcriptome analysis of food habit transition from carnivory to herbivory in a typical vertebrate herbivore, grass carp <i>Ctenopharyngodon idella</i> . <i>BMC Genomics</i> , 2015, 16, 15.	1.2	43
3505	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. <i>Microbial Cell Factories</i> , 2015, 14, 13.	1.9	51
3506	Transcriptome analysis of nitrogen-starvation-responsive genes in rice. <i>BMC Plant Biology</i> , 2015, 15, 31.	1.6	107

#	ARTICLE	IF	CITATIONS
3507	Deficiency of very large G-protein-coupled receptor-1 is a risk factor of tumor-related epilepsy: a whole transcriptome sequencing analysis. <i>Journal of Neuro-Oncology</i> , 2015, 121, 609-616.	1.4	16
3508	Smoothed Variants Explain the Majority of Drug Resistance in Basal Cell Carcinoma. <i>Cancer Cell</i> , 2015, 27, 342-353.	7.7	337
3509	Identification of Novel Long Noncoding RNAs Underlying Vertebrate Cardiovascular Development. <i>Circulation</i> , 2015, 131, 1278-1290.	1.6	185
3510	Analytical workflow profiling gene expression in murine macrophages. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550010.	0.3	8
3511	Transcriptome Analysis of Sexually Dimorphic Chinese White Wax Scale Insects Reveals Key Differences in Developmental Programs and Transcription Factor Expression. <i>Scientific Reports</i> , 2015, 5, 8141.	1.6	31
3512	Disruption of DNA-methylation-dependent long gene repression in Rett syndrome. <i>Nature</i> , 2015, 522, 89-93.	13.7	521
3513	Plant Functional Genomics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	9
3514	Genome Sequencing of the Perciform Fish <i>Larimichthys crocea</i> Provides Insights into Molecular and Genetic Mechanisms of Stress Adaptation. <i>PLoS Genetics</i> , 2015, 11, e1005118.	1.5	230
3515	Acetylation Regulates Survival of <i>Salmonella enterica</i> Serovar Typhimurium under Acid Stress. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5675-5682.	1.4	37
3516	Phenotype and transcriptome analysis reveals chloroplast development and pigment biosynthesis together influenced the leaf color formation in mutants of <i>Anthurium andraeanum</i> "Sonata"™. <i>Frontiers in Plant Science</i> , 2015, 6, 139.	1.7	99
3517	Transcriptome-based gene profiling provides novel insights into the characteristics of radish root response to Cr stress with next-generation sequencing. <i>Frontiers in Plant Science</i> , 2015, 6, 202.	1.7	65
3518	Sensing Cardiac Electrical Activity With a Cardiac Myocyte "Targeted Optogenetic Voltage Indicator. <i>Circulation Research</i> , 2015, 117, 401-412.	2.0	57
3519	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic <i>Escherichia coli</i> prototype isolates. <i>Frontiers in Microbiology</i> , 2015, 6, 569.	1.5	32
3521	Comparative genomics reveals conserved positioning of essential genomic clusters in highly rearranged <i>Thermococcales</i> chromosomes. <i>Biochimie</i> , 2015, 118, 313-321.	1.3	15
3522	Integrated analysis of miRNA and mRNA expression profiles in development of porcine testes. <i>RSC Advances</i> , 2015, 5, 63439-63449.	1.7	32
3523	edgeRun: an R package for sensitive, functionally relevant differential expression discovery using an unconditional exact test. <i>Bioinformatics</i> , 2015, 31, 2589-2590.	1.8	53
3524	C-It-Loci: a knowledge database for tissue-enriched loci. <i>Bioinformatics</i> , 2015, 31, 3537-3543.	1.8	30
3525	Molecular Mechanisms of Enhanced Bacterial Growth on Hexadecane with Red Clay. <i>Microbial Ecology</i> , 2015, 70, 912-921.	1.4	14

#	ARTICLE	IF	CITATIONS
3526	RNA-seq reveals the critical role of OtpR in regulating <i>Brucella melitensis</i> metabolism and virulence under acidic stress. <i>Scientific Reports</i> , 2015, 5, 10864.	1.6	18
3527	Investigation of heart proteome of different consomic mouse strains. Testing the effect of polymorphisms on the proteome-wide trans-variation of proteins. <i>EuPA Open Proteomics</i> , 2015, 7, 27-42.	2.5	0
3528	Transcriptome-based discovery of AP2/ERF transcription factors related to temperature stress in tea plant ( <i>Camellia sinensis</i> ). <i>Functional and Integrative Genomics</i> , 2015, 15, 741-752.	1.4	73
3529	Identification of volatile and softening-related genes using digital gene expression profiles in melting peach. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	31
3530	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	1.8	76
3531	Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. <i>Genome Biology</i> , 2015, 16, 150.	13.9	126
3532	Applications of Deep Sequencing to Developmental Systems. , 2015, , 37-48.		1
3533	scaRNAs regulate splicing and vertebrate heart development. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2015, 1852, 1619-1629.	1.8	22
3534	De novo assembly and analysis of tissue-specific transcriptomes revealed the tissue-specific genes and profile of immunity from <i>Strongylocentrotus intermedius</i> . <i>Fish and Shellfish Immunology</i> , 2015, 46, 723-736.	1.6	21
3535	Molecular Testing in Myelodysplastic Syndromes for the Practicing Oncologist: Will the Progress Fulfill the Promise?. <i>Oncologist</i> , 2015, 20, 1069-1076.	1.9	20
3536	Comparative transcriptome analyses of drought-resistant and -susceptible <i>Brassica napus</i> L. and development of EST-SSR markers by RNA-Seq. <i>Journal of Plant Biology</i> , 2015, 58, 259-269.	0.9	48
3537	A pivotal role of KrÄppel-like factor 5 in regulation of cancer stem-like cells in hepatocellular carcinoma. <i>Cancer Biology and Therapy</i> , 2015, 16, 1453-1461.	1.5	22
3538	Nonfunctional ingestion of plant miRNAs in silkworm revealed by digital droplet PCR and transcriptome analysis. <i>Scientific Reports</i> , 2015, 5, 12290.	1.6	27
3539	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 3728-3737.	0.4	518
3540	Transcriptomic response to low salinity stress in gills of the Pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Marine Genomics</i> , 2015, 24, 297-304.	0.4	40
3541	Genomics and drug profiling of fatal TCF3-HLF <sup>+</sup> positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <i>Nature Genetics</i> , 2015, 47, 1020-1029.	9.4	190
3542	De novo transcriptome characterization of the ghost moth, <i>Thitarodes pui</i> , and elevation-based differences in the gene expression of its larvae. <i>Gene</i> , 2015, 574, 95-105.	1.0	10
3543	Detection and quantitative estimation of spurious double stranded DNA formation during reverse transcription in bacteria using tagRNA-seq. <i>RNA Biology</i> , 2015, 12, 1067-1069.	1.5	3

#	ARTICLE	IF	CITATIONS
3544	Global identification of the genetic networks and cis-regulatory elements of the cold response in zebrafish. <i>Nucleic Acids Research</i> , 2015, 43, 9198-9213.	6.5	38
3545	Matching Kidneys and Urines: Establishing Noninvasive Surrogates of Intrarenal Events in Primary Glomerulonephritis. <i>Seminars in Nephrology</i> , 2015, 35, 256-265.	0.6	1
3546	Comparative Analysis of Anther Transcriptome Profiles of Two Different Rice Male Sterile Lines Genotypes under Cold Stress. <i>International Journal of Molecular Sciences</i> , 2015, 16, 11398-11416.	1.8	73
3547	Genetic Influence on CNS Gene Expression: Impact on Behavior†. , 2015, , .		0
3548	Complete Dosage Compensation in <i>Anopheles stephensi</i> and the Evolution of Sex-Biased Genes in Mosquitoes. <i>Genome Biology and Evolution</i> , 2015, 7, 1914-1924.	1.1	40
3549	Transcriptome Profiling and Identification of Transcription Factors in Ramie ( <i>Boehmeria nivea</i> L. Gaud) in Response to PEG Treatment, Using Illumina Paired-End Sequencing Technology. <i>International Journal of Molecular Sciences</i> , 2015, 16, 3493-3511.	1.8	38
3550	Effects of Tris(1,3-dichloro-2-propyl) Phosphate (TDCPP) in <i>Tetrahymena Thermophila</i> : Targeting the Ribosome. <i>Scientific Reports</i> , 2015, 5, 10562.	1.6	34
3551	A Long Non-coding RNA, LncMyoD, Regulates Skeletal Muscle Differentiation by Blocking IMP2-Mediated mRNA Translation. <i>Developmental Cell</i> , 2015, 34, 181-191.	3.1	248
3552	Differential Expression of HERV-K (HML-2) Proviruses in Cells and Virions of the Teratocarcinoma Cell Line Tera-1. <i>Viruses</i> , 2015, 7, 939-968.	1.5	65
3553	Floral Transcriptome Analyses of Four <i>Paphiopedilum</i> Orchids with Distinct Flowering Behaviors and Development of Simple Sequence Repeat Markers. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1928-1952.	1.0	8
3554	Effects of 17 $\beta$ -methyltestosterone on transcriptome, gonadal histology and sex steroid hormones in rare minnow <i>Gobiocypris rarus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 15, 20-27.	0.4	17
3555	The global transcriptional landscape of <i>Bacillus amyloliquefaciens</i> XH7 and high-throughput screening of strong promoters based on RNA-seq data. <i>Gene</i> , 2015, 571, 252-262.	1.0	34
3556	Tick Salivary Sialostatin L Represses the Initiation of Immune Responses by Targeting IRF4-Dependent Transcription in Murine Mast Cells. <i>Journal of Immunology</i> , 2015, 195, 621-631.	0.4	35
3557	Filamentous phages prevalent in <i>Pseudoalteromonas</i> spp. confer properties advantageous to host survival in Arctic sea ice. <i>ISME Journal</i> , 2015, 9, 871-881.	4.4	69
3558	Transcriptome analysis of the compatible interaction of tomato with <i>Verticillium dahliae</i> using RNA-sequencing. <i>Frontiers in Plant Science</i> , 2015, 6, 428.	1.7	65
3559	Exploring the Secrets of Long Noncoding RNAs. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5467-5496.	1.8	125
3560	Exploration of molecular pathways mediating electric field-directed schwann cell migration by RNA-seq. <i>Journal of Cellular Physiology</i> , 2015, 230, 1515-1524.	2.0	25
3561	High-throughput sequencing reveals differing immune responses in the intestinal mucosa of two inbred lines afflicted with necrotic enteritis. <i>Veterinary Immunology and Immunopathology</i> , 2015, 166, 116-124.	0.5	21

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3562	Global Genome and Transcriptome Analyses of <i>Magnaporthe oryzae</i> Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. <i>PLoS Pathogens</i> , 2015, 11, e1004801.	2.1	148
3563	Validation of suitable reference genes for gene expression analysis in the halophyte <i>Salicornia europaea</i> by real-time quantitative PCR. <i>Frontiers in Plant Science</i> , 2014, 5, 788.	1.7	81
3564	Transcriptomic insights into antagonistic effects of gibberellin and abscisic acid on petal growth in <i>Gerbera hybrida</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 168.	1.7	35
3565	The intracellular domains of Notch1 and 2 are functionally equivalent during development and carcinogenesis. <i>Development (Cambridge)</i> , 2015, 142, 2452-63.	1.2	71
3566	Effects of low temperature on mRNA and small RNA transcriptomes in <i>Solanum lycopersicoides</i> leaf revealed by RNA-Seq. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 768-773.	1.0	22
3567	Transcriptomic and proteomic analysis of pre-diapause and non-diapause eggs of migratory locust, <i>Locusta migratoria</i> L. (Orthoptera: Acridoidea). <i>Scientific Reports</i> , 2015, 5, 11402.	1.6	79
3568	Antisense RNA Controls LRP1 Sense Transcript Expression through Interaction with a Chromatin-Associated Protein, HMGB2. <i>Cell Reports</i> , 2015, 11, 967-976.	2.9	75
3569	How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. <i>Nucleic Acids Research</i> , 2015, 43, 7664-7674.	6.5	90
3570	Abiotic Stress Tolerance and Sustainable Agriculture: A Functional Genomics Perspective. , 2015, , 439-472.		4
3571	Deep sequencing analysis of microRNA expression in human melanocyte and melanoma cell lines. <i>Gene</i> , 2015, 572, 135-145.	1.0	15
3572	p53-Regulated Networks of Protein, mRNA, miRNA, and lncRNA Expression Revealed by Integrated Pulsed Stable Isotope Labeling With Amino Acids in Cell Culture (pSILAC) and Next Generation Sequencing (NGS) Analyses. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2609-2629.	2.5	59
3573	Spirotetramat resistance adaption analysis of <i>Aphis gossypii</i> Glover by transcriptomic survey. <i>Pesticide Biochemistry and Physiology</i> , 2015, 124, 73-80.	1.6	41
3574	Alternative preprocessing of RNA-Sequencing data in The Cancer Genome Atlas leads to improved analysis results. <i>Bioinformatics</i> , 2015, 31, 3666-3672.	1.8	196
3575	Transcriptional profiling analysis of genic male sterile "fertile <i>Capsicum annum</i> reveal candidate genes for pollen development and maturation by RNA-Seq technology. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 122, 465-476.	1.2	16
3576	Towards understanding the molecular basis of cockroach tergal gland morphogenesis. A transcriptomic approach. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 63, 104-112.	1.2	8
3577	Unraveling adaptation of <i>Pontibacter korensis</i> to radiation and infertility in desert through complete genome and comparative transcriptomic analysis. <i>Scientific Reports</i> , 2015, 5, 10929.	1.6	8
3578	Small C-terminal Domain Phosphatase 3 Dephosphorylates the Linker Sites of Receptor-regulated Smads (R-Smads) to Ensure Transforming Growth Factor $\beta^2$ (TGF $\beta^2$ )-mediated Germ Layer Induction in <i>Xenopus</i> Embryos. <i>Journal of Biological Chemistry</i> , 2015, 290, 17239-17249.	1.6	6
3579	Isolation of strong constitutive promoters from <i>Lactococcus lactis</i> subsp. <i>lactis</i> N8. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv107.	0.7	42

#	ARTICLE	IF	CITATIONS
3580	Differential Analysis of the Cytochrome p450 Acaricide-Resistance Genes in <i>Panonychus citri</i> (Trombidiformes: Tetranychidae) Strains. <i>Florida Entomologist</i> , 2015, 98, 318-329.	0.2	4
3581	Next-generation transcriptome analysis in transgenic birch overexpressing and suppressing APETALA1 sheds lights in reproduction development and diterpenoid biosynthesis. <i>Plant Cell Reports</i> , 2015, 34, 1663-1680.	2.8	6
3582	Distinct iron architecture in SF3B1-mutant myelodysplastic syndrome patients is linked to an SLC25A37 splice variant with a retained intron. <i>Leukemia</i> , 2015, 29, 188-195.	3.3	52
3583	Analysis of intronic and exonic reads in RNA-seq data characterizes transcriptional and post-transcriptional regulation. <i>Nature Biotechnology</i> , 2015, 33, 722-729.	9.4	248
3584	Unique somatic and malignant expression patterns implicate PIWI-interacting RNAs in cancer-type specific biology. <i>Scientific Reports</i> , 2015, 5, 10423.	1.6	139
3585	Identification of a critical determinant that enables efficient fatty acid synthesis in oleaginous fungi. <i>Scientific Reports</i> , 2015, 5, 11247.	1.6	83
3586	Functional organization of the human 4D Nucleome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8002-8007.	3.3	102
3587	Right Ventricular Long Noncoding RNA Expression in Human Heart Failure. <i>Pulmonary Circulation</i> , 2015, 5, 135-161.	0.8	39
3588	Biosynthesis of monoterpene scent compounds in roses. <i>Science</i> , 2015, 349, 81-83.	6.0	177
3589	Identification and expression pattern of candidate olfactory genes in <i>Chrysoperla sinica</i> by antennal transcriptome analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 15, 28-38.	0.4	25
3590	De Novo Transcriptome Sequencing of Low Temperature-Treated <i>Phlox subulata</i> and Analysis of the Genes Involved in Cold Stress. <i>International Journal of Molecular Sciences</i> , 2015, 16, 9732-9748.	1.8	17
3591	MicroRNAs in the pathobiology of sarcomas. <i>Laboratory Investigation</i> , 2015, 95, 987-994.	1.7	5
3592	Omics Technologies Used in Systems Biology. , 2015, , 57-83.		7
3593	Transcriptome profiling analysis of naked carp ( <i>Gymnocypris przewalskii</i> ) provides insights into the immune-related genes in highland fish. <i>Fish and Shellfish Immunology</i> , 2015, 46, 366-377.	1.6	36
3594	Identification of Missing Proteins Defined by Chromosome-Centric Proteome Project in the Cytoplasmic Detergent-Insoluble Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3693-3709.	1.8	29
3595	Whole-body transcriptome of selectively bred, resistant-, control-, and susceptible-line rainbow trout following experimental challenge with <i>Flavobacterium psychrophilum</i> . <i>Frontiers in Genetics</i> , 2014, 5, 453.	1.1	74
3596	Involvement of glycolysis/gluconeogenesis and signaling regulatory pathways in <i>Saccharomyces cerevisiae</i> biofilms during fermentation. <i>Frontiers in Microbiology</i> , 2015, 6, 139.	1.5	36
3597	Tales from the crypt and coral reef: the successes and challenges of identifying new herpesviruses using metagenomics. <i>Frontiers in Microbiology</i> , 2015, 6, 188.	1.5	12

#	ARTICLE	IF	CITATIONS
3598	Identification and Validation of Evolutionarily Conserved Unusually Short Pre-mRNA Introns in the Human Genome. <i>International Journal of Molecular Sciences</i> , 2015, 16, 10376-10388.	1.8	11
3599	The kinase ABL phosphorylates the microprocessor subunit DGCR8 to stimulate primary microRNA processing in response to DNA damage. <i>Science Signaling</i> , 2015, 8, ra64.	1.6	18
3600	Embryonic Stem Cell Specific "Master" Replication Origins at the Heart of the Loss of Pluripotency. <i>PLoS Computational Biology</i> , 2015, 11, e1003969.	1.5	22
3601	Si-CSP9 regulates the integument and moulting process of larvae in the red imported fire ant, <i>Solenopsis invicta</i> . <i>Scientific Reports</i> , 2015, 5, 9245.	1.6	44
3602	Myogenesis in the Genomics Era. <i>Journal of Molecular Biology</i> , 2015, 427, 2023-2038.	2.0	10
3603	<i>Polyester</i> : simulating RNA-seq datasets with differential transcript expression. <i>Bioinformatics</i> , 2015, 31, 2778-2784.	1.8	250
3604	Immunoglobulin transcript sequence and somatic hypermutation computation from unselected RNA-seq reads in chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4322-4327.	3.3	38
3605	Transcriptomic analysis of degraded forensic body fluids. <i>Forensic Science International: Genetics</i> , 2015, 17, 35-42.	1.6	33
3606	Cytotoxicity of cardiotonic steroids in sensitive and multidrug-resistant leukemia cells and the link with Na <sup>+</sup> /K <sup>+</sup> -ATPase. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2015, 150, 97-111.	1.2	40
3607	The influence of budA deletion on glucose metabolism related in 2,3-butanediol production by <i>Klebsiella pneumoniae</i> . <i>Enzyme and Microbial Technology</i> , 2015, 73-74, 1-8.	1.6	4
3608	The transcriptomic and proteomic basis for the evolution of a novel venom phenotype within the Timber Rattlesnake ( <i>Crotalus horridus</i> ). <i>Toxicon</i> , 2015, 98, 34-48.	0.8	73
3609	Carotenoid composition of the flowers of <i>Mimulus lewisii</i> and related species: Implications regarding the prevalence and origin of two unique, allenic pigments. <i>Archives of Biochemistry and Biophysics</i> , 2015, 573, 32-39.	1.4	12
3610	Characterization of the transcriptome of the Asian gypsy moth <i>Lymantria dispar</i> identifies numerous transcripts associated with insecticide resistance. <i>Pesticide Biochemistry and Physiology</i> , 2015, 119, 54-61.	1.6	29
3611	Transcriptome analysis of the mammary gland from GH transgenic goats during involution. <i>Gene</i> , 2015, 565, 228-234.	1.0	19
3612	The Type VI Secretion System Modulates Flagellar Gene Expression and Secretion in <i>Citrobacter freundii</i> and Contributes to Adhesion and Cytotoxicity to Host Cells. <i>Infection and Immunity</i> , 2015, 83, 2596-2604.	1.0	36
3613	RNA-Seq-based transcriptome analysis of stem development and dwarfing regulation in <i>Agapanthus praecox</i> ssp. <i>orientalis</i> (Leighton) Leighton. <i>Gene</i> , 2015, 565, 252-267.	1.0	33
3614	Comparative analysis of the hepatopancreas transcriptome of grass carp ( <i>Ctenopharyngodon idellus</i> ) fed with lard oil and fish oil diets. <i>Gene</i> , 2015, 565, 192-200.	1.0	52
3615	Systems Biology Tools for Methyloprophs. <i>Springer Protocols</i> , 2015, , 97-118.	0.1	4

#	ARTICLE	IF	CITATIONS
3616	Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. <i>Scientific Reports</i> , 2014, 4, 5297.	1.6	132
3617	High-density linkage mapping aided by transcriptomics documents ZW sex determination system in the Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Heredity</i> , 2015, 115, 206-215.	1.2	102
3618	Transcriptome comparison of Cabernet Sauvignon grape berries from two regions with distinct climate. <i>Journal of Plant Physiology</i> , 2015, 178, 43-54.	1.6	29
3619	Transcriptome analysis of the variations between autotetraploid <i>Paulownia tomentosa</i> and its diploid using high-throughput sequencing. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1627-1638.	1.0	12
3620	Comparative transcriptome analysis of the petal degeneration mutant pdm in Chinese cabbage ( <i>Brassica campestris</i> ssp. <i>pekinensis</i> ) using RNA-Seq. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1833-1847.	1.0	30
3621	Comparative transcriptome of rhizome and leaf in <i>Ligusticum Chuanxiong</i> . <i>Plant Systematics and Evolution</i> , 2015, 301, 2073-2085.	0.3	9
3622	Wild soybean roots depend on specific transcription factors and oxidation reduction related genes in response to alkaline stress. <i>Functional and Integrative Genomics</i> , 2015, 15, 651-660.	1.4	51
3623	Investigation of possible molecular mechanisms underlying the regulation of adhesion in <i>Vibrio alginolyticus</i> with comparative transcriptome analysis. <i>Antonie Van Leeuwenhoek</i> , 2015, 107, 1197-1206.	0.7	34
3624	Hex1-related transcriptome of <i>Trichoderma atroviride</i> reveals expression patterns of ABC transporters associated with tolerance to dichlorvos. <i>Biotechnology Letters</i> , 2015, 37, 1421-1429.	1.1	22
3625	Apple russetting as seen through the RNA-seq lens: strong alterations in the exocarp cell wall. <i>Plant Molecular Biology</i> , 2015, 88, 21-40.	2.0	94
3626	Pirin1 Is a Non-Circadian Regulated Transcript and Protein, but Highly Responsive to Light/Dark Periods in the Seed-to-Seedling Transition in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1336-1348.	1.0	1
3627	A Buckwheat ( <i>Fagopyrum esculentum</i> ) DRE-Binding Transcription Factor Gene, FeDREB1, Enhances Freezing and Drought Tolerance of Transgenic <i>Arabidopsis</i> . <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1510-1525.	1.0	52
3628	De novo characterization of the alligator weed ( <i>Alternanthera philoxeroides</i> ) transcriptome illuminates gene expression under potassium deprivation. <i>Journal of Genetics</i> , 2015, 94, 95-104.	0.4	16
3629	Gene expression profiling for seed protein and oil synthesis during early seed development in soybean. <i>Genes and Genomics</i> , 2015, 37, 409-418.	0.5	12
3630	Systems Biology Approaches Applied to Regenerative Medicine. <i>Current Pathobiology Reports</i> , 2015, 3, 37-45.	1.6	9
3631	Transcriptome analysis reveals the oxidative stress response in <i>Saccharomyces cerevisiae</i> . <i>RSC Advances</i> , 2015, 5, 22923-22934.	1.7	22
3632	RNA-Seq analysis and transcriptome assembly for blackberry ( <i>Rubus</i> sp. Var. <i>Lochness</i> ) fruit. <i>BMC Genomics</i> , 2015, 16, 5.	1.2	62
3633	Genome-wide survey and expression analysis of F-box genes in chickpea. <i>BMC Genomics</i> , 2015, 16, 67.	1.2	68



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3634	A comprehensive evaluation of ensembl, RefSeq, and UCSC annotations in the context of RNA-seq read mapping and gene quantification. <i>BMC Genomics</i> , 2015, 16, 97.	1.2	118
3635	Comparative transcriptome profiling of a rice line carrying Xa39 and its parents triggered by <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> provides novel insights into the broad-spectrum hypersensitive response. <i>BMC Genomics</i> , 2015, 16, 111.	1.2	23
3636	Transcript profiling of <i>Populus tomentosa</i> genes in normal, tension, and opposite wood by RNA-seq. <i>BMC Genomics</i> , 2015, 16, 164.	1.2	58
3637	Global gene expression patterns of grass carp following compensatory growth. <i>BMC Genomics</i> , 2015, 16, 184.	1.2	37
3638	Transcriptomic analysis of <i>Litchi chinensis</i> pericarp during maturation with a focus on chlorophyll degradation and flavonoid biosynthesis. <i>BMC Genomics</i> , 2015, 16, 225.	1.2	74
3639	Transcriptome responses to <i>Ralstonia solanacearum</i> infection in the roots of the wild potato <i>Solanum commersonii</i> . <i>BMC Genomics</i> , 2015, 16, 246.	1.2	85
3640	NexGenEx-Tom: a gene expression platform to investigate the functionalities of the tomato genome. <i>BMC Plant Biology</i> , 2015, 15, 48.	1.6	16
3641	Transcriptomic analysis of differentially expressed genes in an orange-pericarp mutant and wild type in pummelo ( <i>Citrus grandis</i> ). <i>BMC Plant Biology</i> , 2015, 15, 44.	1.6	35
3642	Genome-wide analyses identify KLF4 as an important negative regulator in T-cell acute lymphoblastic leukemia through directly inhibiting T-cell associated genes. <i>Molecular Cancer</i> , 2015, 14, 26.	7.9	27
3643	RNA sequencing reveals distinct mechanisms underlying BET inhibitor JQ1-mediated modulation of the LPS-induced activation of BV-2 microglial cells. <i>Journal of Neuroinflammation</i> , 2015, 12, 36.	3.1	38
3644	Average genome size estimation improves comparative metagenomics and sheds light on the functional ecology of the human microbiome. <i>Genome Biology</i> , 2015, 16, 51.	3.8	241
3645	A transcriptomic analysis of <i>Neurospora crassa</i> using five major crop residues and the novel role of the sporulation regulator <i>rca-1</i> in lignocellulase production. <i>Biotechnology for Biofuels</i> , 2015, 8, 21.	6.2	25
3646	Transcriptomic analysis revealed the mechanism of oil dynamic accumulation during developing Siberian apricot ( <i>Prunus sibirica</i> L.) seed kernels for the development of woody biodiesel. <i>Biotechnology for Biofuels</i> , 2015, 8, 29.	6.2	28
3647	Genome-wide analysis of the endoplasmic reticulum stress response during lignocellulase production in <i>Neurospora crassa</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 66.	6.2	60
3648	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. <i>Epigenetics and Chromatin</i> , 2015, 8, 13.	1.8	10
3649	Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. <i>Biology of Reproduction</i> , 2015, 92, 95.	1.2	32
3650	De novo transcriptome sequencing of <i>Agropyron cristatum</i> to identify available gene resources for the enhancement of wheat. <i>Genomics</i> , 2015, 106, 129-136.	1.3	50
3651	Transcriptome of an entomophthoralean fungus ( <i>Pandora formicae</i> ) shows molecular machinery adjusted for successful host exploitation and transmission. <i>Journal of Invertebrate Pathology</i> , 2015, 128, 47-56.	1.5	42

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3652	Identification of innovative potential quality markers in rocket and melon fresh-cut produce. <i>Food Chemistry</i> , 2015, 188, 225-233.	4.2	32
3653	Single Cell Transcriptome Amplification with MALBAC. <i>PLoS ONE</i> , 2015, 10, e0120889.	1.1	44
3654	Isoform-level brain expression profiling of the spermidine/spermine N1-Acetyltransferase1 ( SAT1 ) gene in major depression and suicide. <i>Neurobiology of Disease</i> , 2015, 79, 123-134.	2.1	28
3655	Transcriptome analysis of the brain of the silkworm <i>Bombyx mori</i> infected with <i>Bombyx mori</i> nucleopolyhedrovirus: A new insight into the molecular mechanism of enhanced locomotor activity induced by viral infection. <i>Journal of Invertebrate Pathology</i> , 2015, 128, 37-43.	1.5	30
3656	Accumulation of long-lived mRNAs associated with germination in embryos during seed development of rice. <i>Journal of Experimental Botany</i> , 2015, 66, 4035-4046.	2.4	40
3657	Dissection of the style's response to pollination using transcriptome profiling in self-compatible ( <i>Solanum pimpinellifolium</i> ) and self-incompatible ( <i>Solanum chilense</i> ) tomato species. <i>BMC Plant Biology</i> , 2015, 15, 119.	1.6	20
3658	Genome-wide analysis of small nucleolar RNAs of <i>Leishmania major</i> reveals a rich repertoire of RNAs involved in modification and processing of rRNA. <i>RNA Biology</i> , 2015, 12, 1222-1255.	1.5	29
3659	Genome-wide transcriptome profiling provides insights into floral bud development of summer-flowering <i>Camellia azalea</i> . <i>Scientific Reports</i> , 2015, 5, 9729.	1.6	72
3660	Transcriptome-Wide Analysis of SAME Superfamily to Novelty Phosphoethanolamine N-Methyltransferase Copy in <i>Lonicera japonica</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 521-534.	1.8	9
3661	RNA Nanotechnology and Therapeutics. <i>Methods in Molecular Biology</i> , 2015, , .	0.4	3
3662	The draft genome of the grass carp ( <i>Ctenopharyngodon idellus</i> ) provides insights into its evolution and vegetarian adaptation. <i>Nature Genetics</i> , 2015, 47, 625-631.	9.4	352
3663	Identification of AGO3-Associated miRNAs and Computational Prediction of Their Targets in the Green Alga <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2015, 200, 105-121.	1.2	28
3664	Omics: Potential Role in Early-Phase Drug Development. , 2015, , 189-222.		0
3665	Comprehensive transcriptome analysis using synthetic long-read sequencing reveals molecular co-association of distant splicing events. <i>Nature Biotechnology</i> , 2015, 33, 736-742.	9.4	205
3666	Shape analysis of high-throughput transcriptomics experiment data. <i>Biostatistics</i> , 2015, 16, 627-640.	0.9	4
3668	FlyBase: introduction of the <i>Drosophila melanogaster</i> Release 6 reference genome assembly and large-scale migration of genome annotations. <i>Nucleic Acids Research</i> , 2015, 43, D690-D697.	6.5	387
3669	Simultaneous generation of many RNA-seq libraries in a single reaction. <i>Nature Methods</i> , 2015, 12, 323-325.	9.0	256
3670	Significant accumulation of persistent organic pollutants and dysregulation in multiple DNA damage repair pathways in the electronic-waste-exposed populations. <i>Environmental Research</i> , 2015, 137, 458-466.	3.7	21

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3671	High-throughput RNA profiling via up-front sample parallelization. <i>Nature Methods</i> , 2015, 12, 343-346.	9.0	18
3672	Right Ventricular Myocardial Biomarkers in Human Heart Failure. <i>Journal of Cardiac Failure</i> , 2015, 21, 398-411.	0.7	49
3673	Histone Lysine Methyltransferase Ezh1 Promotes TLR-Triggered Inflammatory Cytokine Production by Suppressing Tollip. <i>Journal of Immunology</i> , 2015, 194, 2838-2846.	0.4	47
3674	Duplex-specific nuclease-mediated bioanalysis. <i>Trends in Biotechnology</i> , 2015, 33, 180-188.	4.9	86
3675	Systematic identification and characterization of long intergenic non-coding RNAs in fetal porcine skeletal muscle development. <i>Scientific Reports</i> , 2015, 5, 8957.	1.6	154
3676	Long Noncoding RNAs in Cardiovascular Diseases. <i>Circulation Research</i> , 2015, 116, 737-750.	2.0	641
3677	A retrovirus packages nascent host noncoding RNAs from a novel surveillance pathway. <i>Genes and Development</i> , 2015, 29, 646-657.	2.7	40
3678	RNA Sequencing of Laser-Capture Microdissected Compartments of the Maize Kernel Identifies Regulatory Modules Associated with Endosperm Cell Differentiation. <i>Plant Cell</i> , 2015, 27, 513-531.	3.1	206
3679	The multigene family of fungal laccases and their expression in the white rot basidiomycete <i>Flammulina velutipes</i> . <i>Gene</i> , 2015, 563, 142-149.	1.0	60
3680	Identification of genes involved in the drought adaptation and recovery in <i>Portulaca oleracea</i> by differential display. <i>Plant Physiology and Biochemistry</i> , 2015, 90, 38-49.	2.8	13
3681	Thermophilic microbial cellulose decomposition and methanogenesis pathways recharacterized by metatranscriptomic and metagenomic analysis. <i>Scientific Reports</i> , 2014, 4, 6708.	1.6	62
3682	Root-applied brassinolide can alleviate the NaCl injuries on cotton. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	13
3683	Constitutive expression of DaCBF7, an Antarctic vascular plant <i>Deschampsia antarctica</i> CBF homolog, resulted in improved cold tolerance in transgenic rice plants. <i>Plant Science</i> , 2015, 236, 61-74.	1.7	87
3684	Renal C3 Complement Component: Feed Forward to Diabetic Kidney Disease. <i>American Journal of Nephrology</i> , 2015, 41, 48-56.	1.4	41
3685	Functionally defined therapeutic targets in diffuse intrinsic pontine glioma. <i>Nature Medicine</i> , 2015, 21, 555-559.	15.2	473
3686	Identification of genes involved in biosynthesis of mannan polysaccharides in <i>Dendrobium officinale</i> by RNA-seq analysis. <i>Plant Molecular Biology</i> , 2015, 88, 219-231.	2.0	79
3687	Screening and transcriptome analysis of water deficiency tolerant germplasms in peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	8
3688	Renal Mechanisms of Association between Fibroblast Growth Factor 1 and Blood Pressure. <i>Journal of the American Society of Nephrology: JASN</i> , 2015, 26, 3151-3160.	3.0	20

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3689	De Novo Assembly and Characterization of Narrow-Ridged Finless Porpoise Renal Transcriptome and Identification of Candidate Genes Involved in Osmoregulation. <i>International Journal of Molecular Sciences</i> , 2015, 16, 2220-2238.	1.8	12
3690	<i>Lvr</i> targeting by <i>Mir125a</i> and <i>Mir351</i> modulates autophagy associated with <i>Ewsr1</i> deficiency. <i>Autophagy</i> , 2015, 11, 796-811.	4.3	24
3691	The Transcriptome and Terpene Profile of <i>Eucalyptus grandis</i> Reveals Mechanisms of Defense Against the Insect Pest, <i>Leptocybe invasa</i> . <i>Plant and Cell Physiology</i> , 2015, 56, 1418-1428.	1.5	55
3692	Chondroitin Sulfate N-acetylgalactosaminyltransferase-2 Contributes to the Replication of Infectious Bursal Disease Virus via Interaction with the Capsid Protein VP2. <i>Viruses</i> , 2015, 7, 1474-1491.	1.5	7
3693	BioXpress: an integrated RNA-seq-derived gene expression database for pan-cancer analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	72
3694	FEATnotator: A tool for integrated annotation of sequence features and variation, facilitating interpretation in genomics experiments. <i>Methods</i> , 2015, 79-80, 11-17.	1.9	7
3695	Transcriptomic analyses reveal species-specific light-induced anthocyanin biosynthesis in <i>chrysanthemum</i> . <i>BMC Genomics</i> , 2015, 16, 202.	1.2	86
3696	Potential use of phytocystatins in crop improvement, with a particular focus on legumes. <i>Journal of Experimental Botany</i> , 2015, 66, 3559-3570.	2.4	48
3697	The variation game: Cracking complex genetic disorders with NGS and omics data. <i>Methods</i> , 2015, 79-80, 18-31.	1.9	22
3698	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
3699	Silica Microcapsules for Long-Term, Robust, and Reliable Room Temperature RNA Preservation. <i>Advanced Healthcare Materials</i> , 2015, 4, 1332-1338.	3.9	17
3700	The red coral ( <i>Corallium rubrum</i> ) transcriptome: a new resource for population genetics and local adaptation studies. <i>Molecular Ecology Resources</i> , 2015, 15, 1205-1215.	2.2	47
3701	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
3702	Identification of the transcriptionally active cytochrome P450 repertoire in <i>Coffea arabica</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 2399-2412.	0.3	4
3703	Next-generation gene discovery for variants of large impact on lipid traits. <i>Current Opinion in Lipidology</i> , 2015, 26, 114-119.	1.2	5
3704	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <i>Genome Medicine</i> , 2015, 7, 22.	3.6	45
3705	Proteogenomics of the human hippocampus: The road ahead. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 788-797.	1.1	23
3706	Efflux as a Glutaraldehyde Resistance Mechanism in <i>Pseudomonas fluorescens</i> and <i>Pseudomonas aeruginosa</i> Biofilms. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 3433-3440.	1.4	64

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3707	Computational approaches towards understanding human long non-coding RNA biology. <i>Bioinformatics</i> , 2015, 31, 2241-2251.	1.8	71
3708	Side-by-side secretion of Late Palaeozoic diverged courtship pheromones in an aquatic salamander. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142960.	1.2	19
3709	Plasticity of DNA methylation in a nerve injury model of pain. <i>Epigenetics</i> , 2015, 10, 200-212.	1.3	27
3710	RNA sequencing atopic dermatitis transcriptome profiling provides insights into novel disease mechanisms with potential therapeutic implications. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 1218-1227.	1.5	229
3711	Genome-wide identification and characterization of teleost-specific microRNAs within zebrafish. <i>Gene</i> , 2015, 561, 181-189.	1.0	8
3712	The coupling of glycolysis and the Rubisco-based pathway through the non-oxidative pentose phosphate pathway to achieve low carbon dioxide emission fermentation. <i>Bioresource Technology</i> , 2015, 187, 189-197.	4.8	31
3713	De novo transcriptome sequencing to identify the sex-determination genes in <i>Hyriopsis schlegelii</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2015, 79, 1257-1265.	0.6	30
3714	Understanding the molecular mechanisms of human microtia via a pig model of <i>HOXA1</i> syndrome. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 611-622.	1.2	17
3715	Next-generation sequencing data analysis on cloud computing. <i>Genes and Genomics</i> , 2015, 37, 489-501.	0.5	21
3716	Comparative transcriptome profiling of two maize near-isogenic lines differing in the allelic state for bacterial brown spot disease resistance. <i>Journal of Integrative Agriculture</i> , 2015, 14, 610-621.	1.7	8
3717	Estrogen alters the profile of the transcriptome in river snail <i>Bellamya aeruginosa</i> . <i>Ecotoxicology</i> , 2015, 24, 330-338.	1.1	8
3718	Blocking Yersiniabactin Import Attenuates Extraintestinal Pathogenic <i>Escherichia coli</i> in Cystitis and Pyelonephritis and Represents a Novel Target To Prevent Urinary Tract Infection. <i>Infection and Immunity</i> , 2015, 83, 1443-1450.	1.0	48
3719	Early and delayed long-term transcriptional changes and short-term transient responses during cold acclimation in olive leaves. <i>DNA Research</i> , 2015, 22, 1-11.	1.5	67
3720	Transcriptomic and proteomic analyses of splenic immune mechanisms of rainbow trout ( <i>Oncorhynchus mykiss</i> ) infected by <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> . <i>Journal of Proteomics</i> , 2015, 122, 41-54.	1.2	99
3721	Comprehensive evaluation of the effectiveness of gene expression signatures to predict complete response to neoadjuvant chemoradiotherapy and guide surgical intervention in rectal cancer. <i>Cancer Genetics</i> , 2015, 208, 319-326.	0.2	45
3722	A cost-effective RNA sequencing protocol for large-scale gene expression studies. <i>Scientific Reports</i> , 2015, 5, 9570.	1.6	84
3723	RNA Sequencing and Analysis. <i>Cold Spring Harbor Protocols</i> , 2015, 2015, pdb.top084970.	0.2	538
3724	Defining cell types and states with single-cell genomics. <i>Genome Research</i> , 2015, 25, 1491-1498.	2.4	636

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3725	Plant transcriptomics and responses to environmental stress: an overview. <i>Journal of Genetics</i> , 2015, 94, 525-537.	0.4	50
3726	Shared Pathways Among Autism Candidate Genes Determined by Co-expression Network Analysis of the Developing Human Brain Transcriptome. <i>Journal of Molecular Neuroscience</i> , 2015, 57, 580-594.	1.1	54
3727	PBX3 is targeted by multiple miRNAs and is essential for liver tumour-initiating cells. <i>Nature Communications</i> , 2015, 6, 8271.	5.8	61
3728	<i>Anopheles gambiae</i> Ag55 cell line as a model for <i>Lysinibacillus sphaericus</i> Bin toxin action. <i>Journal of Invertebrate Pathology</i> , 2015, 132, 105-110.	1.5	5
3729	An Epigenetic Role for Disrupted Paternal Gene Expression in Postzygotic Seed Abortion in Arabidopsis Interspecific Hybrids. <i>Molecular Plant</i> , 2015, 8, 1766-1775.	3.9	39
3730	Harnessing Next Generation Sequencing in Climate Change: RNA-Seq Analysis of Heat Stress-Responsive Genes in Wheat ( <i>Triticum aestivum</i> L.). <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 632-647.	1.0	50
3731	mRIN for direct assessment of genome-wide and gene-specific mRNA integrity from large-scale RNA-sequencing data. <i>Nature Communications</i> , 2015, 6, 7816.	5.8	59
3732	HIV-1 Nef promotes infection by excluding SERINC5 from virion incorporation. <i>Nature</i> , 2015, 526, 212-217.	13.7	376
3733	Single nucleotide resolution RNA-seq uncovers new regulatory mechanisms in the opportunistic pathogen <i>Streptococcus agalactiae</i> . <i>BMC Genomics</i> , 2015, 16, 419.	1.2	53
3734	The <i>Medicago sativa</i> gene index 1.2: a web-accessible gene expression atlas for investigating expression differences between <i>Medicago sativa</i> subspecies. <i>BMC Genomics</i> , 2015, 16, 502.	1.2	54
3735	Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant ( <i>Camellia sinensis</i> ). <i>BMC Genomics</i> , 2015, 16, 560.	1.2	174
3736	Whole transcriptomic analysis of the plant-beneficial rhizobacterium <i>Bacillus amyloliquefaciens</i> SQR9 during enhanced biofilm formation regulated by maize root exudates. <i>BMC Genomics</i> , 2015, 16, 685.	1.2	139
3737	Transcriptomic and phytochemical analysis of the biosynthesis of characteristic constituents in tea ( <i>Camellia sinensis</i> ) compared with oil tea ( <i>Camellia oleifera</i> ). <i>BMC Plant Biology</i> , 2015, 15, 190.	1.6	128
3738	CXCL14, CXCR7 expression and CXCR4 splice variant ratio associate with survival and metastases in Ewing sarcoma patients. <i>European Journal of Cancer</i> , 2015, 51, 2624-2633.	1.3	30
3739	Survey of protein-DNA interactions in <i>Aspergillus oryzae</i> on a genomic scale. <i>Nucleic Acids Research</i> , 2015, 43, 4429-4446.	6.5	9
3740	Apoptosis transcriptional mechanism of feline infectious peritonitis virus infected cells. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2015, 20, 1457-1470.	2.2	10
3741	Integrated analysis of miRNA, gene, and pathway regulatory networks in hepatic cancer stem cells. <i>Journal of Translational Medicine</i> , 2015, 13, 259.	1.8	20
3742	Differential gene expression analysis of early-ripening mutants of grape ( <i>Vitis vinifera</i> L.). <i>Scientia Horticulturae</i> , 2015, 194, 7-17.	1.7	1

#	ARTICLE	IF	CITATIONS
3743	Metabolic Coevolution in the Bacterial Symbiosis of Whiteflies and Related Plant Sap-Feeding Insects. <i>Genome Biology and Evolution</i> , 2015, 7, 2635-2647.	1.1	161
3744	Estimation of isoform expression in RNA-seq data using a hierarchical Bayesian model. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1542001.	0.3	4
3745	Dynamic transcriptional symmetry-breaking in pre-implantation mammalian embryo development revealed by single-cell RNA-seq. <i>Development (Cambridge)</i> , 2015, 142, 3468-77.	1.2	75
3746	Next-generation sequencing, assembly, and comparative analyses of the latex transcriptomes from two elite <i>Hevea brasiliensis</i> varieties. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	10
3747	Transcriptomic analysis reveals the potential antioxidant pathways regulated by multiprotein bridging factor 1 ( <i>BbMBF1</i> ) in the fungal entomopathogen <i>Beauveria bassiana</i> . <i>Biocontrol Science and Technology</i> , 2015, 25, 1346-1358.	0.5	3
3748	Transcriptome analysis reveals flavonoid biosynthesis regulation and simple sequence repeats in yam ( <i>Dioscorea alata</i> L.) tubers. <i>BMC Genomics</i> , 2015, 16, 346.	1.2	45
3749	Transcriptome profiling provides new insights into the formation of floral scent in <i>Hedychium coronarium</i> . <i>BMC Genomics</i> , 2015, 16, 470.	1.2	70
3750	Identification of Immunity-Related Genes in the Larvae of <i>Protaetia brevitarsis seulensis</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overl 2015, 15, 142.	0.6	19
3751	Cdt1-binding protein GRWD1 is a novel histone-binding protein that facilitates MCM loading through its influence on chromatin architecture. <i>Nucleic Acids Research</i> , 2015, 43, 5898-5911.	6.5	59
3752	Modelling the conditional regulatory activity of methylated and bivalent promoters. <i>Epigenetics and Chromatin</i> , 2015, 8, 21.	1.8	6
3753	Quality Control and Analysis of NGS RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2015, 1326, 217-232.	0.4	1
3754	Host adaption to the bacteriophage carrier state of <i>Campylobacter jejuni</i> . <i>Research in Microbiology</i> , 2015, 166, 504-515.	1.0	25
3755	Transcriptome analysis of an apple ( <i>Malus domestica</i> ) yellow fruit somatic mutation identifies a gene network module highly associated with anthocyanin and epigenetic regulation. <i>Journal of Experimental Botany</i> , 2015, 66, 7359-7376.	2.4	253
3756	Functional genomics of human brain development and implications for autism spectrum disorders. <i>Translational Psychiatry</i> , 2015, 5, e665-e665.	2.4	24
3757	Transcriptome and expression profiling analysis link patterns of gene expression to antennal responses in <i>Spodoptera litura</i> . <i>BMC Genomics</i> , 2015, 16, 269.	1.2	34
3758	De novo transcriptome characterization and gene expression profiling of the desiccation tolerant moss <i>Bryum argenteum</i> following rehydration. <i>BMC Genomics</i> , 2015, 16, 416.	1.2	73
3759	Dynamic Transcriptional Regulation of Fis in Salmonella During the Exponential Phase. <i>Current Microbiology</i> , 2015, 71, 713-718.	1.0	0
3760	An RNA-Seq analysis of the pear ( <i>Pyrus communis</i> L.) transcriptome, with a focus on genes associated with dwarf. <i>Plant Gene</i> , 2015, 4, 69-77.	1.4	20

#	ARTICLE	IF	CITATIONS
3761	The evolutionary landscape of intergenic trans-splicing events in insects. <i>Nature Communications</i> , 2015, 6, 8734.	5.8	17
3762	Transcriptional regulation of xylose utilization in <i>Enterococcus mundtii</i> QU 25. <i>RSC Advances</i> , 2015, 5, 93283-93292.	1.7	4
3763	RNA-Seq analysis identifies genes associated with differential reproductive success under drought-stress in accessions of wild barley <i>Hordeum spontaneum</i> . <i>BMC Plant Biology</i> , 2015, 15, 134.	1.6	62
3764	Phenylpropanoid metabolism, hormone biosynthesis and signal transduction-related genes play crucial roles in the resistance of <i>Paulownia fortunei</i> to paulownia witches' broom phytoplasma infection. <i>Genes and Genomics</i> , 2015, 37, 913-929.	0.5	28
3765	Celiac Disease. <i>Methods in Molecular Biology</i> , 2015, 1326, v.	0.4	1
3766	Transcriptome sequencing of microglial cells stimulated with TLR3 and TLR4 ligands. <i>BMC Genomics</i> , 2015, 16, 517.	1.2	71
3767	Alterations in <i>Mc1r</i> gene expression are associated with regressive pigmentation in <i>Astyanax</i> cavefish. <i>Development Genes and Evolution</i> , 2015, 225, 367-375.	0.4	35
3768	FoxP1 orchestration of ASD-relevant signaling pathways in the striatum. <i>Genes and Development</i> , 2015, 29, 2081-2096.	2.7	91
3769	Variation analysis of transcriptome changes reveals cochlear genes and their associated functions in cochlear susceptibility to acoustic overstimulation. <i>Hearing Research</i> , 2015, 330, 78-89.	0.9	19
3770	A genome-wide survey of glycolytic genes in diploid Asian cotton ( <i>Gossypium arboreum</i> ). <i>Plant Gene</i> , 2015, 4, 1-9.	1.4	3
3771	Genome-wide transcriptomic analysis of a superior biomass-degrading strain of <i>A. fumigatus</i> revealed active lignocellulose-degrading genes. <i>BMC Genomics</i> , 2015, 16, 459.	1.2	52
3772	Detection of a Distinctive Genomic Signature in Rhabdoid Glioblastoma, A Rare Disease Entity Identified by Whole Exome Sequencing and Whole Transcriptome Sequencing. <i>Translational Oncology</i> , 2015, 8, 279-287.	1.7	11
3773	A comparison of the low temperature transcriptomes of two tomato genotypes that differ in freezing tolerance: <i>Solanum lycopersicum</i> and <i>Solanum habrochaites</i> . <i>BMC Plant Biology</i> , 2015, 15, 132.	1.6	77
3774	TARDIS, a targeted RNA directional sequencing method for rare RNA discovery. <i>Nature Protocols</i> , 2015, 10, 1915-1938.	5.5	6
3775	Transcriptomic Analysis of Shiga-Toxigenic Bacteriophage Carriage Reveals a Profound Regulatory Effect on Acid Resistance in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 8118-8125.	1.4	60
3776	Deep sequencing-based characterization of transcriptome of trifoliolate orange ( <i>Poncirus trifoliata</i> (L.) TJ ETQq1 1 0.784314 rgBT /Overdo	1.2	97
3777	Bifidobacteria grown on human milk oligosaccharides downregulate the expression of inflammation-related genes in Caco-2 cells. <i>BMC Microbiology</i> , 2015, 15, 172.	1.3	67
3778	CD44 Isoform Status Predicts Response to Treatment with Anti-CD44 Antibody in Cancer Patients. <i>Clinical Cancer Research</i> , 2015, 21, 2753-2762.	3.2	42



#	ARTICLE	IF	CITATIONS
3779	Comprehensive transcriptome and improved genome annotation of <i>Bacillus licheniformis</i> . FEBS Letters, 2015, 589, 2372-2381.	1.3	19
3780	Carboxyl-modified single-walled carbon nanotubes negatively affect bacterial growth and denitrification activity. Scientific Reports, 2014, 4, 5653.	1.6	38
3781	Transcriptome comparison of the sex pheromone glands from two sibling <i>Helicoverpa</i> species with opposite sex pheromone components. Scientific Reports, 2015, 5, 9324.	1.6	32
3782	The Histone Demethylase Jumonji Coordinates Cellular Senescence Including Secretion of Neural Stem Cell-Attracting Cytokines. Molecular Cancer Research, 2015, 13, 636-650.	1.5	40
3783	BioWardrobe: an integrated platform for analysis of epigenomics and transcriptomics data. Genome Biology, 2015, 16, 158.	3.8	74
3784	RNA splicing regulated by RBFOX1 is essential for cardiac function in zebrafish. Journal of Cell Science, 2015, 128, 3030-40.	1.2	16
3785	Novel insights into RNP granules by employing the trypanosome's microtubule skeleton as a molecular sieve. Nucleic Acids Research, 2015, 43, 8013-8032.	6.5	74
3786	(p)ppGpp, a Small Nucleotide Regulator, Directs the Metabolic Fate of Glucose in <i>Vibrio cholerae</i> . Journal of Biological Chemistry, 2015, 290, 13178-13190.	1.6	14
3787	The use of exome capture RNA-seq for highly degraded RNA with application to clinical cancer sequencing. Genome Research, 2015, 25, 1372-1381.	2.4	139
3788	The <i>Importin KAP8 (Pse1Kap121)</i> is required for nuclear import of the cellulase transcriptional regulator <i>XYR1</i> , asexual sporulation and stress resistance in <i>Trichoderma reesei</i> . Molecular Microbiology, 2015, 96, 405-418.	1.2	22
3789	Genome sequence of the Asian Tiger mosquito, <i>Aedes albopictus</i> , reveals insights into its biology, genetics, and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5907-15.	3.3	251
3790	Transcriptome sequencing and characterization for <i>Kappaphycus alvarezii</i> . European Journal of Phycology, 2015, 50, 400-407.	0.9	9
3791	A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. BMC Bioinformatics, 2015, 16, 262.	1.2	7
3792	Reducing amplification artifacts in high multiplex amplicon sequencing by using molecular barcodes. BMC Genomics, 2015, 16, 589.	1.2	107
3793	A chromatin code for alternative splicing involving a putative association between CTCF and HP1 proteins. BMC Biology, 2015, 13, 31.	1.7	52
3794	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed <i>Alopecurus myosuroides</i> (black-grass). BMC Genomics, 2015, 16, 590.	1.2	66
3795	Uncovering co-expression gene network modules regulating fruit acidity in diverse apples. BMC Genomics, 2015, 16, 612.	1.2	68
3796	Transcriptomic changes following synthesis of a <i>Populus</i> full-sib diploid and allotriploid population with different heterozygosities driven by three types of 2n female gamete. Plant Molecular Biology, 2015, 89, 493-510.	2.0	14

#	ARTICLE	IF	CITATIONS
3797	Meloidogyne javanica fatty acid- and retinol-binding protein (Mj-FAR-1) regulates expression of lipid-, cell wall-, stress- and phenylpropanoid-related genes during nematode infection of tomato. BMC Genomics, 2015, 16, 272.	1.2	48
3798	Systems approach for exploring the intricate associations between sweetness, color and aroma in melon fruits. BMC Plant Biology, 2015, 15, 71.	1.6	39
3799	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640.	4.6	72
3800	De novo sequencing and characterization of the Bradysia odoriphaga (Diptera: Sciaridae) larval transcriptome. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 20-27.	0.4	13
3801	Genes involved in sex pheromone biosynthesis of Ephestia cautella, an important food storage pest, are determined by transcriptome sequencing. BMC Genomics, 2015, 16, 532.	1.2	38
3802	Comparative transcriptome profiling of Pyropia yezoensis (Ueda) M.S. Hwang & H.G. Choi in response to temperature stresses. BMC Genomics, 2015, 16, 463.	1.2	73
3803	Genome-wide analysis of the gene families of resistance gene analogues in cotton and their response to Verticillium wilt. BMC Plant Biology, 2015, 15, 148.	1.6	64
3804	Transcriptomic Approaches to Neural Repair. Journal of Neuroscience, 2015, 35, 13860-13867.	1.7	28
3805	Transcription Profiles Reveal Sugar and Hormone Signaling Pathways Mediating Flower Induction in Apple ( <i>Malus domestica</i> Borkh.). Plant and Cell Physiology, 2015, 56, 2052-2068.	1.5	118
3806	High-wire act: the poised genome and cellular memory. FEBS Journal, 2015, 282, 1675-1691.	2.2	19
3807	Transcriptome sequencing and analysis of rubber tree (Hevea brasiliensis Muell.) to discover putative genes associated with tapping panel dryness (TPD). BMC Genomics, 2015, 16, 398.	1.2	39
3808	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. Nucleic Acids Research, 2015, 43, 6787-6798.	6.5	94
3809	Functional diversity of CTCFs is encoded in their binding motifs. BMC Genomics, 2015, 16, 649.	1.2	10
3810	deGPS is a powerful tool for detecting differential expression in RNA-sequencing studies. BMC Genomics, 2015, 16, 455.	1.2	21
3811	Next-Generation Transcriptome Profiling of the Salmon Louse Caligus rogercresseyi Exposed to Deltamethrin (AlphaMax <sup>®</sup> , <sup>®</sup> ): Discovery of Relevant Genes and Sex-Related Differences. Marine Biotechnology, 2015, 17, 793-810.	1.1	17
3812	Fast and accurate approximate inference of transcript expression from RNA-seq data. Bioinformatics, 2015, 31, 3881-3889.	1.8	33
3813	Systematic assessment of reference genes for RT-qPCR across plant species under salt stress and drought stress. Acta Physiologiae Plantarum, 2015, 37, 1.	1.0	6
3814	Homology in the Age of Developmental Genomics. , 2015, , 25-43.		6

#	ARTICLE	IF	CITATIONS
3815	Suppression Subtractive Hybridization Versus Next-Generation Sequencing in Plant Genetic Engineering: Challenges and Perspectives. <i>Molecular Biotechnology</i> , 2015, 57, 880-903.	1.3	21
3816	Assessing the consistency of public human tissue RNA-seq data sets. <i>Briefings in Bioinformatics</i> , 2015, 16, 941-949.	3.2	19
3817	The paralogous R3 MYB proteins CAPRICE, TRIPTYCHON and ENHANCER OF TRY AND CPC1 play pleiotropic and partly non-redundant roles in the phosphate starvation response of <i>Arabidopsis</i> roots. <i>Journal of Experimental Botany</i> , 2015, 66, 4821-4834.	2.4	44
3818	Genome wide interactions of wild-type and activator bypass forms of <i>Yf54</i> . <i>Nucleic Acids Research</i> , 2015, 43, 7280-7291.	6.5	20
3819	Molecular profiling of activated olfactory neurons identifies odorant receptors for odors in vivo. <i>Nature Neuroscience</i> , 2015, 18, 1446-1454.	7.1	106
3820	Natural variation in <i>ARF18</i> gene simultaneously affects seed weight and silique length in polyploid rapeseed. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5123-32.	3.3	185
3821	Loss of diphthamide pre-activates NF- $\kappa$ B and death receptor pathways and renders MCF7 cells hypersensitive to tumor necrosis factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10732-10737.	3.3	37
3822	<i>PpYUC11</i> , a strong candidate gene for the stony hard phenotype in peach ( <i>Prunus persica</i> L.) Tj ETQq1 1 0.784314 rgBT 7031-7044.	2.4	160
3823	Regulation of gene expression dynamics during developmental transitions by the Ikaros transcription factor. <i>Genes and Development</i> , 2015, 29, 1801-1816.	2.7	29
3824	Identification of hub glyco genes and their nsSNP analysis from mouse RNA-Seq data. <i>Gene</i> , 2015, 574, 235-246.	1.0	2
3825	Integrative network modeling approaches to personalized cancer medicine. <i>Personalized Medicine</i> , 2015, 12, 245-257.	0.8	12
3826	The mechanism of the acclimation of <i>Nannochloropsis oceanica</i> to freshwater deduced from its transcriptome profiles. <i>Journal of Ocean University of China</i> , 2015, 14, 922-930.	0.6	7
3827	Modulating Molecular Chaperones Improves Mitochondrial Bioenergetics and Decreases the Inflammatory Transcriptome in Diabetic Sensory Neurons. <i>ACS Chemical Neuroscience</i> , 2015, 6, 1637-1648.	1.7	53
3828	Transcriptome analysis of grass carp ( <i>Ctenopharyngodon idella</i> ) fed with animal and plant diets. <i>Gene</i> , 2015, 574, 371-379.	1.0	14
3829	Super-enhancers: Asset management in immune cell genomes. <i>Trends in Immunology</i> , 2015, 36, 519-526.	2.9	36
3830	Decoding breast cancer tissue-stroma interactions using species-specific sequencing. <i>Breast Cancer Research</i> , 2015, 17, 109.	2.2	11
3831	The mRNA related ceRNA-ceRNA landscape and significance across 20 major cancer types. <i>Nucleic Acids Research</i> , 2015, 43, 8169-8182.	6.5	170
3832	Overexpression of ARGOS Genes Modifies Plant Sensitivity to Ethylene, Leading to Improved Drought Tolerance in Both <i>Arabidopsis</i> and Maize. <i>Plant Physiology</i> , 2015, 169, 266-282.	2.3	182

#	ARTICLE	IF	CITATIONS
3833	Transcriptional Regulation of the Pancreatic Islet: Implications for Islet Function. <i>Current Diabetes Reports</i> , 2015, 15, 66.	1.7	11
3834	Tissue-Based Proteogenomics Reveals that Human Testis Endows Plentiful Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3583-3594.	1.8	45
3835	Integrative genome-wide analysis reveals HLP1, a novel RNA-binding protein, regulates plant flowering by targeting alternative polyadenylation. <i>Cell Research</i> , 2015, 25, 864-876.	5.7	94
3836	Digital gene expression analysis of <i>Helicoverpa armigera</i> in the early stage of infection with <i>Helicoverpa armigera</i> nucleopolyhedrovirus. <i>Journal of Invertebrate Pathology</i> , 2015, 132, 66-76.	1.5	7
3837	Errors in RNA-Seq quantification affect genes of relevance to human disease. <i>Genome Biology</i> , 2015, 16, 177.	3.8	153
3838	Defining the three cell lineages of the human blastocyst by single-cell RNA-seq. <i>Development (Cambridge)</i> , 2015, 142, 3151-65.	1.2	343
3839	Discovery of ML358, a Selective Small Molecule Inhibitor of the SKN-1 Pathway Involved in Drug Detoxification and Resistance in Nematodes. <i>ACS Chemical Biology</i> , 2015, 10, 1871-1879.	1.6	9
3840	Transcriptional plasticity promotes primary and acquired resistance to BET inhibition. <i>Nature</i> , 2015, 525, 543-547.	13.7	414
3841	Predator strike shapes antipredator phenotype through new genetic interactions in water striders. <i>Nature Communications</i> , 2015, 6, 8153.	5.8	30
3842	RNA-seq analysis of the whole transcriptome of MDA-MB-231 mammary carcinoma cells exposed to the antimetastatic drug NAMI-A. <i>Metallomics</i> , 2015, 7, 1439-1450.	1.0	15
3843	Metatranscriptomic discovery of plant biomass-degrading capacity from grass carp intestinal microbiomes. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv107.	1.3	51
3844	Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. <i>Chromosome Research</i> , 2015, 23, 753-766.	1.0	49
3845	Transcriptional Changes in nAChRs, Interactive Proteins and P450s in <i>Locusta migratoria manilensis</i> (Orthoptera: Acrididae) CNS in Response to High and Low Oral Doses of Imidacloprid. <i>Journal of Insect Science</i> , 2015, 15, 102.	0.6	14
3846	Transcriptome response to heat stress in a chicken hepatocellular carcinoma cell line. <i>Cell Stress and Chaperones</i> , 2015, 20, 939-950.	1.2	58
3847	Genome-wide analysis of DNA methylation in the sexual stage of the insect pathogenic fungus <i>Cordyceps militaris</i> . <i>Fungal Biology</i> , 2015, 119, 1246-1254.	1.1	39
3848	Transcriptome analysis of a CHO cell line expressing a recombinant therapeutic protein treated with inducers of protein expression. <i>Journal of Biotechnology</i> , 2015, 212, 106-115.	1.9	36
3849	Fibrocytes Regulate Wilms Tumor 1-Positive Cell Accumulation in Severe Fibrotic Lung Disease. <i>Journal of Immunology</i> , 2015, 195, 3978-3991.	0.4	29
3850	Transcriptome analysis of the genes related to the morphological changes of <i>Paulownia tomentosa</i> plantlets infected with phytoplasma. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	21

#	ARTICLE	IF	CITATIONS
3851	Endogenous cellulolytic enzyme systems in the longhorn beetle <i>Mesosa myops</i> (Insecta: Coleoptera) studied by transcriptomic analysis. <i>Acta Biochimica Et Biophysica Sinica</i> , 2015, 47, 741-748.	0.9	18
3852	Embryonic gene expression of <i>Coregonus palaea</i> (whitefish) under pathogen stress as analyzed by high-throughput RNA-sequencing. <i>Fish and Shellfish Immunology</i> , 2015, 47, 130-140.	1.6	7
3853	De novo characterization of <i>Panax japonicus</i> C. A. Mey transcriptome and genes related to triterpenoid saponin biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2015, 466, 450-455.	1.0	24
3854	Comparative transcriptome analysis of <i>Chrysanthemum nankingense</i> in response to nitrogen deficiency. <i>Scientia Horticulturae</i> , 2015, 195, 101-107.	1.7	16
3855	Effects of Space Environment on Genome, Transcriptome, and Proteome of <i>Klebsiella pneumoniae</i> . <i>Archives of Medical Research</i> , 2015, 46, 609-618.	1.5	9
3856	Space station image captures a red tide ciliate bloom at high spectral and spatial resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14783-14787.	3.3	52
3857	Identification of soybean herbivory-regulated genes and a transgenic investigation of their potential in insect resistance. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 123, 321-340.	1.2	13
3858	Branched-chain amino acid catabolism is a conserved regulator of physiological ageing. <i>Nature Communications</i> , 2015, 6, 10043.	5.8	132
3859	Translational profiling identifies a cascade of damage initiated in motor neurons and spreading to glia in mutant SOD1-mediated ALS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6993-7002.	3.3	165
3860	A peculiar lamin in a peculiar mammal: Expression of lamin LIII in platypus ( <i>Ornithorhynchus anatinus</i> ). <i>European Journal of Cell Biology</i> , 2015, 94, 522-530.	1.6	1
3861	Mitochondrial divergence between slow- and fast-aging garter snakes. <i>Experimental Gerontology</i> , 2015, 71, 135-146.	1.2	15
3862	Transcriptomics in cancer diagnostics: developments in technology, clinical research and commercialization. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 1589-1603.	1.5	39
3863	G9a is essential for epigenetic silencing of K <sup>+</sup> channel genes in acute-to-chronic pain transition. <i>Nature Neuroscience</i> , 2015, 18, 1746-1755.	7.1	159
3864	Evaluating whole transcriptome amplification for gene profiling experiments using RNA-Seq. <i>BMC Biotechnology</i> , 2015, 15, 65.	1.7	23
3865	Comparative whole genome transcriptome and metabolome analyses of five <i>Klebsiella pneumoniae</i> strains. <i>Bioprocess and Biosystems Engineering</i> , 2015, 38, 2201-2219.	1.7	2
3866	Expression patterns, molecular markers and genetic diversity of insect-susceptible and resistant <i>Barbarea</i> genotypes by comparative transcriptome analysis. <i>BMC Genomics</i> , 2015, 16, 486.	1.2	16
3867	Prokaryotic Metatranscriptomics. <i>Springer Protocols</i> , 2015, , 69-98.	0.1	1
3868	Computational challenges, tools, and resources for analyzing and post-transcriptional events in high throughput. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 291-310.	3.2	16

#	ARTICLE	IF	CITATIONS
3869	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , 2015, 105, 83-89.	1.3	220
3870	Simultaneous transcriptome analysis of <i>Colletotrichum gloeosporioides</i> and tomato fruit pathosystem reveals novel fungal pathogenicity and fruit defense strategies. <i>New Phytologist</i> , 2015, 205, 801-815.	3.5	170
3871	Using RNA-seq and targeted nucleases to identify mechanisms of drug resistance in acute myeloid leukemia. <i>Scientific Reports</i> , 2014, 4, 6048.	1.6	29
3872	Technical Variations in Low-Input RNA-seq Methodologies. <i>Scientific Reports</i> , 2014, 4, 3678.	1.6	75
3873	Advancing Small-Molecule-Based Chemical Biology with Next-Generation Sequencing Technologies. <i>ChemBioChem</i> , 2015, 16, 20-38.	1.3	27
3874	Variation in transcriptome size: are we getting the message?. <i>Chromosoma</i> , 2015, 124, 27-43.	1.0	62
3875	Genome-wide identification of RNA editing in hepatocellular carcinoma. <i>Genomics</i> , 2015, 105, 76-82.	1.3	40
3876	Diminishing returns in next-generation sequencing (NGS) transcriptome data. <i>Gene</i> , 2015, 557, 82-87.	1.0	28
3877	Maternal Germline-Specific Genes in the Asian Malaria Mosquito <i>Anopheles stephensi</i> : Characterization and Application for Disease Control. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 157-166.	0.8	14
3878	<i>Systems and Synthetic Biology</i> . , 2015, , .		7
3879	Population Genomics Analysis of Legume Host Preference for Specific Rhizobial Genotypes in the <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> Symbioses. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 310-318.	1.4	17
3880	Clonal evolution revealed by whole genome sequencing in a case of primary myelofibrosis transformed to secondary acute myeloid leukemia. <i>Leukemia</i> , 2015, 29, 869-876.	3.3	44
3881	A Naturally Occurring Single Amino Acid Replacement in Multiple Gene Regulator of Group A <i>Streptococcus</i> Significantly Increases Virulence. <i>American Journal of Pathology</i> , 2015, 185, 462-471.	1.9	19
3882	Transcriptomic comparison of thiamethoxam-resistance adaptation in resistant and susceptible strains of <i>Aphis gossypii</i> Glover. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 13, 10-15.	0.4	35
3883	An RNA-Sequencing Study of the Genes and Metabolic Pathways Involved in <i>Aspergillus niger</i> Weathering of Potassium Feldspar. <i>Geomicrobiology Journal</i> , 2015, 32, 689-700.	1.0	23
3884	Epigenetic mechanisms in diabetic complications and metabolic memory. <i>Diabetologia</i> , 2015, 58, 443-455.	2.9	366
3885	Competition between target sites of regulators shapes post-transcriptional gene regulation. <i>Nature Reviews Genetics</i> , 2015, 16, 113-126.	7.7	220
3886	Genome-wide identification and comparative expression analysis reveal a rapid expansion and functional divergence of duplicated genes in the WRKY gene family of cabbage, <i>Brassica oleracea</i> var. <i>capitata</i> . <i>Gene</i> , 2015, 557, 35-42.	1.0	51

#	ARTICLE	IF	CITATIONS
3887	Transcriptome analysis reveals diversified adaptation of <i>Stipa purpurea</i> along a drought gradient on the Tibetan Plateau. <i>Functional and Integrative Genomics</i> , 2015, 15, 295-307.	1.4	36
3888	Deep sequencing analysis of the <i>Kineococcus radiotolerans</i> transcriptome in response to ionizing radiation. <i>Microbiological Research</i> , 2015, 170, 248-254.	2.5	8
3889	Digital gene expression analysis in hemocytes of the white shrimp <i>Litopenaeus vannamei</i> in response to low salinity stress. <i>Fish and Shellfish Immunology</i> , 2015, 42, 400-407.	1.6	54
3890	Global Transcriptional Start Site Mapping Using Differential RNA Sequencing Reveals Novel Antisense RNAs in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2015, 197, 18-28.	1.0	287
3891	Genome-wide analysis of local chromatin packing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2015, 25, 246-256.	2.4	254
3892	MarVis-Pathway: integrative and exploratory pathway analysis of non-targeted metabolomics data. <i>Metabolomics</i> , 2015, 11, 764-777.	1.4	72
3893	Mining diverse small RNA species in the deep transcriptome. <i>Trends in Biochemical Sciences</i> , 2015, 40, 4-7.	3.7	60
3896	RNA-Seq-Based Transcriptome Profiling of Early Nitrogen Deficiency Response in Cucumber Seedlings Provides New Insight into the Putative Nitrogen Regulatory Network. <i>Plant and Cell Physiology</i> , 2015, 56, 455-467.	1.5	90
3897	Functional Conservation of Both CDS- and 3' UTR-Located MicroRNA Binding Sites between Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 623-628.	3.5	42
3898	Transcriptional adaptation of <i>Shigella flexneri</i> during adherence to epithelial cells. <i>Journal of Basic Microbiology</i> , 2015, 55, 186-194.	1.8	6
3899	Infection of <i>Ustilaginoidea virens</i> intercepts rice seed formation but activates grain-filling-related genes. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 577-590.	4.1	67
3900	IsoSCM: improved and alternative 3' UTR annotation using multiple change-point inference. <i>Rna</i> , 2015, 21, 14-27.	1.6	54
3901	Bayesian Hierarchical Model for Differential Gene Expression Using RNA-Seq Data. <i>Statistics in Biosciences</i> , 2015, 7, 48-67.	0.6	4
3902	A multi-Poisson dynamic mixture model to cluster developmental patterns of gene expression by RNA-seq. <i>Briefings in Bioinformatics</i> , 2015, 16, 205-215.	3.2	6
3903	Transcriptomic reprogramming of genus <i>Paracoccidioides</i> in dimorphism and host niches. <i>Fungal Genetics and Biology</i> , 2015, 81, 98-109.	0.9	16
3904	Antisense transcription at the TRPM2 locus as a novel prognostic marker and therapeutic target in prostate cancer. <i>Oncogene</i> , 2015, 34, 2094-2102.	2.6	72
3905	RNA-seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 613-624.	4.1	202
3906	Transcriptome and metabolome analyses of sugar and organic acid metabolism in Ponkan ( <i>Citrus TJ ETQq1</i> ). <i>Overlooked</i> 1.0 0.784314 rgBT/105	1.0	105

#	ARTICLE	IF	CITATIONS
3907	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 232-248.	1.4	183
3908	Transcriptomic and proteomic analysis reveals mechanisms of embryo abortion during chrysanthemum cross breeding. <i>Scientific Reports</i> , 2015, 4, 6536.	1.6	36
3909	A highly sensitive and accurate gene expression analysis by sequencing (â€œbead-seqâ€) for a single cell. <i>Analytical Biochemistry</i> , 2015, 471, 9-16.	1.1	18
3910	Probing of a Human Proteome Microarray With a Recombinant Pathogen Protein Reveals a Novel Mechanism by Which Hookworms Suppress B-Cell Receptor Signaling. <i>Journal of Infectious Diseases</i> , 2015, 211, 416-425.	1.9	47
3911	Global Transcriptome Profiling of Genes that Are Differentially Regulated During Differentiation of Mouse Embryonic Neural Stem Cells into Astrocytes. <i>Journal of Molecular Neuroscience</i> , 2015, 55, 109-125.	1.1	31
3912	Copper trafficking in the CsoR regulon of <i>Streptomyces lividans</i> . <i>Metallomics</i> , 2015, 7, 145-155.	1.0	18
3913	Transcriptomic and Physiological Insights into the Robustness of Long Filamentous Cells of <i>Methanosaeta harundinacea</i> , Prevalent in Upflow Anaerobic Sludge Blanket Granules. <i>Applied and Environmental Microbiology</i> , 2015, 81, 831-839.	1.4	15
3914	WemIQ: an accurate and robust isoform quantification method for RNA-seq data. <i>Bioinformatics</i> , 2015, 31, 878-885.	1.8	23
3915	Comparative transcriptomic analysis provides insights into the molecular basis of the metamorphosis and nutrition metabolism change from zoeae to megalopae in <i>Eriocheir sinensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 13, 1-9.	0.4	27
3916	Tissue-specific mtDNA abundance from exome data and its correlation with mitochondrial transcription, mass and respiratory activity. <i>Mitochondrion</i> , 2015, 20, 13-21.	1.6	146
3917	Comparative proteomic and transcriptomic profile of <i>Staphylococcus epidermidis</i> biofilms grown in glucose-enriched medium. <i>Talanta</i> , 2015, 132, 705-712.	2.9	14
3918	The genome of the Pacific oyster <i>Crassostrea gigas</i> brings new insights on the massive expansion of the C1q gene family in Bivalvia. <i>Developmental and Comparative Immunology</i> , 2015, 49, 59-71.	1.0	95
3919	High-resolution chromatin immunoprecipitation (ChIP) sequencing reveals novel binding targets and prognostic role for SOX11 in mantle cell lymphoma. <i>Oncogene</i> , 2015, 34, 1231-1240.	2.6	60
3920	Transcription of Inflammatory Genes: Long Noncoding RNA and Beyond. <i>Journal of Interferon and Cytokine Research</i> , 2015, 35, 79-88.	0.5	29
3921	Genome-wide DNA Methylation Profiles and Their Relationships with mRNA and the microRNA Transcriptome in Bovine Muscle Tissue ( <i>Bos taurine</i> ). <i>Scientific Reports</i> , 2015, 4, 6546.	1.6	97
3922	PROPER: comprehensive power evaluation for differential expression using RNA-seq. <i>Bioinformatics</i> , 2015, 31, 233-241.	1.8	80
3923	Transcriptomic study of the red palm weevil <i>Rhynchophorus ferrugineus</i> embryogenesis. <i>Insect Science</i> , 2015, 22, 65-82.	1.5	15
3924	Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. <i>Briefings in Functional Genomics</i> , 2015, 14, 130-142.	1.3	186



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3925	Rcount: simple and flexible RNA-Seq read counting. <i>Bioinformatics</i> , 2015, 31, 436-437.	1.8	36
3926	Predictive modelling of gene expression from transcriptional regulatory elements. <i>Briefings in Bioinformatics</i> , 2015, 16, 616-628.	3.2	33
3927	Bioinformatics approaches to single-blastomere transcriptomics. <i>Molecular Human Reproduction</i> , 2015, 21, 115-125.	1.3	3
3928	The Neuronal Activity-Driven Transcriptome. <i>Molecular Neurobiology</i> , 2015, 51, 1071-1088.	1.9	104
3929	Analysis of the Drought Stress-Responsive Transcriptome of Black Cottonwood ( <i>Populus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td (	1.0	40
3930	Characterization of the "Xiangshui"™ lemon transcriptome by de novo assembly to discover genes associated with self-incompatibility. <i>Molecular Genetics and Genomics</i> , 2015, 290, 365-375.	1.0	39
3931	How do hosts react to endosymbionts? A new insight into the molecular mechanisms underlying the <i>Wolbachia</i> host association. <i>Insect Molecular Biology</i> , 2015, 24, 1-12.	1.0	27
3932	Diverse strategies conferring extreme cadmium (Cd) tolerance in the dark septate endophyte (DSE), <i>Exophiala pisciphila</i> : Evidence from RNA-seq data. <i>Microbiological Research</i> , 2015, 170, 27-35.	2.5	73
3933	Comprehensive transcriptome profiling of squamous cell carcinoma of horn in <i>Bos indicus</i> . <i>Veterinary and Comparative Oncology</i> , 2016, 14, 122-136.	0.8	12
3934	Genome-wide analysis of mechanosensitive channel of small conductance (MscS)-like gene family in common bean. <i>African Journal of Biotechnology</i> , 2016, 15, 580-592.	0.3	6
3935	Next-Generation Sequencing. , 2016, , 68-79.		4
3938	Symbiont modulates expression of specific gene categories in <i>Angomonas deanei</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2016, 111, 686-691.	0.8	6
3939	Orthology Guided Transcriptome Assembly of Italian Ryegrass and Meadow Fescue for Single-Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0017.	1.6	9
3940	Hemizyosity Enhances Purifying Selection: Lack of Fast-Z Evolution in Two Satyrine Butterflies. <i>Genome Biology and Evolution</i> , 2016, 8, 3108-3119.	1.1	31
3941	Cell type-specific transcriptome profiling in mammalian brains. <i>Frontiers in Bioscience - Landmark</i> , 2016, 21, 973-985.	3.0	6
3942	Reverse Genetics and High Throughput Sequencing Methodologies for Plant Functional Genomics. <i>Current Genomics</i> , 2016, 17, 460-475.	0.7	27
3943	Effects of Antioxidants in Human Cancers: Differential Effects on Non-Coding Intronic RNA Expression. <i>Antioxidants</i> , 2016, 5, 1.	2.2	62
3944	The Kinome of Edible and Medicinal Fungus <i>Wolfiporia cocos</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1495.	1.5	19

#	ARTICLE	IF	CITATIONS
3945	Transcriptome Analysis of Ramie ( <i>Boehmeria nivea</i> L. Gaud.) in Response to Ramie Moth ( <i>Cocytodes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	9
3946	Upregulated long intergenic noncoding RNA KRT18P55 acts as a novel biomarker for the progression of intestinal-type gastric cancer. <i>OncoTargets and Therapy</i> , 2016, 9, 445.	1.0	5
3947	Immune-Related Gene Expression Patterns in GPV- or H9N2-Infected Goose Spleens. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1990.	1.8	11
3948	The Protein Elicitor PevD1 Enhances Resistance to Pathogens and Promotes Growth in <i>Arabidopsis</i> . <i>International Journal of Biological Sciences</i> , 2016, 12, 931-943.	2.6	27
3949	RNA sequencing analysis to capture the transcriptome landscape during skin ulceration syndrome progression in sea cucumber <i>Apostichopus japonicus</i> . <i>BMC Genomics</i> , 2016, 17, 459.	1.2	40
3950	Evidence of selection for an accessible nucleosomal array in human. <i>BMC Genomics</i> , 2016, 17, 526.	1.2	25
3951	Transcriptomics of liver and muscle in Holstein cows genetically divergent for fertility highlight differences in nutrient partitioning and inflammation processes. <i>BMC Genomics</i> , 2016, 17, 603.	1.2	18
3952	RNA-Seq analysis reveals new evidence for inflammation-related changes in aged kidney. <i>Oncotarget</i> , 2016, 7, 30037-30048.	0.8	14
3953	Transcriptome sequencing identified hub genes for hepatocellular carcinoma by weighted-gene co-expression analysis. <i>Oncotarget</i> , 2016, 7, 38487-38499.	0.8	22
3954	Sexually Dimorphic Gene Expression Associated with Growth and Reproduction of Tongue Sole ( <i>Cynoglossus semilaevis</i> ) Revealed by Brain Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1402.	1.8	15
3955	RNA Sequencing and Transcriptome Analyses for <i>Cercis Gigantea</i> . <i>Current Bioinformatics</i> , 2016, 11, 32-39.	0.7	0
3956	Genome-wide identification and expression analysis of CIPK genes in diploid cottons. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	9
3957	Comparative analysis of the liver tissue transcriptomes of Mongolian and Lanzhou fat-tailed sheep. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	11
3958	Comparative transcriptome analysis reveals three potential antiviral signaling pathways in lymph organ tissue of the red swamp crayfish, <i>Procambarus clarkii</i> . <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	11
3959	Impact of Gene Annotation on RNA-seq Data Analysis. , 2016, , .		4
3960	The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. <i>BMC Genomics</i> , 2016, 17, 702.	1.2	32
3961	Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. <i>BMC Genomics</i> , 2016, 17, 761.	1.2	11
3962	A quantitative transcriptomic analysis of the physiological significance of mTOR signaling in goat fetal fibroblasts. <i>BMC Genomics</i> , 2016, 17, 879.	1.2	3

#	ARTICLE	IF	CITATIONS
3963	A new method for estimating the number of non-differentially expressed genes. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	2
3964	Aberrantly expressed microRNAs in the context of bladder tumorigenesis. <i>Investigative and Clinical Urology</i> , 2016, 57, S52.	1.0	14
3965	Cloning and abiotic stress resistance analyses of a new proline-glycine-alanine-histidine-rich protein gene from <i>Ipomoea batatas</i> (L.) Lam.. <i>Turkish Journal of Biology</i> , 2016, 40, 1148-1157.	2.1	2
3966	Bioinformatic analyses of GRAS genes in <i>Betula kirghisorum</i> based on transcriptome data. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	1
3967	Simulated linear test applied to quantitative proteomics. <i>Bioinformatics</i> , 2016, 32, i702-i709.	1.8	1
3968	Regulatory polymorphisms modulate the expression of HLA class II molecules and promote autoimmunity. <i>ELife</i> , 2016, 5, .	2.8	113
3969	RNA-seq profiling of mRNA associated with hypertrophic cardiomyopathy. <i>Molecular Medicine Reports</i> , 2016, 14, 5573-5586.	1.1	18
3970	Abnormal Expressions of DNA Glycosylase Genes NEIL1, NEIL2, and NEIL3 Are Associated with Somatic Mutation Loads in Human Cancer. <i>Oxidative Medicine and Cellular Longevity</i> , 2016, 2016, 1-10.	1.9	39
3971	Analysis of Gene Expression in an Inbred Line of Soft-Shell Clams ( <i>Mya arenaria</i> ) Displaying Growth Heterosis: Regulation of Structural Genes and the NOD2 Pathway. <i>International Journal of Genomics</i> , 2016, 2016, 1-10.	0.8	2
3972	The Impact of Serum Amyloid P-Component on Gene Expression in RAW264.7 Mouse Macrophages. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	7
3973	Transcriptome Analysis of Bovine Ovarian Follicles at Predeviation and Onset of Deviation Stages of a Follicular Wave. <i>International Journal of Genomics</i> , 2016, 2016, 1-9.	0.8	10
3974	Differential Gene Expression during Larval Metamorphic Development in the Pearl Oyster, <i>Pinctada fucata</i> , Based on Transcriptome Analysis. <i>International Journal of Genomics</i> , 2016, 2016, 1-15.	0.8	9
3975	<i>De Novo</i> Assembly and Comparative Transcriptome Analysis Provide Insight into Lysine Biosynthesis in <i>Toona sinensis</i> Roem. <i>International Journal of Genomics</i> , 2016, 2016, 1-9.	0.8	6
3976	Genome-Wide Transcriptome Analysis of Cadmium Stress in Rice. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	50
3977	De Novo Sequencing and Characterization of the Transcriptome of Dwarf Polish Wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50 1	0.8	8
3978	Genome-Wide Analysis of the Lysine Biosynthesis Pathway Network during Maize Seed Development. <i>PLoS ONE</i> , 2016, 11, e0148287.	1.1	5
3979	Akt-mTORC1 signaling regulates Acly to integrate metabolic input to control of macrophage activation. <i>ELife</i> , 2016, 5, .	2.8	324
3980	Digital gene expression analysis with sample multiplexing and PCR duplicate detection: A straightforward protocol. <i>BioTechniques</i> , 2016, 61, 26-32.	0.8	4

#	ARTICLE	IF	CITATIONS
3981	Transcriptome Analysis of HepG2 Cells Expressing ORF3 from Swine Hepatitis E Virus to Determine the Effects of ORF3 on Host Cells. <i>BioMed Research International</i> , 2016, 2016, 1-8.	0.9	5
3982	Discovery of clubroot-resistant genes in <i>Brassica napus</i> by transcriptome sequencing. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	7
3983	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	0.8	1,848
3984	Advancements in Omics Sciences. , 2016, , 67-108.		3
3985	Transcriptomic Profiling Using Next Generation Sequencing - Advances, Advantages, and Challenges. , 0, , .		8
3986	ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences. <i>BMC Genomics</i> , 2016, 17, 541.	1.2	31
3987	RNA-Seq and iTRAQ Reveal the Dwarfing Mechanism of Dwarf Polish Wheat ( <i>Triticum polonicum</i> ) Tj ETQq0 0,0 rgBT /Overlock 10	2.6	17
3988	An Integrated Analysis of the Genome-Wide Profiles of DNA Methylation and mRNA Expression Defining the Side Population of a Human Malignant Mesothelioma Cell Line. <i>Journal of Cancer</i> , 2016, 7, 1668-1679.	1.2	22
3989	Impact of RNA degradation on fusion detection by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 814.	1.2	34
3990	Single Cell Isolation and Analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2016, 4, 116.	1.8	257
3991	Functional Genomic Analysis of <i>Aspergillus flavus</i> Interacting with Resistant and Susceptible Peanut. <i>Toxins</i> , 2016, 8, 46.	1.5	33
3992	Colubrid Venom Composition: An -Omics Perspective. <i>Toxins</i> , 2016, 8, 230.	1.5	61
3993	Fish Transcriptomics. , 2016, , 205-214.		0
3994	Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. <i>Frontiers in Genetics</i> , 2016, 7, 42.	1.1	10
3995	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016, 7, 172.	1.1	12
3996	RNA-seq Profiling Reveals Novel Target Genes of LexA in the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Frontiers in Microbiology</i> , 2016, 7, 193.	1.5	44
3997	Exopolysaccharides Play a Role in the Swarming of the Benthic Bacterium <i>Pseudoalteromonas</i> sp. SM9913. <i>Frontiers in Microbiology</i> , 2016, 7, 473.	1.5	14
3998	Genome-Wide Detection of Predicted Non-coding RNAs Related to the Adhesion Process in <i>Vibrio alginolyticus</i> Using High-Throughput Sequencing. <i>Frontiers in Microbiology</i> , 2016, 7, 619.	1.5	14

#	ARTICLE	IF	CITATIONS
3999	Genome Structure of the Symbiont <i>Bifidobacterium pseudocatenulatum</i> CECT 7765 and Gene Expression Profiling in Response to Lactulose-Derived Oligosaccharides. <i>Frontiers in Microbiology</i> , 2016, 7, 624.	1.5	12
4000	Transcriptomic Analysis Reveals Adaptive Responses of an <i>Enterobacteriaceae</i> Strain LSJC7 to Arsenic Exposure. <i>Frontiers in Microbiology</i> , 2016, 7, 636.	1.5	38
4001	De novo Transcriptome Analysis of <i>Rhizoctonia solani</i> AG1 IA Strain Early Invasion in <i>Zoysia japonica</i> Root. <i>Frontiers in Microbiology</i> , 2016, 7, 708.	1.5	18
4002	Genome-Wide Transcriptional Profiling Reveals Two Distinct Outcomes in Central Nervous System Infections of Rabies Virus. <i>Frontiers in Microbiology</i> , 2016, 7, 751.	1.5	21
4003	Transcriptomic Analysis of <i>Staphylococcus epidermidis</i> Biofilm-Released Cells upon Interaction with Human Blood Circulating Immune Cells and Soluble Factors. <i>Frontiers in Microbiology</i> , 2016, 7, 1143.	1.5	7
4004	Comparative Transcriptomic Analysis Reveals Novel Insights into the Adaptive Response of <i>Skeletonema costatum</i> to Changing Ambient Phosphorus. <i>Frontiers in Microbiology</i> , 2016, 07, 1476.	1.5	43
4005	Molecular Keys to the <i>Janthinobacterium</i> and <i>Duganella</i> spp. Interaction with the Plant Pathogen <i>Fusarium graminearum</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1668.	1.5	66
4006	Genome-Wide Discovery of Putative sRNAs in <i>Paracoccus denitrificans</i> Expressed under Nitrous Oxide Emitting Conditions. <i>Frontiers in Microbiology</i> , 2016, 7, 1806.	1.5	16
4007	Sulfur Metabolism Pathways in <i>Sulfobacillus acidophilus</i> TPY, A Gram-Positive Moderate Thermoacidophile from a Hydrothermal Vent. <i>Frontiers in Microbiology</i> , 2016, 7, 1861.	1.5	8
4008	Characterization of the Olfactory Receptors Expressed in Human Spermatozoa. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 73.	1.6	74
4009	Pseudo-Reference-Based Assembly of Vertebrate Transcriptomes. <i>Genes</i> , 2016, 7, 10.	1.0	2
4010	Comparative Transcriptome Profile of the Cytoplasmic Male Sterile and Fertile Floral Buds of Radish ( <i>Raphanus sativus</i> L.). <i>International Journal of Molecular Sciences</i> , 2016, 17, 42.	1.8	29
4011	De Novo Transcriptome Assembly in <i>Shiraia bambusicola</i> to Investigate Putative Genes Involved in the Biosynthesis of Hypocrellin A. <i>International Journal of Molecular Sciences</i> , 2016, 17, 311.	1.8	45
4012	Effects of Endobacterium ( <i>Stenotrophomonas maltophilia</i> ) on Pathogenesis-Related Gene Expression of Pine Wood Nematode ( <i>Bursaphelenchus xylophilus</i> ) and Pine Wilt Disease. <i>International Journal of Molecular Sciences</i> , 2016, 17, 778.	1.8	20
4013	De Novo Assembly and Characterization of the Transcriptome of Grasshopper <i>Shirakiacris shirakii</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1110.	1.8	10
4014	Omics-Based Strategies in Precision Medicine: Toward a Paradigm Shift in Inborn Errors of Metabolism Investigations. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1555.	1.8	135
4015	Digital Gene Expression Profiling to Explore Differentially Expressed Genes Associated with Terpenoid Biosynthesis during Fruit Development in <i>Litsea cubeba</i> . <i>Molecules</i> , 2016, 21, 1251.	1.7	9
4016	Comparative Transcriptomic Analysis of Grape Berry in Response to Root Restriction during Developmental Stages. <i>Molecules</i> , 2016, 21, 1431.	1.7	21

#	ARTICLE	IF	CITATIONS
4017	Organ- and Growing Stage-Specific Expression of Solanesol Biosynthesis Genes in <i>Nicotiana tabacum</i> Reveals Their Association with Solanesol Content. <i>Molecules</i> , 2016, 21, 1536.	1.7	10
4018	Statistical inference for time course RNA-Seq data using a negative binomial mixed-effect model. <i>BMC Bioinformatics</i> , 2016, 17, 324.	1.2	21
4019	Superior anti-tumor activity of the MDM2 antagonist idasanutlin and the Bcl-2 inhibitor venetoclax in p53 wild-type acute myeloid leukemia models. <i>Journal of Hematology and Oncology</i> , 2016, 9, 50.	6.9	73
4020	RNA expression of TLR10 in normal equine tissues. <i>BMC Research Notes</i> , 2016, 9, 353.	0.6	7
4021	Transcriptome-Wide Analysis of Hepatitis B Virus-Mediated Changes to Normal Hepatocyte Gene Expression. <i>PLoS Pathogens</i> , 2016, 12, e1005438.	2.1	43
4022	Discharging tRNAs: a tug of war between translation and detoxification in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, 8324-8334.	6.5	46
4023	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. <i>PLoS Genetics</i> , 2016, 12, e1006433.	1.5	136
4024	Transcriptome Analysis of Flower Sex Differentiation in <i>Jatropha curcas</i> L. Using RNA Sequencing. <i>PLoS ONE</i> , 2016, 11, e0145613.	1.1	31
4025	GPCRs Direct Germline Development and Somatic Gonad Function in Planarians. <i>PLoS Biology</i> , 2016, 14, e1002457.	2.6	42
4026	Histone H3 Variant Regulates RNA Polymerase II Transcription Termination and Dual Strand Transcription of siRNA Loci in <i>Trypanosoma brucei</i> . <i>PLoS Genetics</i> , 2016, 12, e1005758.	1.5	55
4027	The Transcription Factor <i>Nfatc2</i> Regulates $\beta$ -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. <i>PLoS Genetics</i> , 2016, 12, e1006466.	1.5	40
4028	Identification of <i>Aedes aegypti</i> Long Intergenic Non-coding RNAs and Their Association with Wolbachia and Dengue Virus Infection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005069.	1.3	85
4029	RNA-Seq Reveals OTA-Related Gene Transcriptional Changes in <i>Aspergillus carbonarius</i> . <i>PLoS ONE</i> , 2016, 11, e0147089.	1.1	23
4030	Transcriptomic Profile of Whole Blood Cells from Elderly Subjects Fed Probiotic Bacteria <i>Lactobacillus rhamnosus</i> GG ATCC 53103 (LGG) in a Phase I Open Label Study. <i>PLoS ONE</i> , 2016, 11, e0147426.	1.1	16
4031	Identification of Putative Chemosensory Receptor Genes from the <i>Athetis dissimilis</i> Antennal Transcriptome. <i>PLoS ONE</i> , 2016, 11, e0147768.	1.1	21
4032	Differential Gene Expression Patterns in Chicken Cardiomyocytes during Hydrogen Peroxide-Induced Apoptosis. <i>PLoS ONE</i> , 2016, 11, e0147950.	1.1	8
4033	Transcriptome Profiling of Resistance to <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> in Cabbage ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	36
4034	Identification and Comparative Study of Chemosensory Genes Related to Host Selection by Legs Transcriptome Analysis in the Tea Geometrid <i>Ectropis obliqua</i> . <i>PLoS ONE</i> , 2016, 11, e0149591.	1.1	47

#	ARTICLE	IF	CITATIONS
4035	Genome-Wide Investigation Using sRNA-Seq, Degradome-Seq and Transcriptome-Seq Reveals Regulatory Networks of microRNAs and Their Target Genes in Soybean during Soybean mosaic virus Infection. PLoS ONE, 2016, 11, e0150582.	1.1	30
4036	Transcriptome Profiling of Two Asparagus Bean ( <i>Vigna unguiculata</i> subsp. <i>sesquipedalis</i> ) Cultivars Differing in Chilling Tolerance under Cold Stress. PLoS ONE, 2016, 11, e0151105.	1.1	26
4037	Expanding the Role of FurA as Essential Global Regulator in Cyanobacteria. PLoS ONE, 2016, 11, e0151384.	1.1	33
4038	Gene Expression Profile in the Long-Living Lotus: Insights into the Heat Stress Response Mechanism. PLoS ONE, 2016, 11, e0152540.	1.1	10
4039	Molecular Characterization and Global Expression Analysis of Lectin Receptor Kinases in Bread Wheat ( <i>Triticum aestivum</i> ). PLoS ONE, 2016, 11, e0153925.	1.1	73
4040	Comparative Transcriptome Analysis Reveals Different Silk Yields of Two Silkworm Strains. PLoS ONE, 2016, 11, e0155329.	1.1	26
4041	Utilization of a Conidia-Deficient Mutant to Study Sexual Development in <i>Fusarium graminearum</i> . PLoS ONE, 2016, 11, e0155671.	1.1	19
4042	Transcriptome Analysis and Gene Identification in the Pulmonary Artery of Broilers with Ascites Syndrome. PLoS ONE, 2016, 11, e0156045.	1.1	22
4043	Insights into Sexual Precocity of Female Oriental River Prawn <i>Macrobrachium nipponense</i> through Transcriptome Analysis. PLoS ONE, 2016, 11, e0157173.	1.1	13
4044	A Mechanistic Beta-Binomial Probability Model for mRNA Sequencing Data. PLoS ONE, 2016, 11, e0157828.	1.1	8
4045	Transcriptomic Analysis of Multipurpose Timber Yielding Tree <i>Neolamarckia cadamba</i> during Xylogenesis Using RNA-Seq. PLoS ONE, 2016, 11, e0159407.	1.1	26
4046	Transcriptome Profile of Near-Isogenic Soybean Lines for $\beta^2$ -Conglycinin $\beta^2$ -Subunit Deficiency during Seed Maturation. PLoS ONE, 2016, 11, e0159723.	1.1	17
4047	De Novo Assembly and Comparative Transcriptome Analyses of Red and Green Morphs of Sweet Basil Grown in Full Sunlight. PLoS ONE, 2016, 11, e0160370.	1.1	25
4048	Transcriptome Characterization of <i>Dendrolimus punctatus</i> and Expression Profiles at Different Developmental Stages. PLoS ONE, 2016, 11, e0161667.	1.1	29
4049	Identification and Expression Analysis of Candidate Odorant-Binding Protein and Chemosensory Protein Genes by Antennal Transcriptome of <i>Sitobion avenae</i> . PLoS ONE, 2016, 11, e0161839.	1.1	99
4050	The Involvement of Mig1 from <i>Xanthophyllomyces dendrorhous</i> in Catabolic Repression: An Active Mechanism Contributing to the Regulation of Carotenoid Production. PLoS ONE, 2016, 11, e0162838.	1.1	24
4051	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. PLoS ONE, 2016, 11, e0162868.	1.1	93
4052	The RNA Chaperone Hfq Is Involved in Colony Morphology, Nutrient Utilization and Oxidative and Envelope Stress Response in <i>Vibrio alginolyticus</i> . PLoS ONE, 2016, 11, e0163689.	1.1	38

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4053	Ovarian Transcriptome Analysis of Vitellogenic and Non-Vitellogenic Female Banana Shrimp ( <i>Fenneropenaeus merguensis</i> ). <i>PLoS ONE</i> , 2016, 11, e0164724.	1.1	24
4054	Genome-Wide Transcriptome Analysis of CD36 Overexpression in HepG2.2.15 Cells to Explore Its Regulatory Role in Metabolism and the Hepatitis B Virus Life Cycle. <i>PLoS ONE</i> , 2016, 11, e0164787.	1.1	8
4055	Transcriptome Analysis of the Midgut of the Chinese Oak Silkworm <i>Antheraea pernyi</i> Infected with <i>Antheraea pernyi</i> Nucleopolyhedrovirus. <i>PLoS ONE</i> , 2016, 11, e0165959.	1.1	11
4056	Transcriptional Responses and Gentiopicroside Biosynthesis in Methyl Jasmonate-Treated <i>Gentiana macrophylla</i> Seedlings. <i>PLoS ONE</i> , 2016, 11, e0166493.	1.1	14
4057	Transcriptome and Multivariable Data Analysis of <i>Corynebacterium glutamicum</i> under Different Dissolved Oxygen Conditions in Bioreactors. <i>PLoS ONE</i> , 2016, 11, e0167156.	1.1	19
4058	InFusion: Advancing Discovery of Fusion Genes and Chimeric Transcripts from Deep RNA-Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0167417.	1.1	62
4059	The Epstein-Barr Virus Immune-evasins BCRF1 and BPLF1 Are Expressed by a Mechanism Independent of the Canonical Late Pre-initiation Complex. <i>PLoS Pathogens</i> , 2016, 12, e1006008.	2.1	29
4060	Understanding the Diversity of <i>Aspergillus</i> by Next-Generation Sequencing. , 2016, , 29-40.		1
4061	Transcriptome Analysis of Differentially Expressed Genes Involved in Proanthocyanidin Accumulation in the Rhizomes of <i>Fagopyrum dibotrys</i> and an Irradiation-Induced Mutant. <i>Frontiers in Physiology</i> , 2016, 7, 100.	1.3	16
4062	Modulation of Mammary Gland Development and Milk Production by Growth Hormone Expression in GH Transgenic Goats. <i>Frontiers in Physiology</i> , 2016, 7, 278.	1.3	27
4063	Multi-Omics Approach Identifies Molecular Mechanisms of Plant-Fungus Mycorrhizal Interaction. <i>Frontiers in Plant Science</i> , 2015, 6, 1061.	1.7	39
4064	Transcriptome Analysis of <i>Brassica rapa</i> Near-Isogenic Lines Carrying Clubroot-Resistant and "Susceptible Alleles in Response to <i>Plasmodiophora brassicae</i> during Early Infection. <i>Frontiers in Plant Science</i> , 2015, 6, 1183.	1.7	118
4065	Extensive Transcriptome Changes Underlying the Flower Color Intensity Variation in <i>Paeonia ostii</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 1205.	1.7	44
4066	Heat Shock Factor Genes of Tall Fescue and Perennial Ryegrass in Response to Temperature Stress by RNA-Seq Analysis. <i>Frontiers in Plant Science</i> , 2015, 6, 1226.	1.7	39
4067	Physiological Characterization and Comparative Transcriptome Analysis of a Slow-Growing Reduced-Thylakoid Mutant of Chinese Cabbage ( <i>Brassica campestris</i> ssp. <i>pekinensis</i> ). <i>Frontiers in Plant Science</i> , 2016, 7, 3.	1.7	9
4068	Transcriptomic Analysis Reveals the Metabolic Mechanism of L-Ascorbic Acid in <i>Ziziphus jujuba</i> Mill.. <i>Frontiers in Plant Science</i> , 2016, 7, 122.	1.7	19
4069	Transcriptome Analysis of Soybean Leaf Abscission Identifies Transcriptional Regulators of Organ Polarity and Cell Fate. <i>Frontiers in Plant Science</i> , 2016, 7, 125.	1.7	26
4070	Extreme Hypoxic Conditions Induce Selective Molecular Responses and Metabolic Reset in Detached Apple Fruit. <i>Frontiers in Plant Science</i> , 2016, 7, 146.	1.7	48



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4071	Transcriptome Characterization of <i>Gnetum parvifolium</i> Reveals Candidate Genes Involved in Important Secondary Metabolic Pathways of Flavonoids and Stilbenoids. <i>Frontiers in Plant Science</i> , 2016, 7, 174.	1.7	42
4072	De novo Transcriptome Analysis of <i>Sinapis alba</i> in Revealing the Glucosinolate and Phytochelatin Pathways. <i>Frontiers in Plant Science</i> , 2016, 7, 259.	1.7	19
4073	Transcriptome Analyses Reveal the Involvement of Both C and N Termini of Cryptochrome 1 in Its Regulation of Phytohormone-Responsive Gene Expression in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 294.	1.7	21
4074	Validation and Comparison of Reference Genes for qPCR Normalization of <i>Celery</i> ( <i>Apium graveolens</i> ) at Different Development Stages. <i>Frontiers in Plant Science</i> , 2016, 7, 313.	1.7	77
4075	De novo Sequencing of the Leaf Transcriptome Reveals Complex Light-Responsive Regulatory Networks in <i>Camellia sinensis</i> cv. Baijiguan. <i>Frontiers in Plant Science</i> , 2016, 7, 332.	1.7	58
4076	Changes in Transcript Related to Osmosis and Intracellular Ion Homeostasis in <i>Paulownia tomentosa</i> under Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 384.	1.7	18
4077	Genome-Wide Identification of <i>Jatropha curcas</i> Aquaporin Genes and the Comparative Analysis Provides Insights into the Gene Family Expansion and Evolution in <i>Hevea brasiliensis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 395.	1.7	54
4078	Transcriptome Analysis of Differentially Expressed Genes Provides Insight into Stolon Formation in <i>Tulipa edulis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 409.	1.7	27
4079	Integrated Systems Biology Analysis of Transcriptomes Reveals Candidate Genes for Acidity Control in Developing Fruits of Sweet Orange ( <i>Citrus sinensis</i> L. Osbeck). <i>Frontiers in Plant Science</i> , 2016, 7, 486.	1.7	32
4080	Genome-Wide Analysis of Gene Regulatory Networks of the FVE-HDA6-FLD Complex in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 555.	1.7	37
4081	Different Gene Expression Patterns between Leaves and Flowers in <i>Lonicera japonica</i> Revealed by Transcriptome Analysis. <i>Frontiers in Plant Science</i> , 2016, 7, 637.	1.7	9
4082	Transcriptomic Analysis Identifies Differentially Expressed Genes (DEGs) Associated with Bolting and Flowering in Radish ( <i>Raphanus sativus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 682.	1.7	26
4083	Transcriptome Profiling of Light-Regulated Anthocyanin Biosynthesis in the Pericarp of Litchi. <i>Frontiers in Plant Science</i> , 2016, 07, 963.	1.7	62
4084	The <i>Rosa chinensis</i> cv. <i>Viridiflora</i> Phyllody Phenotype Is Associated with Misexpression of Flower Organ Identity Genes. <i>Frontiers in Plant Science</i> , 2016, 7, 996.	1.7	17
4085	Comprehensive Analysis of the Triterpenoid Saponins Biosynthetic Pathway in <i>Anemone flaccida</i> by Transcriptome and Proteome Profiling. <i>Frontiers in Plant Science</i> , 2016, 7, 1094.	1.7	32
4086	Temporal-Spatial Transcriptome Analyses Provide Insights into the Development of Petaloid Androecium in <i>Canna indica</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1194.	1.7	12
4087	Comparative Transcriptome Analysis of Latex Reveals Molecular Mechanisms Underlying Increased Rubber Yield in <i>Hevea brasiliensis</i> Self-Rooting Juvenile Clones. <i>Frontiers in Plant Science</i> , 2016, 7, 1204.	1.7	21
4088	Transcriptome Profiling of Taproot Reveals Complex Regulatory Networks during Taproot Thickening in Radish ( <i>Raphanus sativus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1210.	1.7	29

#	ARTICLE	IF	CITATIONS
4089	Comparative Transcriptome Analysis of Primary Roots of Brassica napus Seedlings with Extremely Different Primary Root Lengths Using RNA Sequencing. <i>Frontiers in Plant Science</i> , 2016, 7, 1238.	1.7	18
4090	Mining for Candidate Genes in an Introgression Line by Using RNA Sequencing: The Anthocyanin Overaccumulation Phenotype in Brassica. <i>Frontiers in Plant Science</i> , 2016, 7, 1245.	1.7	30
4091	Transcriptome Analysis of Pepper ( <i>Capsicum annuum</i> ) Revealed a Role of 24-Epibrassinolide in Response to Chilling. <i>Frontiers in Plant Science</i> , 2016, 7, 1281.	1.7	51
4092	Comparative Transcriptome Analysis Identifies Putative Genes Involved in the Biosynthesis of Xanthanolides in <i>Xanthium strumarium</i> L.. <i>Frontiers in Plant Science</i> , 2016, 7, 1317.	1.7	9
4093	Genomic Dissection and Expression Profiling Revealed Functional Divergence in <i>Triticum aestivum</i> Leucine Rich Repeat Receptor Like Kinases (TaLRRKs). <i>Frontiers in Plant Science</i> , 2016, 7, 1374.	1.7	68
4094	Transcriptome Analysis of Stem and Globally Comparison with Other Tissues in Brassica napus. <i>Frontiers in Plant Science</i> , 2016, 7, 1403.	1.7	49
4095	Transcriptome Sequencing Identified Genes and Gene Ontologies Associated with Early Freezing Tolerance in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1477.	1.7	43
4096	Transcriptome Analysis of Green Peach Aphid ( <i>Myzus persicae</i> ): Insight into Developmental Regulation and Inter-Species Divergence. <i>Frontiers in Plant Science</i> , 2016, 7, 1562.	1.7	16
4097	Transcriptome Sequencing and Expression Analysis of Cadmium (Cd) Transport and Detoxification Related Genes in Cd-Accumulating <i>Salix integra</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1577.	1.7	54
4098	Transcriptome Dynamics in Mango Fruit Peel Reveals Mechanisms of Chilling Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 1579.	1.7	69
4099	Differential Gene Expression in <i>Rhododendron fortunei</i> Roots Colonized by an Ericoid Mycorrhizal Fungus and Increased Nitrogen Absorption and Plant Growth. <i>Frontiers in Plant Science</i> , 2016, 7, 1594.	1.7	21
4100	Insights from the Cold Transcriptome and Metabolome of <i>Dendrobium officinale</i> : Global Reprogramming of Metabolic and Gene Regulation Networks during Cold Acclimation. <i>Frontiers in Plant Science</i> , 2016, 7, 1653.	1.7	75
4101	The Mechanisms of Maize Resistance to <i>Fusarium verticillioides</i> by Comprehensive Analysis of RNA-seq Data. <i>Frontiers in Plant Science</i> , 2016, 7, 1654.	1.7	61
4102	Ability to Remove Na <sup>+</sup> and Retain K <sup>+</sup> Correlates with Salt Tolerance in Two Maize Inbred Lines Seedlings. <i>Frontiers in Plant Science</i> , 2016, 7, 1716.	1.7	72
4103	Studying Secondary Growth and Bast Fiber Development: The Hemp Hypocotyl Peeks behind the Wall. <i>Frontiers in Plant Science</i> , 2016, 7, 1733.	1.7	62
4104	Transcriptional Profiling of Rice Treated with MoHrip1 Reveal the Function of Protein Elicitor in Enhancement of Disease Resistance and Plant Growth. <i>Frontiers in Plant Science</i> , 2016, 7, 1818.	1.7	16
4105	Genome-Wide Identification, Localization, and Expression Analysis of Proanthocyanidin-Associated Genes in Brassica. <i>Frontiers in Plant Science</i> , 2016, 7, 1831.	1.7	14
4106	Transcriptome Analysis Highlights Defense and Signaling Pathways Mediated by Rice pi21 Gene with Partial Resistance to <i>Magnaporthe oryzae</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1834.	1.7	40

#	ARTICLE	IF	CITATIONS
4107	Characterization and Comparative Expression Profiling of Browning Response in <i>Medinilla formosana</i> after Cutting. <i>Frontiers in Plant Science</i> , 2016, 7, 1897.	1.7	9
4108	OsSGL, a Novel DUF1645 Domain-Containing Protein, Confers Enhanced Drought Tolerance in Transgenic Rice and <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2001.	1.7	46
4109	Comparative structural analysis of Bru1 region homeologs in <i>Saccharum spontaneum</i> and <i>S. officinarum</i> . <i>BMC Genomics</i> , 2016, 17, 446.	1.2	8
4110	Comparison of Genotypic and Expression Data to Determine Distinctness among Inbred Lines of Maize for Granting of Plant Variety Protection. <i>Crop Science</i> , 2016, 56, 1443-1459.	0.8	6
4111	From Big Data Analytics and Network Inference to Systems Modeling. , 2016, , 113-144.		0
4112	eQTL mapping. , 0, , 208-228.		0
4113	De novo transcriptome analysis of tobacco seedlings and identification of the early response gene network under low-potassium stress. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	6
4114	Next-Generation Sequencing " An Overview of the History, Tools, and "Omic" Applications. , 0, , .		94
4115	Bioinformatics for RNA-Seq Data Analysis. , 2016, , .		6
4116	A comparative analytical assay of gene regulatory networks inferred using microarray and RNA-seq datasets. <i>Bioinformatics</i> , 2016, 12, 340-341.	0.2	10
4117	Prognostic significance of PLIN1 expression in human breast cancer. <i>Oncotarget</i> , 2016, 7, 54488-54502.	0.8	38
4118	Integrated analysis of miRNAs and transcriptomes in <i>Aedes albopictus</i> midgut reveals the differential expression profiles of immune-related genes during dengue virus serotype-2 infection. <i>Insect Science</i> , 2016, 23, 377-385.	1.5	22
4119	Transcriptome analysis in heart failure. <i>Current Opinion in Cardiology</i> , 2016, 31, 242-248.	0.8	11
4120	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. <i>Genome Research</i> , 2016, 26, 1124-1133.	2.4	19
4121	Transcriptomic analysis of the hippocampus from six inbred strains of mice suggests a basis for sex-specific susceptibility and severity of neurological disorders. <i>Journal of Comparative Neurology</i> , 2016, 524, 2696-2710.	0.9	24
4122	Identification of differentially expressed genes associated with differential body size in mandarin fish ( <i>Siniperca chuatsi</i> ). <i>Genetica</i> , 2016, 144, 445-455.	0.5	9
4123	Metabolic activity in dormant conidia of <i>Aspergillus niger</i> and developmental changes during conidial outgrowth. <i>Fungal Genetics and Biology</i> , 2016, 94, 23-31.	0.9	59
4124	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. <i>Bioinformatics</i> , 2016, 32, 3345-3347.	1.8	11

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4125	Transcriptomic responses to different doses of cyclozaprid involved in detoxification and stress response in the whitebacked planthopper, <i>Sogatella furcifera</i> . <i>Entomologia Experimentalis Et Applicata</i> , 2016, 158, 248-257.	0.7	22
4126	Identification of <i>FLS1</i> expands the repertoire of genes for resistance to Fusarium wilt in tomato to three resistance gene classes. <i>Molecular Plant Pathology</i> , 2016, 17, 448-463.	2.0	125
4127	Nascent Genomic Evolution and Allopatric Speciation of <i>Myroides profundus</i> D25 in Its Transition from Land to Ocean. <i>MBio</i> , 2016, 7, e01946-15.	1.8	7
4128	Chronic toxicological effects of $\beta$ -diketone antibiotics on <i>Zebrafish</i> ( <i>Danio rerio</i> ) using transcriptome profiling of deep sequencing. <i>Environmental Toxicology</i> , 2016, 31, 1357-1371.	2.1	15
4129	De novo transcriptome sequencing of blue honeysuckle fruit ( <i>Lonicera caerulea</i> L.) and analysis of major genes involved in anthocyanin biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	7
4130	Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice. <i>Nature Genetics</i> , 2016, 48, 919-926.	9.4	119
4131	ADAR-Mediated RNA Editing Predicts Progression and Prognosis of Gastric Cancer. <i>Gastroenterology</i> , 2016, 151, 637-650.e10.	0.6	127
4132	RNA-seq analysis reveals new candidate genes for drip loss in a Pietrain–ADuroc–ALandrace–AYorkshire population. <i>Animal Genetics</i> , 2016, 47, 192-199.	0.6	11
4133	Identification of genes in longissimus dorsi muscle differentially expressed between Wannanhua and Yorkshire pigs using RNA-seq. <i>Animal Genetics</i> , 2016, 47, 324-333.	0.6	40
4134	Position-effect variegation revisited: HUSHing up heterochromatin in human cells. <i>BioEssays</i> , 2016, 38, 333-343.	1.2	36
4135	Systems Biology Approaches for Host–Fungal Interactions: An Expanding Multi-Omics Frontier. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 127-138.	1.0	34
4136	PCAN: Probabilistic Correlation Analysis of Two Non-Normal Data Sets. <i>Biometrics</i> , 2016, 72, 1358-1368.	0.8	7
4137	<i>ETV6-LPXN</i> fusion transcript generated by t(11;12)(q12.1;p13) in a patient with relapsing acute myeloid leukemia with <i>NUP98-HOXA9</i> . <i>Genes Chromosomes and Cancer</i> , 2016, 55, 242-250.	1.5	14
4138	A novel <i>Gal</i> -responsive regulator discovered in the rice blast fungus <i>Pyricularia oryzae</i> ( <i>Magnaporthe oryzae</i> ). <i>FEBS Letters</i> , 2016, 590, 550-558.	1.3	22
4139	Integrating transcriptome and proteome profiling: Strategies and applications. <i>Proteomics</i> , 2016, 16, 2533-2544.	1.3	147
4140	Comparative transcriptome analysis of differentially expressed genes between the curly and normal leaves of <i>Cymbidium goeringii</i> var. <i>longibracteatum</i> . <i>Genes and Genomics</i> , 2016, 38, 985-998.	0.5	7
4141	Current analysis of host–parasite interactions with a focus on next generation sequencing data. <i>Zoology</i> , 2016, 119, 298-306.	0.6	33
4142	multiDE: a dimension reduced model based statistical method for differential expression analysis using RNA-sequencing data with multiple treatment conditions. <i>BMC Bioinformatics</i> , 2016, 17, 248.	1.2	5

#	ARTICLE	IF	CITATIONS
4143	Transcriptome sequencing reveals genetic mechanisms underlying the transition between the laying and brooding phases and gene expression changes associated with divergent reproductive phenotypes in chickens. <i>Molecular Biology Reports</i> , 2016, 43, 977-989.	1.0	29
4144	MicroRNAs in Cardiovascular Disease. <i>Cardiology in Review</i> , 2016, 24, 110-118.	0.6	22
4145	<scp>SCR</scp>96, a small cysteine-rich secretory protein of <scp><i>P</i></scp><i>hytophthora cactorum</i>, can trigger cell death in the Solanaceae and is important for pathogenicity and oxidative stress tolerance. <i>Molecular Plant Pathology</i> , 2016, 17, 577-587.	2.0	42
4146	Analysis of digital gene expression profiling in hemocytes of white shrimp <i>Litopenaeus vannamei</i> under nitrite stress. <i>Fish and Shellfish Immunology</i> , 2016, 56, 1-11.	1.6	55
4147	Identification of major Toxoneuron nigriceps venom proteins using an integrated transcriptomic/proteomic approach. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 49-61.	1.2	44
4148	Systems level analysis of the <i>Chlamydomonas reinhardtii</i> metabolic network reveals variability in evolutionary co-conservation. <i>Molecular BioSystems</i> , 2016, 12, 2394-2407.	2.9	12
4149	Reconstruction and applications of consensus yeast metabolic network based on <scp>RNA</scp> sequencing. <i>FEBS Open Bio</i> , 2016, 6, 264-275.	1.0	4
4150	<scp>MAPK</scp> cascade-mediated regulation of pathogenicity, conidiation and tolerance to abiotic stresses in the entomopathogenic fungus <scp><i>M</i></scp><i>etarhizium robertsii</i>. <i>Environmental Microbiology</i> , 2016, 18, 1048-1062.	1.8	54
4151	Sensory and immune genes identification and analysis in a widely used parasitoid wasp <i>Trichogramma dendrolimi</i> (Hymenoptera: Trichogrammatidae). <i>Insect Science</i> , 2016, 23, 417-429.	1.5	13
4152	Genome-wide gene expression and DNA methylation differences in abnormally cloned and normally natural mating piglets. <i>Animal Genetics</i> , 2016, 47, 436-450.	0.6	12
4153	Exploring complex pheromone biosynthetic processes in the bumblebee male labial gland by RNA sequencing. <i>Insect Molecular Biology</i> , 2016, 25, 295-314.	1.0	12
4154	Transcriptome analysis of near-isogenic lines provides molecular insights into starch biosynthesis in maize kernel. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 713-723.	4.1	15
4155	Alternative splicing enhances transcriptome complexity in desiccating seeds. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 947-958.	4.1	26
4156	Differentially expressed genes associated with adaptation to different thermal environments in three sympatric Cuban <i>Anolis</i> lizards. <i>Molecular Ecology</i> , 2016, 25, 2273-2285.	2.0	36
4157	A transcriptomics investigation into pine reproductive organ development. <i>New Phytologist</i> , 2016, 209, 1278-1289.	3.5	34
4158	Expression and diversification analysis reveals transposable elements play important roles in the origin of <scp>L</scp>ycopersicon-specific lnc<scp>RNA</scp>s in tomato. <i>New Phytologist</i> , 2016, 209, 1442-1455.	3.5	87
4159	AshSP17, a creeping bentgrass small heat shock protein modulates plant photosynthesis and ABA-dependent and independent signalling to attenuate plant response to abiotic stress. <i>Plant, Cell and Environment</i> , 2016, 39, 1320-1337.	2.8	82
4160	Transcriptomic analysis of differentially expressed genes in the floral transition of the summer flowering chrysanthemum. <i>BMC Genomics</i> , 2016, 17, 673.	1.2	27

#	ARTICLE	IF	CITATIONS
4161	Improved Placement of Multi-mapping Small RNAs. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2103-2111.	0.8	263
4162	Improvement of genome assembly completeness and identification of novel full-length protein-coding genes by RNA-seq in the giant panda genome. <i>Scientific Reports</i> , 2016, 5, 18019.	1.6	12
4163	Integrative analysis of transcriptomics and proteomics of skeletal muscles of the Chinese indigenous Shaziling pig compared with the Yorkshire breed. <i>BMC Genetics</i> , 2016, 17, 80.	2.7	58
4164	Quorum sensing systems differentially regulate the production of phenazine-1-carboxylic acid in the rhizobacterium <i>Pseudomonas aeruginosa</i> PA1201. <i>Scientific Reports</i> , 2016, 6, 30352.	1.6	32
4165	Analysis of miRNAs and their target genes associated with lipid metabolism in duck liver. <i>Scientific Reports</i> , 2016, 6, 27418.	1.6	18
4166	Genome-wide analysis of miRNAs in the ovaries of Jining Grey and Laiwu Black goats to explore the regulation of fecundity. <i>Scientific Reports</i> , 2016, 6, 37983.	1.6	44
4167	An Expanded Maize Gene Expression Atlas based on RNA Sequencing and its Use to Explore Root Development. <i>Plant Genome</i> , 2016, 9, plantgenome2015.04.0025.	1.6	289
4168	Identification of candidate thermotolerance genes during early seedling stage in upland cotton ( <i>Gossypium hirsutum</i> L.) revealed by comparative transcriptome analysis. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	1
4169	Regulation of carotenogenesis in the red yeast <i>Xanthophyllomyces dendrorhous</i> : the role of the transcriptional co-repressor complex Cyc8-Tup1 involved in catabolic repression. <i>Microbial Cell Factories</i> , 2016, 15, 193.	1.9	17
4170	Identification and expression analysis of an olfactory receptor gene family in green plant bug <i>Apolygus lucorum</i> (Meyer-D&A14r). <i>Scientific Reports</i> , 2016, 6, 37870.	1.6	41
4171	Identifying ultrasensitive HGF dose-response functions in a 3D mammalian system for synthetic morphogenesis. <i>Scientific Reports</i> , 2016, 6, 39178.	1.6	7
4172	A Network of Splice Isoforms for the Mouse. <i>Scientific Reports</i> , 2016, 6, 24507.	1.6	17
4173	In-depth comparative transcriptome analysis of intestines of red swamp crayfish, <i>Procambarus clarkii</i> , infected with WSSV. <i>Scientific Reports</i> , 2016, 6, 26780.	1.6	30
4174	A novel mutant allele of SSI2 confers a better balance between disease resistance and plant growth inhibition on <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2016, 16, 208.	1.6	21
4175	A novel scoring estimator to screening for oncogenic chimeric transcripts in cancer transcriptome sequencing. , 2016, , .		0
4176	Genomic and transcriptomic profiling of resistant CEM/ADR-5000 and sensitive CCRF-CEM leukaemia cells for unravelling the full complexity of multi-factorial multidrug resistance. <i>Scientific Reports</i> , 2016, 6, 36754.	1.6	41
4177	Gene expression changes triggered by end-of-day far-red light treatment on early developmental stages of <i>Eustoma grandiflorum</i> (Raf.) Shinn.. <i>Scientific Reports</i> , 2016, 5, 17864.	1.6	8
4178	Deep transcriptomic profiling reveals the similarity between endothelial cells cultured under static and oscillatory shear stress conditions. <i>Physiological Genomics</i> , 2016, 48, 660-666.	1.0	23

#	ARTICLE	IF	CITATIONS
4179	Transcriptomic Analysis of Differentially Expressed Genes During Larval Development of <i>Rapana venosa</i> by Digital Gene Expression Profiling. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2181-2193.	0.8	25
4180	Overexpression of sonic hedgehog in the triple negative breast cancer: clinicopathological characteristics of high burden breast cancer patients from Bangladesh. <i>Scientific Reports</i> , 2016, 6, 18830.	1.6	50
4181	Neurons That Underlie <i>Drosophila melanogaster</i> Reproductive Behaviors: Detection of a Large Male-Bias in Gene Expression in fruitless-Expressing Neurons. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2455-2465.	0.8	20
4182	Transcriptome analyses reveal molecular mechanism underlying tapping panel dryness of rubber tree ( <i>Hevea brasiliensis</i> ). <i>Scientific Reports</i> , 2016, 6, 23540.	1.6	35
4183	Homoeologue expression insights into the basis of growth heterosis at the intersection of ploidy and hybridity in Cyprinidae. <i>Scientific Reports</i> , 2016, 6, 27040.	1.6	29
4184	Transcriptional identification and characterization of differentially expressed genes associated with embryogenesis in radish ( <i>Raphanus sativus</i> L.). <i>Scientific Reports</i> , 2016, 6, 21652.	1.6	42
4185	Analysis of <i>Drosophila p8</i> and <i>p52</i> mutants reveals distinct roles for the maintenance of TFIIH stability and male germ cell differentiation. <i>Open Biology</i> , 2016, 6, 160222.	1.5	5
4186	Transcriptome Analysis of the Signalling Networks in Coronatine-Induced Secondary Laticifer Differentiation from Vascular Cambia in Rubber Trees. <i>Scientific Reports</i> , 2016, 6, 36384.	1.6	25
4187	Identification of vernalization responsive genes in the winter wheat cultivar Jing841 by transcriptome sequencing. <i>Journal of Genetics</i> , 2016, 95, 957-964.	0.4	7
4188	A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. <i>BMC Genomics</i> , 2016, 17, 1025.	1.2	35
4189	Deciphering the transcriptomic response of <i>Fusarium verticillioides</i> in relation to nitrogen availability and the development of sugarcane pokkah boeng disease. <i>Scientific Reports</i> , 2016, 6, 29692.	1.6	23
4190	Gene-specific correlation of <i>RNA</i> and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016, 12, 883.	3.2	347
4191	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	1.6	155
4192	Transcriptomic analysis of mouse liver reveals a potential hepato-enteric pathogenic mechanism in acute <i>Toxoplasma gondii</i> infection. <i>Parasites and Vectors</i> , 2016, 9, 427.	1.0	73
4193	Landscape and Fruit Developmental Regulation of Alternative Splicing in Tomato by Genome-Wide Analysis. <i>Horticultural Plant Journal</i> , 2016, 2, 338-350.	2.3	11
4194	Transcriptomics. , 2016, , 160-165.		15
4195	CD14 in the TLRs signaling pathway is associated with the resistance to <i>E. coli</i> F18 in Chinese domestic weaned piglets. <i>Scientific Reports</i> , 2016, 6, 24611.	1.6	22
4196	Identification of novel targets of diabetic nephropathy and PEDF peptide treatment using RNA-seq. <i>BMC Genomics</i> , 2016, 17, 936.	1.2	30

#	ARTICLE	IF	CITATIONS
4197	Corrigendum to: Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 1205.	1.1	0
4198	Transcriptome analysis revealed the dynamic oil accumulation in <i>Symplocos paniculata</i> fruit. <i>BMC Genomics</i> , 2016, 17, 929.	1.2	15
4199	Impact of external pneumatic compression target inflation pressure on transcriptome-wide RNA expression in skeletal muscle. <i>Physiological Reports</i> , 2016, 4, e13029.	0.7	19
4200	Digital gene expression profiling analysis of duodenum transcriptomes in SD rats administered ferrous sulfate or ferrous glycine chelate by gavage. <i>Scientific Reports</i> , 2016, 6, 37923.	1.6	17
4202	Evolutionary and functional analysis of mulberry type III polyketide synthases. <i>BMC Genomics</i> , 2016, 17, 540.	1.2	20
4203	Differential expression analyses for single-cell RNA-seq: old questions on new data. <i>Quantitative Biology</i> , 2016, 4, 243-260.	0.3	31
4204	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. <i>Integrative and Comparative Biology</i> , 2016, 56, 1067-1079.	0.9	20
4205	FARNA: knowledgebase of inferred functions of non-coding RNA transcripts. <i>Nucleic Acids Research</i> , 2017, 45, gkw973.	6.5	30
4206	Combined transcriptome and metabolome analyses to understand the dynamic responses of rice plants to attack by the rice stem borer <i>Chilo suppressalis</i> (Lepidoptera: Crambidae). <i>BMC Plant Biology</i> , 2016, 16, 259.	1.6	68
4207	Modeling Enzyme Processivity Reveals that RNA-Seq Libraries Are Biased in Characteristic and Correctable Ways. <i>Cell Systems</i> , 2016, 3, 467-479.e12.	2.9	20
4208	A novel long intergenic noncoding <i>scRNA</i> indispensable for the cleavage of mouse two-cell embryos. <i>EMBO Reports</i> , 2016, 17, 1452-1470.	2.0	55
4209	Transcriptome analysis of root development in bottle gourd ( <i>Lagenaria siceraria</i> ). <i>Acta Horticulturae</i> , 2016, , 41-48.	0.1	2
4210	Transcriptome analysis revealed chimeric RNAs, single nucleotide polymorphisms and allele-specific expression in porcine prenatal skeletal muscle. <i>Scientific Reports</i> , 2016, 6, 29039.	1.6	8
4211	Transcriptomic comparison between <i>Brassica oleracea</i> and rice ( <i>Oryza sativa</i> ) reveals diverse modulations on cell death in response to <i>Sclerotinia sclerotiorum</i> . <i>Scientific Reports</i> , 2016, 6, 33706.	1.6	11
4212	RNA-seq transcriptome analysis of a <i>Pseudomonas</i> strain with diversified catalytic properties growth under different culture medium. <i>MicrobiologyOpen</i> , 2016, 5, 626-636.	1.2	18
4213	Heat shock protein 90 is required for sexual and asexual development, virulence, and heat shock response in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2016, 6, 28154.	1.6	70
4214	Overexpression of ADP-glucose pyrophosphorylase in both leaf and seed tissue synergistically increase biomass and seed number in rice ( <i>Oryza sativa</i> ssp. <i>japonica</i> ). <i>Functional Plant Biology</i> , 2016, 43, 1194.	1.1	17
4215	Comparative transcriptome profiling of two <i>Brassica napus</i> cultivars under chromium toxicity and its alleviation by reduced glutathione. <i>BMC Genomics</i> , 2016, 17, 885.	1.2	69



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4216	Comparative transcript profiling of maize inbreds in response to long-term phosphorus deficiency stress. <i>Plant Physiology and Biochemistry</i> , 2016, 109, 467-481.	2.8	34
4217	Effect of ovarian hormones on the healthy equine uterus: a global gene expression analysis. <i>Reproduction, Fertility and Development</i> , 2016, 28, 1810.	0.1	7
4218	A strategy to identify housekeeping genes suitable for analysis in breast cancer diseases. <i>BMC Genomics</i> , 2016, 17, 639.	1.2	47
4219	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers <sup>1</sup> . <i>Journal of Animal Science</i> , 2016, 94, 3693-3702.	0.2	27
4220	Receptor MER Tyrosine Kinase Proto-oncogene (MERTK) Is Not Required for Transfer of Bis-retinoids to the Retinal Pigmented Epithelium. <i>Journal of Biological Chemistry</i> , 2016, 291, 26937-26949.	1.6	17
4221	High-throughput sequencing reveals differential regulation of miRNAs in fenoxaprop-P-ethyl-resistant <i>Beckmannia syzigachne</i> . <i>Scientific Reports</i> , 2016, 6, 28725.	1.6	19
4222	Genome-wide profiling of transfer RNAs and their role as novel prognostic markers for breast cancer. <i>Scientific Reports</i> , 2016, 6, 32843.	1.6	40
4223	Gene expression profiling analysis reveals a crucial gene regulating metabolism in adventitious roots of neem ( <i>Azadirachta indica</i> ). <i>RSC Advances</i> , 2016, 6, 114889-114898.	1.7	4
4224	Seven gene deletions in seven days: Fast generation of <i>Escherichia coli</i> strains tolerant to acetate and osmotic stress. <i>Scientific Reports</i> , 2016, 5, 17874.	1.6	84
4225	Identification of candidate genes associated with porcine meat color traits by genome-wide transcriptome analysis. <i>Scientific Reports</i> , 2016, 6, 35224.	1.6	36
4226	The effect of quercetin on genetic expression of the commensal gut microbes <i>Bifidobacterium catenulatum</i> , <i>Enterococcus caccae</i> and <i>Ruminococcus gauvreauii</i> . <i>Anaerobe</i> , 2016, 42, 130-141.	1.0	38
4227	Comprehensive analysis of multi-tissue transcriptome data and the genome-wide investigation of GRAS family in <i>Phyllostachys edulis</i> . <i>Scientific Reports</i> , 2016, 6, 27640.	1.6	11
4228	Morphological observation, RNA-Seq quantification, and expression profiling: novel insight into grafting-responsive carotenoid biosynthesis in watermelon grafted onto pumpkin rootstock. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 216-227.	0.9	15
4229	Sex Differences in <i>Drosophila</i> Somatic Gene Expression: Variation and Regulation by <i>doublesex</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1799-1808.	0.8	33
4230	Toxic gain of function from mutant <i>FUS</i> protein is crucial to trigger cell autonomous motor neuron loss. <i>EMBO Journal</i> , 2016, 35, 1077-1097.	3.5	187
4231	The Spermatophore in <i>Glossina morsitans morsitans</i> : Insights into Male Contributions to Reproduction. <i>Scientific Reports</i> , 2016, 6, 20334.	1.6	40
4232	Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods, and Challenges. <i>Human Heredity</i> , 2016, 81, 88-105.	0.4	3
4233	Comparative transcriptome profiling and SSR marker identification in three Jerusalem artichoke ( <i>Helianthus tuberosus</i> L.) cultivars exhibiting phenotypic variation. <i>Plant Biotechnology Reports</i> , 2016, 10, 447-461.	0.9	9

#	ARTICLE	IF	CITATIONS
4234	Comparative transcriptome and metabolome provides new insights into the regulatory mechanisms of accelerated senescence in litchi fruit after cold storage. <i>Scientific Reports</i> , 2016, 6, 19356.	1.6	48
4235	Integrative approaches for data analysis in systems biology: Current advances. , 2016, , .		3
4236	Development of <i>Streptomyces</i> sp. FR-008 as an emerging chassis. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 207-214.	1.8	36
4237	Fertility and genomics: comparison of gene expression in contrasting reproductive tissues of female cattle. <i>Reproduction, Fertility and Development</i> , 2016, 28, 11.	0.1	11
4238	Undiscovered Physiology of Transcript and Protein Networks. , 2016, 6, 1851-1872.		0
4239	Genome-wide transcriptomic analysis uncovers the molecular basis underlying early flowering and apetalous characteristic in <i>Brassica napus</i> L. <i>Scientific Reports</i> , 2016, 6, 30576.	1.6	24
4240	The retardant effect of 2-Tridecanone, mediated by Cytochrome P450, on the Development of Cotton bollworm, <i>Helicoverpa armigera</i> . <i>BMC Genomics</i> , 2016, 17, 954.	1.2	32
4241	ERDS-pe: A paired hidden Markov model for copy number variant detection from whole-exome sequencing data. , 2016, , .		3
4242	Multivariate approach to the analysis of correlated RNA-seq data. , 2016, , .		1
4243	DeepSplice: Deep classification of novel splice junctions revealed by RNA-seq. , 2016, , .		16
4244	A novel transcription factor gene FHS1 is involved in the DNA damage response in <i>Fusarium graminearum</i> . <i>Scientific Reports</i> , 2016, 6, 21572.	1.6	20
4245	Impacts of environment on gene expression and epigenetic modification in grazing animals. <i>Journal of Animal Science</i> , 2016, 94, 63-73.	0.2	1
4246	Comparative transcriptional profile of the fish parasite <i>Cryptocaryon irritans</i> . <i>Parasites and Vectors</i> , 2016, 9, 630.	1.0	35
4247	Rewiring a secondary metabolite pathway towards itaconic acid production in <i>Aspergillus niger</i> . <i>Microbial Cell Factories</i> , 2016, 15, 130.	1.9	64
4248	Deconvolution of base pair level RNA-Seq read counts for quantification of transcript expression levels. <i>Annals of Applied Statistics</i> , 2016, 10, .	0.5	1
4249	Role and mechanism of the AMPK pathway in waterborne Zn exposure influencing the hepatic energy metabolism of <i>Synechogobius hasta</i> . <i>Scientific Reports</i> , 2016, 6, 38716.	1.6	34
4250	â€œMatreshkaâ€•genes with alternative reading frames. <i>Russian Journal of Genetics</i> , 2016, 52, 125-140.	0.2	0
4251	RNA-Seq analysis of immune-relevant genes in <i>Lateolabrax japonicus</i> during <i>Vibrio anguillarum</i> infection. <i>Fish and Shellfish Immunology</i> , 2016, 52, 57-64.	1.6	33

#	ARTICLE	IF	CITATIONS
4252	Transcriptomic profiling of chemical exposure reveals roles of Yap1 in protecting yeast cells from oxidative and other types of stresses. <i>Yeast</i> , 2016, 33, 5-19.	0.8	8
4254	Gene Expression and Profiling. <i>Translational Bioinformatics</i> , 2016, , 59-82.	0.0	0
4255	Comparative transcriptome analyses indicate enhanced cellular protection against FMDV in PK15 cells pretreated with IFN- $\beta$ . <i>Gene</i> , 2016, 586, 206-215.	1.0	8
4256	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	6.5	44
4257	Transcriptomic changes in the ovaries of scallop <i>Chlamys farreri</i> exposed to benzo[a]pyrene. <i>Genes and Genomics</i> , 2016, 38, 509-518.	0.5	9
4258	RNA sequencing analysis to demonstrate Erk dependent and independent functions of Mek. <i>Genomics Data</i> , 2016, 7, 73-75.	1.3	2
4259	Decoding transcriptional enhancers: Evolving from annotation to functional interpretation. <i>Seminars in Cell and Developmental Biology</i> , 2016, 57, 40-50.	2.3	11
4260	Drought stress tolerance strategies revealed by RNA-Seq in two sorghum genotypes with contrasting WUE. <i>BMC Plant Biology</i> , 2016, 16, 115.	1.6	165
4261	c-Myc and viral cofactor Kaposin B co-operate to elicit angiogenesis through modulating miRNome traits of endothelial cells. <i>BMC Systems Biology</i> , 2016, 10, 1.	3.0	56
4262	Transcriptome analysis revealed the drought-responsive genes in Tibetan hulless barley. <i>BMC Genomics</i> , 2016, 17, 386.	1.2	81
4263	Comparative fatty acid transcriptomic test and iTRAQ-based proteomic analysis in <i>Haematococcus pluvialis</i> upon salicylic acid (SA) and jasmonic acid (JA) inductions. <i>Algal Research</i> , 2016, 17, 277-284.	2.4	19
4264	Identification of Regulatory DNA Elements Using Genome-wide Mapping of DNase I Hypersensitive Sites during Tomato Fruit Development. <i>Molecular Plant</i> , 2016, 9, 1168-1182.	3.9	24
4265	De novo transcriptome analysis in radish ( <i>Raphanus sativus</i> L.) and identification of critical genes involved in bolting and flowering. <i>BMC Genomics</i> , 2016, 17, 389.	1.2	53
4266	Drought-responsive WRKY transcription factor genes TaWRKY1 and TaWRKY33 from wheat confer drought and/or heat resistance in <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2016, 16, 116.	1.6	293
4267	Molecular etiology of an indolent lymphoproliferative disorder determined by whole-genome sequencing. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000679.	0.5	3
4268	The lncRNA SLNCR1 Mediates Melanoma Invasion through a Conserved SRA1-like Region. <i>Cell Reports</i> , 2016, 15, 2025-2037.	2.9	97
4269	Transcriptome sequencing identified wax-related genes controlling the glossy phenotype formation of 'Ganqi 3', a bud mutant derived from wild-type 'Newhall' navel orange. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	19
4270	Transcriptome based identification and tissue expression profiles of chemosensory genes in <i>Blattella germanica</i> (Blattaria: Blattellidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 18, 30-43.	0.4	19

#	ARTICLE	IF	CITATIONS
4271	Maize OXIDATIVE STRESS2 Homologs Enhance Cadmium Tolerance in Arabidopsis through Activation of a Putative SAM-Dependent Methyltransferase Gene. <i>Plant Physiology</i> , 2016, 171, 1675-1685.	2.3	30
4272	Transcriptomic Responses of the Interactions between <i>Clostridium cellulovorans</i> 743B and <i>Rhodospseudomonas palustris</i> CGA009 in a Cellulose-Grown Coculture for Enhanced Hydrogen Production. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4546-4559.	1.4	22
4273	<i>De novo</i> assembly of transcriptome from next-generation sequencing data. <i>Quantitative Biology</i> , 2016, 4, 94-105.	0.3	5
4274	Transcriptomic and proteomic analyses provide new insights into the regulation mechanism of low-temperature-induced leafy head formation in Chinese cabbage. <i>Journal of Proteomics</i> , 2016, 144, 1-10.	1.2	37
4275	Response of the hepatic transcriptome to aflatoxin B1 in ducklings. <i>Toxicol</i> , 2016, 111, 69-76.	0.8	36
4276	Aberrant PD-L1 expression through 3'-UTR disruption in multiple cancers. <i>Nature</i> , 2016, 534, 402-406.	13.7	536
4277	Transcriptome analysis reveals the effects of sugar metabolism and auxin and cytokinin signaling pathways on root growth and development of grafted apple. <i>BMC Genomics</i> , 2016, 17, 150.	1.2	52
4278	Compressive mapping for next-generation sequencing. <i>Nature Biotechnology</i> , 2016, 34, 374-376.	9.4	33
4279	Genome-wide analysis of PHD family transcription factors in carrot ( <i>Daucus carota</i> L.) reveals evolution and response to abiotic stress. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	9
4280	Transcriptomic features associated with energy production in the muscles of Pacific bluefin tuna and Pacific cod. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 1114-1124.	0.6	6
4281	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	3.8	166
4282	Improvement and transcriptome analysis of root architecture by overexpression of <i>Fraxinus pennsylvanica</i> DREB2A transcription factor in <i>Robinia pseudoacacia</i> L. 'Idaho'™. <i>Plant Biotechnology Journal</i> , 2016, 14, 1456-1469.	4.1	20
4283	Splicing-independent loading of TREX on nascent RNA is required for efficient expression of dual-strand piRNA clusters in <i>Drosophila</i> . <i>Genes and Development</i> , 2016, 30, 840-855.	2.7	71
4284	An RNA-seq based reference transcriptome for Citrus. <i>Plant Biotechnology Journal</i> , 2016, 14, 938-950.	4.1	21
4285	Near-optimal probabilistic RNA-seq quantification. <i>Nature Biotechnology</i> , 2016, 34, 525-527.	9.4	7,322
4286	Transcriptome-wide sequencing provides insights into geocarpy in peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2016, 14, 1215-1224.	4.1	30
4287	Effects of drought and salt-stresses on gene expression in <i>Caragana korshinskii</i> seedlings revealed by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 200.	1.2	47
4288	Transcriptome profiling reveals differentially expressed genes associated with wizened flower bud formation in Chinese pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2016, 91, 227-235.	0.9	4

#	ARTICLE	IF	CITATIONS
4289	Identification of gene expression changes in rabbit uterus during embryo implantation. <i>Genomics</i> , 2016, 107, 216-221.	1.3	13
4290	Expression profile analysis of head and neck squamous cell carcinomas using data from The Cancer Genome Atlas. <i>Molecular Medicine Reports</i> , 2016, 13, 4259-4265.	1.1	22
4291	Long noncoding RNAs related to the odontogenic potential of dental mesenchymal cells in mice. <i>Archives of Oral Biology</i> , 2016, 67, 1-8.	0.8	14
4292	Characterization of Glycolytic Pathway Genes Using RNA-Seq in Developing Kernels of <i>Eucommia ulmoides</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3712-3731.	2.4	17
4293	Comparison of transcriptomes of wild-type and isothiazolone-resistant <i>Pseudomonas aeruginosa</i> by using RNA-seq. <i>Molecular Biology Reports</i> , 2016, 43, 527-540.	1.0	5
4294	BpMADS12 gene role in lignin biosynthesis of <i>Betula platyphylla</i> Suk by transcriptome analysis. <i>Journal of Forestry Research</i> , 2016, 27, 1111-1120.	1.7	13
4295	High light exposure on seed coat increases lipid accumulation in seeds of castor bean ( <i>Ricinus</i> ). <i>Trends in Plant Science</i> , 2016, 11, 10-18.	1.6	18
4296	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	25
4297	BMAL1 regulates transcription initiation and activates circadian clock gene expression in mammals. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 1019-1025.	1.0	10
4298	Comparing human and macaque placental transcriptomes to disentangle preterm birth pathology from gestational age effects. <i>Placenta</i> , 2016, 41, 74-82.	0.7	19
4299	Smooth Muscle Enriched Long Noncoding RNA ( <i>SMILR</i> ) Regulates Cell Proliferation. <i>Circulation</i> , 2016, 133, 2050-2065.	1.6	182
4300	A homeobox protein, NKX6.1, up-regulates interleukin-6 expression for cell growth in basal-like breast cancer cells. <i>Experimental Cell Research</i> , 2016, 343, 177-189.	1.2	6
4301	RNA Extraction from a Mycobacterium under Ultrahigh Electric Field Intensity in a Microfluidic Device. <i>Analytical Chemistry</i> , 2016, 88, 5053-5057.	3.2	12
4302	Differential gene expression in porcine SK6 cells infected with wild-type and SAP domain-mutant foot-and-mouth disease virus. <i>Virologica Sinica</i> , 2016, 31, 249-257.	1.2	5
4303	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in <i>Escherichia coli</i> O157:H7 (EHEC). <i>BMC Genomics</i> , 2016, 17, 133.	1.2	42
4304	The Properties of Long Noncoding RNAs That Regulate Chromatin. <i>Annual Review of Genomics and Human Genetics</i> , 2016, 17, 69-94.	2.5	75
4305	Differential transcriptome analysis of leaves of tea plant ( <i>Camellia sinensis</i> ) provides comprehensive insights into the defense responses to <i>Ectropis oblique</i> attack using RNA-Seq. <i>Functional and Integrative Genomics</i> , 2016, 16, 383-398.	1.4	98
4306	Global comparative analysis of expressed genes in ovules and leaves of <i>Ginkgo biloba</i> L.. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	12

#	ARTICLE	IF	CITATIONS
4307	MMR: a tool for read multi-mapper resolution. <i>Bioinformatics</i> , 2016, 32, 770-772.	1.8	39
4308	Transcriptome analysis reveals the molecular mechanisms underlying growth superiority in a novel grouper hybrid ( <i>Epinephelus fuscogutatus</i> × <i>E. lanceolatus</i> ). <i>BMC Genetics</i> , 2016, 17, 24.	2.7	94
4309	Identification of transcriptome involved in atrazine detoxification and degradation in alfalfa ( <i>Medicago sativa</i> ) exposed to realistic environmental contamination. <i>Ecotoxicology and Environmental Safety</i> , 2016, 130, 103-112.	2.9	42
4310	The Cotton Mitogen-Activated Protein Kinase Kinase 3 Functions in Drought Tolerance by Regulating Stomatal Responses and Root Growth. <i>Plant and Cell Physiology</i> , 2016, 57, 1629-1642.	1.5	83
4311	Genomics and Personalized Medicine. , 2016, , 187-219.		0
4312	Strategies for clinical trials in type 1 diabetes. <i>Journal of Autoimmunity</i> , 2016, 71, 88-96.	3.0	20
4313	The De-Etiolated 1 Homolog of Arabidopsis Modulates the ABA Signaling Pathway and ABA Biosynthesis in Rice. <i>Plant Physiology</i> , 2016, 171, 1259-1276.	2.3	16
4314	Detection and validation of one stable fiber strength QTL on c9 in tetraploid cotton. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1625-1638.	1.0	19
4315	Thymic Mesenchymal Cells Have a Distinct Transcriptomic Profile. <i>Journal of Immunology</i> , 2016, 196, 4760-4770.	0.4	19
4316	Comparative transcriptome analysis of fertile and sterile buds from a genetically male sterile line of Chinese cabbage. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2016, 52, 130-139.	0.9	21
4317	Protrusion-localized STAT3 mRNA promotes metastasis of highly metastatic hepatocellular carcinoma cells in vitro. <i>Acta Pharmacologica Sinica</i> , 2016, 37, 805-813.	2.8	9
4318	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016, 165, 535-550.	13.5	2,216
4319	A benchmark for RNA-seq quantification pipelines. <i>Genome Biology</i> , 2016, 17, 74.	3.8	160
4320	Tobacco mosaic virus-directed reprogramming of auxin/indole acetic acid protein transcriptional responses enhances virus phloem loading. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2740-9.	3.3	55
4321	Molecular mechanism of ethylene stimulation of latex yield in rubber tree ( <i>Hevea brasiliensis</i> ) revealed by de novo sequencing and transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 257.	1.2	33
4322	Traffic light rules: Chromatin states direct miRNA-mediated network motifs running by integrating epigenome and regulatome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 1475-1488.	1.1	9
4323	Regulatory Differences in Natal Down Development between Altricial Zebra Finch and Precocial Chicken. <i>Molecular Biology and Evolution</i> , 2016, 33, 2030-2043.	3.5	14
4324	Next-generation sequencing revolution through big data analytics. <i>Frontiers in Life Science: Frontiers of Interdisciplinary Research in the Life Sciences</i> , 2016, 9, 119-149.	1.1	40

#	ARTICLE	IF	CITATIONS
4325	Mining for heat-stress responsive genes by large scale gene expression data from <i>Betula luminifera</i> . <i>Euphytica</i> , 2016, 210, 245-257.	0.6	1
4326	Transcriptomic analysis of <i>Arabidopsis</i> overexpressing flowering locus T driven by a meristem-specific promoter that induces early flowering. <i>Gene</i> , 2016, 587, 120-131.	1.0	9
4327	Genome-wide identification of the mildew resistance locus O (MLO) gene family in novel cereal model species <i>Brachypodium distachyon</i> . <i>European Journal of Plant Pathology</i> , 2016, 145, 239-253.	0.8	28
4328	Acclimation of Antarctic <i>Chlamydomonas</i> to the sea-ice environment: a transcriptomic analysis. <i>Extremophiles</i> , 2016, 20, 437-450.	0.9	32
4329	Transcriptomic analysis of <i>Pseudostellariae Radix</i> from different fields using RNA-seq. <i>Gene</i> , 2016, 588, 7-18.	1.0	20
4330	Up-regulating the abscisic acid inactivation gene <i>ZmABA8ox1</i> contributes to seed germination heterosis by promoting cell expansion. <i>Journal of Experimental Botany</i> , 2016, 67, 2889-2900.	2.4	17
4331	<i>Olig2</i> is expressed late in human eosinophil development and controls <i>Siglec-8</i> expression. <i>Journal of Leukocyte Biology</i> , 2016, 100, 711-723.	1.5	24
4332	Comparative transcriptome analysis revealed distinct gene set expression associated with anthocyanin biosynthesis in response to short-wavelength light in turnip. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	8
4333	Macrophage Susceptibility to Emactuzumab (RG7155) Treatment. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 3077-3086.	1.9	57
4334	Editor's Highlight: Dose-Response Analysis of RNA-Seq Profiles in Archival Formalin-Fixed Paraffin-Embedded Samples. <i>Toxicological Sciences</i> , 2016, 154, 202-213.	1.4	31
4335	Wnt-signalling pathways and microRNAs network in carcinogenesis: experimental and bioinformatics approaches. <i>Molecular Cancer</i> , 2016, 15, 56.	7.9	55
4336	ReadXplorer 2: detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016, 32, 3702-3708.	1.8	96
4338	RNA-Seq Library Construction Methods for Transcriptome Analysis. <i>Current Protocols in Plant Biology</i> , 2016, 1, 197-215.	2.8	8
4339	CHD8 haploinsufficiency results in autistic-like phenotypes in mice. <i>Nature</i> , 2016, 537, 675-679.	13.7	268
4340	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. <i>Epigenetics</i> , 2016, 11, 804-818.	1.3	35
4342	Identification of zinc finger protein <i>Bcl6</i> as a novel regulator of early adipose commitment. <i>Open Biology</i> , 2016, 6, 160065.	1.5	18
4343	A systems biology approach reveals major metabolic changes in the thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> in response to the carbon source L-glucose versus D-glucose. <i>Molecular Microbiology</i> , 2016, 102, 882-908.	1.2	69
4344	Transcriptome comparison between newly emerged and sexually matured bees of <i>Apis mellifera</i> . <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 893-897.	0.4	4

#	ARTICLE	IF	CITATIONS
4345	Histomorphometric and transcriptomic features characterize silk glands' development during the molt to intermolt transition process in silkworm. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 95-108.	1.2	16
4346	Cryptophyte farming by symbiotic ciliate host detected in situ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12208-12213.	3.3	32
4347	Insights into the adaptive response of <i>Arabidopsis thaliana</i> to prolonged thermal stress by ribosomal profiling and RNA-Seq. <i>BMC Plant Biology</i> , 2016, 16, 221.	1.6	55
4348	Detecting cognizable trends of gene expression in a time series RNA-sequencing experiment: a bootstrap approach. <i>Journal of Genetics</i> , 2016, 95, 587-593.	0.4	1
4349	MacoNPV baculovirus midgut-specific gene expression during infection of the bertha armyworm, <i>Mamestra configurata</i> . <i>Virology</i> , 2016, 499, 1-8.	1.1	2
4350	Transferable model for chromosome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12168-12173.	3.3	291
4351	De novo transcriptome sequencing of pakchoi ( <i>Brassica rapa</i> L. <i>chinensis</i> ) reveals the key genes related to the response of heat stress. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	8
4355	Multi-perspective quality control of Illumina RNA sequencing data analysis. <i>Briefings in Functional Genomics</i> , 2017, 16, elw035.	1.3	68
4356	Combination analysis of genome-wide association and transcriptome sequencing of residual feed intake in quality chickens. <i>BMC Genomics</i> , 2016, 17, 594.	1.2	52
4357	Proton-pump inhibitor omeprazole attenuates hyperoxia induced lung injury. <i>Journal of Translational Medicine</i> , 2016, 14, 247.	1.8	18
4358	Supporting data for characterization of non-coding RNAs associated with the Neuronal growth regulator 1 (NEGR1) adhesion protein. <i>Data in Brief</i> , 2016, 7, 381-385.	0.5	2
4359	De novo assembly and characterization of antennal transcriptome reveal chemosensory system in <i>Nysius ericae</i> . <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 1077-1087.	0.4	19
4360	Diversity of insulin-like peptide signaling system proteins in <i>Calanus finmarchicus</i> (Crustacea). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267</i> <i>Endocrinology</i> , 2016, 236, 157-173.	0.8	35
4362	Transcriptomic analysis for elucidating the physiological effects of 5-aminolevulinic acid accumulation on <i>Corynebacterium glutamicum</i> . <i>Microbiological Research</i> , 2016, 192, 292-299.	2.5	8
4363	Agroinfiltration contributes to VP1 recombinant protein degradation. <i>Bioengineered</i> , 2016, 7, 459-477.	1.4	10
4364	Comprehensive transcriptome-based characterization of differentially expressed genes involved in microsporogenesis of radish CMS line and its maintainer. <i>Functional and Integrative Genomics</i> , 2016, 16, 529-543.	1.4	12
4365	Nitrate Protects Cucumber Plants Against <i>Fusarium oxysporum</i> by Regulating Citrate Exudation. <i>Plant and Cell Physiology</i> , 2016, 57, 2001-2012.	1.5	37
4366	Transcriptional Control in Marine Copiotrophic and Oligotrophic Bacteria with Streamlined Genomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6010-6018.	1.4	45



#	ARTICLE	IF	CITATIONS
4367	Transcriptome analysis of male and female mature gonads of Japanese scallop <i>Patinopecten yessoensis</i> . <i>Genes and Genomics</i> , 2016, 38, 1041-1052.	0.5	18
4368	RNA-seq analysis of <i>Paris polyphylla</i> var. <i>yunnanensis</i> roots identified candidate genes for saponin synthesis. <i>Plant Diversity</i> , 2016, 38, 163-170.	1.8	18
4369	Differential gene expression according to race and host plant in the pea aphid. <i>Molecular Ecology</i> , 2016, 25, 4197-4215.	2.0	59
4370	Precultivation of <i>Bacillus coagulans</i> DSM2314 in the presence of furfural decreases inhibitory effects of lignocellulosic by-products during l(+)-lactic acid fermentation. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 10307-10319.	1.7	15
4371	On the study of microbial transcriptomes using second- and third-generation sequencing technologies. <i>Journal of Microbiology</i> , 2016, 54, 527-536.	1.3	12
4372	Transcriptional effects of metal-rich acid drainage water from the abandoned L��kken Mine on Atlantic salmon ( <i>Salmo salar</i> ) smolt. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2016, 79, 612-632.	1.1	3
4373	De novo assembly and transcriptome characterization of major growth-related genes in various tissues of <i>Penaeus monodon</i> . <i>Aquaculture</i> , 2016, 464, 545-553.	1.7	27
4374	Transcriptomic Analysis of Chloroquine-Sensitive and Chloroquine-Resistant Strains of <i>Plasmodium falciparum</i> : Toward Malaria Diagnostics and Therapeutics for Global Health. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 424-432.	1.0	12
4375	Transcriptome comparison of resistant and susceptible sesame ( <i>Sesamum indicum</i> L.) varieties inoculated with <i>Fusarium oxysporum</i> f. sp. <i>Sesami</i> . <i>Plant Breeding</i> , 2016, 135, 627-635.	1.0	11
4376	Transcriptome analysis of Dlm mutants reveals the potential formation mechanism of lesion mimic in wheat. <i>European Journal of Plant Pathology</i> , 2016, 146, 987-997.	0.8	6
4377	Spliced synthetic genes as internal controls in RNA sequencing experiments. <i>Nature Methods</i> , 2016, 13, 792-798.	9.0	123
4378	Genomics of Natural Populations: How Differentially Expressed Genes Shape the Evolution of Chromosomal Inversions in <i>Drosophila pseudoobscura</i> . <i>Genetics</i> , 2016, 204, 287-301.	1.2	61
4379	Combination scaffolds of salmon fibrin, hyaluronic acid, and laminin for human neural stem cell and vascular tissue engineering. <i>Acta Biomaterialia</i> , 2016, 43, 122-138.	4.1	125
4380	Transcriptomic responses of <i>Perna viridis</i> embryo to Benzo(a)pyrene exposure elucidated by RNA sequencing. <i>Chemosphere</i> , 2016, 163, 125-132.	4.2	24
4381	Breathing air to save energy – new insights into the ecophysiological role of high-affinity [NiFe]-hydrogenase in <i>Streptomyces avermitilis</i> . <i>MicrobiologyOpen</i> , 2016, 5, 47-59.	1.2	57
4382	Fluorescence-Activated Cell Sorting and Gene Expression Profiling of GFP-Positive Cells from Transgenic Zebrafish Lines. <i>Methods in Molecular Biology</i> , 2016, 1451, 93-106.	0.4	1
4383	Global analysis of transcriptome in dorsal root ganglia following peripheral nerve injury in rats. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 206-212.	1.0	47
4384	A Cyclic di-GMP-binding Adaptor Protein Interacts with Histidine Kinase to Regulate Two-component Signaling. <i>Journal of Biological Chemistry</i> , 2016, 291, 16112-16123.	1.6	40

#	ARTICLE	IF	CITATIONS
4385	Pathway Analysis for RNA-Seq Data Using a Score-Based Approach. <i>Biometrics</i> , 2016, 72, 165-174.	0.8	3
4386	Natural bone fragmentation in the blind cave-dwelling fish, <i>Astyanax mexicanus</i> : candidate gene identification through integrative comparative genomics. <i>Evolution &amp; Development</i> , 2016, 18, 7-18.	1.1	16
4387	High-throughput sequencing reveals key genes and immune homeostatic pathways activated in myeloid dendritic cells by <i>Porphyromonas gingivalis</i> 381 and its fimbrial mutants. <i>Molecular Oral Microbiology</i> , 2016, 31, 78-93.	1.3	24
4388	RNA sequencing reveals retinal transcriptome changes in STZ-induced diabetic rats. <i>Molecular Medicine Reports</i> , 2016, 13, 2101-2109.	1.1	14
4389	RNA sequencing provides insights into the toxicogenomic response of ZF4 cells to methyl methanesulfonate. <i>Journal of Applied Toxicology</i> , 2016, 36, 94-104.	1.4	8
4390	Cry1Ab-expressing rice did not influence expression of fecundity-related genes in the wolf spider <i>Pardosa pseudoannulata</i> . <i>Gene</i> , 2016, 592, 1-7.	1.0	12
4391	Gene expression classification using epigenetic features and DNA sequence composition in the human embryonic stem cell line H1. <i>Gene</i> , 2016, 592, 227-234.	1.0	10
4392	Non-coding RNAs and Inter-kingdom Communication. , 2016, , .		5
4393	Transcriptome sequencing provides insights into the metabolic pathways of patchouli alcohol and pogostone in <i>Pogostemon cablin</i> (Blanco) Benth.. <i>Genes and Genomics</i> , 2016, 38, 1031-1039.	0.5	15
4394	Metabolic Reprogramming Regulates the Proliferative and Inflammatory Phenotype of Adventitial Fibroblasts in Pulmonary Hypertension Through the Transcriptional Corepressor C-Terminal Binding Protein-1. <i>Circulation</i> , 2016, 134, 1105-1121.	1.6	107
4395	Drought Stress Tolerance in Plants: Insights from Transcriptomic Studies. , 2016, , 153-185.		4
4396	Transcriptome analysis reveals that constant heat stress modifies the metabolism and structure of the porcine longissimus dorsi skeletal muscle. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2101-2115.	1.0	36
4397	Genome-wide identification of salinity responsive HSP70s in common bean. <i>Molecular Biology Reports</i> , 2016, 43, 1251-1266.	1.0	31
4398	Transcriptomic analysis reveals key early events of narciclasine signaling in <i>Arabidopsis</i> root apex. <i>Plant Cell Reports</i> , 2016, 35, 2381-2401.	2.8	6
4399	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mammalian retinas. <i>Human Molecular Genetics</i> , 2016, 25, ddw268.	1.4	36
4401	RNA-seq analysis revealed ROS-mediated related genes involved in cadmium detoxification in the razor clam <i>Sinonovacula constricta</i> . <i>Fish and Shellfish Immunology</i> , 2016, 57, 350-361.	1.6	20
4402	Exploiting the potential of next-generation sequencing in genomic medicine. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 1037-1047.	1.5	5
4403	Studying Oogenesis in a Non-model Organism Using Transcriptomics: Assembling, Annotating, and Analyzing Your Data. <i>Methods in Molecular Biology</i> , 2016, 1457, 129-143.	0.4	0

#	ARTICLE	IF	CITATIONS
4404	Acute tumour response to a bispecific Ang-2-VEGF-A antibody: insights from multiparametric MRI and gene expression profiling. <i>British Journal of Cancer</i> , 2016, 115, 691-702.	2.9	19
4405	A robust (re-)annotation approach to generate unbiased mapping references for RNA-seq-based analyses of differential expression across closely related species. <i>BMC Genomics</i> , 2016, 17, 392.	1.2	26
4406	RNA-Seq as a Tool to Study the Tumor Microenvironment. <i>Methods in Molecular Biology</i> , 2016, 1458, 311-337.	0.4	7
4407	Nutritional functions of the funiculus in <i>Brassica napus</i> seed maturation revealed by transcriptome and dynamic metabolite profile analyses. <i>Plant Molecular Biology</i> , 2016, 92, 539-553.	2.0	10
4408	Real-time kinetics of cadmium transport and transcriptomic analysis in low cadmium accumulator <i>Miscanthus sacchariflorus</i> . <i>Planta</i> , 2016, 244, 1289-1302.	1.6	18
4409	Antennal transcriptome analysis and expression profiles of odorant binding proteins in <i>Eogystia hippophaecolus</i> (Lepidoptera: Cossidae). <i>BMC Genomics</i> , 2016, 17, 651.	1.2	36
4411	Differentiation-inducing and anti-proliferative activities of isoliquiritigenin and all-trans-retinoic acid on B16F0 melanoma cells: Mechanisms profiling by RNA-seq. <i>Gene</i> , 2016, 592, 86-98.	1.0	19
4412	De Novo Sequencing and Analysis of the Transcriptome of the Wild Eggplant Species <i>Solanum Aculeatissimum</i> in Response to <i>Verticillium dahliae</i> . <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1193-1203.	1.0	42
4414	A novel nitrogen-dependent gene associates with the lesion mimic trait in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2075-2084.	1.8	15
4415	Predicting gene expression level by the transcription factor binding signals in human embryonic stem cells. <i>BioSystems</i> , 2016, 150, 92-98.	0.9	12
4416	Transcriptome expression analysis of candidate milk genes affecting cheese-related traits in 2 sheep breeds. <i>Journal of Dairy Science</i> , 2016, 99, 6381-6390.	1.4	29
4417	Critical re-evaluation of neuroglobin expression reveals conserved patterns among mammals. <i>Neuroscience</i> , 2016, 337, 339-354.	1.1	38
4418	Comparative transcriptome analysis reveals a global insight into molecular processes regulating citrate accumulation in sweet orange ( <i>Citrus sinensis</i> ). <i>Physiologia Plantarum</i> , 2016, 158, 463-482.	2.6	37
4419	Insights From Genomics Into Spatial and Temporal Variation in <i>Batrachochytrium dendrobatidis</i> . <i>Progress in Molecular Biology and Translational Science</i> , 2016, 142, 269-290.	0.9	9
4420	Increased acid resistance of the archaeon, <i>Metallosphaera sedula</i> by adaptive laboratory evolution. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 1455-1465.	1.4	27
4421	Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. <i>Nature Protocols</i> , 2016, 11, 1650-1667.	5.5	4,743
4422	Assembly and Application to the Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , 139-158.	0.3	0
4423	The Transcriptional Foundations of Sp110-mediated Macrophage (RAW264.7) Resistance to <i>Mycobacterium tuberculosis</i> H37Ra. <i>Scientific Reports</i> , 2016, 6, 22041.	1.6	26

#	ARTICLE	IF	CITATIONS
4424	Applications of integrative OMICs approaches to gene regulation studies. <i>Quantitative Biology</i> , 2016, 4, 283-301.	0.3	6
4425	The impact of amplification on differential expression analyses by RNA-seq. <i>Scientific Reports</i> , 2016, 6, 25533.	1.6	200
4426	Comparative transcriptome analysis of basal and zygote-located tip regions of peanut ovaries provides insight into the mechanism of light regulation in peanut embryo and pod development. <i>BMC Genomics</i> , 2016, 17, 606.	1.2	27
4427	The Essential Role of H19 Contributing to Cisplatin Resistance by Regulating Glutathione Metabolism in High-Grade Serous Ovarian Cancer. <i>Scientific Reports</i> , 2016, 6, 26093.	1.6	116
4428	mRNA changes in nucleus accumbens related to methamphetamine addiction in mice. <i>Scientific Reports</i> , 2016, 6, 36993.	1.6	41
4429	Centrifuge: rapid and sensitive classification of metagenomic sequences. <i>Genome Research</i> , 2016, 26, 1721-1729.	2.4	1,025
4430	Candidate egg case silk genes for the spider <i>Argiope argentata</i> from differential gene expression analyses. <i>Insect Molecular Biology</i> , 2016, 25, 757-768.	1.0	11
4431	Identification of Differential Gene Expression Patterns after Acute Exposure to High and Low Doses of Low-LET Ionizing Radiation in a Reconstituted Human Skin Tissue. <i>Radiation Research</i> , 2016, 186, 531.	0.7	18
4432	De novo transcriptome sequencing in <i>Monsonia burkeana</i> revealed putative genes for key metabolic pathways involved in tea quality and medicinal value. <i>3 Biotech</i> , 2016, 6, 250.	1.1	3
4433	Genomic identification of WRKY transcription factors in carrot ( <i>Daucus carota</i> ) and analysis of evolution and homologous groups for plants. <i>Scientific Reports</i> , 2016, 6, 23101.	1.6	68
4434	Integrated omics study of lipid droplets from <i>Plasmodiophora brassicae</i> . <i>Scientific Reports</i> , 2016, 6, 36965.	1.6	59
4435	Strigolactone-Induced Putative Secreted Protein 1 Is Required for the Establishment of Symbiosis by the Arbuscular Mycorrhizal Fungus <i>Rhizophagus irregularis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 277-286.	1.4	136
4436	Association of the molecular regulation of ear leaf senescence/stress response and photosynthesis/metabolism with heterosis at the reproductive stage in maize. <i>Scientific Reports</i> , 2016, 6, 29843.	1.6	23
4437	The Tomato Genome. <i>Compendium of Plant Genomes</i> , 2016, , .	0.3	9
4438	GRK6 regulates ROS response and maintains hematopoietic stem cell self-renewal. <i>Cell Death and Disease</i> , 2016, 7, e2478-e2478.	2.7	22
4439	Identification of reference genes for quantitative expression analysis using large-scale RNA-seq data of <i>Arabidopsis thaliana</i> and model crop plants. <i>Genes and Genetic Systems</i> , 2016, 91, 111-125.	0.2	24
4440	Transcriptome altered by latent human cytomegalovirus infection on THP-1 cells using RNA-seq. <i>Gene</i> , 2016, 594, 144-150.	1.0	24
4441	Multi-tiered Reorganization of the Genome during B Cell Affinity Maturation Anchored by a Germinal Center-Specific Locus Control Region. <i>Immunity</i> , 2016, 45, 497-512.	6.6	112

#	ARTICLE	IF	CITATIONS
4442	Transcriptome and digital gene expression analysis of herbaceous peony ( <i>Paeonia lactiflora</i> Pall.) to screen thermo-tolerant related differently expressed genes. <i>Genes and Genomics</i> , 2016, 38, 1201-1215.	0.5	21
4443	MdMyb93 is a regulator of suberin deposition in russeted apple fruit skins. <i>New Phytologist</i> , 2016, 212, 977-991.	3.5	113
4444	Short communication: In vivo screening platform for bacteriocins using <i>Caenorhabditis elegans</i> to control mastitis-causing pathogens. <i>Journal of Dairy Science</i> , 2016, 99, 8614-8621.	1.4	11
4445	Comparative transcriptomic analyses of two bighead carp ( <i>Hypophthalmichthys nobilis</i> ) groups with different growth rates. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 20, 111-117.	0.4	10
4446	Long non-coding RNAs in human early embryonic development and their potential in ART. <i>Human Reproduction Update</i> , 2016, 23, 19-40.	5.2	108
4447	New Insights into the Formation of Viable but Nonculturable <i>Escherichia coli</i> O157:H7 Induced by High-Pressure CO <sub>2</sub> . <i>MBio</i> , 2016, 7, .	1.8	82
4448	De novo transcriptomic analysis and development of EST-SSR markers in the Siberian tiger ( <i>Panthera Tigris</i> ). <i>PLoS ONE</i> , 2016, 11, e0157005.	1.8	5
4450	Transcriptomic analysis of different stages of pigeon ovaries by RNA-seq. <i>Molecular Reproduction and Development</i> , 2016, 83, 640-648.	1.0	13
4451	Tomato plants increase their tolerance to low temperature in a chilling acclimation process entailing comprehensive transcriptional and metabolic adjustments. <i>Plant, Cell and Environment</i> , 2016, 39, 2303-2318.	2.8	91
4452	Genome-wide analysis of LTR-retrotransposon expression in leaves of <i>Populus trichocarpa</i> water-deprived plants. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	17
4453	Transcriptome profiling of <i>Camelina sativa</i> to identify genes involved in triacylglycerol biosynthesis and accumulation in the developing seeds. <i>Biotechnology for Biofuels</i> , 2016, 9, 136.	6.2	53
4454	Survive or die? A molecular insight into salt-dependant signaling network. <i>Environmental and Experimental Botany</i> , 2016, 132, 140-153.	2.0	16
4455	Transcriptome analysis of woodland strawberry ( <i>Fragaria vesca</i> ) response to the infection by Strawberry vein banding virus (SVBV). <i>Virology Journal</i> , 2016, 13, 128.	1.4	24
4457	Cellular identity at the single-cell level. <i>Molecular BioSystems</i> , 2016, 12, 2965-2979.	2.9	17
4458	A multilevel investigation to discover why <i>Kandelia candel</i> thrives in high salinity. <i>Plant, Cell and Environment</i> , 2016, 39, 2486-2497.	2.8	31
4459	In-silico discovery of cancer-specific peptide-HLA complexes for targeted therapy. <i>BMC Bioinformatics</i> , 2016, 17, 286.	1.2	15
4460	Using FlyBase, a Database of <i>Drosophila</i> Genes and Genomes. <i>Methods in Molecular Biology</i> , 2016, 1478, 1-31.	0.4	45
4461	Activation of PPAR $\beta$ by a Natural Flavonoid Modulator, Apigenin Ameliorates Obesity-Related Inflammation Via Regulation of Macrophage Polarization. <i>EBioMedicine</i> , 2016, 9, 61-76.	2.7	127

#	ARTICLE	IF	CITATIONS
4462	Guidelines for the selection of functional assays to evaluate the hallmarks of cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2016, 1866, 300-319.	3.3	89
4463	Thermophilic archaea activate butane via alkyl-coenzyme M formation. <i>Nature</i> , 2016, 539, 396-401.	13.7	279
4464	Regulation of transcriptional elongation in pluripotency and cell differentiation by the PHD-finger protein Phf5a. <i>Nature Cell Biology</i> , 2016, 18, 1127-1138.	4.6	57
4465	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). <i>Nature Communications</i> , 2016, 7, 12339.	5.8	69
4466	RNA-seq analysis for detecting quantitative trait-associated genes. <i>Scientific Reports</i> , 2016, 6, 24375.	1.6	35
4467	Transcriptome Analysis Reveals Candidate Genes Involved in Blister Blight defense in Tea ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBJ / Overlock	1.6	78
4468	Oil Biosynthesis in Underground Oil-Rich Storage Vegetative Tissue: Comparison of <i>Cyperus esculentus</i> Tuber with Oil Seeds and Fruits. <i>Plant and Cell Physiology</i> , 2016, 57, 2519-2540.	1.5	33
4469	The lipid sensor GPR120 promotes brown fat activation and FGF21 release from adipocytes. <i>Nature Communications</i> , 2016, 7, 13479.	5.8	180
4470	Transcriptome profiling of the salt-stress response in <i>Triticum aestivum</i> cv. Kharchia Local. <i>Scientific Reports</i> , 2016, 6, 27752.	1.6	82
4471	Shedding light on cell compartmentation in the candidate phylum Poribacteria by high resolution visualisation and transcriptional profiling. <i>Scientific Reports</i> , 2016, 6, 35860.	1.6	31
4472	Elucidating a molecular mechanism that the deterioration of porcine meat quality responds to increased cortisol based on transcriptome sequencing. <i>Scientific Reports</i> , 2016, 6, 36589.	1.6	18
4473	SUMO-specific protease 3 is a key regulator for hepatic lipid metabolism in non-alcoholic fatty liver disease. <i>Scientific Reports</i> , 2016, 6, 37351.	1.6	11
4474	Partial exhaustion of CD8 T cells and clinical response to teplizumab in new-onset type 1 diabetes. <i>Science Immunology</i> , 2016, 1, .	5.6	169
4475	Improving GENCODE reference gene annotation using a high-stringency proteogenomics workflow. <i>Nature Communications</i> , 2016, 7, 11778.	5.8	68
4476	MYC/MIZ1-dependent gene repression inversely coordinates the circadian clock with cell cycle and proliferation. <i>Nature Communications</i> , 2016, 7, 11807.	5.8	103
4477	(3-oxo-hexanoyl)-homoserine lactone has a critical contribution to the quorum-sensing-dependent regulation in phytopathogen <i>Pseudomonas syringae</i> pv. <i>tabaci</i> 11528. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw265.	0.7	9
4478	Metagenomic Analysis of Genes Encoding Nutrient Cycling Pathways in the Microbiota of Deep-Sea and Shallow-Water Sponges. <i>Marine Biotechnology</i> , 2016, 18, 659-671.	1.1	27
4479	Chromosome-specific sequencing reveals an extensive dispensable genome component in wheat. <i>Scientific Reports</i> , 2016, 6, 36398.	1.6	24

#	ARTICLE	IF	CITATIONS
4480	Expression Variations of miRNAs and mRNAs in Rice ( <i>Oryza sativa</i> ). <i>Genome Biology and Evolution</i> , 2016, 8, 3529-3544.	1.1	32
4481	Discovery of putative capsaicin biosynthetic genes by RNA-Seq and digital gene expression analysis of pepper. <i>Scientific Reports</i> , 2016, 6, 34121.	1.6	37
4482	LSCplus: a fast solution for improving long read accuracy by short read alignment. <i>BMC Bioinformatics</i> , 2016, 17, 451.	1.2	19
4483	Hippocampal Transcriptome Profile of Persistent Memory Rescue in a Mouse Model of THRA1 Mutation-Mediated Resistance to Thyroid Hormone. <i>Scientific Reports</i> , 2016, 6, 18617.	1.6	6
4484	Identification and developmental expression profiling of putative alkaloid biosynthetic genes in <i>Corydalis yanhusuo</i> bulbs. <i>Scientific Reports</i> , 2016, 6, 19460.	1.6	18
4485	Tracking Cancer Genetic Evolution using OncoTrack. <i>Scientific Reports</i> , 2016, 6, 29647.	1.6	5
4486	Transcriptome analysis of follicles reveals the importance of autophagy and hormones in regulating broodiness of Zhedong white goose. <i>Scientific Reports</i> , 2016, 6, 36877.	1.6	34
4487	Comparative transcriptome profiling of chilling stress responsiveness in grafted watermelon seedlings. <i>Plant Physiology and Biochemistry</i> , 2016, 109, 561-570.	2.8	34
4488	Distinct transcriptome profiles reveal gene expression patterns during fruit development and maturation in five main cultivated species of pear ( <i>Pyrus L.</i> ). <i>Scientific Reports</i> , 2016, 6, 28130.	1.6	59
4489	Seasonal induction of alternative principal pathway for rose flower scent. <i>Scientific Reports</i> , 2016, 6, 20234.	1.6	42
4490	Blood miRNomes and transcriptomes reveal novel longevity mechanisms in the long-lived bat, <i>Myotis myotis</i> . <i>BMC Genomics</i> , 2016, 17, 906.	1.2	47
4491	Identification of candidate genes related to calanolide biosynthesis by transcriptome sequencing of <i>Calophyllum brasiliense</i> (Calophyllaceae). <i>BMC Plant Biology</i> , 2016, 16, 177.	1.6	7
4492	Chromosome doubling to overcome the chrysanthemum cross barrier based on insight from transcriptomic and proteomic analyses. <i>BMC Genomics</i> , 2016, 17, 585.	1.2	12
4493	AtPRMT5 Regulates Shoot Regeneration through Mediating Histone H4R3 Dimethylation on KRPs and Pre-mRNA Splicing of RKP in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2016, 9, 1634-1646.	3.9	33
4494	Long non-coding RNAs: spatial amplifiers that control nuclear structure and gene expression. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 756-770.	16.1	510
4495	RNA-binding protein CPEB1 remodels host and viral RNA landscapes. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1101-1110.	3.6	40
4496	<i>Peltaster fructicola</i> genome reveals evolution from an invasive phytopathogen to an ectophytic parasite. <i>Scientific Reports</i> , 2016, 6, 22926.	1.6	21
4497	Overexpression of the Eggplant ( <i>Solanum melongena</i> ) NAC Family Transcription Factor SmNAC Suppresses Resistance to Bacterial Wilt. <i>Scientific Reports</i> , 2016, 6, 31568.	1.6	31

#	ARTICLE	IF	CITATIONS
4498	Integrated application of transcriptomics and metabolomics yields insights into population-asynchronous ovary development in <i>Coilia nasus</i> . <i>Scientific Reports</i> , 2016, 6, 31835.	1.6	37
4499	Nutrient reduction induced stringent responses promote bacterial quorum-sensing divergence for population fitness. <i>Scientific Reports</i> , 2016, 6, 34925.	1.6	29
4500	RNA-binding profiles of <i>Drosophila</i> CPEB proteins Orb and Orb2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7030-E7038.	3.3	49
4501	Trends in the Evolution of Snake Toxins Underscored by an Integrative Omics Approach to Profile the Venom of the Colubrid <i>Phalotris mertensi</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2266-2287.	1.1	29
4502	Expression and chromatin structures of cellulolytic enzyme gene regulated by heterochromatin protein 1. <i>Biotechnology for Biofuels</i> , 2016, 9, 206.	6.2	29
4503	Measuring circulating placental RNAs to non-invasively assess the placental transcriptome and to predict pregnancy complications. <i>Prenatal Diagnosis</i> , 2016, 36, 997-1008.	1.1	31
4504	Transcriptomic analysis of heteromorphic stamens in <i>Cassia bispicalaris</i> L.. <i>Scientific Reports</i> , 2016, 6, 31600.	1.6	3
4505	Prosteatotic and Protective Components in a Unique Model of Fatty Liver: Gut Microbiota and Suppressed Complement System. <i>Scientific Reports</i> , 2016, 6, 31763.	1.6	47
4506	A polydnal genome of <i>Microplitis bicoloratus</i> bracovirus and molecular interactions between the host and virus involved in NF- $\kappa$ B signaling. <i>Archives of Virology</i> , 2016, 161, 3095-3124.	0.9	23
4507	Aberrant Meiotic Prophase I Leads to Genic Male Sterility in the Novel TE5A Mutant of <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 33955.	1.6	10
4508	Characterization and Comparative Analysis of the Milk Transcriptome in Two Dairy Sheep Breeds using RNA Sequencing. <i>Scientific Reports</i> , 2016, 5, 18399.	1.6	88
4509	Transcriptome assembly and expression profiling of molecular responses to cadmium toxicity in hepatopancreas of the freshwater crab <i>Sinopotamon henanense</i> . <i>Scientific Reports</i> , 2016, 6, 19405.	1.6	63
4510	Analysis of tigecycline resistance development in clinical <i>Acinetobacter baumannii</i> isolates through a combined genomic and transcriptomic approach. <i>Scientific Reports</i> , 2016, 6, 26930.	1.6	31
4511	Computational Methods for Integration of Biological Data. <i>Europeanization and Globalization</i> , 2016, , 137-178.	0.1	2
4512	Computational Methods for Quality Check, Preprocessing and Normalization of RNA-Seq Data for Systems Biology and Analysis. , 2016, , 61-77.		2
4513	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. <i>Scientific Reports</i> , 2016, 6, 25521.	1.6	13
4514	RNA-Seq reveals 10 novel promising candidate genes affecting milk protein concentration in the Chinese Holstein population. <i>Scientific Reports</i> , 2016, 6, 26813.	1.6	85
4515	Gene Body Methylation and Transcriptional Regulation: Statistical Modelling and More. , 2016, , 212-230.		0



#	ARTICLE	IF	CITATIONS
4516	Revealing the vectors of cellular identity with single-cell genomics. <i>Nature Biotechnology</i> , 2016, 34, 1145-1160.	9.4	534
4517	Vancomycin susceptibility in methicillin-resistant <i>Staphylococcus aureus</i> is mediated by YycH1 activation of the WalRK essential two-component regulatory system. <i>Scientific Reports</i> , 2016, 6, 30823.	1.6	48
4518	Systems-wide analysis of manganese deficiency-induced changes in gene activity of <i>Arabidopsis</i> roots. <i>Scientific Reports</i> , 2016, 6, 35846.	1.6	17
4519	Transcriptomic analysis on the formation of the viable putative non-culturable state of beer-spoilage <i>Lactobacillus acetotolerans</i> . <i>Scientific Reports</i> , 2016, 6, 36753.	1.6	74
4520	Integrative transcriptome, proteome, phosphoproteome and genetic mapping reveals new aspects in a fiberless mutant of cotton. <i>Scientific Reports</i> , 2016, 6, 24485.	1.6	19
4521	Comparative analysis of the integument transcriptomes of the black dilute mutant and the wild-type silkworm <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2016, 6, 26114.	1.6	18
4522	Mycobacteriophage SWU1 gp39 can potentiate multiple antibiotics against <i>Mycobacterium</i> via altering the cell wall permeability. <i>Scientific Reports</i> , 2016, 6, 28701.	1.6	32
4523	Genome-wide analysis of alternative splicing during human heart development. <i>Scientific Reports</i> , 2016, 6, 35520.	1.6	29
4524	Dynamic translation regulation in <i>Caulobacter</i> cell cycle control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6859-E6867.	3.3	57
4525	Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. <i>Scientific Reports</i> , 2016, 6, 21597.	1.6	123
4526	Complementary Post Transcriptional Regulatory Information is Detected by PUNCH-P and Ribosome Profiling. <i>Scientific Reports</i> , 2016, 6, 21635.	1.6	25
4527	miARma-Seq: a comprehensive tool for miRNA, mRNA and circRNA analysis. <i>Scientific Reports</i> , 2016, 6, 25749.	1.6	114
4528	Electric fish genomics: Progress, prospects, and new tools for neuroethology. <i>Journal of Physiology (Paris)</i> , 2016, 110, 259-272.	2.1	10
4529	Biogeography and environmental genomics of the <i>Roseobacter</i> -affiliated pelagic CHAB-I-5 lineage. <i>Nature Microbiology</i> , 2016, 1, 16063.	5.9	36
4530	Flexibility in the structure of spiral flowers and its underlying mechanisms. <i>Nature Plants</i> , 2016, 2, 15188.	4.7	88
4531	Transcriptome and Degradome Sequencing Reveals Dormancy Mechanisms of <i>Cunninghamia lanceolata</i> Seeds. <i>Plant Physiology</i> , 2016, 172, 2347-2362.	2.3	33
4532	A computationally constructed ceRNA interaction network based on a comparison of the SHEE and SHEEC cell lines. <i>Cellular and Molecular Biology Letters</i> , 2016, 21, 21.	2.7	30
4533	Adipose triglyceride lipase (Atgl) mediates the antibiotic jinggangmycin-stimulated reproduction in the brown planthopper, <i>Nilaparvata lugens</i> Stål. <i>Scientific Reports</i> , 2016, 6, 18984.	1.6	14

#	ARTICLE	IF	CITATIONS
4534	Differential expression of genes in the alate and apterous morphs of the brown citrus aphid, <i>Toxoptera citricida</i> . <i>Scientific Reports</i> , 2016, 6, 32099.	1.6	34
4535	Transcriptome Comparison Analysis of <i>Ostrinia furnacalis</i> in Four Developmental Stages. <i>Scientific Reports</i> , 2016, 6, 35008.	1.6	21
4536	Universal stress protein Rv2624c alters abundance of arginine and enhances intracellular survival by ATP binding in mycobacteria. <i>Scientific Reports</i> , 2016, 6, 35462.	1.6	15
4539	Identification of chemicals that mimic transcriptional changes associated with autism, brain aging and neurodegeneration. <i>Nature Communications</i> , 2016, 7, 11173.	5.8	101
4540	Normalization of human RNA-seq experiments using chimpanzee RNA as a spike-in standard. <i>Scientific Reports</i> , 2016, 6, 31923.	1.6	0
4541	Reproductive switching analysis of <i>Daphnia similoides</i> between sexual female and parthenogenetic female by transcriptome comparison. <i>Scientific Reports</i> , 2016, 6, 34241.	1.6	31
4542	A specialized flavone biosynthetic pathway has evolved in the medicinal plant, <i>Scutellaria baicalensis</i> . <i>Science Advances</i> , 2016, 2, e1501780.	4.7	165
4543	Transcriptomic responses of a simplified soil microcosm to a plant pathogen and its biocontrol agent reveal a complex reaction to harsh habitat. <i>BMC Genomics</i> , 2016, 17, 838.	1.2	13
4544	Transcriptome analysis of dormant tomites of the marine fish ectoparasitic ciliate <i>Cryptocaryon irritans</i> under low temperature. <i>Parasites and Vectors</i> , 2016, 9, 280.	1.0	19
4545	TPhP exposure disturbs carbohydrate metabolism, lipid metabolism, and the DNA damage repair system in zebrafish liver. <i>Scientific Reports</i> , 2016, 6, 21827.	1.6	92
4546	To Be a Flower or Fruiting Branch: Insights Revealed by mRNA and Small RNA Transcriptomes from Different Cotton Developmental Stages. <i>Scientific Reports</i> , 2016, 6, 23212.	1.6	21
4547	Identification of Changes in Gene expression of rats after Sensory and Motor Nerves Injury. <i>Scientific Reports</i> , 2016, 6, 26579.	1.6	6
4548	Genome-wide identification of endogenous RNA-directed DNA methylation loci associated with abundant 21-nucleotide siRNAs in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2016, 6, 36247.	1.6	26
4549	Whole-transcriptome analysis of differentially expressed genes in the ray florets and disc florets of <i>Chrysanthemum morifolium</i> . <i>BMC Genomics</i> , 2016, 17, 398.	1.2	39
4550	From green to red: large-scale transcriptome comparison of a bud sport in poplar ( <i>Populus deltoides</i> ). <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	7
4551	Integrated analysis of DNA methylation and RNA-sequencing data in Down syndrome. <i>Molecular Medicine Reports</i> , 2016, 14, 4309-4314.	1.1	3
4552	Correction of the Bias Derived from the Number of Exons in Exon-Level Enrichment Analysis. <i>Japanese Journal of Biometrics</i> , 2016, 36, 63-84.	0.0	0
4553	A Meiotic Drive Element in the Maize Pathogen <i>Fusarium verticillioides</i> Is Located Within a 102 kb Region of Chromosome V. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2543-2552.	0.8	8

#	ARTICLE	IF	CITATIONS
4554	DNA methylation profiling of primary neuroblastoma tumors using methyl-CpG-binding domain sequencing. <i>Scientific Data</i> , 2016, 3, 160004.	2.4	11
4555	Exploration of nucleosome positioning patterns in transcription factor function. <i>Scientific Reports</i> , 2016, 6, 19620.	1.6	14
4556	Genomic features of uncultured methylotrophs in activated-sludge microbiomes grown under different enrichment procedures. <i>Scientific Reports</i> , 2016, 6, 26650.	1.6	7
4557	Antennal transcriptome and differential expression of olfactory genes in the yellow peach moth, <i>Conogethes punctiferalis</i> (Lepidoptera: Crambidae). <i>Scientific Reports</i> , 2016, 6, 29067.	1.6	50
4558	Contrasting diets reveal metabolic plasticity in the tree-killing beetle, <i>Anoplophora glabripennis</i> (Cerambycidae: Lamiinae). <i>Scientific Reports</i> , 2016, 6, 33813.	1.6	21
4559	De novo sequencing and analysis of the transcriptome of <i>Panax ginseng</i> in the leaf-expansion period. <i>Molecular Medicine Reports</i> , 2016, 14, 1404-1412.	1.1	13
4560	The Immature Fiber Mutant Phenotype of Cotton ( <i>Gossypium hirsutum</i> ) Is Linked to a 22-bp Frame-Shift Deletion in a Mitochondria Targeted Pentatricopeptide Repeat Gene. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1627-1633.	0.8	24
4561	Whole Transcriptome Analysis of Hypertension Induced Cardiac Injury Using Deep Sequencing. <i>Cellular Physiology and Biochemistry</i> , 2016, 38, 670-682.	1.1	9
4562	FOXE3 contributes to Peters anomaly through transcriptional regulation of an autophagy-associated protein termed DNAJB1. <i>Nature Communications</i> , 2016, 7, 10953.	5.8	35
4563	A new method of finding groups of coexpressed genes and conditions of coexpression. <i>BMC Bioinformatics</i> , 2016, 17, 486.	1.2	2
4564	Evaluation of the External RNA Controls Consortium (ERCC) reference material using a modified Latin square design. <i>BMC Biotechnology</i> , 2016, 16, 54.	1.7	41
4565	A fuzzy method for RNA-Seq differential expression analysis in presence of multireads. <i>BMC Bioinformatics</i> , 2016, 17, 345.	1.2	25
4566	PARRoT- a homology-based strategy to quantify and compare RNA-sequencing from non-model organisms. <i>BMC Bioinformatics</i> , 2016, 17, 513.	1.2	6
4567	Genome-wide analysis of gene expression reveals gene regulatory networks that regulate chasmogamous and cleistogamous flowering in <i>Pseudostellaria heterophylla</i> (Caryophyllaceae). <i>BMC Genomics</i> , 2016, 17, 382.	1.2	17
4568	Transcriptome analysis in switchgrass discloses ecotype difference in photosynthetic efficiency. <i>BMC Genomics</i> , 2016, 17, 1040.	1.2	9
4569	RNA-Sequencing for profiling goat milk transcriptome in colostrum and mature milk. <i>BMC Veterinary Research</i> , 2016, 12, 264.	0.7	71
4570	Transcriptome analysis of genes involved in anthocyanins biosynthesis and transport in berries of black and white spine grapes ( <i>Vitis davidii</i> ). <i>Hereditas</i> , 2016, 153, 17.	0.5	37
4571	Estimating isoform abundance by Particle Swarm Optimization. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
4572	Identifying peaks in *-seq data using shape information. BMC Bioinformatics, 2016, 17, 206.	1.2	17
4573	Cancer somatic mutations cluster in a subset of regulatory sites predicted from the ENCODE data. Molecular Cancer, 2016, 15, 76.	7.9	3
4574	Identification of microRNAs regulating Escherichia coli F18 infection in Meishan weaned piglets. Biology Direct, 2016, 11, 59.	1.9	15
4575	EpiMINE, a computational program for mining epigenomic data. Epigenetics and Chromatin, 2016, 9, 42.	1.8	12
4576	Preliminary analysis of Psoroptes ovis transcriptome in different developmental stages. Parasites and Vectors, 2016, 9, 570.	1.0	16
4577	An Integrated Approach for RNA-seq Data Normalization. Cancer Informatics, 2016, 15, CIN.S39781.	0.9	10
4578	Functionalities of expressed messenger RNAs revealed from mutant phenotypes. Wiley Interdisciplinary Reviews RNA, 2016, 7, 416-427.	3.2	1
4579	Deletion of the genes <i>waaC</i> , <i>waaF</i> , or <i>waaG</i> in <i>Escherichia coli</i> W3110 disables the flagella biosynthesis. Journal of Basic Microbiology, 2016, 56, 1021-1035.	1.8	21
4580	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. Environmental Microbiology, 2016, 18, 2196-2213.	1.8	66
4581	Regulation of filamentation in the human fungal pathogen <i>Candida tropicalis</i> . Molecular Microbiology, 2016, 99, 528-545.	1.2	34
4582	Transcriptome analysis of genes related to resistance against powdery mildew in wheat-Thinopyrum alien addition disomic line germplasm SN6306. Gene, 2016, 590, 5-17.	1.0	13
4583	Transcriptome sequencing and de novo analysis of Rosa multiflora under cold stress. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	19
4584	Genome-wide transcriptome analysis of hypothalamus in rats with inherited stress-induced arterial hypertension. BMC Genetics, 2016, 17, 13.	2.7	22
4585	De novo transcriptome sequencing and gene expression analysis reveal potential mechanisms of seed abortion in dove tree (Davidia involucreta Baill.). BMC Plant Biology, 2016, 16, 82.	1.6	24
4586	UTR introns, antisense RNA and differentially spliced transcripts between Plasmodium yoelii subspecies. Malaria Journal, 2016, 15, 30.	0.8	13
4587	Histone H3.5 forms an unstable nucleosome and accumulates around transcription start sites in human testis. Epigenetics and Chromatin, 2016, 9, 2.	1.8	53
4588	Transcriptomic analysis of developing embryos of apricot (Prunus armeniaca L.). Horticulture Environment and Biotechnology, 2016, 57, 197-206.	0.7	1
4589	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. , 2016, , .		6

#	ARTICLE	IF	CITATIONS
4590	Increased small intestinal permeability and RNA expression profiles of mucosa from terminal ileum in patients with diarrhoea-predominant irritable bowel syndrome. <i>Digestive and Liver Disease</i> , 2016, 48, 880-887.	0.4	19
4591	Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight. <i>Functional Plant Biology</i> , 2016, 43, 766.	1.1	24
4592	DEG9, a serine protease, modulates cytokinin and light signaling by regulating the level of <i>ARABIDOPSIS</i> RESPONSE REGULATOR 4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3568-76.	3.3	22
4593	Comparative Transcriptome Analysis of Two <i>Ipomoea aquatica</i> Forsk. Cultivars Targeted To Explore Possible Mechanism of Genotype-Dependent Accumulation of Cadmium. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 5241-5250.	2.4	46
4594	Towards clinical application of pronuclear transfer to prevent mitochondrial DNA disease. <i>Nature</i> , 2016, 534, 383-386.	13.7	278
4595	ADAR1 Activation Drives Leukemia Stem Cell Self-Renewal by Impairing Let-7 Biogenesis. <i>Cell Stem Cell</i> , 2016, 19, 177-191.	5.2	182
4596	Heterogeneity in the Histidine-brace Copper Coordination Sphere in Auxiliary Activity Family 10 (AA10) Lytic Polysaccharide Monooxygenases. <i>Journal of Biological Chemistry</i> , 2016, 291, 12838-12850.	1.6	45
4597	Features that define the best ChIP-seq peak calling algorithms. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw035.	3.2	96
4598	Regulation, overexpression, and target gene identification of <i>Potato Homeobox 15</i> ( <i>POTH15</i> ) a class-I <i>KNOX</i> gene in potato. <i>Journal of Experimental Botany</i> , 2016, 67, 4255-4272.	2.4	20
4599	Evolution of Vertebrate Phototransduction: Cascade Activation. <i>Molecular Biology and Evolution</i> , 2016, 33, 2064-2087.	3.5	44
4600	TSCAN: Pseudo-time reconstruction and evaluation in single-cell RNA-seq analysis. <i>Nucleic Acids Research</i> , 2016, 44, e117-e117.	6.5	491
4601	Cotton cytosolic pyruvate kinase GhPK6 participates in fast fiber elongation regulation in a ROS-mediated manner. <i>Planta</i> , 2016, 244, 915-926.	1.6	17
4602	Reconstructing the temporal progression of HIV-1 immune response pathways. <i>Bioinformatics</i> , 2016, 32, i253-i261.	1.8	14
4603	Toward reliable biomarker signatures in the age of liquid biopsies - how to standardize the small RNA-Seq workflow. <i>Nucleic Acids Research</i> , 2016, 44, 5995-6018.	6.5	97
4604	Abscission-related genes revealed by RNA-Seq analysis using self-abscising apple ( <i>Malus</i> 'Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,9	0.9	6
4605	Convergent Evolution of Rumen Microbiomes in High-Altitude Mammals. <i>Current Biology</i> , 2016, 26, 1873-1879.	1.8	281
4606	An optimized protocol for generation and analysis of Ion Proton sequencing reads for RNA-Seq. <i>BMC Genomics</i> , 2016, 17, 403.	1.2	26
4607	Molecular identification and sex distribution of two chemosensory receptor families in <i>Athetis lepigone</i> by antennal transcriptome analysis. <i>Journal of Asia-Pacific Entomology</i> , 2016, 19, 571-580.	0.4	18

#	ARTICLE	IF	CITATIONS
4608	Transcriptional regulation of vascular cambium activity during the transition from juvenile to mature stages in <i>Cunninghamia lanceolata</i> . <i>Journal of Plant Physiology</i> , 2016, 200, 7-17.	1.6	19
4609	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740.	9.0	6,181
4610	Calcium-insensitive splice variants of mammalian E1 subunit of 2-oxoglutarate dehydrogenase complex with tissue-specific patterns of expression. <i>Biochemical Journal</i> , 2016, 473, 1165-1178.	1.7	26
4611	Ablation of Liver X receptors $\text{LXR}\alpha$ and $\text{LXR}\beta$ leads to spontaneous peripheral squamous cell lung cancer in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7614-7619.	3.3	35
4612	Genome-wide identification and comparative analysis of the cation proton antiporters family in pear and four other Rosaceae species. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1727-1742.	1.0	32
4613	A single amino acid mutation in SpoOA results in sporulation deficiency of <i>Paenibacillus polymyxa</i> SC2. <i>Research in Microbiology</i> , 2016, 167, 472-479.	1.0	22
4614	Regulation of neuroendocrine cells and neuron factors in the ovary by zinc oxide nanoparticles. <i>Toxicology Letters</i> , 2016, 256, 19-32.	0.4	38
4615	Distribution and evolution of the serine/aspartate racemase family in invertebrates. <i>Amino Acids</i> , 2016, 48, 387-402.	1.2	38
4616	Sexually biased expression of odorant-binding proteins and chemosensory proteins in Asian corn borer <i>Ostrinia furnacalis</i> (Lepidoptera: Crambidae). <i>Applied Entomology and Zoology</i> , 2016, 51, 373-383.	0.6	4
4617	Transcriptional changes of mouse splenocyte organelle components following acute infection with <i>Toxoplasma gondii</i> . <i>Experimental Parasitology</i> , 2016, 167, 7-16.	0.5	26
4618	The Fast-Evolving <i>phy-2</i> Gene Modulates Sexual Development in Response to Light in the Model Fungus <i>Neurospora crassa</i> . <i>MBio</i> , 2016, 7, e02148.	1.8	37
4619	De novo assembly and transcriptome analysis of sclerotial development in <i>Wolfiporia cocos</i> . <i>Gene</i> , 2016, 588, 149-155.	1.0	16
4620	A global study of transcriptome dynamics in canola ( <i>Brassica napus</i> L.) responsive to <i>Sclerotinia sclerotiorum</i> infection using RNA-Seq. <i>Gene</i> , 2016, 590, 57-67.	1.0	41
4621	The role of melanin pathways in extremotolerance and virulence of <i>Fonsecaea</i> revealed by de novo assembly transcriptomics using illumina paired-end sequencing. <i>Studies in Mycology</i> , 2016, 83, 1-18.	4.5	35
4622	Assessment of individual differences in the rat nucleus accumbens transcriptome following taste-heroin extended access. <i>Brain Research Bulletin</i> , 2016, 123, 71-80.	1.4	30
4623	Transcriptomic responses in the fish intestine. <i>Developmental and Comparative Immunology</i> , 2016, 64, 103-117.	1.0	136
4624	Upregulation of Haploinsufficient Gene Expression in the Brain by Targeting a Long Non-coding RNA Improves Seizure Phenotype in a Model of Dravet Syndrome. <i>EBioMedicine</i> , 2016, 9, 257-277.	2.7	116
4625	Global transcriptional regulation by H-NS and its biological influence on the virulence of Enterohemorrhagic <i>Escherichia coli</i> . <i>Gene</i> , 2016, 588, 115-123.	1.0	13

#	ARTICLE	IF	CITATIONS
4626	Analysis of transcriptome profiling from the brain at maturation and regression phases in starry flounder ( <i>Platichthys stellatus</i> ). <i>Gene Reports</i> , 2016, 4, 45-52.	0.4	1
4627	Transcriptome profiling of the microalga <i>Chlorella pyrenoidosa</i> in response to different carbon dioxide concentrations. <i>Marine Genomics</i> , 2016, 29, 81-87.	0.4	10
4628	Cells with surface expression of CD133 <sup>high</sup> CD71 <sup>low</sup> are enriched for tripotent colony-forming progenitor cells in the adult murine pancreas. <i>Stem Cell Research</i> , 2016, 16, 40-53.	0.3	25
4629	Iron deficiency resistance mechanisms enlightened by gene expression analysis in <i>Paenibacillus riograndensis</i> SBR5. <i>Research in Microbiology</i> , 2016, 167, 501-509.	1.0	7
4630	Long-Term Memory in <i>Drosophila</i> Is Influenced by Histone Deacetylase HDAC4 Interacting with SUMO-Conjugating Enzyme Ubc9. <i>Genetics</i> , 2016, 203, 1249-1264.	1.2	29
4631	Molecular microevolution and epigenetic patterns of the long non-coding gene H19 show its potential function in pig domestication and breed divergence. <i>BMC Evolutionary Biology</i> , 2016, 16, 87.	3.2	13
4632	Genome-wide analysis of tomato NF-Y factors and their role in fruit ripening. <i>BMC Genomics</i> , 2016, 17, 36.	1.2	70
4633	Identification of the genes involved in odorant reception and detection in the palm weevil <i>Rhynchophorus ferrugineus</i> , an important quarantine pest, by antennal transcriptome analysis. <i>BMC Genomics</i> , 2016, 17, 69.	1.2	102
4634	Transcriptomic analysis reveals the gene expression profile that specifically responds to IBA during adventitious rooting in mung bean seedlings. <i>BMC Genomics</i> , 2016, 17, 43.	1.2	31
4635	ChlamyNET: a <i>Chlamydomonas</i> gene co-expression network reveals global properties of the transcriptome and the early setup of key co-expression patterns in the green lineage. <i>BMC Genomics</i> , 2016, 17, 227.	1.2	45
4636	Transcriptome analysis of highly purified mouse spermatogenic cell populations: gene expression signatures switch from meiotic-to postmeiotic-related processes at pachytene stage. <i>BMC Genomics</i> , 2016, 17, 294.	1.2	132
4637	Identification of candidate genes involved in wax deposition in <i>Poa pratensis</i> by RNA-seq. <i>BMC Genomics</i> , 2016, 17, 314.	1.2	11
4638	Transcriptome and comparative gene expression analysis of <i>Phyllostachys edulis</i> in response to high light. <i>BMC Plant Biology</i> , 2016, 16, 34.	1.6	34
4639	Transcriptomic, proteomic and metabolic changes in <i>Arabidopsis thaliana</i> leaves after the onset of illumination. <i>BMC Plant Biology</i> , 2016, 16, 43.	1.6	39
4640	Detection of pup odors by non-canonical adult vomeronasal neurons expressing an odorant receptor gene is influenced by sex and parenting status. <i>BMC Biology</i> , 2016, 14, 12.	1.7	18
4641	Toward precision medicine of breast cancer. <i>Theoretical Biology and Medical Modelling</i> , 2016, 13, 7.	2.1	48
4642	A developing <i>Setaria viridis</i> internode: an experimental system for the study of biomass generation in a C4 model species. <i>Biotechnology for Biofuels</i> , 2016, 9, 45.	6.2	50
4643	Crystal structure and biochemical characterization of the recombinant ThBgl, a GH1 $\beta$ -glucosidase overexpressed in <i>Trichoderma harzianum</i> under biomass degradation conditions. <i>Biotechnology for Biofuels</i> , 2016, 9, 71.	6.2	45

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4644	A complete annotation of the chromosomes of the cellulase producer <i>Trichoderma reesei</i> provides insights in gene clusters, their expression and reveals genes required for fitness. <i>Biotechnology for Biofuels</i> , 2016, 9, 75.	6.2	54
4645	De novo transcriptomic analysis of the female and male adults of the blood fluke <i>Schistosoma turkestanicum</i> . <i>Parasites and Vectors</i> , 2016, 9, 143.	1.0	12
4646	Comparative transcriptomics of the nematode gut identifies global shifts in feeding mode and pathogen susceptibility. <i>BMC Research Notes</i> , 2016, 9, 142.	0.6	19
4647	High-throughput identification of novel conotoxins from the Chinese tubular cone snail ( <i>Conus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 103.3	3.3	52
4648	Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. <i>Microbiome</i> , 2016, 4, 2.	4.9	118
4649	Transcriptome analysis reveals self-incompatibility in the tea plant ( <i>Camellia sinensis</i> ) might be under gametophytic control. <i>BMC Genomics</i> , 2016, 17, 359.	1.2	50
4650	Suppression of microRNA activity amplifies IFN- $\beta$ -induced macrophage activation and promotes anti-tumour immunity. <i>Nature Cell Biology</i> , 2016, 18, 790-802.	4.6	214
4651	Salinity stress induces the production of 2-(2-phenylethyl)chromones and regulates novel classes of responsive genes involved in signal transduction in <i>Aquilaria sinensis</i> calli. <i>BMC Plant Biology</i> , 2016, 16, 119.	1.6	39
4652	f-divergence cutoff index to simultaneously identify differential expression in the integrated transcriptome and proteome. <i>Nucleic Acids Research</i> , 2016, 44, e97-e97.	6.5	7
4653	A Bayesian approach for estimating allele-specific expression from RNA-Seq data with diploid genomes. <i>BMC Genomics</i> , 2016, 17, 2.	1.2	22
4654	Comparison of normalization and differential expression analyses using RNA-Seq data from 726 individual <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2016, 17, 28.	1.2	154
4655	A <i>Colletotrichum graminicola</i> mutant deficient in the establishment of biotrophy reveals early transcriptional events in the maize anthracnose disease interaction. <i>BMC Genomics</i> , 2016, 17, 202.	1.2	33
4656	Transcriptome and metabolome analysis in shoot and root of <i>Valeriana fauriei</i> . <i>BMC Genomics</i> , 2016, 17, 303.	1.2	17
4657	The virulence factor <i>ychO</i> has a pleiotropic action in an Avian Pathogenic <i>Escherichia coli</i> (APEC) strain. <i>BMC Microbiology</i> , 2016, 16, 35.	1.3	13
4658	RNA-Seq analysis uncovers non-coding small RNA system of <i>Mycobacterium neoaurum</i> in the metabolism of sterols to accumulate steroid intermediates. <i>Microbial Cell Factories</i> , 2016, 15, 64.	1.9	19
4659	Block-Constraint Robust Principal Component Analysis and its Application to Integrated Analysis of TCGA Data. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 510-516.	2.2	17
4660	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. <i>Progress in Retinal and Eye Research</i> , 2016, 55, 1-31.	7.3	58
4661	Dorsal root ganglion transcriptome analysis following peripheral nerve injury in mice. <i>Molecular Pain</i> , 2016, 12, 174480691662904.	1.0	90



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4662	RNA-sequencing of WFS1-deficient pancreatic islets. <i>Physiological Reports</i> , 2016, 4, e12750.	0.7	18
4663	Embryonal Control of Yellow Seed Coat Locus <i>ECY1</i> Is Related to Alanine and Phenylalanine Metabolism in the Seed Embryo of <i>Brassica napus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1073-1081.	0.8	15
4664	Alterations to chromatin in intestinal macrophages link IL10 deficiency to inappropriate inflammatory responses. <i>European Journal of Immunology</i> , 2016, 46, 1912-1925.	1.6	30
4665	<i>OsSIDP366</i> , a DUF1644 gene, positively regulates responses to drought and salt stresses in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 492-502.	4.1	54
4666	Manipulation of flowering time and branching by overexpression of the tomato transcription factor Sl ZFP 2. <i>Plant Biotechnology Journal</i> , 2016, 14, 2310-2321.	4.1	26
4667	Global analysis of the developmental dynamics of <i>Gossypium hirsutum</i> based on strand-specific transcriptome. <i>Physiologia Plantarum</i> , 2016, 158, 106-121.	2.6	6
4668	Normalization of transposon-mutant library sequencing datasets to improve identification of conditionally essential genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1642004.	0.3	12
4669	Genome-wide transcriptome analysis of female-sterile rice ovule shed light on its abortive mechanism. <i>Planta</i> , 2016, 244, 1011-1028.	1.6	18
4670	Evaluating the impact of sequencing error correction for RNA-seq data with ERCC RNA spike-in controls. , 2016, 2016, 74-77.		4
4671	Alcohol resistance in <i>Drosophila</i> is modulated by the Toll innate immune pathway. <i>Genes, Brain and Behavior</i> , 2016, 15, 382-394.	1.1	24
4672	A <i>de novo</i> transcriptomic analysis to reveal functional genes in <i>Apolygus lucorum</i> . <i>Insect Science</i> , 2016, 23, 2-14.	1.5	15
4673	Comparing <i>de novo</i> and reference-based transcriptome assembly strategies by applying them to the blood-sucking bug <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 69, 25-33.	1.2	31
4674	Expanding the Limits of Thermoacidophily in the Archaeon <i>Sulfolobus solfataricus</i> by Adaptive Evolution. <i>Applied and Environmental Microbiology</i> , 2016, 82, 857-867.	1.4	30
4675	Venezuelan Equine Encephalitis Virus Induces Apoptosis through the Unfolded Protein Response Activation of EGR1. <i>Journal of Virology</i> , 2016, 90, 3558-3572.	1.5	48
4676	Single-Cell Genomics and Epigenomics. <i>Series in Bioengineering</i> , 2016, , 257-301.	0.3	2
4677	Transcriptome analysis of the <i>Taxodium</i> 'Zhongshanshan 405'™ roots in response to salinity stress. <i>Plant Physiology and Biochemistry</i> , 2016, 100, 156-165.	2.8	31
4678	Compensatory Drift and the Evolutionary Dynamics of Dosage-Sensitive Duplicate Genes. <i>Genetics</i> , 2016, 202, 765-774.	1.2	46
4679	The activation of the NF- $\kappa$ B-JNK pathway is independent of the PI3K-Rac1-JNK pathway involved in the bFGF-regulated human fibroblast cell migration. <i>Journal of Dermatological Science</i> , 2016, 82, 28-37.	1.0	36

#	ARTICLE	IF	CITATIONS
4680	Functional characterization and transcriptome analysis reveal multiple roles for <i>prc</i> in the pathogenicity of the black rot pathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Research in Microbiology</i> , 2016, 167, 299-312.	1.0	19
4681	Metatranscriptomic insights on gene expression and regulatory controls in <i>Candidatus</i> <i>Accumulibacter phosphatis</i> . <i>ISME Journal</i> , 2016, 10, 810-822.	4.4	98
4682	Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. <i>Nature</i> , 2016, 530, 113-116.	13.7	211
4683	Integrated analysis of the prostate cancer small nucleolar transcriptome reveals SNORA55 as a driver of prostate cancer progression. <i>Molecular Oncology</i> , 2016, 10, 693-703.	2.1	48
4684	Chemical Inhibition of Kynureninase Reduces <i>Pseudomonas aeruginosa</i> Quorum Sensing and Virulence Factor Expression. <i>ACS Chemical Biology</i> , 2016, 11, 1106-1117.	1.6	33
4685	De novo comparative transcriptome analysis provides new insights into sucrose induced somatic embryogenesis in camphor tree ( <i>Cinnamomum camphora</i> L.). <i>BMC Genomics</i> , 2016, 17, 26.	1.2	58
4686	Liver transcriptome sequencing and de novo annotation of the large yellow croaker ( <i>Larimichthys</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	86
4687	A Gene Encoding a DUF247 Domain Protein Cosegregates with the <i>S</i> Self-Incompatibility Locus in Perennial Ryegrass. <i>Molecular Biology and Evolution</i> , 2016, 33, 870-884.	3.5	78
4688	Simultaneous exposure to estrogen and androgen resulted in feminization and endocrine disruption. <i>Journal of Endocrinology</i> , 2016, 228, 205-218.	1.2	29
4689	Identification and characterisation of hemocyanin of the fish louse <i>Argulus</i> (Crustacea: Branchiura). <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2016, 186, 161-168.	0.7	10
4690	Expression Characterization of Stress Genes Under High and Low Temperature Stresses in the Pacific Oyster, <i>Crassostrea gigas</i> . <i>Marine Biotechnology</i> , 2016, 18, 176-188.	1.1	73
4691	RNA-seq of human reference RNA samples using a thermostable group II intron reverse transcriptase. <i>Rna</i> , 2016, 22, 597-613.	1.6	80
4692	Transcriptome sequencing discovers genes related to fatty acid biosynthesis in the seeds of <i>Eucommia ulmoides</i> . <i>Genes and Genomics</i> , 2016, 38, 275-283.	0.5	13
4693	Long non-coding RNA expression in primary human monocytes. <i>Genomics</i> , 2016, 108, 37-45.	1.3	20
4694	Global transcriptome profiling analysis reveals insight into saliva-responsive genes in alfalfa. <i>Plant Cell Reports</i> , 2016, 35, 561-571.	2.8	29
4695	RNA-seq reveals the critical role of CspA in regulating <i>Brucella melitensis</i> metabolism and virulence. <i>Science China Life Sciences</i> , 2016, 59, 417-424.	2.3	18
4696	Transcriptome-wide interrogation of RNA secondary structure in living cells with icSHAPE. <i>Nature Protocols</i> , 2016, 11, 273-290.	5.5	147
4697	MMP-9 facilitates selective proteolysis of the histone H3 tail at genes necessary for proficient osteoclastogenesis. <i>Genes and Development</i> , 2016, 30, 208-219.	2.7	87

#	ARTICLE	IF	CITATIONS
4698	De novo characterization of the liver transcriptome of javelin goby <i>Synechogobius hasta</i> and analysis of its transcriptomic profile following waterborne copper exposure. <i>Fish Physiology and Biochemistry</i> , 2016, 42, 979-994.	0.9	21
4699	A long non-coding RNA, BC048612 and a microRNA, miR-203 coordinate the gene expression of neuronal growth regulator 1 (NEGR1) adhesion protein. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 533-543.	1.9	17
4700	Essentials of Single-Cell Analysis. Series in Bioengineering, 2016, , .	0.3	29
4701	Identification of a drought responsive gene encoding a nuclear protein involved in drought and freezing stress tolerance in <i>Arabidopsis</i> . <i>Biologia Plantarum</i> , 2016, 60, 105-112.	1.9	5
4702	Integrative Genomics of Aging. , 2016, , 263-285.		6
4703	Comparative transcriptome analysis of <i>Bombyx mori</i> spinnerets and Filippi's glands suggests their role in silk fiber formation. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 68, 89-99.	1.2	24
4704	Comparison of transcriptome analysis between silk gland of <i>B. mori</i> and <i>B. mandarina</i> using next generation sequencing. <i>Genes and Genomics</i> , 2016, 38, 251-262.	0.5	1
4705	Mechanisms of TiO <sub>2</sub> NPs-induced phoxim metabolism in silkworm ( <i>Bombyx mori</i> ) fat body. <i>Pesticide Biochemistry and Physiology</i> , 2016, 129, 89-94.	1.6	22
4706	Transcriptome analysis of the unfolded protein response in hemocytes of <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2016, 54, 153-163.	1.6	35
4707	De novo assembly and transcriptome analysis of osmoregulation in <i>Litopenaeus vannamei</i> under three cultivated conditions with different salinities. <i>Gene</i> , 2016, 578, 185-193.	1.0	48
4708	Comparative RNA-seq-Based Transcriptome Analysis of the Virulence Characteristics of Methicillin-Resistant and -Susceptible <i>Staphylococcus pseudintermedius</i> Strains Isolated from Small Animals. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 962-967.	1.4	26
4709	ALCOdb: Gene Coexpression Database for Microalgae. <i>Plant and Cell Physiology</i> , 2016, 57, e3-e3.	1.5	35
4710	Expression of biotic stress response genes to <i>Phytophthora infestans</i> inoculation in White Lady, a potato cultivar with race-specific resistance to late blight. <i>Physiological and Molecular Plant Pathology</i> , 2016, 93, 22-28.	1.3	7
4711	Different mechanisms of resistance modulate sulfite tolerance in wine yeasts. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 797-813.	1.7	42
4712	Comparative Transcriptome Analysis between the Fungal Plant Pathogens <i>Sclerotinia sclerotiorum</i> and <i>S. trifoliorum</i> Using RNA Sequencing. <i>Journal of Heredity</i> , 2016, 107, 163-172.	1.0	9
4713	Expression of mitochondria-related genes is elevated in overfeeding-induced goose fatty liver. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2016, 192, 30-37.	0.7	22
4714	Composition and Metabolic Activities of the Bacterial Community in Shrimp Sauce at the Flavor-Forming Stage of Fermentation As Revealed by Metatranscriptome and 16S rRNA Gene Sequencings. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 2591-2603.	2.4	31
4715	Exploring the surfaceome of Ewing sarcoma identifies a new and unique therapeutic target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3603-3608.	3.3	42

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4716	X inactivation and reactivation in X-linked diseases. <i>Seminars in Cell and Developmental Biology</i> , 2016, 56, 78-87.	2.3	43
4717	Translating RNA sequencing into clinical diagnostics: opportunities and challenges. <i>Nature Reviews Genetics</i> , 2016, 17, 257-271.	7.7	558
4718	FRAMA: from RNA-seq data to annotated mRNA assemblies. <i>BMC Genomics</i> , 2016, 17, 54.	1.2	30
4719	Isoform-level ribosome occupancy estimation guided by transcript abundance with Ribomap. <i>Bioinformatics</i> , 2016, 32, 1880-1882.	1.8	31
4720	Recurrent BCOR Internal Tandem Duplication and YWHAE-NUTM2B Fusions in Soft Tissue Undifferentiated Round Cell Sarcoma of Infancy. <i>American Journal of Surgical Pathology</i> , 2016, 40, 1009-1020.	2.1	155
4721	De novo transcriptomic assembly and profiling of <i>Rigidoporus microporus</i> during saprotrophic growth on rubber wood. <i>BMC Genomics</i> , 2016, 17, 234.	1.2	12
4722	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016, 351, 1454-1458.	6.0	880
4723	TRAPLINE: a standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. <i>BMC Bioinformatics</i> , 2016, 17, 21.	1.2	35
4724	scFUS-mediated regulation of alternative RNA processing in neurons: insights from global transcriptome analysis. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 330-340.	3.2	34
4725	It's DE-licious: A Recipe for Differential Expression Analyses of RNA-seq Experiments Using Quasi-Likelihood Methods in edgeR. <i>Methods in Molecular Biology</i> , 2016, 1418, 391-416.	0.4	352
4726	Population-level consequences for wild fish exposed to sublethal concentrations of chemicals – a critical review. <i>Fish and Fisheries</i> , 2016, 17, 545-566.	2.7	119
4727	Transcriptome changes in STSV2-infected <i>Sulfolobus islandicus</i> ...REY15A undergoing continuous CRISPR spacer acquisition. <i>Molecular Microbiology</i> , 2016, 99, 719-728.	1.2	34
4728	Transcriptome analysis of <i>Ophiocordyceps sinensis</i> before and after infection of <i>Thitarodes</i> larvae. <i>Fungal Biology</i> , 2016, 120, 819-826.	1.1	20
4729	A comprehensive transcriptome of early development in yellowtail kingfish ( <i>Seriola lalandi</i> ). <i>Overlaid</i>	2.2	17
4730	Optimization of next-generation sequencing transcriptome annotation for species lacking sequenced genomes. <i>Molecular Ecology Resources</i> , 2016, 16, 446-458.	2.2	23
4731	Blood transcriptome changes after stroke in an African American population. <i>Annals of Clinical and Translational Neurology</i> , 2016, 3, 70-81.	1.7	15
4732	Identification, characterization and target gene analysis of testicular microRNAs in the oriental fruit fly <i>Bactrocera dorsalis</i> . <i>Insect Molecular Biology</i> , 2016, 25, 32-43.	1.0	27
4733	The genomic bases of morphological divergence and reproductive isolation driven by ecological speciation in <i>Senecio</i> (Asteraceae). <i>Journal of Evolutionary Biology</i> , 2016, 29, 98-113.	0.8	36

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4734	Statistical Genomics. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	21
4735	Phylogenetic analysis and differential expression of EF1 $\alpha$ genes in soybean during development, stress and phytohormone treatments. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1505-1522.	1.0	10
4736	Single-cell Transcriptome Study as Big Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 21-30.	3.0	35
4737	Deciphering the main venom components of the ectoparasitic ant-like bethylid wasp, <i>Scleroderma guani</i> . <i>Toxicon</i> , 2016, 113, 32-40.	0.8	16
4738	Characters, functions and clinical perspectives of long non-coding RNAs. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1013-1033.	1.0	63
4739	Omega-3 fatty acids partially revert the metabolic gene expression profile induced by long-term calorie restriction. <i>Experimental Gerontology</i> , 2016, 77, 29-37.	1.2	3
4740	Differential regulation of type III secretion and virulence genes in <i>Bordetella pertussis</i> and <i>Bordetella bronchiseptica</i> by a secreted anti- $\beta$ factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2341-2348.	3.3	54
4741	An empirical Bayes change-point model for identifying 3 $\alpha$ and 5 $\alpha$ alternative splicing by next-generation RNA sequencing. <i>Bioinformatics</i> , 2016, 32, 1823-1831.	1.8	13
4742	De novo assembly and annotation of the salivary gland transcriptome of <i>Rhipicephalus appendiculatus</i> male and female ticks during blood feeding. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 536-548.	1.1	55
4743	Comparative analysis of transcriptomics based hypoxia signatures in head- and neck squamous cell carcinoma. <i>Radiotherapy and Oncology</i> , 2016, 118, 350-358.	0.3	62
4744	Study of Transposable Elements and Their Genomic Impact. <i>Methods in Molecular Biology</i> , 2016, 1400, 1-19.	0.4	7
4745	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016, 15, 339-359.	1.8	26
4746	On the outside looking in: redefining the role of analytical chemistry in the biosciences. <i>Chemical Communications</i> , 2016, 52, 8918-8934.	2.2	23
4747	Bacteria differently regulate mRNA abundance to specifically respond to various stresses. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150069.	1.6	82
4748	Enhanced butanol production by increasing NADH and ATP levels in <i>Clostridium beijerinckii</i> NCIMB 8052 by insertional inactivation of Cbei_4110. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 4985-4996.	1.7	31
4749	Genome-wide transcriptome analysis in the ovaries of two goats identifies differentially expressed genes related to fecundity. <i>Gene</i> , 2016, 582, 69-76.	1.0	30
4750	Transcriptome and analysis on the complement and coagulation cascades pathway of large yellow croaker ( <i>Larimichthys crocea</i> ) to ciliate ectoparasite <i>Cryptocaryon irritans</i> infection. <i>Fish and Shellfish Immunology</i> , 2016, 50, 127-141.	1.6	72
4751	High-throughput transcriptome sequencing analysis provides preliminary insights into the biotransformation mechanism of <i>Rhodospseudomonas palustris</i> treated with alpha-rhamnnetin-3-rhamnoside. <i>Microbiological Research</i> , 2016, 185, 1-12.	2.5	2

#	ARTICLE	IF	CITATIONS
4752	Overexpression of <i>Rosa rugosa</i> anthocyanidin reductase enhances tobacco tolerance to abiotic stress through increased ROS scavenging and modulation of ABA signaling. <i>Plant Science</i> , 2016, 245, 35-49.	1.7	59
4753	HPV status is associated with altered PIWI-interacting RNA expression pattern in head and neck cancer. <i>Oral Oncology</i> , 2016, 55, 43-48.	0.8	41
4754	Plastic and Evolved Responses to Global Change: What Can We Learn from Comparative Transcriptomics?: Table 1.. <i>Journal of Heredity</i> , 2016, 107, 71-81.	1.0	90
4755	Essential Nonredundant Function of the Catalytic Activity of Histone Deacetylase 2 in Mouse Development. <i>Molecular and Cellular Biology</i> , 2016, 36, 462-474.	1.1	17
4756	Unbiased Detection of Respiratory Viruses by Use of RNA Sequencing-Based Metagenomics: a Systematic Comparison to a Commercial PCR Panel. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1000-1007.	1.8	177
4757	RNA-seq transcriptional profiling of <i>Herbaspirillum seropedicae</i> colonizing wheat ( <i>Triticum aestivum</i> ) roots. <i>Plant Molecular Biology</i> , 2016, 90, 589-603.	2.0	55
4758	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
4759	Long noncoding RNAs as regulators of Toll-like receptor signaling and innate immunity. <i>Journal of Leukocyte Biology</i> , 2016, 99, 839-850.	1.5	53
4760	Genome-wide transcriptomic profiles reveal multiple regulatory responses of poplar to <i>Lonsdalea quercina</i> infection. <i>Trees - Structure and Function</i> , 2016, 30, 1389-1402.	0.9	7
4761	Mitochondrial DNA haplogroups modify the risk of osteoarthritis by altering mitochondrial function and intracellular mitochondrial signals. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 829-836.	1.8	38
4762	Genomic Comparison of Two O111:Hâ <sup>~</sup> Enterohemorrhagic <i>Escherichia coli</i> Isolates from a Historic Hemolytic-Uremic Syndrome Outbreak in Australia. <i>Infection and Immunity</i> , 2016, 84, 775-781.	1.0	14
4763	Chronic TCDD exposure results in the dysregulation of gene expression in splenic B-lymphocytes and in the impairments in T-cell and B-cell differentiation in mouse model. <i>Journal of Environmental Sciences</i> , 2016, 39, 218-227.	3.2	7
4764	Characterization of the transcriptome of <i>Achromobacter</i> sp. HZ01 with the outstanding hydrocarbon-degrading ability. <i>Gene</i> , 2016, 584, 185-194.	1.0	24
4765	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw056.	1.3	44
4766	Pulmonary transcriptome analysis in the rabbit model of surgically-induced diaphragmatic hernia treated with fetal tracheal occlusion. <i>DMM Disease Models and Mechanisms</i> , 2016, 9, 221-8.	1.2	18
4767	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2016, 1402, 243-254.	0.4	28
4768	The ribonuclease polynucleotide phosphorylase can interact with small regulatory RNAs in both protective and degradative modes. <i>Rna</i> , 2016, 22, 360-372.	1.6	51
4769	Comparative Transcriptome Analysis of <i>Isoetes Sinensis</i> Under Terrestrial and Submerged Conditions. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 136-145.	1.0	13

#	ARTICLE	IF	CITATIONS
4770	Molecular Plasticity of Male and Female Murine Gonadotropes Revealed by mRNA Sequencing. <i>Endocrinology</i> , 2016, 157, 1082-1093.	1.4	40
4771	A Novel Candidate Gene for Temperature-Dependent Sex Determination in the Common Snapping Turtle. <i>Genetics</i> , 2016, 203, 557-571.	1.2	85
4772	An Outer Membrane Protein Involved in the Uptake of Glucose Is Essential for <i>Cytophaga hutchinsonii</i> Cellulose Utilization. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1933-1944.	1.4	18
4773	Diverse functions of myosin VI elucidated by an isoform-specific $\hat{\pm}$ -helix domain. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 300-308.	3.6	42
4774	Transcriptome sequencing and characterization of ungerminated and germinated spores of <i>Nosema bombycis</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2016, 48, 246-256.	0.9	20
4775	Research Resource: Hormones, Genes, and Athleticism: Effect of Androgens on the Avian Muscular Transcriptome. <i>Molecular Endocrinology</i> , 2016, 30, 254-271.	3.7	37
4776	20 years of Nature Biotechnology research tools. <i>Nature Biotechnology</i> , 2016, 34, 256-261.	9.4	4
4777	Phase variation of a Type IIG restriction-modification enzyme alters site-specific methylation patterns and gene expression in <i>Campylobacter jejuni</i> strain NCTC11168. <i>Nucleic Acids Research</i> , 2016, 44, 4581-4594.	6.5	53
4778	Improvement of soybean transformation via <i>Agrobacterium tumefaciens</i> methods involving $\hat{\pm}$ -aminooxyacetic acid and sonication treatments enlightened by gene expression profile analysis. <i>Plant Cell Reports</i> , 2016, 35, 1259-1271.	2.8	8
4779	Transcriptomics analysis of iPSC-derived neurons and modeling of neuropsychiatric disorders. <i>Molecular and Cellular Neurosciences</i> , 2016, 73, 32-42.	1.0	33
4781	The RNA-binding protein LARP1 is a post-transcriptional regulator of survival and tumorigenesis in ovarian cancer. <i>Nucleic Acids Research</i> , 2016, 44, 1227-1246.	6.5	120
4782	Transcriptome analysis of the germinated seeds identifies low-temperature responsive genes involved in germination process in <i>Ricinus communis</i> . <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	8
4783	RNA Binding Proteins RZ-1B and RZ-1C Play Critical Roles in Regulating Pre-mRNA Splicing and Gene Expression during Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2016, 28, 55-73.	3.1	79
4784	TauCstF-64 Mediates Correct mRNA Polyadenylation and Splicing of Activator and Repressor Isoforms of the Cyclic AMP-Responsive Element Modulator (CREM) in Mouse Testis1. <i>Biology of Reproduction</i> , 2016, 94, 34.	1.2	16
4785	Genome-wide identification and comparative analysis of grafting-responsive mRNA in watermelon grafted onto bottle gourd and squash rootstocks by high-throughput sequencing. <i>Molecular Genetics and Genomics</i> , 2016, 291, 621-633.	1.0	55
4786	Zero-Inflated Beta Regression for Differential Abundance Analysis with Metagenomics Data. <i>Journal of Computational Biology</i> , 2016, 23, 102-110.	0.8	64
4787	Genomic structural variation contributes to phenotypic change of industrial bioethanol yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2016, 16, fov118.	1.1	21
4788	Discovery of the gray phenotype and white-gray-opaque tristable phenotypic transitions in <i>Candida dubliniensis</i> . <i>Virulence</i> , 2016, 7, 230-242.	1.8	15

#	ARTICLE	IF	CITATIONS
4789	The LINK-A lncRNA activates normoxic HIF1 $\alpha$ signalling in triple-negative breast cancer. <i>Nature Cell Biology</i> , 2016, 18, 213-224.	4.6	444
4790	Quantitative BrdU immunoprecipitation method demonstrates that Fkh1 and Fkh2 are rate-limiting activators of replication origins that reprogram replication timing in G1 phase. <i>Genome Research</i> , 2016, 26, 365-375.	2.4	39
4791	Genome-wide analysis of WRKY family of transcription factors in common bean, <i>Phaseolus vulgaris</i> : Chromosomal localization, structure, evolution and expression divergence. <i>Plant Gene</i> , 2016, 5, 22-30.	1.4	22
4792	Coordinated microRNA and messenger RNA expression profiles for understanding sexual dimorphism of gonads and the potential roles of microRNA in the steroidogenesis pathway in Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>Theriogenology</i> , 2016, 85, 970-978.	0.9	46
4793	A Global View of Gene Expression of <i>Aspergillus nidulans</i> on Responding to the Deficiency in Soluble Potassium. <i>Current Microbiology</i> , 2016, 72, 410-419.	1.0	5
4794	Transcriptome analysis of soiny mullet ( <i>Liza haematocheila</i> ) spleen in response to <i>Streptococcus dysgalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2016, 49, 194-204.	1.6	49
4795	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. <i>Proceedings of the IEEE</i> , 2016, 104, 176-197.	16.4	186
4796	Strand-specific RNA-seq analysis of the <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> transcriptome. <i>Molecular BioSystems</i> , 2016, 12, 508-519.	2.9	15
4797	A proteogenomic approach to understand splice isoform functions through sequence and expression-based computational modeling. <i>Briefings in Bioinformatics</i> , 2016, 17, bbv109.	3.2	6
4798	Dynamic transcriptome analysis reveals AP2/ERF transcription factors responsible for cold stress in rapeseed ( <i>Brassica napus</i> L.). <i>Molecular Genetics and Genomics</i> , 2016, 291, 1053-1067.	1.0	58
4799	Establishing a herbicide-metabolizing enzyme library in <i>Beckmannia syzigachne</i> to identify genes associated with metabolic resistance. <i>Journal of Experimental Botany</i> , 2016, 67, 1745-1757.	2.4	77
4800	RNA-Seq Experiment and Data Analysis. <i>Methods in Molecular Biology</i> , 2016, 1366, 99-114.	0.4	3
4801	ETS family protein GABP is a novel co-factor strongly associated with genomic YY1 binding sites in various cell lines. <i>Genes and Genomics</i> , 2016, 38, 119-125.	0.5	3
4802	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21.	0.3	40
4803	Transcriptome analysis of the endangered Chinese giant salamander ( <i>Andrias davidianus</i> ): Immune modulation in response to <i>Aeromonas hydrophila</i> infection. <i>Veterinary Immunology and Immunopathology</i> , 2016, 169, 85-95.	0.5	41
4804	Immune defense is the primary function associated with the differentially expressed genes in the cochlea following acoustic trauma. <i>Hearing Research</i> , 2016, 333, 283-294.	0.9	62
4805	Transcriptomics and physiological analyses reveal co-ordinated alteration of metabolic pathways in <i>Jatropha curcas</i> drought tolerance. <i>Journal of Experimental Botany</i> , 2016, 67, 845-860.	2.4	29
4806	SBR-Blood: systems biology repository for hematopoietic cells. <i>Nucleic Acids Research</i> , 2016, 44, D925-D931.	6.5	4



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4807	De novo sequencing and comprehensive analysis of the mutant transcriptome from purple sweet potato ( <i>Ipomoea batatas</i> L.). <i>Gene</i> , 2016, 575, 641-649.	1.0	18
4808	Deep sequencing reveals transcriptome re-programming of <i>Polygonum multiflorum</i> thunb. roots to the elicitation with methyl jasmonate. <i>Molecular Genetics and Genomics</i> , 2016, 291, 337-348.	1.0	7
4809	Gene transcript profiles in the desert plant <i>Nitraria tangutorum</i> during fruit development and ripening. <i>Molecular Genetics and Genomics</i> , 2016, 291, 383-398.	1.0	4
4810	Immunity comes first: The effect of parasite genotypes on adaptive immunity and immunization in three-spined sticklebacks. <i>Developmental and Comparative Immunology</i> , 2016, 54, 137-144.	1.0	12
4811	Comparative transcriptome analyses of deltamethrin-susceptible and -resistant <i>Culex pipiens pallens</i> by RNA-seq. <i>Molecular Genetics and Genomics</i> , 2016, 291, 309-321.	1.0	45
4812	Transcript profiling analysis reveals crucial genes regulating main metabolism during adventitious root formation in cuttings of <i>Morus alba</i> L.. <i>Plant Growth Regulation</i> , 2016, 79, 251-262.	1.8	11
4813	Nascent RNA folding mitigates transcription-associated mutagenesis. <i>Genome Research</i> , 2016, 26, 50-59.	2.4	21
4814	Transcriptomics and Gene Regulation. <i>Translational Bioinformatics</i> , 2016, , .	0.0	2
4815	Transcriptome-based gene expression profiling identifies differentially expressed genes critical for salt stress response in radish ( <i>Raphanus sativus</i> L.). <i>Plant Cell Reports</i> , 2016, 35, 329-346.	2.8	72
4816	Application of metabolomics to toxicology of drugs of abuse: A mini review of metabolomics approach to acute and chronic toxicity studies. <i>Drug Metabolism and Pharmacokinetics</i> , 2016, 31, 21-26.	1.1	61
4817	Bayesian inference with historical data-based informative priors improves detection of differentially expressed genes. <i>Bioinformatics</i> , 2016, 32, 682-689.	1.8	11
4818	CAMUR: Knowledge extraction from RNA-seq cancer data through equivalent classification rules. <i>Bioinformatics</i> , 2016, 32, 697-704.	1.8	31
4819	Inhibition of Tumor Growth and Metastasis in Pancreatic Cancer Models by Interference With CD44v6 Signaling. <i>Gastroenterology</i> , 2016, 150, 513-525.e10.	0.6	78
4820	Plant Bioinformatics. <i>Methods in Molecular Biology</i> , 2016, , .	0.4	11
4821	Analysis of RNA-Seq Data Using TopHat and Cufflinks. <i>Methods in Molecular Biology</i> , 2016, 1374, 339-361.	0.4	457
4822	RNA-seq transcriptome analysis of extensor digitorum longus and soleus muscles in large white pigs. <i>Molecular Genetics and Genomics</i> , 2016, 291, 687-701.	1.0	25
4823	Transcriptomic analysis of global changes in cytokine expression in mouse spleens following acute <i>Toxoplasma gondii</i> infection. <i>Parasitology Research</i> , 2016, 115, 703-712.	0.6	51
4824	RNA-Seq mediated root transcriptome analysis of <i>Chlorophytum borivilianum</i> for identification of genes involved in saponin biosynthesis. <i>Functional and Integrative Genomics</i> , 2016, 16, 37-55.	1.4	22

#	ARTICLE	IF	CITATIONS
4825	De novo transcriptome analysis of carotenoid and polyunsaturated fatty acid metabolism in <i>Rhodomonas</i> sp.. <i>Journal of Applied Phycology</i> , 2016, 28, 1649-1656.	1.5	10
4826	The Impact of Multiparity on Uterine Gene Expression and Decidualization in Mice. <i>Reproductive Sciences</i> , 2016, 23, 687-694.	1.1	14
4827	Mapping the Transcriptome-Wide Landscape of RBP Binding Sites Using gPAR-CLIP-seq: Bioinformatic Analysis. <i>Methods in Molecular Biology</i> , 2016, 1361, 91-104.	0.4	3
4828	Transcriptome analysis of the pearl oyster ( <i>Pinctada fucata</i> ) hemocytes in response to <i>Vibrio alginolyticus</i> infection. <i>Gene</i> , 2016, 575, 421-428.	1.0	52
4829	The promise of omics-based approaches to cancer prevention. <i>Seminars in Oncology</i> , 2016, 43, 36-48.	0.8	10
4830	Systems Biology Approaches to the Study of Biological Networks Underlying Alzheimer's Disease: Role of miRNAs. <i>Methods in Molecular Biology</i> , 2016, 1303, 349-377.	0.4	19
4831	De novo sequencing transcriptome of endemic <i>Gentiana straminea</i> (Gentianaceae) to identify genes involved in the biosynthesis of active ingredients. <i>Gene</i> , 2016, 575, 160-170.	1.0	16
4832	Widespread and Adaptive Alterations in Genome-Wide Gene Expression Associated with Ecological Divergence of Two <i>Oryza</i> Species. <i>Molecular Biology and Evolution</i> , 2016, 33, 62-78.	3.5	26
4833	Mapping the non-standardized biases of ribosome profiling. <i>Biological Chemistry</i> , 2016, 397, 23-35.	1.2	50
4834	Aquaporins in Boron-Tolerant Barley: Identification, Characterization, and Expression Analysis. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 374-386.	1.0	25
4835	Gene set analysis approaches for RNA-seq data: performance evaluation and application guideline. <i>Briefings in Bioinformatics</i> , 2016, 17, 393-407.	3.2	57
4836	Genome-wide identification of phosphate-deficiency-responsive genes in soybean roots by high-throughput sequencing. <i>Plant and Soil</i> , 2016, 398, 207-227.	1.8	52
4837	RPFdb: a database for genome wide information of translated mRNA generated from ribosome profiling. <i>Nucleic Acids Research</i> , 2016, 44, D254-D258.	6.5	46
4838	Whole transcriptome profiling reveals the RNA content of motor axons. <i>Nucleic Acids Research</i> , 2016, 44, e33-e33.	6.5	111
4839	Identification of immune response-related genes and signalling pathways in spleen of <i>Vibrio parahaemolyticus</i> -infected <i>Epinephelus fuscoguttatus</i> (Forsk.) by next-generation sequencing. <i>Journal of Fish Diseases</i> , 2016, 39, 389-394.	0.9	9
4840	Overlap between Signaling Pathways Responsive to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Infection and Drought Stress in Rice Introgression Line Revealed by RNA-Seq. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 345-356.	2.8	12
4841	Epigenetic Methods in Neuroscience Research. <i>Neuromethods</i> , 2016, , .	0.2	2
4842	Post-Transcriptional Gene Regulation. <i>Methods in Molecular Biology</i> , 2016, 1358, v-viii.	0.4	3

#	ARTICLE	IF	CITATIONS
4843	Hepatic Long Intergenic Noncoding RNAs: High Promoter Conservation and Dynamic, Sex-Dependent Transcriptional Regulation by Growth Hormone. <i>Molecular and Cellular Biology</i> , 2016, 36, 50-69.	1.1	39
4844	Mammalian Genome Plasticity: Expression Analysis of Transposable Elements. <i>Neuromethods</i> , 2016, , 163-174.	0.2	0
4845	Elevated $CO_2$ improves lipid accumulation by increasing carbon metabolism in <i>Chlorella sorokiniana</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 557-566.	4.1	72
4846	The identification and characterization of novel transcripts from RNA-seq data. <i>Briefings in Bioinformatics</i> , 2016, 17, 678-685.	3.2	32
4847	A Class-Information-Based Sparse Component Analysis Method to Identify Differentially Expressed Genes on RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 392-398.	1.9	19
4848	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. <i>Gene</i> , 2016, 575, 90-100.	1.0	10
4849	A Sparse Model Based Detection of Copy Number Variations From Exome Sequencing Data. <i>IEEE Transactions on Biomedical Engineering</i> , 2016, 63, 496-505.	2.5	5
4850	Transcriptome Sequencing Determined Flowering Pathway Genes in <i>Aechmea fasciata</i> Treated with Ethylene. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 316-329.	2.8	22
4851	Transcriptome-wide identification of <i>Camellia sinensis</i> WRKY transcription factors in response to temperature stress. <i>Molecular Genetics and Genomics</i> , 2016, 291, 255-269.	1.0	67
4852	Will solid-state drives accelerate your bioinformatics? In-depth profiling, performance analysis and beyond. <i>Briefings in Bioinformatics</i> , 2016, 17, 713-727.	3.2	12
4853	Comparison of Glomerular and Podocyte mRNA Profiles in Streptozotocin-Induced Diabetes. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 1006-1014.	3.0	37
4854	De novo assembly and characterization of global transcriptome of coconut palm ( <i>Cocos nucifera</i> L.) embryogenic calli using Illumina paired-end sequencing. <i>Protoplasma</i> , 2016, 253, 913-928.	1.0	50
4856	Statistical detection of differentially expressed genes based on RNA-seq: from biological to phylogenetic replicates. <i>Briefings in Bioinformatics</i> , 2016, 17, 243-248.	3.2	13
4857	Systematically evaluating interfaces for RNA-seq analysis from a life scientist perspective. <i>Briefings in Bioinformatics</i> , 2016, 17, 213-223.	3.2	23
4858	Elucidating the mechanisms of transcription regulation during heart development by next-generation sequencing. <i>Journal of Human Genetics</i> , 2016, 61, 5-12.	1.1	3
4859	Genome-wide characterization and expression analysis of common bean bHLH transcription factors in response to excess salt concentration. <i>Molecular Genetics and Genomics</i> , 2016, 291, 129-143.	1.0	82
4860	Combined venomomics, venom gland transcriptomics, bioactivities, and antivenomics of two <i>Bothrops jararaca</i> populations from geographic isolated regions within the Brazilian Atlantic rainforest. <i>Journal of Proteomics</i> , 2016, 135, 73-89.	1.2	110
4861	An atlas of gastric PIWI-interacting RNA transcriptomes and their utility for identifying signatures of gastric cancer recurrence. <i>Gastric Cancer</i> , 2016, 19, 660-665.	2.7	63

#	ARTICLE	IF	CITATIONS
4862	MTD: a mammalian transcriptomic database to explore gene expression and regulation. <i>Briefings in Bioinformatics</i> , 2017, 18, 28-36.	3.2	18
4863	Transcriptomic variation of pharmacogenes in multiple human tissues and lymphoblastoid cell lines. <i>Pharmacogenomics Journal</i> , 2017, 17, 137-145.	0.9	24
4864	Short Read Mapping: An Algorithmic Tour. <i>Proceedings of the IEEE</i> , 2017, 105, 436-458.	16.4	63
4865	Deep sequencing leads to the identification of eukaryotic translation initiation factor 5A as a key element in <i>Rsv1</i> -mediated lethal systemic hypersensitive response to Soybean mosaic virus infection in soybean. <i>Molecular Plant Pathology</i> , 2017, 18, 391-404.	2.0	25
4866	<i>VisExpress</i> : Visual exploration of differential gene expression data. <i>Information Visualization</i> , 2017, 16, 48-73.	1.2	5
4867	An in-depth comparison of the porcine, murine and human inflammasomes; lessons from the porcine genome and transcriptome. <i>Veterinary Microbiology</i> , 2017, 202, 2-15.	0.8	102
4868	Transcriptomic responses of mixed cultures of ascomycete fungi to lignocellulose using dual RNA-seq reveal inter-species antagonism and limited beneficial effects on CAZyme expression. <i>Fungal Genetics and Biology</i> , 2017, 102, 4-21.	0.9	36
4869	Human Mesenchymal Stem Cell Treatment Normalizes Cortical Gene Expression after Traumatic Brain Injury. <i>Journal of Neurotrauma</i> , 2017, 34, 204-212.	1.7	13
4870	Regulation of infection efficiency in a globally abundant marine <i>Bacteriodes</i> virus. <i>ISME Journal</i> , 2017, 11, 284-295.	4.4	40
4871	PBSeq: Modeling base-level bias to estimate gene and isoform expression for RNA-seq data. <i>International Journal of Machine Learning and Cybernetics</i> , 2017, 8, 1247-1258.	2.3	2
4872	Prediction of the <i>in planta</i> <i>Phakopsora pachyrhizi</i> secretome and potential effector families. <i>Molecular Plant Pathology</i> , 2017, 18, 363-377.	2.0	30
4873	De novo assembly of a tadpole shrimp ( <i>Triops newberryi</i> ) transcriptome and preliminary differential gene expression analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 161-171.	2.2	28
4874	A Statistical Method for Detecting Differentially Expressed SNVs Based on Next-Generation RNA-Seq Data. <i>Biometrics</i> , 2017, 73, 42-51.	0.8	2
4875	Going global: the new era of mapping modifications in <i>RNA</i> . <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1367.	3.2	55
4876	Transgenic cotton expressing <i>CYP392A4</i> double-stranded RNA decreases the reproductive ability of <i>Tetranychus cinnabarinus</i> . <i>Insect Science</i> , 2017, 24, 559-568.	1.5	18
4877	Characterization and analysis of a <i>de novo</i> transcriptome from the pygmy grasshopper <i>Tetrix japonica</i> . <i>Molecular Ecology Resources</i> , 2017, 17, 381-392.	2.2	33
4878	Two olfactory receptors <i>OR</i> 2A4/7 and <i>OR</i> 51B5 differentially affect epidermal proliferation and differentiation. <i>Experimental Dermatology</i> , 2017, 26, 58-65.	1.4	67
4879	Arabidopsis late blight: infection of a nonhost plant by <i>Albugo laibachii</i> enables full colonization by <i>Phytophthora infestans</i> . <i>Cellular Microbiology</i> , 2017, 19, e12628.	1.1	44

#	ARTICLE	IF	CITATIONS
4880	Large-scale gene expression reveals different adaptations of <i>Hyalopterus persikonus</i> to winter and summer host plants. <i>Insect Science</i> , 2017, 24, 431-442.	1.5	12
4881	Development of a multiple-hybrid population for genome-wide association studies: theoretical consideration and genetic mapping of flowering traits in maize. <i>Scientific Reports</i> , 2017, 7, 40239.	1.6	29
4882	A note on statistical repeatability and study design for high-throughput assays. <i>Statistics in Medicine</i> , 2017, 36, 790-798.	0.8	9
4883	Secretory pathway optimization of CHO producer cells by co-engineering of the mitochondrial RNA-1978 target genes <i>CerS2</i> and <i>Tbc1D20</i> . <i>Metabolic Engineering</i> , 2017, 40, 69-79.	3.6	22
4884	Differential Effects of Vitamins A and D on the Transcriptional Landscape of Human Monocytes during Infection. <i>Scientific Reports</i> , 2017, 7, 40599.	1.6	25
4885	High-throughput analysis reveals novel maternal germline RNAs crucial for primordial germ cell preservation and proper migration. <i>Development (Cambridge)</i> , 2017, 144, 292-304.	1.2	19
4886	Identification of ecdysteroid receptor-mediated signaling pathways in the hepatopancreas of the red swamp crayfish, <i>Procambarus clarkii</i> . <i>General and Comparative Endocrinology</i> , 2017, 246, 372-381.	0.8	14
4887	Plant toxin Î²-ODAP activates integrin Î²1 and focal adhesion: A critical pathway to cause neurolathyrism. <i>Scientific Reports</i> , 2017, 7, 40677.	1.6	18
4888	Decoding Crucial lncRNAs Implicated in Neurogenesis and Neurological Disorders. <i>Stem Cells and Development</i> , 2017, 26, 541-553.	1.1	16
4889	Antisense transcription of the myotonic dystrophy locus yields low-abundant RNAs with and without (CAG) <sub>n</sub> repeat. <i>RNA Biology</i> , 2017, 14, 1374-1388.	1.5	25
4890	Comparative RNA-seq based transcriptomic analysis of bud dormancy in grape. <i>BMC Plant Biology</i> , 2017, 17, 18.	1.6	87
4891	Application of Î²-glucuronidase ( <i>GusA</i> ) as an effective reporter for extremely acidophilic <i>Acidithiobacillus ferrooxidans</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3283-3294.	1.7	7
4892	LMM5.1 and LMM5.4, two eukaryotic translation elongation factor 1A-like gene family members, negatively affect cell death and disease resistance in rice. <i>Journal of Genetics and Genomics</i> , 2017, 44, 107-118.	1.7	22
4893	A joint-L2,1-norm-constraint-based semi-supervised feature extraction for RNA-Seq data analysis. <i>Neurocomputing</i> , 2017, 228, 263-269.	3.5	27
4894	Expression profile analysis of <i>Isoetes sinensis</i> in response to light-dark shift under terrestrial and submerged conditions. <i>Plant Gene</i> , 2017, 9, 26-33.	1.4	1
4895	Age influences the olfactory profiles of the migratory oriental armyworm <i>Mythimna separata</i> at the molecular level. <i>BMC Genomics</i> , 2017, 18, 32.	1.2	30
4896	Lineage-specific SoxR-mediated Regulation of an Endoribonuclease Protects Non-enteric Bacteria from Redox-active Compounds. <i>Journal of Biological Chemistry</i> , 2017, 292, 121-133.	1.6	19
4897	TCGA2BED: extracting, extending, integrating, and querying The Cancer Genome Atlas. <i>BMC Bioinformatics</i> , 2017, 18, 6.	1.2	33

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4898	Transcriptomic analysis of spleen infected with infectious salmon anemia virus reveals distinct pattern of viral replication on resistant and susceptible Atlantic salmon ( <i>Salmo salar</i> ). <i>Fish and Shellfish Immunology</i> , 2017, 61, 187-193.	1.6	40
4899	Emerging roles for RNA-binding proteins as effectors and regulators of cardiovascular disease. <i>European Heart Journal</i> , 2017, 38, ehw567.	1.0	94
4900	Small RNAome profiling from human skeletal muscle: novel miRNAs and their targets associated with cancer cachexia. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2017, 8, 405-416.	2.9	74
4901	Comparative genome-wide phylogenetic and expression analysis of SBP genes from potato ( <i>Solanum</i> ) Tj ETQq1 1 0,784314 rgBT /Overl P4	1.1	4
4902	Variant Ionotropic Receptors in the Malaria Vector Mosquito <i>Anopheles gambiae</i> Tuned to Amines and Carboxylic Acids. <i>Scientific Reports</i> , 2017, 7, 40297.	1.6	81
4903	GE-mini: a mobile APP for large-scale gene expression visualization. <i>Bioinformatics</i> , 2017, 33, 941-943.	1.8	27
4904	Transcriptome analysis of four poplars exposed to continuous salinity stress. <i>Biochemical Systematics and Ecology</i> , 2017, 70, 311-319.	0.6	4
4905	Gene expression patterns regulating embryogenesis based on the integrated de novo transcriptome assembly of the Japanese flounder. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 58-66.	0.4	3
4906	Cooperative Binding of Transcription Factors Orchestrates Reprogramming. <i>Cell</i> , 2017, 168, 442-459.e20.	13.5	432
4907	Comparative transcriptional survey between self-incompatibility and self-compatibility in <i>Citrus reticulata</i> Blanco. <i>Gene</i> , 2017, 609, 52-61.	1.0	12
4908	Ecotype diversification of an abundant <i>Roseobacter</i> lineage. <i>Environmental Microbiology</i> , 2017, 19, 1625-1638.	1.8	17
4909	Identification and evolutionary analysis of long non-coding RNAs in zebra finch. <i>BMC Genomics</i> , 2017, 18, 117.	1.2	13
4910	Transcriptomic and hormone analyses reveal mechanisms underlying petal elongation in <i>Chrysanthemum morifolium</i> 'Jinba'™. <i>Plant Molecular Biology</i> , 2017, 93, 593-606.	2.0	53
4911	Transcriptome profiling of the floating-leaved aquatic plant <i>Nymphoides peltata</i> in response to flooding stress. <i>BMC Genomics</i> , 2017, 18, 119.	1.2	8
4912	Comparative and integrative analysis of RNA structural profiling data: current practices and emerging questions. <i>Quantitative Biology</i> , 2017, 5, 3-24.	0.3	37
4913	Heme oxygenase 1 defects lead to reduced chlorophyll in <i>Brassica napus</i> . <i>Plant Molecular Biology</i> , 2017, 93, 579-592.	2.0	36
4914	DGE-seq analysis of MUR3-related <i>Arabidopsis</i> mutants provides insight into how dysfunctional xyloglucan affects cell elongation. <i>Plant Science</i> , 2017, 258, 156-169.	1.7	22
4915	A computational interactome for prioritizing genes associated with complex agronomic traits in rice ( <i>Oryza sativa</i> ). <i>Plant Journal</i> , 2017, 90, 177-188.	2.8	44

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4916	A PTK7-targeted antibody-drug conjugate reduces tumor-initiating cells and induces sustained tumor regressions. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	119
4917	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39
4918	Characterization of transcriptome and identification of biomineralization genes in winged pearl oyster ( <i>Pteria penguin</i> ) mantle tissue. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 67-76.	0.4	13
4919	Single-Cell Genomics: Approaches and Utility in Immunology. <i>Trends in Immunology</i> , 2017, 38, 140-149.	2.9	66
4920	Large-scale transcriptome comparison of sunflower genes responsive to <i>Verticillium dahliae</i> . <i>BMC Genomics</i> , 2017, 18, 42.	1.2	39
4921	Genome-wide analysis of p53-regulated transcription in Myc-driven lymphomas. <i>Oncogene</i> , 2017, 36, 2921-2929.	2.6	11
4922	Transcriptomic basis for drought-resistance in <i>Brassica napus</i> L.. <i>Scientific Reports</i> , 2017, 7, 40532.	1.6	63
4923	Blood RNA biomarkers in prodromal PARK4 and REM sleep behavior disorder show role of complexin-1 loss for risk of Parkinson's disease. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 619-631.	1.2	20
4924	Microarray Analysis of Hypertension. <i>Methods in Molecular Biology</i> , 2017, 1527, 41-52.	0.4	5
4925	Transcriptome sequencing analysis of porcine granulosa cells treated with an anti-inhibin antibody. <i>Reproductive Biology</i> , 2017, 17, 79-88.	0.9	6
4926	Integrated analysis of multiomic data reveals the role of the antioxidant network in the quality of sea buckthorn berry. <i>FASEB Journal</i> , 2017, 31, 1929-1938.	0.2	20
4927	Differentially expressed immune-related genes in hemocytes of the pearl oyster <i>Pinctada fucata</i> against allograft identified by transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2017, 62, 247-256.	1.6	39
4928	Identification of Brassinosteroid Target Genes by Chromatin Immunoprecipitation Followed by High-Throughput Sequencing (ChIP-seq) and RNA-Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1564, 63-79.	0.4	10
4929	Development of SNP markers using RNA-seq technology and tetra-primer ARMS-PCR in sweetpotato. <i>Journal of Integrative Agriculture</i> , 2017, 16, 464-470.	1.7	7
4930	Transcriptome analysis and identification of induced genes in the response of <i>Harmonia axyridis</i> to cold hardiness. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 78-89.	0.4	18
4931	Small RNA and mRNA Profiling of Arabidopsis in Response to Phytophthora Infection and PAMP Treatment. <i>Methods in Molecular Biology</i> , 2017, 1578, 273-283.	0.4	1
4932	Transcriptome analysis of the <i>Brassica napus</i> – <i>Leptosphaeria maculans</i> pathosystem identifies receptor, signaling and structural genes underlying plant resistance. <i>Plant Journal</i> , 2017, 90, 573-586.	2.8	89
4933	Transcriptomic profiling provides molecular insights into hydrogen peroxide-induced adventitious rooting in mung bean seedlings. <i>BMC Genomics</i> , 2017, 18, 188.	1.2	31

#	ARTICLE	IF	CITATIONS
4934	The genome of the protozoan parasite <i>Cystoisospora suis</i> and a reverse vaccinology approach to identify vaccine candidates. <i>International Journal for Parasitology</i> , 2017, 47, 189-202.	1.3	28
4935	Mechanism of H <sub>2</sub> S Oxidation by the Dissimilatory Perchlorate-Reducing Microorganism <i>Azospira suillum</i> PS. <i>MBio</i> , 2017, 8, .	1.8	66
4936	Mining Cancer Transcriptomes: Bioinformatic Tools and the Remaining Challenges. <i>Molecular Diagnosis and Therapy</i> , 2017, 21, 249-258.	1.6	13
4937	Histopathology combined with transcriptome analyses reveals the mechanism of resistance to <i>Meloidogyne incognita</i> in <i>Cucumis metuliferus</i> . <i>Journal of Plant Physiology</i> , 2017, 212, 115-124.	1.6	27
4938	The sRNAome mining revealed existence of unique signature small RNAs derived from 5.8SrRNA from <i>Piper nigrum</i> and other plant lineages. <i>Scientific Reports</i> , 2017, 7, 41052.	1.6	15
4939	Negative Autogenous Control of the Master Type III Secretion System Regulator HrpL in <i>Pseudomonas syringae</i> . <i>MBio</i> , 2017, 8, .	1.8	24
4940	Transcriptome of the floral transition in <i>Rosa chinensis</i> 'Old Blush'™. <i>BMC Genomics</i> , 2017, 18, 199.	1.2	36
4941	RNA-seq based detection of differentially expressed genes in the skeletal muscle of Duroc pigs with distinct lipid profiles. <i>Scientific Reports</i> , 2017, 7, 40005.	1.6	46
4942	Transcriptome profilings of two tall fescue ( <i>Festuca arundinacea</i> ) cultivars in response to lead (Pb) stress. <i>BMC Genomics</i> , 2017, 18, 145.	1.2	40
4943	Variant discovery in the sheep milk transcriptome using RNA sequencing. <i>BMC Genomics</i> , 2017, 18, 170.	1.2	44
4944	Molecular characterization of the C-glycosylation for puerarin biosynthesis in <i>Pueraria lobata</i> . <i>Plant Journal</i> , 2017, 90, 535-546.	2.8	86
4945	De novo sequencing and comparative transcriptome analysis of adventitious root development induced by exogenous indole-3-butyric acid in cuttings of tetraploid black locust. <i>BMC Genomics</i> , 2017, 18, 179.	1.2	27
4946	An atlas and analysis of bovine skeletal muscle long noncoding RNA's. <i>Animal Genetics</i> , 2017, 48, 278-286.	0.6	30
4947	Determination of dosage compensation and comparison of gene expression in a triploid hybrid fish. <i>BMC Genomics</i> , 2017, 18, 38.	1.2	22
4948	Heterozygous mutation of eEF1A1b resulted in spermatogenesis arrest and infertility in male tilapia, <i>Oreochromis niloticus</i> . <i>Scientific Reports</i> , 2017, 7, 43733.	1.6	30
4949	Comparative transcriptomic analysis of key genes involved in flavonoid biosynthetic pathway and identification of a flavonol synthase from <i>Artemisia annua</i> L.. <i>Plant Biology</i> , 2017, 19, 618-629.	1.8	14
4950	Identification, expression pattern, and feature analysis of cuticular protein genes in the pine moth <i>Dendrolimus punctatus</i> (Lepidoptera: Lasiocampidae). <i>Insect Biochemistry and Molecular Biology</i> , 2017, 83, 94-106.	1.2	46
4951	Inactivation of NMB0419 , Encoding a Sel1-Like Repeat (SLR) Protein, in <i>Neisseria meningitidis</i> Is Associated with Differential Expression of Genes Belonging to the Fur Regulon and Reduced Intraepithelial Replication. <i>Infection and Immunity</i> , 2017, 85, .	1.0	6



#	ARTICLE	IF	CITATIONS
4952	Transcriptome analysis reveals metabolic alteration due to consecutive monoculture and abiotic stress stimuli in <i>Rehmannia glutinosa</i> Libosch. <i>Plant Cell Reports</i> , 2017, 36, 859-875.	2.8	25
4953	RNA surveillance via nonsense-mediated mRNA decay is crucial for longevity in <i>daf-2/insulin/IGF-1</i> mutant <i>C. elegans</i> . <i>Nature Communications</i> , 2017, 8, 14749.	5.8	59
4954	ZntR positively regulates T6SS4 expression in <i>Yersinia pseudotuberculosis</i> . <i>Journal of Microbiology</i> , 2017, 55, 448-456.	1.3	20
4955	T-ALL and thymocytes: a message of noncoding RNAs. <i>Journal of Hematology and Oncology</i> , 2017, 10, 66.	6.9	24
4956	Comparison of transcriptional expression patterns of carotenoid metabolism in Cabernet Sauvignon™ grapes from two regions with distinct climate. <i>Journal of Plant Physiology</i> , 2017, 213, 75-86.	1.6	33
4957	Genome-wide screening and characterization of long non-coding RNAs involved in flowering development of trifoliate orange ( <i>Poncirus trifoliata</i> L. Raf.). <i>Scientific Reports</i> , 2017, 7, 43226.	1.6	41
4958	Identification of strong promoters based on the transcriptome of <i>Bacillus licheniformis</i> . <i>Biotechnology Letters</i> , 2017, 39, 873-881.	1.1	24
4959	Characterization of microRNAs in orange-spotted grouper ( <i>Epinephelus coioides</i> ) fin cells upon red-spotted grouper nervous necrosis virus infection. <i>Fish and Shellfish Immunology</i> , 2017, 63, 228-236.	1.6	49
4960	Whole-Genome Sequencing of a Family with Hereditary Pulmonary Alveolar Proteinosis Identifies a Rare Structural Variant Involving CSF2RA/CRLF2/IL3RA Gene Disruption. <i>Scientific Reports</i> , 2017, 7, 43469.	1.6	10
4961	ATF61-based fine-tuning of the unfolded protein response enhances therapeutic antibody productivity of Chinese hamster ovary cells. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1310-1318.	1.7	27
4962	Comparative transcriptome analysis of <i>Trueperella pyogenes</i> reveals a novel antimicrobial strategy. <i>Archives of Microbiology</i> , 2017, 199, 649-655.	1.0	10
4963	Transcriptional markers enable identification of rye-grass ( <i>Lolium</i> sp.) plants with non-target-site-based resistance to herbicides inhibiting acetolactate-synthase. <i>Plant Science</i> , 2017, 257, 22-36.	1.7	42
4964	Physiological and transcriptomic analyses reveal a response mechanism to cold stress in <i>Santalum album</i> L. leaves. <i>Scientific Reports</i> , 2017, 7, 42165.	1.6	58
4966	ABA Suppresses Root Hair Growth via the OBP4 Transcriptional Regulator. <i>Plant Physiology</i> , 2017, 173, 1750-1762.	2.3	67
4967	The function and transcriptome analysis of a bZIP transcription factor CgAP1 in <i>Colletotrichum gloeosporioides</i> . <i>Microbiological Research</i> , 2017, 197, 39-48.	2.5	24
4968	Transcriptome profiling of <i>Galaxea fascicularis</i> and its endosymbiont <i>Symbiodinium</i> reveals chronic eutrophication tolerance pathways and metabolic mutualism between partners. <i>Scientific Reports</i> , 2017, 7, 42100.	1.6	26
4969	Lethal Consequences of Overcoming Metabolic Restrictions Imposed on a Cooperative Bacterial Population. <i>MBio</i> , 2017, 8, .	1.8	17
4970	A study on regional differences in decidualization of the mouse uterus. <i>Reproduction</i> , 2017, 153, 645-653.	1.1	13

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4971	Metatranscriptomic Evidence for Direct Interspecies Electron Transfer between <i>Geobacter</i> and <i>Methanotrix</i> Species in Methanogenic Rice Paddy Soils. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	247
4972	Evolution and expression of the fructokinase gene family in <i>Saccharum</i> . <i>BMC Genomics</i> , 2017, 18, 197.	1.2	39
4973	De novo transcriptome and expression profile analyses of the Asian corn borer ( <i>Ostrinia furnacalis</i> ) reveals relevant flubendiamide response genes. <i>BMC Genomics</i> , 2017, 18, 20.	1.2	33
4974	Differentiation of ncRNAs from small mRNAs in <i>Escherichia coli</i> O157:H7 EDL933 (EHEC) by combined RNAseq and RIBOseq – <i>ryhB</i> encodes the regulatory RNA <i>RyhB</i> and a peptide, <i>RyhP</i> . <i>BMC Genomics</i> , 2017, 18, 216.	1.2	43
4975	A Whole-Transcriptome Approach to Evaluating Reference Genes for Quantitative Gene Expression Studies: A Case Study in <i>Mimulus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1085-1095.	0.8	23
4976	Novel Three-Component Phenazine-1-Carboxylic Acid 1,2-Dioxygenase in <i>Sphingomonas wittichii</i> DP58. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	11
4977	Comparative Transcriptomics of Malaria Mosquito Testes: Function, Evolution, and Linkage. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1127-1136.	0.8	9
4978	Genome-wide gene expression patterns in dikaryon of the basidiomycete fungus <i>Pleurotus ostreatus</i> . <i>Brazilian Journal of Microbiology</i> , 2017, 48, 380-390.	0.8	10
4979	Orthogonal Comparison of Molecular Signatures of Kidney Transplants With Subclinical and Clinical Acute Rejection: Equivalent Performance Is Agnostic to Both Technology and Platform. <i>American Journal of Transplantation</i> , 2017, 17, 2103-2116.	2.6	31
4980	The abundance of homoeologue transcripts is disrupted by hybridization and is partially restored by genome doubling in synthetic hexaploid wheat. <i>BMC Genomics</i> , 2017, 18, 149.	1.2	30
4981	Comparative transcriptome analysis provides insight into differentially expressed genes related to cytoplasmic male sterility in broccoli ( <i>Brassica oleracea</i> var. <i>italica</i> ). <i>Scientia Horticulturae</i> , 2017, 217, 234-242.	1.7	18
4982	Transcriptome analysis around the onset of strawberry fruit ripening uncovers an important role of oxidative phosphorylation in ripening. <i>Scientific Reports</i> , 2017, 7, 41477.	1.6	58
4983	Expression map of a complete set of gustatory receptor genes in chemosensory organs of <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 82, 74-82.	1.2	61
4984	An Overview of Next-Generation Sequencing (NGS) Technologies to Study the Molecular Diversity of Genome. , 2017, , 295-317.		1
4985	Nitrate application or P deficiency induce a decline in <i>Medicago truncatula</i> N <sub>2</sub> -fixation by similar changes in the nodule transcriptome. <i>Scientific Reports</i> , 2017, 7, 46264.	1.6	31
4986	Identification of regulatory networks and hub genes controlling soybean seed set and size using RNA sequencing analysis. <i>Journal of Experimental Botany</i> , 2017, 68, erw460.	2.4	105
4987	Finding Transcripts Associated with Prostate Cancer Gleason Stages Using Next Generation Sequencing and Machine Learning Techniques. <i>Lecture Notes in Computer Science</i> , 2017, , 337-348.	1.0	3
4988	RNA-sequencing and pathway analysis reveal alteration of hepatic steroid biosynthesis and retinol metabolism by tributyltin exposure in male rare minnow ( <i>Gobiocypris rarus</i> ). <i>Aquatic Toxicology</i> , 2017, 188, 109-118.	1.9	19

#	ARTICLE	IF	CITATIONS
4989	Network module-based model in the differential expression analysis for RNA-seq. <i>Bioinformatics</i> , 2017, 33, 2699-2705.	1.8	5
4990	H3K4 demethylase KDM5B regulates global dynamics of transcription elongation and alternative splicing in embryonic stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 6427-6441.	6.5	42
4991	Transcriptome analysis of comb and testis from Rose-comb Silky chicken (R1/R1) and Beijing Fatty wild type chicken (r/r). <i>Poultry Science</i> , 2017, 96, 1866-1873.	1.5	13
4992	RNA sequencing for global gene expression associated with muscle growth in a single male modern broiler line compared to a foundational Barred Plymouth Rock chicken line. <i>BMC Genomics</i> , 2017, 18, 82.	1.2	51
4993	Recessive male sterility in cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) caused by loss of function of BoCYP704B1 due to the insertion of a LTR-retrotransposon. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1441-1451.	1.8	29
4994	Analysis of global gene expression profiles during the flowering initiation process of <i>Lilium formolongi</i> . <i>Plant Molecular Biology</i> , 2017, 94, 361-379.	2.0	24
4995	The role of Next-Generation Sequencing in tumoral radiosensitivity prediction. <i>Clinical and Translational Radiation Oncology</i> , 2017, 3, 16-20.	0.9	10
4996	Evolutionary changes in lamin expression in the vertebrate lineage. <i>Nucleus</i> , 2017, 8, 392-403.	0.6	4
4998	Comparative Transcriptome Analysis of Three <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) Organs to Identify Functional Genes in the Male Accessory Glands and Ejaculatory Duct. <i>Florida Entomologist</i> , 2017, 100, 42-51.	0.2	11
4999	miRCat2: accurate prediction of plant and animal microRNAs from next-generation sequencing datasets. <i>Bioinformatics</i> , 2017, 33, 2446-2454.	1.8	49
5000	Characterization of transcriptome in the Indian meal moth <i>Plodia interpunctella</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342	1.0	22
5001	Transcriptome Profiling Reveals the Important Role of Exogenous Nitrogen in Alleviating Cadmium Toxicity in Poplar Plants. <i>Journal of Plant Growth Regulation</i> , 2017, 36, 942-956.	2.8	11
5002	Transcriptomic responses to conspecific and congeneric competition in co-occurring <i>Trifolium</i> . <i>Journal of Ecology</i> , 2017, 105, 602-615.	1.9	27
5003	Transcriptome Dynamics of Dominant Maize Dwarf Dwarf11 (D11) Revealed by RNA-seq and Co-expression Analysis. <i>Plant Molecular Biology Reporter</i> , 2017, 35, 355-365.	1.0	1
5004	Identifying Novel Transcriptional and Epigenetic Features of Nuclear Lamina-associated Genes. <i>Scientific Reports</i> , 2017, 7, 100.	1.6	30
5005	<i>N</i> -acetylhomoserine lactone regulation of genes mediating motility and pathogenicity in <i>Pseudomonas syringae</i> pathovar <i>tabaci</i> 11528. <i>MicrobiologyOpen</i> , 2017, 6, e00440.	1.2	9
5006	Differential gene responses in the embryo of the green mussel <i>Perna viridis</i> exposed to dichlorodiphenyltrichloroethane (DDT). <i>Toxicology Research</i> , 2017, 6, 477-486.	0.9	7
5007	Gain-of-function p53 activates multiple signaling pathways to induce oncogenicity in lung cancer cells. <i>Molecular Oncology</i> , 2017, 11, 696-711.	2.1	15

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5008	Transposable elements in the <i>Anopheles funestus</i> transcriptome. <i>Genetica</i> , 2017, 145, 275-293.	0.5	6
5009	High-Throughput Sequencing and Co-Expression Network Analysis of lncRNAs and mRNAs in Early Brain Injury Following Experimental Subarachnoid Haemorrhage. <i>Scientific Reports</i> , 2017, 7, 46577.	1.6	42
5010	Comparative transcript profiling of fertile and sterile flower buds from multiple-allele-inherited male sterility in Chinese cabbage ( <i>Brassica campestris</i> L. ssp. <i>pekinensis</i> ). <i>Molecular Genetics and Genomics</i> , 2017, 292, 967-990.	1.0	25
5011	Brownian model of transcriptome evolution and phylogenetic network visualization between tissues. <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 34-39.	1.2	5
5012	Transcriptomic analysis of porcine PBMCs in response to FMDV infection. <i>Acta Tropica</i> , 2017, 173, 69-75.	0.9	12
5013	Acot1 is a sensitive indicator for PPAR $\alpha$ activation after perfluorooctanoic acid exposure in primary hepatocytes of Sprague-Dawley rats. <i>Toxicology in Vitro</i> , 2017, 42, 299-307.	1.1	8
5014	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571.	9.0	405
5015	The prohibitin-repressive interaction with E2F1 is rapidly inhibited by androgen signalling in prostate cancer cells. <i>Oncogenesis</i> , 2017, 6, e333-e333.	2.1	18
5016	Comparative transcriptomics in human and mouse. <i>Nature Reviews Genetics</i> , 2017, 18, 425-440.	7.7	168
5017	Metabolic Flux Redirection and Transcriptomic Reprogramming in the Albino Tea Cultivar ‘Yu-Jin-Xiang’™ with an Emphasis on Catechin Production. <i>Scientific Reports</i> , 2017, 7, 45062.	1.6	55
5018	Identification and characterization of the glucose dual-affinity transport system in <i>Neurospora crassa</i> : pleiotropic roles in nutrient transport, signaling, and carbon catabolite repression. <i>Biotechnology for Biofuels</i> , 2017, 10, 17.	6.2	73
5019	Digital gene expression profiling of flax ( <i>Linum usitatissimum</i> L.) stem peel identifies genes enriched in fiber-bearing phloem tissue. <i>Gene</i> , 2017, 626, 32-40.	1.0	23
5020	Benchmarking of RNA-sequencing analysis workflows using whole-transcriptome RT-qPCR expression data. <i>Scientific Reports</i> , 2017, 7, 1559.	1.6	247
5021	Environment-dependent regulation of spliceosome activity by the LSM2-8 complex in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2017, 45, 7416-7431.	6.5	36
5022	UV-B Inhibits Leaf Growth through Changes in Growth Regulating Factors and Gibberellin Levels. <i>Plant Physiology</i> , 2017, 174, 1110-1126.	2.3	79
5023	Comparative transcriptomic analysis of <i>Gardnerella vaginalis</i> biofilms vs. planktonic cultures using RNA-seq. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 3.	2.9	66
5024	Genome of <i>Paulownia</i> ( <i>Paulownia fortunei</i> ) illuminates the related transcripts, miRNA and proteins for salt resistance. <i>Scientific Reports</i> , 2017, 7, 1285.	1.6	13
5025	A Fluorescence in Situ Hybridization Method To Quantify mRNA Translation by Visualizing Ribosome-mRNA Interactions in Single Cells. <i>ACS Central Science</i> , 2017, 3, 425-433.	5.3	27

#	ARTICLE	IF	CITATIONS
5026	SigSeeker: a peak-calling ensemble approach for constructing epigenetic signatures. <i>Bioinformatics</i> , 2017, 33, 2615-2621.	1.8	6
5027	Differential expression analysis for RNAseq using Poisson mixed models. <i>Nucleic Acids Research</i> , 2017, 45, e106-e106.	6.5	60
5028	The specific problems of the experimental design in the high-throughput sequencing studies of transcriptome. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 258-265.	0.4	0
5029	Differential Retention of Gene Functions in a Secondary Metabolite Cluster. <i>Molecular Biology and Evolution</i> , 2017, 34, 2002-2015.	3.5	41
5030	Assessment of Single Cell RNA-Seq Normalization Methods. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2039-2045.	0.8	10
5031	The UEA Small RNA Workbench: A Suite of Computational Tools for Small RNA Analysis. <i>Methods in Molecular Biology</i> , 2017, 1580, 193-224.	0.4	32
5032	The significant expression of TRPV3 in nasal polyps of eosinophilic chronic rhinosinusitis. <i>Allergy International</i> , 2017, 66, 610-616.	1.4	11
5033	<i>Aspergillus flavus</i> aswA , a gene homolog of <i>Aspergillus nidulans</i> oefC , regulates sclerotial development and biosynthesis of sclerotium-associated secondary metabolites. <i>Fungal Genetics and Biology</i> , 2017, 104, 29-37.	0.9	23
5034	Transcriptome-Based Identification of the Desiccation Response Genes in Marine Red Algae <i>Pyropia tenera</i> (Rhodophyta) and Enhancement of Abiotic Stress Tolerance by PtDRG2 in <i>Chlamydomonas</i> . <i>Marine Biotechnology</i> , 2017, 19, 232-245.	1.1	33
5035	Transcriptome profile analysis of cadmium tolerance in Chinese flowering cabbage. <i>Horticulture Environment and Biotechnology</i> , 2017, 58, 56-65.	0.7	8
5036	Transcriptomics of Meat Quality. , 2017, , 259-320.		11
5037	Transcriptome profiling of sulfate deprivation responses in two agarophytes <i>Gracilaria changii</i> and <i>Gracilaria salicornia</i> (Rhodophyta). <i>Scientific Reports</i> , 2017, 7, 46563.	1.6	15
5038	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	3.5	157
5039	High-Dimensional Profiling for Computational Diagnosis. <i>Methods in Molecular Biology</i> , 2017, 1526, 205-229.	0.4	2
5040	The Role of the Histone Methyltransferase Enhancer of Zeste Homolog 2 (EZH2) in the Pathobiological Mechanisms Underlying Inflammatory Bowel Disease (IBD). <i>Journal of Biological Chemistry</i> , 2017, 292, 706-722.	1.6	59
5041	Differential gene expression and filamentation of <i>Listeria monocytogenes</i> 08-5923 exposed to sodium lactate and sodium diacetate. <i>Food Microbiology</i> , 2017, 63, 153-158.	2.1	21
5042	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017, 120, 341-353.	2.0	166
5043	Transcriptome Architecture of Adult Mouse Brain Revealed by Sparse Coding of Genome-Wide In Situ Hybridization Images. <i>Neuroinformatics</i> , 2017, 15, 285-295.	1.5	8

#	ARTICLE	IF	CITATIONS
5044	Coordinated circRNA Biogenesis and Function with NF90/NF110 in Viral Infection. <i>Molecular Cell</i> , 2017, 67, 214-227.e7.	4.5	533
5045	Integrated gene expression profiling and chromatin immunoprecipitation followed by sequencing: Analysis of the C-terminal binding protein in breast cancer. <i>Journal of Obstetrics and Gynaecology Research</i> , 2017, 43, 1472-1480.	0.6	2
5046	A Comparative Transcriptomic Analysis of Development in Two <i>Astyanax</i> Cavefish Populations. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 515-532.	0.6	37
5047	Comparative analysis of pre- and post-parasitic transcriptomes and mining pioneer effectors of <i>Heterodera avenae</i> . <i>Cell and Bioscience</i> , 2017, 7, 11.	2.1	33
5048	Multidimensional Genetic Analysis of Repeated Seizures in the Hybrid Mouse Diversity Panel Reveals a Novel Epileptogenesis Susceptibility Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2545-2558.	0.8	13
5049	Mitochondria-Associated Apoptosis in Human Melanoma Cells Induced by Cardanol Monoene from Cashew Nut Shell Liquid. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 5620-5631.	2.4	18
5050	Lipid production in <i>Nannochloropsis gaditana</i> is doubled by decreasing expression of a single transcriptional regulator. <i>Nature Biotechnology</i> , 2017, 35, 647-652.	9.4	349
5051	Expression profiles of a cytoplasmic male sterile line of <i>Gossypium harknessii</i> and its fertility restorer and maintainer lines revealed by RNA-Seq. <i>Plant Physiology and Biochemistry</i> , 2017, 116, 106-115.	2.8	8
5052	MicroRNAs that affect the Fanconi Anemia/BRCA pathway are downregulated in imatinib-resistant chronic myeloid leukemia patients without detectable BCR-ABL kinase domain mutations. <i>Leukemia Research</i> , 2017, 59, 32-40.	0.4	11
5053	Transcriptome analysis on the exoskeleton formation in early developmental stages and reconstruction scenario in growth-moulting in <i>Litopenaeus vannamei</i> . <i>Scientific Reports</i> , 2017, 7, 1098.	1.6	33
5054	Dissecting molecular and physiological response mechanisms to high solar radiation in cyanic and acyanic leaves: a case study on red and green basil. <i>Journal of Experimental Botany</i> , 2017, 68, 2425-2437.	2.4	42
5055	Transcriptome Profiling of Wheat Inflorescence Development from Spikelet Initiation to Floral Patterning Identified Stage-Specific Regulatory Genes. <i>Plant Physiology</i> , 2017, 174, 1779-1794.	2.3	121
5056	Transcriptome analysis of <i>Spodoptera frugiperda</i> 9 (Sf9) cells infected with baculovirus, AcMNPV or AcMNPV-BmK IT. <i>Biotechnology Letters</i> , 2017, 39, 1129-1139.	1.1	19
5057	Comparative transcriptome analysis of sweet corn seedlings under low-temperature stress. <i>Crop Journal</i> , 2017, 5, 396-406.	2.3	21
5058	Antennal and abdominal transcriptomes reveal chemosensory gene families in the coconut hispine beetle, <i>Brontispa longissima</i> . <i>Scientific Reports</i> , 2017, 7, 2809.	1.6	24
5059	Integrated analysis and transcript abundance modelling of H3K4me3 and H3K27me3 in developing secondary xylem. <i>Scientific Reports</i> , 2017, 7, 3370.	1.6	32
5060	Do changes in gene expression contribute to sexual isolation and reinforcement in the house mouse?. <i>Molecular Ecology</i> , 2017, 26, 5189-5202.	2.0	18
5061	Overexpression of <i>Lsi1</i> in cold-sensitive rice mediates transcriptional regulatory networks and enhances resistance to chilling stress. <i>Plant Science</i> , 2017, 262, 115-126.	1.7	41

#	ARTICLE	IF	CITATIONS
5062	Pseudoalignment for metagenomic read assignment. <i>Bioinformatics</i> , 2017, 33, 2082-2088.	1.8	69
5063	Metatranscriptomics Supports the Mechanism for Biocathode Electroautotrophy by <i>Candidatus</i> <i>Tenderia electrophaga</i> . <i>MSystems</i> , 2017, 2, .	1.7	54
5064	GRIK3: A novel oncogenic protein related to tumor TNM stage, lymph node metastasis, and poor prognosis of GC. <i>Tumor Biology</i> , 2017, 39, 101042831770436.	0.8	13
5065	Different exogenous sugars affect the hormone signal pathway and sugar metabolism in <i>Red Globe</i> ( <i>Vitis vinifera</i> L.) plantlets grown in vitro as shown by transcriptomic analysis. <i>Planta</i> , 2017, 246, 537-552.	1.6	15
5066	Exploring the heat-responsive chaperones and microsatellite markers associated with terminal heat stress tolerance in developing wheat. <i>Functional and Integrative Genomics</i> , 2017, 17, 621-640.	1.4	15
5067	Functional and molecular responses of the blue mussel <i>Mytilus edulis</i> ' hemocytes exposed to cadmium - An <i>In Vitro</i> model and transcriptomic approach. <i>Fish and Shellfish Immunology</i> , 2017, 67, 575-585.	1.6	44
5068	Recognition of long-range enhancer-promoter interactions by adding genomic signatures of segmented regulatory regions. <i>Genomics</i> , 2017, 109, 341-352.	1.3	15
5069	Bioinformatic analysis of bacteria and host cell dual RNA-sequencing experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1115-1129.	3.2	16
5070	Gene dispersion is the key determinant of the read count bias in differential expression analysis of RNA-seq data. <i>BMC Genomics</i> , 2017, 18, 408.	1.2	21
5071	BMP signaling orchestrates a transcriptional network to control the fate of mesenchymal stem cells in mice. <i>Development (Cambridge)</i> , 2017, 144, 2560-2569.	1.2	57
5072	Functional annotation and analysis of the <i>Ornithodoros moubata</i> midgut genes differentially expressed after blood feeding. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 693-708.	1.1	34
5073	Comparative transcriptome analysis of <i>Rimicaris</i> sp. reveals novel molecular features associated with survival in deep-sea hydrothermal vent. <i>Scientific Reports</i> , 2017, 7, 2000.	1.6	28
5074	The draft genome of blunt snout bream ( <i>Megalobrama amblycephala</i> ) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
5075	Comprehensive discovery of subsample gene expression components by information explanation: therapeutic implications in cancer. <i>BMC Medical Genomics</i> , 2017, 10, 12.	0.7	18
5076	A Joint Bayesian Model for Integrating Microarray and RNA Sequencing Transcriptomic Data. <i>Journal of Computational Biology</i> , 2017, 24, 647-662.	0.8	23
5077	De novo assembly and analysis of the <i>Pugionium cornutum</i> (L.) Gaertn. transcriptome and identification of genes involved in the drought response. <i>Gene</i> , 2017, 626, 290-297.	1.0	16
5078	Transcriptome profiling of the <i>Macrobrachium rosenbergii</i> lymphoid organ under the white spot syndrome virus challenge. <i>Fish and Shellfish Immunology</i> , 2017, 67, 27-39.	1.6	38
5079	Chd2 regulates chromatin for proper gene expression toward differentiation in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2017, 45, 8758-8772.	6.5	31

#	ARTICLE	IF	CITATIONS
5080	A Tripeptidyl peptidase 1 is a binding partner of GPHR (Golgi pH regulator) in <i>Dictyostelium</i> . <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 897-907.	1.2	22
5081	Absence of juvenile hormone signalling regulates the dynamic expression profiles of nutritional metabolism genes during diapause preparation in the cabbage beetle <i>Colaphellus bowringi</i> . <i>Insect Molecular Biology</i> , 2017, 26, 530-542.	1.0	33
5082	Gene expression analysis of bovine embryonic disc, trophoblast and parietal hypoblast at the start of gastrulation. <i>Zygote</i> , 2017, 25, 265-278.	0.5	19
5083	Drug-seeking motivation level in male rats determines offspring susceptibility or resistance to cocaine-seeking behaviour. <i>Nature Communications</i> , 2017, 8, 15527.	5.8	70
5084	Metabolic network analysis reveals microbial community interactions in anammox granules. <i>Nature Communications</i> , 2017, 8, 15416.	5.8	489
5085	Single-Cell RNA Sequencing Reveals Expanded Clones of Islet Antigen-Reactive CD4+ T Cells in Peripheral Blood of Subjects with Type 1 Diabetes. <i>Journal of Immunology</i> , 2017, 199, 323-335.	0.4	62
5086	<i>Phylogenomics.</i> , 2017, , .		47
5087	Time-Resolved Proteomics Extends Ribosome Profiling-Based Measurements of Protein Synthesis Dynamics. <i>Cell Systems</i> , 2017, 4, 636-644.e9.	2.9	62
5088	EST-SSR marker development and transcriptome sequencing analysis of different tissues of Korean pine ( <i>Pinus koraiensis</i> Sieb. et Zucc.). <i>Biotechnology and Biotechnological Equipment</i> , 0, , 1-11.	0.5	10
5089	Bayesian Inference of Allele-Specific Gene Expression Indicates Abundant Cis-Regulatory Variation in Natural Flycatcher Populations. <i>Genome Biology and Evolution</i> , 2017, 9, 1266-1279.	1.1	22
5090	Triterpenoid biosynthesis and the transcriptional response elicited by nitric oxide in submerged fermenting <i>Ganoderma lucidum</i> . <i>Process Biochemistry</i> , 2017, 60, 19-26.	1.8	21
5091	Identification of the elementary structural units of the DNA damage response. <i>Nature Communications</i> , 2017, 8, 15760.	5.8	141
5092	Long non-coding RNAs in aging organs and tissues. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2017, 44, 30-37.	0.9	19
5093	Transcriptome analysis of the immune reaction of the pearl oyster <i>Pinctada fucata</i> to xenograft from <i>Pinctada maxima</i> . <i>Fish and Shellfish Immunology</i> , 2017, 67, 331-345.	1.6	29
5094	Effects of drought stress on global gene expression profile in leaf and root samples of Dongxiang wild rice ( <i>Oryza rufipogon</i> ). <i>Bioscience Reports</i> , 2017, 37, .	1.1	29
5095	A Bayesian mixture model for clustering and selection of feature occurrence rates under mean constraints. <i>Statistical Analysis and Data Mining</i> , 2017, 10, 393-409.	1.4	19
5096	Comparative Transcriptomic Analysis of Vernalization- and Cytokinin-Induced Floral Transition in <i>Dendrobium nobile</i> . <i>Scientific Reports</i> , 2017, 7, 45748.	1.6	22
5097	A Survey of Bioinformatics-Based Tools in RNA-Sequencing (RNA-Seq) Data Analysis. <i>Translational Medicine Research</i> , 2017, , 223-248.	0.0	3



#	ARTICLE	IF	CITATIONS
5098	MicroRNAs Associated with Caste Determination and Differentiation in a Primitively Eusocial Insect. <i>Scientific Reports</i> , 2017, 7, 45674.	1.6	32
5099	Unravelling the genetics of inherited retinal dystrophies: Past, present and future. <i>Progress in Retinal and Eye Research</i> , 2017, 59, 53-96.	7.3	85
5100	Placental Up-Regulation of Leptin and ARMS2 is Associated with Growth Discordance in Monochorionic Diamniotic Twin Pregnancies. <i>Twin Research and Human Genetics</i> , 2017, 20, 169-179.	0.3	6
5101	On the design and prospects of direct RNA sequencing. <i>Briefings in Functional Genomics</i> , 2017, 16, 326-335.	1.3	18
5102	Different expression patterns of sperm motility-related genes in testis of diploid and tetraploid cyprinid fish. <i>Biology of Reproduction</i> , 2017, 96, 907-920.	1.2	21
5103	A Direct Test of Selection in Cell Populations Using the Diversity in Gene Expression within Tumors. <i>Molecular Biology and Evolution</i> , 2017, 34, 1730-1742.	3.5	9
5105	A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments. <i>BMC Bioinformatics</i> , 2017, 18, 43.	1.2	23
5106	Characterization of Leaf Transcriptome in <i>Banksia hookeriana</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 49-56.	3.0	14
5107	Comprehensive analysis of differentially expressed genes under salt stress in pear ( <i>Pyrus betulaefolia</i> ) using RNA-Seq. <i>Plant Growth Regulation</i> , 2017, 82, 409-420.	1.8	13
5108	Comparative transcriptome analysis of berry-sizing effects of gibberellin (GA3) on seedless <i>Vitis vinifera</i> L. <i>Genes and Genomics</i> , 2017, 39, 493-507.	0.5	14
5109	De novo sequencing and comparative analysis of leaf transcriptomes of diverse condensed tannin-containing lines of underutilized <i>Psophocarpus tetragonolobus</i> (L.) DC. <i>Scientific Reports</i> , 2017, 7, 44733.	1.6	20
5110	Expression profiling in <i>Pinus radiata</i> infected with <i>Fusarium circinatum</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	31
5111	Enzyme IANtr Regulates Salmonella Invasion Via 1,2-Propanediol And Propionate Catabolism. <i>Scientific Reports</i> , 2017, 7, 44827.	1.6	22
5112	Large-scale gene network analysis reveals the significance of extracellular matrix pathway and homeobox genes in acute myeloid leukemia: an introduction to the Pigengene package and its applications. <i>BMC Medical Genomics</i> , 2017, 10, 16.	0.7	34
5113	Carfilzomib induces leukaemia cell apoptosis via inhibiting <sc>ELK</sc>1</sc> and activating <sc>PP</sc>2A not related to proteasome inhibition. <i>British Journal of Haematology</i> , 2017, 177, 726-740.	1.2	9
5115	Comprehensive processing of high-throughput small RNA sequencing data including quality checking, normalization, and differential expression analysis using the UEA sRNA Workbench. <i>Rna</i> , 2017, 23, 823-835.	1.6	29
5116	Comprehensive Analysis of R2R3-MYB Genes During Adventitious Root Formation in Cuttings of <i>Morus alba</i> . <i>Journal of Plant Growth Regulation</i> , 2017, 36, 290-299.	2.8	8
5117	Identification and expression analysis of WRKY transcription factor genes in response to fungal pathogen and hormone treatments in apple ( <i>Malus domestica</i> ). <i>Journal of Plant Biology</i> , 2017, 60, 215-230.	0.9	36

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5118	Clinical Next-Generation Sequencing. , 2017, , 35-54.		1
5119	Characterization of <i>Brucella abortus</i> mutant strain $\hat{\Gamma}$ 22915, a potential vaccine candidate. <i>Veterinary Research</i> , 2017, 48, 17.	1.1	27
5120	<i>Arabidopsis</i> Transcription Factors SPL1 and SPL12 Confer Plant Thermotolerance at Reproductive Stage. <i>Molecular Plant</i> , 2017, 10, 735-748.	3.9	133
5121	Elucidating fish oil-induced milk fat depression in dairy sheep: Milk somatic cell transcriptome analysis. <i>Scientific Reports</i> , 2017, 7, 45905.	1.6	18
5122	FUNNEL-GSEA: FUNctioNal ELastic-net regression in time-course gene set enrichment analysis. <i>Bioinformatics</i> , 2017, 33, 1944-1952.	1.8	27
5123	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47
5124	Molecular identification of differential expression genes associated with sex pheromone biosynthesis in <i>Spodoptera exigua</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 795-809.	1.0	21
5125	Responses of gonadal transcriptome and physiological analysis following exposure to 17 $\beta$ -ethynylestradiol in adult rare minnow <i>Gobiocypris rarus</i> . <i>Ecotoxicology and Environmental Safety</i> , 2017, 141, 209-215.	2.9	17
5126	Transcriptomic analysis of two <i>Beauveria bassiana</i> strains grown on cuticle extracts of the silkworm uncovers their different metabolic response at early infection stage. <i>Journal of Invertebrate Pathology</i> , 2017, 145, 45-54.	1.5	23
5127	Mutations in <i>Argonaute5</i> Illuminate Epistatic Interactions of the <i>K1</i> and <i>I1</i> Loci Leading to Saddle Seed Color Patterns in <i>Glycine max</i> . <i>Plant Cell</i> , 2017, 29, 708-725.	3.1	51
5128	Transcriptome analysis of bagging-treated red Chinese sand pear peels reveals light-responsive pathway functions in anthocyanin accumulation. <i>Scientific Reports</i> , 2017, 7, 63.	1.6	67
5129	Transcriptome analysis of molecular mechanisms responsible for light-stress response in <i>Mythimna separata</i> (Walker). <i>Scientific Reports</i> , 2017, 7, 45188.	1.6	28
5130	GFFview: A Web Server for Parsing and Visualizing Annotation Information of Eukaryotic Genome. <i>Journal of Computational Biology</i> , 2017, 24, 1060-1064.	0.8	0
5131	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. <i>Cell Systems</i> , 2017, 4, 416-429.e3.	2.9	105
5132	Formation of (E)-nerolidol in tea ( <i>Camellia sinensis</i> ) leaves exposed to multiple stresses during tea manufacturing. <i>Food Chemistry</i> , 2017, 231, 78-86.	4.2	140
5133	Physiological investigation of C 4 -phosphoenolpyruvate-carboxylase-introduced rice line shows that sucrose metabolism is involved in the improved drought tolerance. <i>Plant Physiology and Biochemistry</i> , 2017, 115, 328-342.	2.8	28
5134	StMYB44 negatively regulates phosphate transport by suppressing expression of PHOSPHATE1 in potato. <i>Journal of Experimental Botany</i> , 2017, 68, 1265-1281.	2.4	78
5135	Spatial transcriptome analysis provides insights of key gene(s) involved in steroidal saponin biosynthesis in medicinally important herb <i>Trillium govanianum</i> . <i>Scientific Reports</i> , 2017, 7, 45295.	1.6	48

#	ARTICLE	IF	CITATIONS
5136	Transcriptomics and proteomic studies reveal acaricidal mechanism of octadecanoic acid-3, 4 - tetrahydrofuran diester against <i>Sarcoptes scabiei</i> var. <i>cuniculi</i> . <i>Scientific Reports</i> , 2017, 7, 45479.	1.6	20
5137	De novo transcriptome sequencing and analysis of the juvenile and adult stages of <i>Fasciola gigantica</i> . <i>Infection, Genetics and Evolution</i> , 2017, 51, 33-40.	1.0	18
5138	Hybrid sequencing and map finding (HySeMaFi): optional strategies for extensively deciphering gene splicing and expression in organisms without reference genome. <i>Scientific Reports</i> , 2017, 7, 43793.	1.6	24
5139	Inhibition of Pol I transcription treats murine and human AML by targeting the leukemia-initiating cell population. <i>Blood</i> , 2017, 129, 2882-2895.	0.6	74
5140	The Platelet Transcriptome: Coding RNAs. , 2017, , 227-238.		2
5141	Evaluation of two public genome references for chinese hamster ovary cells in the context of rna-seq based gene expression analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1603-1613.	1.7	12
5142	Extracting Genes Involved in Disease from a Connected Network of Perturbed Biological Processes. <i>Journal of Computational Biology</i> , 2017, 24, 460-469.	0.8	1
5143	Complementary transcriptomic and proteomic analyses reveal regulatory mechanisms of milk protein production in dairy cows consuming different forages. <i>Scientific Reports</i> , 2017, 7, 44234.	1.6	29
5144	Single-Cell Transcriptional Analysis. <i>Annual Review of Analytical Chemistry</i> , 2017, 10, 439-462.	2.8	93
5145	Transcriptional sequencing and analysis of major genes involved in the adventitious root formation of mango cotyledon segments. <i>Planta</i> , 2017, 245, 1193-1213.	1.6	13
5146	Differential gene expression analysis of "Chili"™ ( <i>Pyrus bretschneideri</i> ) fruit pericarp with two types of bagging treatments. <i>Horticulture Research</i> , 2017, 4, 17005.	2.9	25
5147	ChpA Controls Twitching Motility and Broadly Affects Gene Expression in the Biological Control Agent <i>Lysobacter enzymogenes</i> . <i>Current Microbiology</i> , 2017, 74, 566-574.	1.0	10
5148	RNA-seq analysis reveals a key role of brassinolide-regulated pathways in NaCl-stressed cotton. <i>Biologia Plantarum</i> , 2017, 61, 667-674.	1.9	5
5149	Considerations and complications of mapping small RNA high-throughput data to transposable elements. <i>Mobile DNA</i> , 2017, 8, 3.	1.3	11
5150	Comparative transcriptomics analyses of the different growth states of multidrug-resistant <i>Acinetobacter baumannii</i> . <i>Biomedicine and Pharmacotherapy</i> , 2017, 85, 564-574.	2.5	9
5151	Transcriptomic profiles of striped snakehead fish cells (SSN-1) infected with red-spotted grouper nervous necrosis virus (RGNNV) with an emphasis on apoptosis pathway. <i>Fish and Shellfish Immunology</i> , 2017, 60, 346-354.	1.6	43
5152	NanoString, a novel digital color-coded barcode technology: current and future applications in molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2017, 17, 95-103.	1.5	111
5153	Differential gene expression in the endometrium reveals cytoskeletal and immunological genes in lactating dairy cows genetically divergent for fertility traits. <i>Reproduction, Fertility and Development</i> , 2017, 29, 274.	0.1	55

#	ARTICLE	IF	CITATIONS
5154	Double-stranded RNA-binding protein DRB3 negatively regulates anthocyanin biosynthesis by modulating PAP1 expression in <i>Arabidopsis thaliana</i> . <i>Journal of Plant Research</i> , 2017, 130, 45-55.	1.2	9
5155	Transcriptomic alterations in <i>Sitophilus zeamais</i> in response to allyl isothiocyanate fumigation. <i>Pesticide Biochemistry and Physiology</i> , 2017, 137, 62-70.	1.6	14
5156	Gene expression profiling of U2AF2 dependent RNA-protein interactions during CD4 + T cell activation. <i>Genomics Data</i> , 2017, 11, 77-80.	1.3	4
5157	Comprehensive analysis of differently expressed genes and proteins in albino and green plantlets from a wheat anther culture. <i>Biologia Plantarum</i> , 2017, 61, 255-265.	1.9	11
5158	5-hydroxytryptamine synthesized in the aorta-gonad-mesonephros regulates hematopoietic stem and progenitor cell survival. <i>Journal of Experimental Medicine</i> , 2017, 214, 529-545.	4.2	27
5159	Unique Transcriptional Programs Identify Subtypes of AKI. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 1729-1740.	3.0	93
5160	HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2017, 45, D408-D414.	6.5	401
5161	The molecular response of the white-rot fungus <i>Dichomitus squalens</i> to wood and non-woody biomass as examined by transcriptome and exoproteome analyses. <i>Environmental Microbiology</i> , 2017, 19, 1237-1250.	1.8	55
5162	Transcriptome Analysis of Sugarcane Response to the Infection by Sugarcane Steak Mosaic Virus (SCSMV). <i>Tropical Plant Biology</i> , 2017, 10, 45-55.	1.0	21
5163	Transcriptome analysis reveals critical genes and key pathways involved in early phyllotaxy development in maize. <i>Genes and Genomics</i> , 2017, 39, 15-26.	0.5	1
5164	De novo transcriptome analysis reveals insights into different mechanisms of growth and immunity in a Chinese soft-shelled turtle hybrid and the parental varieties. <i>Gene</i> , 2017, 605, 54-62.	1.0	20
5165	<i>UNBRANCHED3</i> regulates branching by modulating cytokinin biosynthesis and signaling in maize and rice. <i>New Phytologist</i> , 2017, 214, 721-733.	3.5	86
5166	Loss of Rearranged L-Myc Fusion (RLF) results in defects in heart development in the mouse. <i>Differentiation</i> , 2017, 94, 8-20.	1.0	10
5167	Jasmonic Acid Enhances Al-Induced Root Growth Inhibition. <i>Plant Physiology</i> , 2017, 173, 1420-1433.	2.3	79
5168	Digital gene expression profiling analysis of DNA repair pathways in colon cancer stem population of HT29 cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 90-100.	0.9	4
5169	<i>Laribacter hongkongensis</i> anaerobic adaptation mediated by arginine metabolism is controlled by the cooperation of FNR and ArgR. <i>Environmental Microbiology</i> , 2017, 19, 1266-1280.	1.8	16
5170	Biomarker detection and categorization in ribonucleic acid sequencing meta-analysis using Bayesian hierarchical models. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2017, 66, 847-867.	0.5	5
5171	Novel BET protein proteolysis-targeting chimera exerts superior lethal activity than bromodomain inhibitor (BETi) against post-myeloproliferative neoplasm secondary (s) AML cells. <i>Leukemia</i> , 2017, 31, 1951-1961.	3.3	151

#	ARTICLE	IF	CITATIONS
5172	Transcriptome analysis of the freshwater pearl mussel ( <i>Cristaria plicata</i> ) mantle unravels genes involved in the formation of shell and pearl. <i>Molecular Genetics and Genomics</i> , 2017, 292, 343-352.	1.0	39
5173	Variation in Reproductive Success Across Captive Populations: Methodological Differences, Potential Biases and Opportunities. <i>Ethology</i> , 2017, 123, 1-29.	0.5	60
5174	Plant Promoter Database (PPDB). <i>Methods in Molecular Biology</i> , 2017, 1533, 299-314.	0.4	5
5175	Transcriptional Profiles Underlying the Effects of Methyl Jasmonate on Apple Ripening. <i>Journal of Plant Growth Regulation</i> , 2017, 36, 271-280.	2.8	16
5176	Curd development associated gene (CDAG1) in cauliflower ( <i>Brassica oleracea</i> L. var. botrytis) could result in enlarged organ size and increased biomass. <i>Plant Science</i> , 2017, 254, 82-94.	1.7	13
5177	Unit-Free and Robust Detection of Differential Expression from RNA-Seq Data. <i>Statistics in Biosciences</i> , 2017, 9, 178-199.	0.6	4
5178	Transcript profiling in the milk of dairy ewes fed extruded linseed. <i>Genomics Data</i> , 2017, 11, 17-19.	1.3	4
5179	Involvement of two glycoside hydrolase family 19 members in colony morphotype and virulence in <i>Flavobacterium columnare</i> . <i>Chinese Journal of Oceanology and Limnology</i> , 2017, 35, 1511-1523.	0.7	2
5180	Hypertranscription in Development, Stem Cells, and Regeneration. <i>Developmental Cell</i> , 2017, 40, 9-21.	3.1	87
5182	<i>Methylophilum fumariolicum</i> SolV, a thermoacidophilic "Knallgas"™ methanotroph with both an oxygen-sensitive and -insensitive hydrogenase. <i>ISME Journal</i> , 2017, 11, 945-958.	4.4	80
5183	Small non-coding RNA transcriptome of the NCI-60 cell line panel. <i>Scientific Data</i> , 2017, 4, 170157.	2.4	20
5184	Transcriptomics and proteomics reveal genetic and biological basis of superior biomass crop <i>Miscanthus</i> . <i>Scientific Reports</i> , 2017, 7, 13777.	1.6	13
5185	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , 2017, 8, 1126.	5.8	54
5186	Profiling of miRNAs and target genes related to cystogenesis in ADPKD mouse models. <i>Scientific Reports</i> , 2017, 7, 14151.	1.6	33
5187	UCLncR: Ultrafast and comprehensive long non-coding RNA detection from RNA-seq. <i>Scientific Reports</i> , 2017, 7, 14196.	1.6	29
5188	Transcriptomic analysis reveals differentially expressed genes and a unique apoptosis pathway in channel catfish ovary cells after infection with the channel catfish virus. <i>Fish and Shellfish Immunology</i> , 2017, 71, 58-68.	1.6	14
5189	FOXO4 expression is associated with the occurrence and outcome of seizures: An RNA-sequencing analysis of low-grade gliomas. <i>Seizure: the Journal of the British Epilepsy Association</i> , 2017, 52, 41-45.	0.9	5
5190	U1 snRNP telescripting regulates a size- and function-stratified human genome. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 993-999.	3.6	93

#	ARTICLE	IF	CITATIONS
5191	Algorithms for Next-Generation Sequencing Data. , 2017, , .		2
5192	De novo transcriptome assembly for pericarp in Litchi chinesis Sonn. cv. Feizixiao and identification of differentially expressed genes in response to Mg Foliar Nutrient. Scientia Horticulturae, 2017, 226, 59-67.	1.7	5
5193	Gene expression profiles of ovarian low-grade serous carcinoma resemble those of fallopian tube epithelium. Gynecologic Oncology, 2017, 147, 634-641.	0.6	15
5194	Molecular-level effects of acupuncture on depression: a genome-wide transcriptome analysis of pituitary gland in rats exposed to chronic restraint stress. Journal of Traditional Chinese Medicine = Chung I Tsa Chih Ying Wen Pan / Sponsored By All-China Association of Traditional Chinese Medicine, Academy of Traditional Chinese Medicine, 2017, 37, 486-495.	0.4	4
5195	Evaluating the toxicity of silicon dioxide nanoparticles on neural stem cells using RNA-Seq. RSC Advances, 2017, 7, 47552-47564.	1.7	14
5196	Spatial organization of silybin biosynthesis in milk thistle [ <i>Silybum marianum</i> (L.) Gaertn]. Plant Journal, 2017, 92, 995-1004.	2.8	41
5197	Root RNA-seq analysis reveals a distinct transcriptome landscape between clubroot-susceptible and clubroot-resistant Chinese cabbage lines after Plasmodiophora brassicae infection. Plant and Soil, 2017, 421, 93-105.	1.8	46
5198	DNA sequencing at 40: past, present and future. Nature, 2017, 550, 345-353.	13.7	729
5199	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico â€œDead Zoneâ€. MBio, 2017, 8, .	1.8	80
5200	A Novel Method to Detect Bias in Short Read NGS Data. Journal of Integrative Bioinformatics, 2017, 14, .	1.0	3
5201	Inherent humic substance promotes microbial denitrification of landfill leachate via shifting bacterial community, improving enzyme activity and up-regulating gene. Scientific Reports, 2017, 7, 12215.	1.6	33
5202	FLT1 and transcriptome-wide polyadenylation site (PAS) analysis in preeclampsia. Scientific Reports, 2017, 7, 12139.	1.6	38
5203	SMYD5 Controls Heterochromatin and Chromosome Integrity during Embryonic Stem Cell Differentiation. Cancer Research, 2017, 77, 6729-6745.	0.4	23
5204	Antennal transcriptome and expression analyses of olfactory genes in the sweetpotato weevil Cylas formicarius. Scientific Reports, 2017, 7, 11073.	1.6	40
5205	MicroRNA expression in a phosphaturic mesenchymal tumour. Bone Reports, 2017, 7, 63-69.	0.2	7
5206	Integrated profiling of global metabolomic and transcriptomic responses to viral hemorrhagic septicemia virus infection in olive flounder. Fish and Shellfish Immunology, 2017, 71, 220-229.	1.6	25
5207	Transcriptome analysis of hepatopancreas of Procambarus clarkii challenged with polyriboinosinic polyribocytidylic acid (poly I:C). Fish and Shellfish Immunology, 2017, 71, 144-150.	1.6	28
5208	Transcriptome sequencing and annotation of the halophytic microalga Dunaliella salina. Journal of Zhejiang University: Science B, 2017, 18, 833-844.	1.3	21

#	ARTICLE	IF	CITATIONS
5209	Genome-wide characterization of differential transcript usage in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 92, 1218-1231.	2.8	31
5210	Deep Sequencing Reveals the Significant Involvement of cAMP-Related Signaling Pathways Following Sciatic Nerve Crush. <i>Neurochemical Research</i> , 2017, 42, 3603-3611.	1.6	1
5211	Transcriptomic profiles of <i>Clostridium ljungdahlii</i> during lithotrophic growth with syngas or H <sub>2</sub> and CO <sub>2</sub> compared to organotrophic growth with fructose. <i>Scientific Reports</i> , 2017, 7, 13135.	1.6	33
5212	RNA-seq Analysis in Plant-Fungus Interactions. , 2017, , 1-25.		0
5213	RNA sequencing analysis of activated macrophages treated with the anti-HIV ABX464 in intestinal inflammation. <i>Scientific Data</i> , 2017, 4, 170150.	2.4	5
5214	The novel ethylene-responsive factor CsERF025 affects the development of fruit bending in cucumber. <i>Plant Molecular Biology</i> , 2017, 95, 519-531.	2.0	15
5215	Untranslated Parts of Genes Interpreted: Making Heads or Tails of High-Throughput Transcriptomic Data via Computational Methods. <i>BioEssays</i> , 2017, 39, 1700090.	1.2	14
5216	Comparative transcriptomic analysis of high and low egg-producing duck ovaries. <i>Poultry Science</i> , 2017, 96, 4378-4388.	1.5	48
5217	Similarity between soybean and <i>Arabidopsis</i> seed methylomes and loss of non-CG methylation does not affect seed development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9730-E9739.	3.3	111
5218	PDM3, a pentatricopeptide repeat-containing protein, affects chloroplast development. <i>Journal of Experimental Botany</i> , 2017, 68, 5615-5627.	2.4	41
5219	Transcriptome profiling of red swamp crayfish ( <i>Procambarus clarkii</i> ) hepatopancreas in response to lipopolysaccharide (LPS) infection. <i>Fish and Shellfish Immunology</i> , 2017, 71, 423-433.	1.6	33
5220	Analyzing homoeolog expression provides insights into the rediploidization event in gynogenetic hybrids of <i>Carassius auratus</i> red var. <i>Cyprinus carpio</i> . <i>Scientific Reports</i> , 2017, 7, 13679.	1.6	12
5221	Transcriptome-wide profiling and expression analysis of two accessions of <i>Paulownia australis</i> under salt stress. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	8
5222	A Loss-of-Function Splice Acceptor Variant in <i>IGF2</i> Is Protective for Type 2 Diabetes. <i>Diabetes</i> , 2017, 66, 2903-2914.	0.3	52
5223	Different substrate regimes determine transcriptional profiles and gene co-expression in <i>Methanosarcina barkeri</i> (DSM 800). <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7303-7316.	1.7	6
5224	The Promises and Challenges of Genomic Studies of Human Centromeres. <i>Progress in Molecular and Subcellular Biology</i> , 2017, 56, 285-304.	0.9	15
5225	Transcriptome analysis of the response of Burmese python to digestion. <i>GigaScience</i> , 2017, 6, 1-18.	3.3	17
5226	Transcriptomic analysis of <i>Camellia oleifera</i> in response to drought stress using high throughput RNA-seq. <i>Russian Journal of Plant Physiology</i> , 2017, 64, 728-737.	0.5	6

#	ARTICLE	IF	CITATIONS
5227	Regulation of Peripheral Myelination through Transcriptional Buffering of Egr2 by an Antisense Long Non-coding RNA. <i>Cell Reports</i> , 2017, 20, 1950-1963.	2.9	32
5228	RNA-Seq analysis of differentially expressed genes in rice under photooxidation. <i>Russian Journal of Plant Physiology</i> , 2017, 64, 698-706.	0.5	3
5230	Differential transcriptome of tolerogenic versus inflammatory dendritic cells points to modulated T1D genetic risk and enriched immune regulation. <i>Genes and Immunity</i> , 2017, 18, 176-183.	2.2	32
5231	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage <i>acL</i> . <i>MSystems</i> , 2017, 2, .	1.7	21
5232	Dissecting the Satellite DNA Landscape in Three Cactophilic <i>Drosophila</i> Sequenced Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2831-2843.	0.8	27
5233	Enteric dysbiosis-linked gut barrier disruption triggers early renal injury induced by chronic high salt feeding in mice. <i>Experimental and Molecular Medicine</i> , 2017, 49, e370-e370.	3.2	77
5234	Discovery of novel stroke-responsive lncRNAs in the mouse cortex using genome-wide RNA-seq. <i>Neurobiology of Disease</i> , 2017, 108, 204-212.	2.1	50
5235	Identification and characterization of <i>Vibrio vulnificus</i> plpA encoding a phospholipase A2 essential for pathogenesis. <i>Journal of Biological Chemistry</i> , 2017, 292, 17129-17143.	1.6	48
5236	De novo transcriptome analysis in <i>Dendrobium</i> and identification of critical genes associated with flowering. <i>Plant Physiology and Biochemistry</i> , 2017, 119, 319-327.	2.8	23
5237	Cadmium effects on DNA and protein metabolism in oyster ( <i>Crassostrea gigas</i> ) revealed by proteomic analyses. <i>Scientific Reports</i> , 2017, 7, 11716.	1.6	53
5238	Transcriptome characterization of HPG axis from Chinese sea perch <i>Lateolabrax maculatus</i> . <i>Journal of Fish Biology</i> , 2017, 91, 1407-1418.	0.7	7
5239	Improving de novo metatranscriptome assembly via machine learning algorithms. <i>International Journal of Computational Biology and Drug Design</i> , 2017, 10, 91.	0.3	3
5240	Needs and opportunities in bio-design automation: four areas for focus. <i>Current Opinion in Chemical Biology</i> , 2017, 40, 111-118.	2.8	25
5241	Defined Sensing Mechanisms and Signaling Pathways Contribute to the Global Inflammatory Gene Expression Output Elicited by Ionizing Radiation. <i>Immunity</i> , 2017, 47, 421-434.e3.	6.6	43
5242	Transcriptome and phytohormone analysis reveals a comprehensive phytohormone and pathogen defence response in pear self-/cross-pollination. <i>Plant Cell Reports</i> , 2017, 36, 1785-1799.	2.8	32
5243	Comparative study of the leaf transcriptomes and ionoms of <i>Juglans regia</i> and its wild relative species <i>Juglans cathayensis</i> . <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	6
5244	Genome editing reveals a role for OCT4 in human embryogenesis. <i>Nature</i> , 2017, 550, 67-73.	13.7	315
5245	A Driving Bioinformatics Approach to Explore Co-regulation of AOX Gene Family Members During Growth and Development. <i>Methods in Molecular Biology</i> , 2017, 1670, 219-224.	0.4	2



#	ARTICLE	IF	CITATIONS
5246	Transcriptomics analysis of salt stress tolerance in the roots of the mangrove <i>Avicennia officinalis</i> . <i>Scientific Reports</i> , 2017, 7, 10031.	1.6	77
5247	Ameliorative effects of melatonin on dark-induced leaf senescence in gardenia ( <i>Gardenia jasminoides</i> ) Tj ETQq1 1 0,784314 rgBT /Over 1.6 94	1.6	94
5248	Early X chromosome inactivation during human preimplantation development revealed by single-cell RNA-sequencing. <i>Scientific Reports</i> , 2017, 7, 10794.	1.6	78
5249	Bias and Correction in RNA-seq Data for Marine Species. <i>Marine Biotechnology</i> , 2017, 19, 541-550.	1.1	16
5250	Deep sequencing of antennal transcriptome from <i>Callosobruchus chinensis</i> to characterize odorant binding protein and chemosensory protein genes. <i>Journal of Stored Products Research</i> , 2017, 74, 13-21.	1.2	16
5251	Identification of immunity-related genes in <i>Plutella xylostella</i> in response to fungal peptide destruxin A: RNA-Seq and DGE analysis. <i>Scientific Reports</i> , 2017, 7, 10966.	1.6	30
5252	Molecular basis of peripheral olfactory sensing during oviposition in the behavior of the parasitic wasp <i>Anastatus japonicus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 89, 58-70.	1.2	27
5253	Acidophilic green algal genome provides insights into adaptation to an acidic environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8304-E8313.	3.3	93
5254	PAcluster: Clustering polyadenylation site data using canonical correlation analysis. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1750018.	0.3	3
5255	Procedures of Mitochondria Purification and Gene Expression to Study Alternative Respiratory and Uncoupling Pathways in Fruits. <i>Methods in Molecular Biology</i> , 2017, 1670, 143-165.	0.4	1
5256	A Genome-Wide Identification of the WRKY Family Genes and a Survey of Potential WRKY Target Genes in <i>Dendrobium officinale</i> . <i>Scientific Reports</i> , 2017, 7, 9200.	1.6	28
5257	Data Analysis Pipeline for RNA-seq Experiments: From Differential Expression to Cryptic Splicing. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 11.15.1-11.15.21.	25.8	35
5258	The <i>Apostasia</i> genome and the evolution of orchids. <i>Nature</i> , 2017, 549, 379-383.	18.7	305
5259	De novo assembly of leaf transcriptome, functional annotation and genomic resources development in <i>Prosopis cineraria</i> , a multipurpose tree of Indian Thar Desert. <i>Plant Gene</i> , 2017, 12, 88-97.	1.4	12
5260	Differential immune-related gene expression in the spleens of duck Tembusu virus-infected goslings. <i>Veterinary Microbiology</i> , 2017, 212, 39-47.	0.8	32
5261	Overexpression of RING Domain E3 Ligase <i>ZmXerico1</i> Confers Drought Tolerance through Regulation of ABA Homeostasis. <i>Plant Physiology</i> , 2017, 175, 1350-1369.	2.3	49
5262	Mitotic transcription and waves of gene reactivation during mitotic exit. <i>Science</i> , 2017, 358, 119-122.	6.0	201
5263	Novel endogenous retrovirus-derived transcript expressed in the bovine placenta is regulated by WNT signaling. <i>Biochemical Journal</i> , 2017, 474, 3499-3512.	1.7	8

#	ARTICLE	IF	CITATIONS
5264	Probabilistic Models for Error Correction of Nonuniform Sequencing Data. , 2017, , 131-145.		0
5265	Detoxification of Atrazine by Low Molecular Weight Thiols in Alfalfa (<i>Medicago sativa</i>). Chemical Research in Toxicology, 2017, 30, 1835-1846.	1.7	24
5266	Structural and developmental expression of Ss-riok-2, an RIO protein kinase encoding gene of Strongyloides stercoralis. Scientific Reports, 2017, 7, 8693.	1.6	6
5267	Discovering Condition-Specific Gene Co-Expression Patterns Using Gaussian Mixture Models: A Cancer Case Study. Scientific Reports, 2017, 7, 8617.	1.6	44
5268	Trans-omics approaches used to characterise fish nutritional biorhythms in leopard coral grouper (Plectropomus leopardus). Scientific Reports, 2017, 7, 9372.	1.6	24
5269	A time series transcriptome analysis of cassava (Manihot esculenta Crantz) varieties challenged with Ugandan cassava brown streak virus. Scientific Reports, 2017, 7, 9747.	1.6	36
5270	The maize WRKY transcription factor ZmWRKY17 negatively regulates salt stress tolerance in transgenic Arabidopsis plants. Planta, 2017, 246, 1215-1231.	1.6	124
5271	Hepatopancreas transcriptome analysis of Chinese mitten crab (Eriocheir sinensis) with white hepatopancreas syndrome. Fish and Shellfish Immunology, 2017, 70, 302-307.	1.6	27
5272	Non-coding RNAs participate in the regulatory network of CLDN4 via ceRNA mediated miRNA evasion. Nature Communications, 2017, 8, 289.	5.8	255
5273	Prominent topologically associated domains differentiate global chromatin packing in rice from Arabidopsis. Nature Plants, 2017, 3, 742-748.	4.7	200
5274	6S RNA is involved in acid resistance and invasion of epithelial cells in <i>Salmonella enterica</i> serovar Typhimurium. Future Microbiology, 2017, 12, 1045-1057.	1.0	19
5275	Deciphering transcriptome profile of the yellow catfish (Pelteobagrus fulvidraco) in response to Edwardsiella ictaluri. Fish and Shellfish Immunology, 2017, 70, 593-608.	1.6	24
5276	Pro- and anti-inflammatory responses of peripheral blood mononuclear cells induced by Staphylococcus aureus and Pseudomonas aeruginosa phages. Scientific Reports, 2017, 7, 8004.	1.6	179
5277	Unravelling a stearidonic acid-rich triacylglycerol biosynthetic pathway in the developing seeds of Buglossoides arvensis: A transcriptomic landscape. Scientific Reports, 2017, 7, 10473.	1.6	14
5278	Beyond Read-Counts: Ribo-seq Data Analysis to Understand the Functions of the Transcriptome. Trends in Genetics, 2017, 33, 728-744.	2.9	101
5279	Human protein secretory pathway genes are expressed in a tissue-specific pattern to match processing demands of the secretome. Npj Systems Biology and Applications, 2017, 3, 22.	1.4	32
5280	RNA-Seq analysis on chicken taste sensory organs: An ideal system to study organogenesis. Scientific Reports, 2017, 7, 9131.	1.6	14
5281	The Combination of RNA and Protein Profiling Reveals the Response to Nitrogen Depletion in Thalassiosira pseudonana. Scientific Reports, 2017, 7, 8989.	1.6	23

#	ARTICLE	IF	CITATIONS
5282	Prosapip1-Dependent Synaptic Adaptations in the Nucleus Accumbens Drive Alcohol Intake, Seeking, and Reward. <i>Neuron</i> , 2017, 96, 145-159.e8.	3.8	49
5283	Comprehensive transcriptome profiling of <i>Salvia miltiorrhiza</i> for discovery of genes associated with the biosynthesis of tanshinones and phenolic acids. <i>Scientific Reports</i> , 2017, 7, 10554.	1.6	77
5284	powsimR: power analysis for bulk and single cell RNA-seq experiments. <i>Bioinformatics</i> , 2017, 33, 3486-3488.	1.8	141
5285	Delineating biological and technical variance in single cell expression data. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 90, 161-166.	1.2	17
5286	Transcriptome analysis of yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) liver challenged with polyriboinosinic polyribocytidylic acid (poly I:C). <i>Fish and Shellfish Immunology</i> , 2017, 68, 395-403.	1.6	25
5287	Integrated Venomics and Venom Gland Transcriptome Analysis of Juvenile and Adult Mexican Rattlesnakes <i>Crotalus simus</i> , <i>C. tzabcan</i> , and <i>C. culminatus</i> Revealed miRNA-modulated Ontogenetic Shifts. <i>Journal of Proteome Research</i> , 2017, 16, 3370-3390.	1.8	82
5288	Identification of potential genes that contributed to the variation in the taxoid contents between two <i>Taxus</i> species ( <i>Taxus media</i> and <i>Taxus mairei</i> ). <i>Tree Physiology</i> , 2017, 37, 1659-1671.	1.4	72
5289	Gene expression changes in honey bees induced by sublethal imidacloprid exposure during the larval stage. <i>Insect Biochemistry and Molecular Biology</i> , 2017, 88, 12-20.	1.2	77
5290	Global transcriptome analysis identifies differentially expressed genes related to lipid metabolism in Wagyu and Holstein cattle. <i>Scientific Reports</i> , 2017, 7, 5278.	1.6	66
5291	Do social insects support Haig's kin theory for the evolution of genomic imprinting?. <i>Epigenetics</i> , 2017, 12, 725-742.	1.3	25
5292	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2017, 29, 1836-1863.	3.1	90
5293	Transcriptomic profile analysis of mouse neural tube development by RNA-seq. <i>IUBMB Life</i> , 2017, 69, 706-719.	1.5	20
5294	Transcriptional profiling of <i>Rickettsia prowazekii</i> coding and non-coding transcripts during in vitro host-pathogen and vector-pathogen interactions. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 827-836.	1.1	26
5295	Linking Auxin with Photosynthetic Rate via Leaf Venation. <i>Plant Physiology</i> , 2017, 175, 351-360.	2.3	52
5296	Transcriptomic insights into the alternative splicing-mediated adaptation of the entomopathogenic fungus <i>Beauveria bassiana</i> to host niches: autophagy-related gene 8 as an example. <i>Environmental Microbiology</i> , 2017, 19, 4126-4139.	1.8	20
5297	Transcriptome analysis reveals temperature-regulated antiviral response in turbot <i>Scophthalmus maximus</i> . <i>Fish and Shellfish Immunology</i> , 2017, 68, 359-367.	1.6	21
5298	miRNAs in the alga <i>Chlamydomonas reinhardtii</i> are not phylogenetically conserved and play a limited role in responses to nutrient deprivation. <i>Scientific Reports</i> , 2017, 7, 5462.	1.6	19
5299	A phase diagram for gene selection and disease classification. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2017, 167, 208-213.	1.8	5

#	ARTICLE	IF	CITATIONS
5300	Preliminary evidence for snail deformation from a Eutrophic lake. <i>Environmental Toxicology and Pharmacology</i> , 2017, 53, 219-226.	2.0	9
5301	The CINSARC signature as a prognostic marker for clinical outcome in multiple neoplasms. <i>Scientific Reports</i> , 2017, 7, 5480.	1.6	24
5302	Transcriptome analysis and discovery of genes involved in immune pathways in large yellow croaker ( <i>Larimichthys crocea</i> ) under high stocking density stress. <i>Fish and Shellfish Immunology</i> , 2017, 68, 332-340.	1.6	31
5303	Zoantharian mitochondrial genomes contain unique complex group I introns and highly conserved intergenic regions. <i>Gene</i> , 2017, 628, 24-31.	1.0	17
5304	Integrative analysis of mRNA and miRNA expression profiles in oral lichen planus: preliminary results. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2017, 124, 390-402.e17.	0.2	22
5305	Papain-like cysteine protease encoding genes in rubber ( <i>Hevea brasiliensis</i> ): comparative genomics, phylogenetic, and transcriptional profiling analysis. <i>Planta</i> , 2017, 246, 999-1018.	1.6	41
5306	Tumor Purity as an Underlying Key Factor in Glioma. <i>Clinical Cancer Research</i> , 2017, 23, 6279-6291.	3.2	372
5307	Comparative transcriptome data for commercial maturity and physiological maturity of "Royal Gala" apple fruit under room temperature storage condition. <i>Scientia Horticulturae</i> , 2017, 225, 386-393.	1.7	8
5308	Genomic insights into specialized metabolism in the marine actinomycete <i>Salinispora</i> . <i>Environmental Microbiology</i> , 2017, 19, 3660-3673.	1.8	69
5309	Metagenomic Analysis of Dairy Bacteriophages: Extraction Method and Pilot Study on Whey Samples Derived from Using Undefined and Defined Mesophilic Starter Cultures. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	23
5310	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
5311	A novel bZIP protein, Gsb1, is required for oxidative stress response, mating, and virulence in the human pathogen <i>Cryptococcus neoformans</i> . <i>Scientific Reports</i> , 2017, 7, 4044.	1.6	9
5312	Neuron-autonomous transcriptome changes upon ischemia/reperfusion injury. <i>Scientific Reports</i> , 2017, 7, 5800.	1.6	15
5313	Widespread alternative exon usage in clinically distinct subtypes of Invasive Ductal Carcinoma. <i>Scientific Reports</i> , 2017, 7, 5568.	1.6	37
5314	Comparative transcriptome analysis of the floral transition in <i>Rosa chinensis</i> "Old Blush" and <i>R. odorata</i> var. <i>gigantea</i> . <i>Scientific Reports</i> , 2017, 7, 6068.	1.6	16
5315	Transcriptome Analysis of Rice Seedling Roots in Response to Potassium Deficiency. <i>Scientific Reports</i> , 2017, 7, 5523.	1.6	32
5316	Deletion of the <i>celA</i> gene in <i>Aspergillus nidulans</i> triggers overexpression of secondary metabolite biosynthetic genes. <i>Scientific Reports</i> , 2017, 7, 5978.	1.6	8
5317	Maize ( <i>Zea mays</i> L.) genome size indicated by 180-bp knob abundance is associated with flowering time. <i>Scientific Reports</i> , 2017, 7, 5954.	1.6	24

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5318	Physiological and transcriptome analysis of He-Ne laser pretreated wheat seedlings in response to drought stress. <i>Scientific Reports</i> , 2017, 7, 6108.	1.6	40
5319	The Rice Phytochrome Genes, PHYA and PHYB, Have Synergistic Effects on Anther Development and Pollen Viability. <i>Scientific Reports</i> , 2017, 7, 6439.	1.6	24
5320	Genomewide Analysis of Clp1 Function in Transcription in Budding Yeast. <i>Scientific Reports</i> , 2017, 7, 6894.	1.6	2
5321	Niche-specific gene expression in a parasitic nematode; increased expression of immunomodulators in <i>Teladorsagia circumcincta</i> larvae derived from host mucosa. <i>Scientific Reports</i> , 2017, 7, 7214.	1.6	17
5322	The <i>Caenorhabditis elegans</i> Female-Like State: Decoupling the Transcriptomic Effects of Aging and Sperm Status. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2969-2977.	0.8	28
5323	Lack of human cytomegalovirus expression in single cells from glioblastoma tumors and cell lines. <i>Journal of NeuroVirology</i> , 2017, 23, 671-678.	1.0	16
5324	Variation-preserving normalization unveils blind spots in gene expression profiling. <i>Scientific Reports</i> , 2017, 7, 42460.	1.6	19
5325	Construction and Optimization of a Large Gene Coexpression Network in Maize Using RNA-Seq Data. <i>Plant Physiology</i> , 2017, 175, 568-583.	2.3	55
5326	PMK-1 p38 MAPK promotes cadmium stress resistance, the expression of SKN-1/Nrf and DAF-16 target genes, and protein biosynthesis in <i>Caenorhabditis elegans</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 1341-1361.	1.0	19
5327	Transcriptome comparative analysis of two <i>Camellia</i> species reveals lipid metabolism during mature seed natural drying. <i>Trees - Structure and Function</i> , 2017, 31, 1827-1848.	0.9	8
5328	Using RNA-Seq to Discover Genetic Polymorphisms That Produce Hidden Splice Variants. <i>Methods in Molecular Biology</i> , 2017, 1648, 129-142.	0.4	2
5329	Unravelling the relationship between the tsetse fly and its obligate symbiont <i>Wigglesworthia</i> : transcriptomic and metabolomic landscapes reveal highly integrated physiological networks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170360.	1.2	53
5330	Expression of Transient Receptor Potential Channels in the Purified Human Pancreatic Î <sup>2</sup> -Cells. <i>Pancreas</i> , 2017, 46, 97-101.	0.5	25
5331	Genome-wide transcriptome analysis of hippocampus in rats indicated that TLR/NLR signaling pathway was involved in the pathogenesis of depressive disorder induced by chronic restraint stress. <i>Brain Research Bulletin</i> , 2017, 134, 195-204.	1.4	29
5332	Rapid alkalization factor (RALF) genes are related to genic male sterility in Chinese cabbage ( <i>Brassica</i> ) Tj ETQqO 0,0,rgBT /Oyerlock 10	1.7	4
5333	The Phosphatidylinositol 3-Kinase Pathway as a Potential Therapeutic Target in Bladder Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6580-6591.	3.2	43
5334	An InDel in the Promoter of <i>AI-ACTIVATED MALATE TRANSPORTER9</i> Selected during Tomato Domestication Determines Fruit Malate Contents and Aluminum Tolerance. <i>Plant Cell</i> , 2017, 29, 2249-2268.	3.1	207
5335	Comparison of transcriptome profiles by <i>Fusarium oxysporum</i> inoculation between <i>Fusarium</i> yellows resistant and susceptible lines in <i>Brassica rapa</i> L.. <i>Plant Cell Reports</i> , 2017, 36, 1841-1854.	2.8	20

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5336	De novo assembly and characterization of seabass <i>Lateolabrax japonicus</i> transcriptome and expression of hepatic genes following different dietary phosphorus/calcium levels. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 24, 51-59.	0.4	4
5337	Transcriptome analysis of San Pedro-type fig ( <i>Ficus carica</i> L.) parthenocarpic breba and non-parthenocarpic main crop reveals divergent phytohormone-related gene expression. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	21
5338	Paternal nicotine exposure defines different behavior in subsequent generation via hyper-methylation of mmu-miR-15b. <i>Scientific Reports</i> , 2017, 7, 7286.	1.6	53
5339	Response of <i>Methylocystis</i> sp. Strain SC2 to Salt Stress: Physiology, Global Transcriptome, and Amino Acid Profiles. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	25
5340	RNA-seq based transcriptomic analysis of CPPU treated grape berries and emission of volatile compounds. <i>Journal of Plant Physiology</i> , 2017, 218, 155-166.	1.6	32
5341	Transcriptional risk scores link GWAS to eQTLs and predict complications in Crohn's disease. <i>Nature Genetics</i> , 2017, 49, 1517-1521.	9.4	146
5342	Intrinsic BET inhibitor resistance in SPOP-mutated prostate cancer is mediated by BET protein stabilization and AKT/mTORC1 activation. <i>Nature Medicine</i> , 2017, 23, 1055-1062.	15.2	225
5343	Metabolic and spatio-taxonomic response of uncultivated seafloor bacteria following the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2017, 11, 2569-2583.	4.4	39
5344	Characterization of the Adult Head Transcriptome and Identification of Migration and Olfaction Genes in the Oriental Armyworm <i>Mythimna separate</i> . <i>Scientific Reports</i> , 2017, 7, 2324.	1.6	5
5345	Genome-wide RNA-Sequencing analysis identifies a distinct fibrosis gene signature in the conjunctiva after glaucoma surgery. <i>Scientific Reports</i> , 2017, 7, 5644.	1.6	16
5346	Transcriptional Variation of Diverse Enteropathogenic <i>Escherichia coli</i> Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017, 2, .	1.7	12
5347	Identification of candidate genes involved in fatty acids degradation at the late maturity stage in <i>Brassica napus</i> based on transcriptomic analysis. <i>Plant Growth Regulation</i> , 2017, 83, 385-396.	1.8	8
5348	Myeloid Cell-Derived Reactive Oxygen Species Induce Epithelial Mutagenesis. <i>Cancer Cell</i> , 2017, 32, 869-883.e5.	7.7	232
5349	SPOTs fill a major gap in RNA quantification. <i>Nature Methods</i> , 2017, 14, 1137-1138.	9.0	0
5350	Comparative transcriptomics as a guide to natural product discovery and biosynthetic gene cluster functionality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11121-E11130.	3.3	94
5351	Expression Profiles of Wuschel-Related Homeobox Gene Family in Pineapple ( <i>Ananas comosus</i> L). <i>Tropical Plant Biology</i> , 2017, 10, 204-215.	1.0	14
5352	Ensemble Modeling Approach Targeting Heterogeneous RNA-Seq data: Application to Melanoma Pseudogenes. <i>Scientific Reports</i> , 2017, 7, 17344.	1.6	2
5353	Protein quantitative trait locus study in obesity during weight-loss identifies a leptin regulator. <i>Nature Communications</i> , 2017, 8, 2084.	5.8	66

#	ARTICLE	IF	CITATIONS
5354	Single-cell gene expression patterns in lupus monocytes independently indicate disease activity, interferon and therapy. <i>Lupus Science and Medicine</i> , 2017, 4, e000202.	1.1	39
5355	MALE STERILE6021 (MS6021) is required for the development of anther cuticle and pollen exine in maize. <i>Scientific Reports</i> , 2017, 7, 16736.	1.6	30
5356	Accurate assembly of transcripts through phase-preserving graph decomposition. <i>Nature Biotechnology</i> , 2017, 35, 1167-1169.	9.4	162
5357	Profiling the transcriptome with RNA SPOTs. <i>Nature Methods</i> , 2017, 14, 1153-1155.	9.0	93
5358	Molecular and cellular reorganization of neural circuits in the human lineage. <i>Science</i> , 2017, 358, 1027-1032.	6.0	192
5359	Comparative genomic hybridization and transcriptome sequencing reveal that two genes, Osl_14279 (LOC_Os03g62620) and Osl_10794 (LOC_Os03g14950) regulate the mutation in the $\beta$ -rl rice mutant. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 745-754.	1.4	4
5360	Transcribed ultraconserved region 339 promotes carcinogenesis by modulating tumor suppressor microRNAs. <i>Nature Communications</i> , 2017, 8, 1801.	5.8	36
5361	OCT4 supports extended LIF-independent self-renewal and maintenance of transcriptional and epigenetic networks in embryonic stem cells. <i>Scientific Reports</i> , 2017, 7, 16360.	1.6	10
5362	Identification of differentially expressed miRNAs in the fatty liver of Landes goose ( <i>Anser anser</i> ). <i>Scientific Reports</i> , 2017, 7, 16296.	1.6	13
5363	Transcriptomic analysis of the regulation of stalk development in flowering Chinese cabbage ( <i>Brassica campestris</i> ) by RNA sequencing. <i>Scientific Reports</i> , 2017, 7, 15517.	1.6	19
5364	Evolution of flower color pattern through selection on regulatory small RNAs. <i>Science</i> , 2017, 358, 925-928.	6.0	48
5365	Alternative transcription start site selection in Mr-OPY2 controls lifestyle transitions in the fungus <i>Metarhizium robertsii</i> . <i>Nature Communications</i> , 2017, 8, 1565.	5.8	39
5366	Insights into gene expression profiles induced by Socs3 depletion in keratinocytes. <i>Scientific Reports</i> , 2017, 7, 15830.	1.6	6
5367	Physiological characterization, transcriptomic profiling, and microsatellite marker mining of <i>Lycium ruthenicum</i> . <i>Journal of Zhejiang University: Science B</i> , 2017, 18, 1002-1021.	1.3	12
5368	Modifying SAMseq to account for asymmetry in the distribution of effect sizes when identifying differentially expressed genes. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 291-312.	0.2	1
5369	Transcriptome studies of granulosa cells at different stages of ovarian follicular development in buffalo. <i>Animal Reproduction Science</i> , 2017, 187, 181-192.	0.5	8
5370	Binding to SMN2 pre-mRNA-protein complex elicits specificity for small molecule splicing modifiers. <i>Nature Communications</i> , 2017, 8, 1476.	5.8	155
5371	A Comparison of mRNA Sequencing with Random Primed and $\beta$ -Directed Libraries. <i>Scientific Reports</i> , 2017, 7, 14626.	1.6	52

#	ARTICLE	IF	CITATIONS
5372	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1961-1969.	3.4	95
5373	Bayesian estimation of differential transcript usage from RNA-seq data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 367-386.	0.2	5
5374	Comprehensive Transcriptome Analysis of Phytohormone Biosynthesis and Signaling Genes in the Flowers of Chinese Chinquapin ( <i>Castanea henryi</i> ). <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 10332-10349.	2.4	34
5375	Pyruvate Accumulation Is the First Line of Cell Defense against Heat Stress in a Fungus. <i>MBio</i> , 2017, 8, .	1.8	52
5376	Structure-mediated modulation of mRNA abundance by A-to-I editing. <i>Nature Communications</i> , 2017, 8, 1255.	5.8	65
5377	Identification of miRNAs involved in DRG neurite outgrowth and their putative targets. <i>FEBS Letters</i> , 2017, 591, 2091-2105.	1.3	25
5378	Hypoxia is a Key Driver of Alternative Splicing in Human Breast Cancer Cells. <i>Scientific Reports</i> , 2017, 7, 4108.	1.6	61
5379	Integrating genome and transcriptome profiling for elucidating the mechanism of muscle growth and lipid deposition in Pekin ducks. <i>Scientific Reports</i> , 2017, 7, 3837.	1.6	17
5380	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. <i>Scientific Reports</i> , 2017, 7, 4200.	1.6	139
5381	MicroRNA-196 Regulates HOX Gene Expression in Human Gluteal Adipose Tissue. <i>Obesity</i> , 2017, 25, 1375-1383.	1.5	21
5382	Transcriptomic responses involved in enhanced production of hypocrellin A by addition of Triton X-100 in submerged cultures of <i>Shiraia bambusicola</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 1415-1429.	1.4	41
5383	RNAseq-based transcriptome comparison of <i>Saccharomyces cerevisiae</i> strains isolated from diverse fermentative environments. <i>International Journal of Food Microbiology</i> , 2017, 257, 262-270.	2.1	11
5384	Transcriptomic profiling of hemp bast fibres at different developmental stages. <i>Scientific Reports</i> , 2017, 7, 4961.	1.6	71
5385	Attack-Phase <i>Bdellovibrio bacteriovorus</i> Responses to Extracellular Nutrients Are Analogous to Those Seen During Late Intraperiplasmic Growth. <i>Microbial Ecology</i> , 2017, 74, 937-946.	1.4	19
5386	Tobacco mosaic virus infection disproportionately impacts phloem associated transcriptomes in <i>Arabidopsis thaliana</i> and <i>Nicotiana benthamiana</i> . <i>Virology</i> , 2017, 510, 76-89.	1.1	17
5387	RNA-Seq reveals differential expression patterns of genes associated with carotenoid accumulation in loquat. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	3
5388	Genome-wide differential mRNA expression profiles in follicles of two breeds and at two stages of estrus cycle of gilts. <i>Scientific Reports</i> , 2017, 7, 5052.	1.6	23
5389	<i>Hop</i> <i>stunt viroid</i> : Effect on Host ( <i>Humulus lupulus</i> ) Transcriptome and Its Interactions With Hop Powdery Mildew ( <i>Podosphaera macularis</i> ). <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 842-851.	1.4	29



#	ARTICLE	IF	CITATIONS
5390	Profile and functional analysis of small RNAs derived from <i>Aspergillus fumigatus</i> infected with double-stranded RNA mycoviruses. <i>BMC Genomics</i> , 2017, 18, 416.	1.2	30
5391	Personalized RNA mutanome vaccines mobilize poly-specific therapeutic immunity against cancer. <i>Nature</i> , 2017, 547, 222-226.	13.7	1,806
5392	Comparative transcriptome analysis on the synthesis pathway of honey bee ( <i>Apis mellifera</i> ) mandibular gland secretions. <i>Scientific Reports</i> , 2017, 7, 4530.	1.6	35
5393	Iterative Systems Biology for Medicine â€” Time for advancing from network signatures to mechanistic equations. <i>Current Opinion in Systems Biology</i> , 2017, 3, 111-118.	1.3	4
5394	sRNA and cis-antisense sRNA identification in <i>Staphylococcus aureus</i> highlights an unusual sRNA gene cluster with one encoding a secreted peptide. <i>Scientific Reports</i> , 2017, 7, 4565.	1.6	25
5395	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	1.6	21
5396	Long non-coding RNA expression profile in cytogenetically normal acute myeloid leukemia identifies a distinct signature and a new biomarker in NPM1-mutated patients. <i>Haematologica</i> , 2017, 102, 1718-1726.	1.7	32
5397	Identification, phylogeny, and transcript profiling of aquaporin genes in response to abiotic stress in <i>Tamarix hispida</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	7
5398	Foodomics evaluation of bioactive compounds in foods. <i>TrAC - Trends in Analytical Chemistry</i> , 2017, 96, 2-13.	5.8	68
5399	Transcriptional determination and functional specificity of myeloid cells: making sense of diversity. <i>Nature Reviews Immunology</i> , 2017, 17, 595-607.	10.6	75
5400	Verification of mutagen function of Zeocin in <i>Nannochloropsis oceanica</i> through transcriptome analysis. <i>Journal of Ocean University of China</i> , 2017, 16, 501-508.	0.6	15
5401	Longissimus lumborum muscle transcriptome analysis of Laiwu and Yorkshire pigs differing in intramuscular fat content. <i>Genes and Genomics</i> , 2017, 39, 759-766.	0.5	34
5402	A scalable and memory-efficient algorithm for de novo transcriptome assembly of non-model organisms. <i>BMC Genomics</i> , 2017, 18, 387.	1.2	7
5403	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017, 18, 109.	1.2	7
5404	Automated multigroup outlier identification in molecular high-throughput data using bagplots and gemplots. <i>BMC Bioinformatics</i> , 2017, 18, 232.	1.2	28
5405	QueryOR: a comprehensive web platform for genetic variant analysis and prioritization. <i>BMC Bioinformatics</i> , 2017, 18, 225.	1.2	20
5406	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. <i>BMC Bioinformatics</i> , 2017, 18, 301.	1.2	40
5407	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. <i>BMC Genomics</i> , 2017, 18, 1044.	1.2	14

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5408	Conserved expression of transposon-derived non-coding transcripts in primate stem cells. <i>BMC Genomics</i> , 2017, 18, 214.	1.2	40
5409	Reduced changes in protein compared to mRNA levels across non-proliferating tissues. <i>BMC Genomics</i> , 2017, 18, 305.	1.2	77
5410	Transcriptome profiling of litchi leaves in response to low temperature reveals candidate regulatory genes and key metabolic events during floral induction. <i>BMC Genomics</i> , 2017, 18, 363.	1.2	13
5411	Genomic and transcriptomic analyses reveal distinct biological functions for cold shock proteins (VpaCspA and VpaCspD) in <i>Vibrio parahaemolyticus</i> CHN25 during low-temperature survival. <i>BMC Genomics</i> , 2017, 18, 436.	1.2	35
5412	Differentially expressed genes from RNA-Seq and functional enrichment results are affected by the choice of single-end versus paired-end reads and stranded versus non-stranded protocols. <i>BMC Genomics</i> , 2017, 18, 399.	1.2	23
5413	Identification of candidate genes for fiber length quantitative trait loci through RNA-Seq and linkage and physical mapping in cotton. <i>BMC Genomics</i> , 2017, 18, 427.	1.2	32
5414	Differences in responses of grass carp to different types of grass carp reovirus (GCRV) and the mechanism of hemorrhage revealed by transcriptome sequencing. <i>BMC Genomics</i> , 2017, 18, 452.	1.2	58
5415	A comprehensive assessment of RNA-seq protocols for degraded and low-quantity samples. <i>BMC Genomics</i> , 2017, 18, 442.	1.2	111
5416	Identification and analysis of the stigma and embryo sac-preferential/specific genes in rice pistils. <i>BMC Plant Biology</i> , 2017, 17, 60.	1.6	9
5417	Transcriptome profiling of <i>Elymus sibiricus</i> , an important forage grass in Qinghai-Tibet plateau, reveals novel insights into candidate genes that potentially connected to seed shattering. <i>BMC Plant Biology</i> , 2017, 17, 78.	1.6	16
5418	Revelation of mRNAs and proteins in porcine milk exosomes by transcriptomic and proteomic analysis. <i>BMC Veterinary Research</i> , 2017, 13, 101.	0.7	42
5419	Progesterone signalling in broiler skeletal muscle is associated with divergent feed efficiency. <i>BMC Systems Biology</i> , 2017, 11, 29.	3.0	29
5420	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. <i>BMC Medical Genomics</i> , 2017, 10, 27.	0.7	29
5421	Whole blood gene expression in adolescent chronic fatigue syndrome: an exploratory cross-sectional study suggesting altered B cell differentiation and survival. <i>Journal of Translational Medicine</i> , 2017, 15, 102.	1.8	44
5422	SMYD5 regulates H4K20me3-marked heterochromatin to safeguard ES cell self-renewal and prevent spurious differentiation. <i>Epigenetics and Chromatin</i> , 2017, 10, 8.	1.8	45
5423	Transcriptome analysis explores genes related to shikonin biosynthesis in <i>Lithospermeae</i> plants and provides insights into <i>Boraginales</i> ™ evolutionary history. <i>Scientific Reports</i> , 2017, 7, 4477.	1.6	26
5424	An RNA Recognition Motif-Containing Protein Functions in Meiotic Silencing by Unpaired DNA. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2871-2882.	0.8	13
5425	Exploration of ZEA cytotoxicity to mouse endometrial stromal cells and RNA-seq analysis. <i>Journal of Biochemical and Molecular Toxicology</i> , 2017, 31, e21874.	1.4	7

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5426	Transcriptomic profiling of soybean in response to UV-B and <i>Xanthomonas axonopodis</i> treatment reveals shared gene components in stress defense pathways. <i>Genes and Genomics</i> , 2017, 39, 225-236.	0.5	2
5427	Resistance-breaking population of <i>Meloidogyne incognita</i> utilizes plant peroxidase to scavenge reactive oxygen species, thereby promoting parasitism on tomato carrying Mi-1 gene. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 1-7.	1.0	14
5428	Genome-wide identification and expression analysis of sulphate transporter (SULTR) genes under sulfur deficiency in <i>Brachypodium distachyon</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 263-273.	0.9	5
5429	<i>Cancer Genomics.</i> , 2017, , 43-63.		0
5431	Polyacrylamide gel as a culture substrate improves in vitro oocyte growth from porcine early antral follicles. <i>Molecular Reproduction and Development</i> , 2017, 84, 44-54.	1.0	18
5432	Novel insights into the regulatory roles of gene <i>hshB</i> in <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Research in Microbiology</i> , 2017, 168, 165-173.	1.0	9
5433	The Cartography of $\text{UV}$ -induced $\text{DNA}$ Damage Formation and $\text{DNA}$ Repair. <i>Photochemistry and Photobiology</i> , 2017, 93, 199-206.	1.3	26
5434	The <i>Arabidopsis</i> <i>UGT87A2</i> , a stress-inducible family 1 glycosyltransferase, is involved in the plant adaptation to abiotic stresses. <i>Physiologia Plantarum</i> , 2017, 159, 416-432.	2.6	50
5435	Identification, annotation and expression analysis of 29 Rho GTPase genes from channel catfish ( <i>Ictalurus punctatus</i> ) after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2017, 67, 445-451.	1.0	9
5436	Clustering of mRNA-Seq data based on alternative splicing patterns. <i>Biostatistics</i> , 2017, 18, 295-307.	0.9	7
5437	Characterising genes associated with flowering time in carrot ( <i>Daucus carota</i> L.) using transcriptome analysis. <i>Plant Biology</i> , 2017, 19, 286-297.	1.8	15
5438	T-Cell Differentiation. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	19
5439	Single-Cell RNA Sequencing of Human T Cells. <i>Methods in Molecular Biology</i> , 2017, 1514, 203-239.	0.4	26
5440	A deep insight into the whole transcriptome of midguts, ovaries and salivary glands of the <i>Amblyomma sculptum</i> tick. <i>Parasitology International</i> , 2017, 66, 64-73.	0.6	34
5441	Recessive mutations in the kinase ZAK cause a congenital myopathy with fibre type disproportion. <i>Brain</i> , 2017, 140, 37-48.	3.7	28
5442	Transcriptome profiling of the hypothalamus and pituitary at gonadal maturation and regression phases in marbled flounder ( <i>Pseudopleuronectes yokohamae</i> ). <i>Genes and Genomics</i> , 2017, 39, 713-722.	0.5	0
5443	Biological effect of aqueous C60 aggregates on <i>Scenedesmus obliquus</i> revealed by transcriptomics and non-targeted metabolomics. <i>Journal of Hazardous Materials</i> , 2017, 324, 221-229.	6.5	58
5444	CD8 <sup>+</sup> T Cells and Macrophages Regulate Pathogenesis in a Mouse Model of Middle East Respiratory Syndrome. <i>Journal of Virology</i> , 2017, 91, .	1.5	52

#	ARTICLE	IF	CITATIONS
5445	Complete Transcriptome RNA-Seq. <i>Methods in Molecular Biology</i> , 2017, 1513, 141-162.	0.4	2
5446	Efficient Approach to Correct Read Alignment for Pseudogene Abundance Estimates. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 522-533.	1.9	4
5447	Transcriptome analysis of mud crab ( <i>Scylla paramamosain</i> ) gills in response to Mud crab reovirus (MCRV). <i>Fish and Shellfish Immunology</i> , 2017, 60, 545-553.	1.6	39
5448	Whole-transcriptome brain expression and exon-usage profiling in major depression and suicide: evidence for altered glial, endothelial and ATPase activity. <i>Molecular Psychiatry</i> , 2017, 22, 760-773.	4.1	164
5449	Enhancing inhibitory synaptic function reverses spatial memory deficits in Shank2 mutant mice. <i>Neuropharmacology</i> , 2017, 112, 104-112.	2.0	56
5450	RNA-sequencing analysis reveals the hepatotoxic mechanism of perfluoroalkyl alternatives, HFPO2 and HFPO4, following exposure in mice. <i>Journal of Applied Toxicology</i> , 2017, 37, 436-444.	1.4	58
5451	Different waves of effector genes with contrasted genomic location are expressed by <i>Leptosphaeria maculans</i> during cotyledon and stem colonization of oilseed rape. <i>Molecular Plant Pathology</i> , 2017, 18, 1113-1126.	2.0	46
5452	Maize susceptibility to <i>Ustilago maydis</i> is influenced by genetic and chemical perturbation of carbohydrate allocation. <i>Molecular Plant Pathology</i> , 2017, 18, 1222-1237.	2.0	35
5453	Human Adipose-Derived Stem Cells Expanded Under Ambient Oxygen Concentration Accumulate Oxidative DNA Lesions and Experience Procarcinogenic DNA Replication Stress. <i>Stem Cells Translational Medicine</i> , 2017, 6, 68-76.	1.6	15
5454	Analysis of Microarray and RNA-seq Expression Profiling Data. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top093104.	0.2	37
5455	Bioinformatic Analysis of Epidemiological and Pathological Data. , 2017, , 91-104.		1
5456	Using RNA-Seq SNP data to reveal potential causal mutations related to pig production traits and RNA editing. <i>Animal Genetics</i> , 2017, 48, 151-165.	0.6	22
5457	Anaerobic metabolism and thermal tolerance: The importance of opine pathways on survival of a gastropod after cardiac dysfunction. <i>Integrative Zoology</i> , 2017, 12, 361-370.	1.3	31
5458	Comparative transcriptomics reveals genes involved in metabolic and immune pathways in the digestive gland of scallop <i>Chlamys farreri</i> following cadmium exposure. <i>Chinese Journal of Oceanology and Limnology</i> , 2017, 35, 603-612.	0.7	6
5459	Comparative transcriptome analysis of barley ( <i>Hordeum vulgare</i> L.) glossy mutant using RNA-Seq. <i>Revista Brasileira De Botanica</i> , 2017, 40, 247-256.	0.5	7
5460	Comprehensive reconstruction and in silico analysis of <i>Aspergillus niger</i> genome-scale metabolic network model that accounts for 1210 ORFs. <i>Biotechnology and Bioengineering</i> , 2017, 114, 685-695.	1.7	33
5461	Maximum-Likelihood Adaptive Filter for Partially Observed Boolean Dynamical Systems. <i>IEEE Transactions on Signal Processing</i> , 2017, 65, 359-371.	3.2	93
5462	Rapid Functional and Sequence Differentiation of a Tandemly Repeated Species-Specific Multigene Family in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 51-65.	3.5	11

#	ARTICLE	IF	CITATIONS
5463	Clinical Applications of Next-Generation Sequencing in Cancer Diagnosis. <i>Pathology and Oncology Research</i> , 2017, 23, 225-234.	0.9	65
5464	The effect of iron dextran on the transcriptome of pig hippocampus. <i>Genes and Genomics</i> , 2017, 39, 1-14.	0.5	19
5465	Probiotic <i>Enterococcus faecalis</i> Symbioflor <sup>®</sup> down regulates virulence genes of EHEC in vitro and decrease pathogenicity in a <i>Caenorhabditis elegans</i> model. <i>Archives of Microbiology</i> , 2017, 199, 203-213.	1.0	21
5466	Genomic Energy Landscapes. <i>Biophysical Journal</i> , 2017, 112, 427-433.	0.2	50
5467	Gene Expression Profiling Stratifies IDH1-Mutant Glioma with Distinct Prognoses. <i>Molecular Neurobiology</i> , 2017, 54, 5996-6005.	1.9	41
5468	Is the growth of microorganisms limited by carbon availability during chalcopyrite bioleaching?. <i>Hydrometallurgy</i> , 2017, 168, 13-20.	1.8	19
5469	Analyses of effects of $\beta$ -cembratrien-diol on cell morphology and transcriptome of <i>Valsa mali</i> var. <i>mali</i> . <i>Food Chemistry</i> , 2017, 214, 110-118.	4.2	32
5470	Transcriptome analysis of peach [ <i>Prunus persica</i> (L.) Batsch] stigma in response to low-temperature stress with digital gene expression profiling. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 141-148.	0.9	17
5471	Comparative transcriptome analysis of transcription factors in different maize varieties under salt stress conditions. <i>Plant Growth Regulation</i> , 2017, 81, 183-195.	1.8	35
5472	Deep sequencing of the transcriptome reveals distinct flavonoid metabolism features of black tartary buckwheat ( <i>Fagopyrum tataricum</i> Garetn.). <i>Progress in Biophysics and Molecular Biology</i> , 2017, 124, 49-60.	1.4	34
5473	Potts Hamiltonian models of protein co-variation, free energy landscapes, and evolutionary fitness. <i>Current Opinion in Structural Biology</i> , 2017, 43, 55-62.	2.6	73
5474	Transcriptional and translational regulation by RNA thermometers, riboswitches and the sRNA DsrA in <i>Escherichia coli</i> O157:H7 Sakai under combined cold and osmotic stress adaptation. <i>FEMS Microbiology Letters</i> , 2017, 364, fnw262.	0.7	15
5476	The mechanism of improved intracellular organic selenium and glutathione contents in selenium-enriched <i>Candida utilis</i> by acid stress. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2131-2141.	1.7	12
5477	Dysregulated circadian rhythm pathway in human osteoarthritis: NR1D1 and BMAL1 suppression alters TGF- $\beta$ 2 signaling in chondrocytes. <i>Osteoarthritis and Cartilage</i> , 2017, 25, 943-951.	0.6	62
5478	Estimation of long terminal repeat element content in the <i>Helicoverpa zea</i> genome from high-throughput sequencing of bacterial artificial chromosome pools. <i>Genome</i> , 2017, 60, 310-324.	0.9	7
5479	Establishing Informative Prior for Gene Expression Variance from Public Databases. <i>Statistics in Biosciences</i> , 2017, 9, 160-177.	0.6	0
5480	Host transcriptomic responses to pneumonic plague reveal that <i>Yersinia pestis</i> inhibits both the initial adaptive and innate immune responses in mice. <i>International Journal of Medical Microbiology</i> , 2017, 307, 64-74.	1.5	20
5481	Transcriptome profiles of embryos before and after cleavage in <i>Eriocheir sinensis</i> : identification of developmental genes at the earliest stages. <i>Chinese Journal of Oceanology and Limnology</i> , 2017, 35, 770-781.	0.7	6

#	ARTICLE	IF	CITATIONS
5482	Comparative transcriptome analysis of the hepatopancreas of <i>Eriocheir sinensis</i> following oral gavage with enrofloxacin. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 435-444.	0.7	4
5483	Sucrose synthase FaSS1 plays an important role in the regulation of strawberry fruit ripening. <i>Plant Growth Regulation</i> , 2017, 81, 175-181.	1.8	37
5484	Deleting the mouse Hsd17b1 gene results in a hypomorphic Naglu allele and a phenotype mimicking a lysosomal storage disease. <i>Scientific Reports</i> , 2017, 7, 16406.	1.6	13
5485	Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P. <i>Nucleic Acids Research</i> , 2017, 45, 13004-13015.	6.5	18
5486	Gene expression profiling of the unfed nymphal <i>Dermacentor silvarum</i> (Acari: Ixodidae) in response to low temperature. <i>Systematic and Applied Acarology</i> , 2017, 22, 2178.	0.5	5
5487	A Simple Process of RNA-Sequence Analyses by Hisat2, Htseq and DESeq2. , 2017, , .		25
5488	Illumina-based de novo transcriptome sequencing and analysis of Chinese forest musk deer. <i>Journal of Genetics</i> , 2017, 96, 1033-1040.	0.4	11
5489	Phylogenomics: The Evolution of Common Bean as Seen from the Perspective of All of Its Genes. <i>Compendium of Plant Genomes</i> , 2017, , 263-287.	0.3	0
5490	Genome-wide analysis shows that RNase G plays a global role in the stability of mRNAs in <i>Stenotrophomonas maltophilia</i> . <i>Scientific Reports</i> , 2017, 7, 16016.	1.6	6
5491	Transcriptome profiles reveal cold acclimation and freezing tolerance of susceptible and tolerant hulless barley genotypes. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	16
5492	Transcriptomic profiling of <i>Alternaria longipes</i> invasion in tobacco reveals pathogenesis regulated by ALHK1, a group III histidine kinase. <i>Scientific Reports</i> , 2017, 7, 16083.	1.6	6
5493	Transcriptome-wide analysis of natural antisense transcripts shows their potential role in breast cancer. <i>Scientific Reports</i> , 2017, 7, 17452.	1.6	39
5494	Elucidating the 16S rRNA 3' boundaries and defining optimal SD/aSD pairing in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> using RNA-Seq data. <i>Scientific Reports</i> , 2017, 7, 17639.	1.6	22
5495	Biotoxicity of Cry1Ab protein on wolf spider <i>Pardosa pseudoannulata</i> . <i>Ecotoxicology</i> , 2017, 26, 1336-1343.	1.1	4
5496	Genomes, Transcriptomes, Proteomes, and Bioinformatics. , 2017, , 629-653.		0
5497	Comparative whole-genome analysis reveals artificial selection effects on <i>Ustilago esculenta</i> genome. <i>DNA Research</i> , 2017, 24, 635-648.	1.5	58
5498	Complementary Proteome and Transcriptome Profiling in Developing Grains of a Notched-Belly Rice Mutant Reveals Key Pathways Involved in Chalkiness Formation. <i>Plant and Cell Physiology</i> , 2017, 58, 560-573.	1.5	34
5499	Prostate-specific PTen deletion in mice activates inflammatory microRNA expression pathways in the epithelium early in hyperplasia development. <i>Oncogenesis</i> , 2017, 6, 400.	2.1	10

#	ARTICLE	IF	CITATIONS
5500	The muscle development transcriptome landscape of ovariectomized goat. <i>Royal Society Open Science</i> , 2017, 4, 171415.	1.1	13
5501	Sublethal effects of imidacloprid on targeting muscle and ribosomal protein related genes in the honey bee <i>Apis mellifera</i> L.. <i>Scientific Reports</i> , 2017, 7, 15943.	1.6	36
5502	Small RNA profiling in <i>Chlamydomonas</i> : insights into chloroplast RNA metabolism. <i>Nucleic Acids Research</i> , 2017, 45, 10783-10799.	6.5	54
5503	Molecular Response of the Acidophilic Iron Oxidizer <i>Ferrovum</i> sp. JA12 to the Exposure to Elevated Concentrations of Ferrous Iron. <i>Solid State Phenomena</i> , 0, 262, 482-486.	0.3	1
5504	Pathways to understanding the genomic aetiology of osteoarthritis. <i>Human Molecular Genetics</i> , 2017, 26, R193-R201.	1.4	38
5505	Genome-wide expression analysis of transcripts, microRNAs, and the degradome in <i>Paulownia tomentosa</i> under drought stress. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	4
5506	RNA-seq of serial kidney biopsies obtained during progression of chronic kidney disease from dogs with X-linked hereditary nephropathy. <i>Scientific Reports</i> , 2017, 7, 16776.	1.6	12
5508	Software Dedicated to Virus Sequence Analysis <i>Bioinformatics Goes Viral</i> , <i>Advances in Virus Research</i> , 2017, 99, 233-257.	0.9	19
5509	Genome-wide analysis of rice cis-natural antisense transcription under cadmium exposure using strand-specific RNA-Seq. <i>BMC Genomics</i> , 2017, 18, 761.	1.2	9
5510	Robust transcriptional signatures for low-input RNA samples based on relative expression orderings. <i>BMC Genomics</i> , 2017, 18, 913.	1.2	45
5511	Sigma factor FaSigE positively regulates strawberry fruit ripening by ABA. <i>Plant Growth Regulation</i> , 2017, 83, 417-427.	1.8	14
5512	Global transcriptional landscape and promoter mapping of the gut commensal <i>Bifidobacterium breve</i> UCC2003. <i>BMC Genomics</i> , 2017, 18, 991.	1.2	24
5513	Recent advances in molecular techniques for the identification of phytopathogenic fungi – a mini review. <i>Journal of Plant Interactions</i> , 2017, 12, 493-504.	1.0	68
5514	Cavatica: A pipeline for identifying author adoption trends among software or methods. , 2017, , .		0
5515	Molecular response of gall induction by aphid <i>Schlechtendalia chinensis</i> (Bell) attack on <i>Rhus chinensis</i> Mill. <i>Journal of Plant Interactions</i> , 2017, 12, 465-479.	1.0	22
5516	A reference gene set construction using RNA-seq of multiple tissues of Chinese giant salamander, <i>Andrias davidianus</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	21
5517	Evaluation of peak calling approaches for genome-wide MBD2-based Methyl-Seq profiling. , 2017, , .		1
5518	Transcriptomic profiles of human foreskin fibroblast cells in response to orf virus. <i>Oncotarget</i> , 2017, 8, 58668-58685.	0.8	8

#	ARTICLE	IF	CITATIONS
5519	Transcriptome profile of one-month-old lambsâ€™ granulosa cells after superstimulation. Asian-Australasian Journal of Animal Sciences, 2017, 30, 20-33.	2.4	14
5520	PREDICTION OF CHRONIC BACTERIAL INFECTION BY IDENTIFICATION OF INTER CELLULAR RESPONSES OF GENETIC FUSION CENTERS. Asian Journal of Pharmaceutical and Clinical Research, 2017, 10, 417.	0.3	0
5521	Analysis of clustered RNA-seq data. International Journal of Data Mining and Bioinformatics, 2017, 19, 19.	0.1	0
5522	Histological and transcriptomic effects of 17Î±-methyltestosterone on zebrafish gonad development. BMC Genomics, 2017, 18, 557.	1.2	52
5523	Characterization of the cytochrome P450 monooxygenase genes (P450ome) from the carotenogenic yeast Xanthophyllomyces dendrorhous. BMC Genomics, 2017, 18, 540.	1.2	42
5524	Transcriptome Profiling in Systems Vascular Medicine. Frontiers in Pharmacology, 2017, 8, 563.	1.6	22
5525	Modification of Flight and Locomotion Performances, Respiratory Metabolism, and Transcriptome Expression in the Lady Beetle Harmonia axyridis through Sublethal Pesticide Exposure. Frontiers in Physiology, 2017, 8, 33.	1.3	30
5526	Comparative Investigation of Copper Tolerance and Identification of Putative Tolerance Related Genes in Tardigrades. Frontiers in Physiology, 2017, 8, 95.	1.3	23
5527	Transcriptomic Profiles Reveal the Interactions of Cd/Zn in Dwarf Polish Wheat (Triticum polonicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.3	38
5528	Identification and Expression Profiling of Chemosensory Genes in Dendrolimus punctatus Walker. Frontiers in Physiology, 2017, 8, 471.	1.3	37
5529	Molecular Ecological Basis of Grasshopper (Oedaleus asiaticus) Phenotypic Plasticity under Environmental Selection. Frontiers in Physiology, 2017, 8, 770.	1.3	9
5530	Chemosensory Gene Families in Ectropis grisescens and Candidates for Detection of Type-II Sex Pheromones. Frontiers in Physiology, 2017, 8, 953.	1.3	40
5531	Transcriptome Analysis of Secondary Metabolism Pathway, Transcription Factors, and Transporters in Response to Methyl Jasmonate in Lycoris aurea. Frontiers in Plant Science, 2016, 7, 1971.	1.7	55
5532	Genome-Wide Transcriptional Profiling to Elucidate Key Candidates Involved in Bud Burst and Rattling Growth in a Subtropical Bamboo (Dendrocalamus hamiltonii). Frontiers in Plant Science, 2016, 7, 2038.	1.7	25
5533	Transcriptomics Analysis of Apple Leaves in Response to Alternaria alternata Apple Pathotype Infection. Frontiers in Plant Science, 2017, 8, 22.	1.7	72
5534	Transcriptome Analyses Reveal Candidate Genes Potentially Involved in Al Stress Response in Alfalfa. Frontiers in Plant Science, 2017, 8, 26.	1.7	27
5535	Overexpression of MpCYS4, A Phytocystatin Gene from Malus prunifolia (Willd.) Borkh., Enhances Stomatal Closure to Confer Drought Tolerance in Transgenic Arabidopsis and Apple. Frontiers in Plant Science, 2017, 8, 33.	1.7	48
5536	An RNA-Seq Analysis of Grape Plantlets Grown in vitro Reveals Different Responses to Blue, Green, Red LED Light, and White Fluorescent Light. Frontiers in Plant Science, 2017, 8, 78.	1.7	59



#	ARTICLE	IF	CITATIONS
5537	Digital Gene Expression Analysis Provides Insight into the Transcript Profile of the Genes Involved in Aporphine Alkaloid Biosynthesis in Lotus ( <i>Nelumbo nucifera</i> ). <i>Frontiers in Plant Science</i> , 2017, 8, 80.	1.7	26
5538	RNA-Seq of Guar ( <i>Cyamopsis tetragonoloba</i> , L. Taub.) Leaves: De novo Transcriptome Assembly, Functional Annotation and Development of Genomic Resources. <i>Frontiers in Plant Science</i> , 2017, 8, 91.	1.7	54
5539	Transcriptomic Analysis Reveals New Insights into High-Temperature-Dependent Glume-Unclosing in an Elite Rice Male Sterile Line. <i>Frontiers in Plant Science</i> , 2017, 8, 112.	1.7	18
5540	De novo Transcriptome Assembly of <i>Phomopsis liquidambari</i> Provides Insights into Genes Associated with Different Lifestyles in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 121.	1.7	19
5541	The Comparison of Expressed Candidate Secreted Proteins from Two Arbuscular Mycorrhizal Fungi Unravels Common and Specific Molecular Tools to Invade Different Host Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 124.	1.7	100
5542	Deep Sequencing of Suppression Subtractive Hybridisation Drought and Recovery Libraries of the Non-model Crop <i>Trifolium repens</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 213.	1.7	6
5543	Transcriptional Responses of Chilean Quinoa ( <i>Chenopodium quinoa</i> Willd.) Under Water Deficit Conditions Uncovers ABA-Independent Expression Patterns. <i>Frontiers in Plant Science</i> , 2017, 8, 216.	1.7	60
5544	Transcriptomic Analysis of Thermally Stressed <i>Symbiodinium</i> Reveals Differential Expression of Stress and Metabolism Genes. <i>Frontiers in Plant Science</i> , 2017, 8, 271.	1.7	94
5545	Transcriptomic Profiling of the Maize ( <i>Zea mays</i> L.) Leaf Response to Abiotic Stresses at the Seedling Stage. <i>Frontiers in Plant Science</i> , 2017, 8, 290.	1.7	77
5546	Root Adaptive Responses to Aluminum-Treatment Revealed by RNA-Seq in Two Citrus Species With Different Aluminum-Tolerance. <i>Frontiers in Plant Science</i> , 2017, 8, 330.	1.7	40
5547	Transcriptome Analysis of a Female-sterile Mutant (fsm) in Chinese Cabbage ( <i>Brassica campestris</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	10
5548	De novo Sequencing and Transcriptome Analysis Reveal Key Genes Regulating Steroid Metabolism in Leaves, Roots, Adventitious Roots and Calli of <i>Periploca sepium</i> Bunge. <i>Frontiers in Plant Science</i> , 2017, 8, 594.	1.7	8
5549	Large Differences in Gene Expression Responses to Drought and Heat Stress between Elite Barley Cultivar Scarlett and a Spanish Landrace. <i>Frontiers in Plant Science</i> , 2017, 8, 647.	1.7	54
5550	Ectopic Expression of CDF3 Genes in Tomato Enhances Biomass Production and Yield under Salinity Stress Conditions. <i>Frontiers in Plant Science</i> , 2017, 8, 660.	1.7	45
5551	miR397/Laccase Gene Mediated Network Improves Tolerance to Fenoxaprop-P-ethyl in <i>Beckmannia syzigachne</i> and <i>Oryza sativa</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 879.	1.7	26
5552	Alteration in Auxin Homeostasis and Signaling by Overexpression Of PINOID Kinase Causes Leaf Growth Defects in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1009.	1.7	27
5553	Identification of Genes Associated with Lemon Floral Transition and Flower Development during Floral Inductive Water Deficits: A Hypothetical Model. <i>Frontiers in Plant Science</i> , 2017, 8, 1013.	1.7	32
5554	Lack of S-RNase-Based Gametophytic Self-Incompatibility in Orchids Suggests That This System Evolved after the Monocot-Eudicot Split. <i>Frontiers in Plant Science</i> , 2017, 8, 1106.	1.7	17

#	ARTICLE	IF	CITATIONS
5555	Transcriptome Analysis of Al-Induced Genes in Buckwheat ( <i>Fagopyrum esculentum</i> Moench) Root Apex: New Insight into Al Toxicity and Resistance Mechanisms in an Al Accumulating Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1141.	1.7	53
5556	Searching for an Accurate Marker-Based Prediction of an Individual Quantitative Trait in Molecular Plant Breeding. <i>Frontiers in Plant Science</i> , 2017, 8, 1182.	1.7	24
5557	Antarctic Moss Multiprotein Bridging Factor 1c Overexpression in <i>Arabidopsis</i> Resulted in Enhanced Tolerance to Salt Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 1206.	1.7	32
5558	Perturbation of Auxin Homeostasis and Signaling by PINOID Overexpression Induces Stress Responses in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1308.	1.7	14
5559	Root Transcriptomic Analysis Revealing the Importance of Energy Metabolism to the Development of Deep Roots in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1314.	1.7	27
5560	Phenotypic and Comparative Transcriptome Analysis of Different Ploidy Plants in <i>Dendrocalamus latiflorus</i> Munro. <i>Frontiers in Plant Science</i> , 2017, 8, 1371.	1.7	14
5561	Transcriptome Profiling to Identify Genes Involved in Mesosulfuron-Methyl Resistance in <i>Alopecurus aequalis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1391.	1.7	66
5562	Gene Regulatory Network for Tapetum Development in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1559.	1.7	64
5563	HvPap-1 C1A Protease Participates Differentially in the Barley Response to a Pathogen and an Herbivore. <i>Frontiers in Plant Science</i> , 2017, 8, 1585.	1.7	18
5564	50/50 Expressional Odds of Retention Signifies the Distinction between Retained Introns and Constitutively Spliced Introns in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1728.	1.7	2
5565	Transcriptome and Metabolome Analyses Provide Insights into the Occurrence of Peel Roughing Disorder on Satsuma Mandarin ( <i>Citrus unshiu</i> Marc.) Fruit. <i>Frontiers in Plant Science</i> , 2017, 8, 1907.	1.7	10
5566	Dissecting the Variations of Ripening Progression and Flavonoid Metabolism in Grape Berries Grown under Double Cropping System. <i>Frontiers in Plant Science</i> , 2017, 8, 1912.	1.7	27
5567	Transcriptomic Response of Resistant (PI613981 "Malus sieversii) and Susceptible ("Royal Gala") Genotypes of Apple to Blue Mold ( <i>Penicillium expansum</i> ) Infection. <i>Frontiers in Plant Science</i> , 2017, 8, 1981.	1.7	40
5568	Regulation of Fig ( <i>Ficus carica</i> L.) Fruit Color: Metabolomic and Transcriptomic Analyses of the Flavonoid Biosynthetic Pathway. <i>Frontiers in Plant Science</i> , 2017, 8, 1990.	1.7	156
5569	Reduced Glutathione Mediates Pheno-Ultrastructure, Kinome and Transportome in Chromium-Induced <i>Brassica napus</i> L.. <i>Frontiers in Plant Science</i> , 2017, 8, 2037.	1.7	42
5570	A Novel AP2/ERF Transcription Factor CR1 Regulates the Accumulation of Vindoline and Serpentine in <i>Catharanthus roseus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2082.	1.7	46
5571	Immune-Response Patterns and Next Generation Sequencing Diagnostics for the Detection of Mycoses in Patients with Septic Shock"Results of a Combined Clinical and Experimental Investigation. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1796.	1.8	52
5572	Transcriptome Analysis of Male <i>Drosophila melanogaster</i> Exposed to Ethylparaben Using Digital Gene Expression Profiling. <i>Journal of Insect Science</i> , 2017, 17, .	0.6	8

#	ARTICLE	IF	CITATIONS
5573	Comparative Transcriptomic Analysis Reveals Candidate Genes and Pathways Involved in Larval Settlement of the Barnacle <i>Megabalanus volcانو</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 2253.	1.8	11
5574	Genome-Wide Transcriptome Analysis Reveals Conserved and Distinct Molecular Mechanisms of Al Resistance in Buckwheat ( <i>Fagopyrum esculentum</i> Moench) Leaves. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1859.	1.8	18
5575	The impact of RNA sequence library construction protocols on transcriptomic profiling of leukemia. <i>BMC Genomics</i> , 2017, 18, 629.	1.2	42
5576	Computational prediction of protein-coding regions in human transcriptomes: An application to the elderly. , 2017, , .		1
5577	The MalR type regulator AcrC is a transcriptional repressor of acarbose biosynthetic genes in <i>Actinoplanes</i> sp. SE50/110. <i>BMC Genomics</i> , 2017, 18, 562.	1.2	15
5578	Chemosensory genes in the antennal transcriptome of two syrphid species, <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Syrphidae). <i>BMC Genomics</i> , 2017, 18, 586.	1.2	64
5579	Complementary RNA-Sequencing Based Transcriptomics and iTRAQ Proteomics Reveal the Mechanism of the Alleviation of Quinclorac Stress by Salicylic Acid in <i>Oryza sativa</i> ssp. <i>japonica</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 1975.	1.8	41
5580	Characterization of the Asiatic Acid Glucosyltransferase, UGT73AH1, Involved in Asiaticoside Biosynthesis in <i>Centella asiatica</i> (L.) Urban. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2630.	1.8	33
5581	Using Network Extracted Ontologies to Identify Novel Genes with Roles in Appressorium Development in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Microorganisms</i> , 2017, 5, 3.	1.6	12
5582	Transcriptomic Analysis of Leaf in Tree Peony Reveals Differentially Expressed Pigments Genes. <i>Molecules</i> , 2017, 22, 324.	1.7	32
5583	Transcriptomic Analysis Reveals Transcription Factors Related to Leaf Anthocyanin Biosynthesis in <i>Paeonia qiui</i> . <i>Molecules</i> , 2017, 22, 2186.	1.7	31
5584	A Next-Generation Sequencing Approach Uncovers Viral Transcripts Incorporated in Poxvirus Virions. <i>Viruses</i> , 2017, 9, 296.	1.5	10
5585	Comparative transcriptome analysis of cotton fiber development of Upland cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 20. <i>BMC Genomics</i> , 2017, 18, 705.	1.2	46
5586	Roles of Long Noncoding RNAs in Recurrence and Metastasis of Radiotherapy-Resistant Cancer Stem Cells. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1903.	1.8	66
5587	Comparative transcriptome profile of the leaf elongation zone of wild barley ( <i>Hordeum spontaneum</i> ) eibi1 mutant and its isogenic wild type. <i>Genetics and Molecular Biology</i> , 2017, 40, 834-843.	0.6	0
5588	Weighted Gene Co-expression Network Analysis of the Dioscin Rich Medicinal Plant <i>Dioscorea nipponica</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 789.	1.7	21
5589	Forward and Reverse Genetics to Model Human Diseases in the Mouse. , 2017, , 727-752.		1
5590	Transcriptome Characterization of the Chinese Fir ( <i>Cunninghamia lanceolata</i> (Lamb.) Hook.) and Expression Analysis of Candidate Phosphate Transporter Genes. <i>Forests</i> , 2017, 8, 420.	0.9	6

#	ARTICLE	IF	CITATIONS
5591	Fine Mapping and Transcriptome Analysis Reveal Candidate Genes Associated with Hybrid Lethality in Cabbage ( <i>Brassica Oleracea</i> ). <i>Genes</i> , 2017, 8, 147.	1.0	15
5592	Identification of Gene Expression Changes in the Aorta of ApoE Null Mice Fed a High-Fat Diet. <i>Genes</i> , 2017, 8, 289.	1.0	5
5593	Characterization of the Transcriptome and Gene Expression of Tetraploid Black Locust Cuttings in Response to Etiolation. <i>Genes</i> , 2017, 8, 345.	1.0	18
5594	RNA-Seq Analyses for Two Silkworm Strains Reveals Insight into Their Susceptibility and Resistance to <i>Beauveria bassiana</i> Infection. <i>International Journal of Molecular Sciences</i> , 2017, 18, 234.	1.8	17
5595	Next-Generation Sequencing in Oncology: Genetic Diagnosis, Risk Prediction and Cancer Classification. <i>International Journal of Molecular Sciences</i> , 2017, 18, 308.	1.8	353
5596	Overexpression of Transforming Acidic Coiled Coil-Containing Protein 3 Reflects Malignant Characteristics and Poor Prognosis of Glioma. <i>International Journal of Molecular Sciences</i> , 2017, 18, 235.	1.8	9
5597	Radiogenomic Analysis of Oncological Data: A Technical Survey. <i>International Journal of Molecular Sciences</i> , 2017, 18, 805.	1.8	102
5598	Transcriptome Sequencing of <i>Dianthus spiculifolius</i> and Analysis of the Genes Involved in Responses to Combined Cold and Drought Stress. <i>International Journal of Molecular Sciences</i> , 2017, 18, 849.	1.8	44
5599	Transcriptomic Analysis of Calcium Remodeling in Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2017, 18, 922.	1.8	38
5600	B-Myb Is Up-Regulated and Promotes Cell Growth and Motility in Non-Small Cell Lung Cancer. <i>International Journal of Molecular Sciences</i> , 2017, 18, 860.	1.8	33
5601	The Eukaryote-Like Serine/Threonine Kinase STK Regulates the Growth and Metabolism of Zoonotic <i>Streptococcus suis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 66.	1.8	52
5602	Bronchial Epithelial Cells from Cystic Fibrosis Patients Express a Specific Long Non-coding RNA Signature upon <i>Pseudomonas aeruginosa</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 218.	1.8	31
5603	Transcriptomic Analysis on Responses of Murine Lungs to <i>Pasteurella multocida</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 251.	1.8	49
5604	Population Dynamics and Transcriptomic Responses of <i>Chorthippus albonemus</i> (Orthoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.1	4
5605	Dysbindin Deficiency Modifies the Expression of GABA Neuron and Ion Permeation Transcripts in the Developing Hippocampus. <i>Frontiers in Genetics</i> , 2017, 8, 28.	1.1	21
5606	IL-10 Dysregulation in Acute Mountain Sickness Revealed by Transcriptome Analysis. <i>Frontiers in Immunology</i> , 2017, 8, 628.	2.2	42
5607	Distinct Transcriptional and Alternative Splicing Signatures of Decidual CD4+ T Cells in Early Human Pregnancy. <i>Frontiers in Immunology</i> , 2017, 8, 682.	2.2	47
5608	Multi-Omics Analyses of the Development and Function of Natural Killer Cells. <i>Frontiers in Immunology</i> , 2017, 8, 1095.	2.2	20

#	ARTICLE	IF	CITATIONS
5609	Characterization and Identification of Differentially Expressed Genes Involved in Thermal Adaptation of the Hong Kong Oyster <i>Crassostrea hongkongensis</i> by Digital Gene Expression Profiling. <i>Frontiers in Marine Science</i> , 2017, 4, .	1.2	26
5610	Metatranscriptomics Reveals the Active Bacterial and Eukaryotic Fibrolytic Communities in the Rumen of Dairy Cow Fed a Mixed Diet. <i>Frontiers in Microbiology</i> , 2017, 8, 67.	1.5	131
5611	Characterization of the Genomic Diversity of Norovirus in Linked Patients Using a Metagenomic Deep Sequencing Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 73.	1.5	34
5612	Exo-miRExplorer: A Comprehensive Resource for Exploring and Comparatively Analyzing Exogenous MicroRNAs. <i>Frontiers in Microbiology</i> , 2017, 8, 126.	1.5	6
5613	Transcriptome Analysis of <i>Arabidopsis thaliana</i> in Response to <i>Plasmodiophora brassicae</i> during Early Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 673.	1.5	60
5614	Effects of Inhibitors on the Transcriptional Profiling of <i>Gluconobacter oxydans</i> NL71 Genes after Biooxidation of Xylose into Xylonate. <i>Frontiers in Microbiology</i> , 2017, 8, 716.	1.5	16
5615	Genome-Wide Transcriptome Analysis Reveals Extensive Alternative Splicing Events in the Protoscolecetes of <i>Echinococcus granulosus</i> and <i>Echinococcus multilocularis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 929.	1.5	22
5616	The Shift of the Intestinal Microbiome in the Innate Immunity-Deficient Mutant <i>rde-1</i> Strain of <i>C. elegans</i> upon Orsay Virus Infection. <i>Frontiers in Microbiology</i> , 2017, 8, 933.	1.5	4
5617	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. <i>Frontiers in Microbiology</i> , 2017, 8, 1079.	1.5	97
5618	Metatranscriptomics Reveals the Functions and Enzyme Profiles of the Microbial Community in Chinese Nong-Flavor Liquor Starter. <i>Frontiers in Microbiology</i> , 2017, 8, 1747.	1.5	68
5619	A Laboratory Methodology for Dual RNA-Sequencing of Bacteria and their Host Cells In Vitro. <i>Frontiers in Microbiology</i> , 2017, 8, 1830.	1.5	19
5620	Ammonia Oxidation and Nitrite Reduction in the Verrucomicrobial Methanotroph <i>Methylacidiphilum fumarolicum</i> SolV. <i>Frontiers in Microbiology</i> , 2017, 8, 1901.	1.5	45
5621	pH Stress-Induced Cooperation between <i>Rhodococcus ruber</i> YYL and <i>Bacillus cereus</i> MLY1 in Biodegradation of Tetrahydrofuran. <i>Frontiers in Microbiology</i> , 2017, 8, 2297.	1.5	25
5622	Transcriptomic Analyses of <i>Scrippsiella trochoidea</i> Reveals Processes Regulating Encystment and Dormancy in the Life Cycle of a Dinoflagellate, with a Particular Attention to the Role of Abscisic Acid. <i>Frontiers in Microbiology</i> , 2017, 8, 2450.	1.5	35
5623	<i>Zygosaccharomyces bailii</i> Is a Potential Producer of Various Flavor Compounds in Chinese Maotai-Flavor Liquor Fermentation. <i>Frontiers in Microbiology</i> , 2017, 8, 2609.	1.5	46
5624	Brain Transcriptome Sequencing of a Natural Model of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 64.	1.7	14
5625	The FOXP2-Driven Network in Developmental Disorders and Neurodegeneration. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 212.	1.8	38
5626	Transcriptome Analysis of Hypothalamic Gene Expression during Daily Torpor in Djungarian Hamsters ( <i>Phodopus sungorus</i> ). <i>Frontiers in Neuroscience</i> , 2017, 11, 122.	1.4	19

#	ARTICLE	IF	CITATIONS
5627	Screening the Molecular Framework Underlying Local Dendritic mRNA Translation. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 45.	1.4	6
5628	Antidepressant Mechanism Research of Acupuncture: Insights from a Genome-Wide Transcriptome Analysis of Frontal Cortex in Rats with Chronic Restraint Stress. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-13.	0.5	24
5629	Asymptotic Approaches to Discovering Cancer Genomic Signatures. <i>Handbook of Statistics</i> , 2017, , 23-36.	0.4	1
5630	A Review of Recent Advancement in Integrating Omics Data with Literature Mining towards Biomedical Discoveries. <i>International Journal of Genomics</i> , 2017, 2017, 1-10.	0.8	37
5631	Transcriptome Analysis of Orange Head Chinese Cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> ) and Molecular Marker Development. <i>International Journal of Genomics</i> , 2017, 2017, 1-8.	0.8	5
5632	RNA-seq Based Transcription Characterization of Fusion Breakpoints as a Potential Estimator for Its Oncogenic Potential. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	11
5633	Integrating miRNA and mRNA Expression Profiling Uncovers miRNAs Underlying Fat Deposition in Sheep. <i>BioMed Research International</i> , 2017, 2017, 1-11.	0.9	38
5634	Transcriptome Analysis of Two Different Developmental Stages of <i>Paeonia lactiflora</i> Seeds. <i>International Journal of Genomics</i> , 2017, 2017, 1-10.	0.8	8
5635	Expression Profiling of Long Noncoding RNA Splice Variants in Human Microvascular Endothelial Cells: Lipopolysaccharide Effects <i>In Vitro</i> . <i>Mediators of Inflammation</i> , 2017, 2017, 1-18.	1.4	36
5636	Comparative RNA-Sequence Transcriptome Analysis of Phenolic Acid Metabolism in <i>Salvia miltiorrhiza</i> , a Traditional Chinese Medicine Model Plant. <i>International Journal of Genomics</i> , 2017, 2017, 1-10.	0.8	21
5637	Comparative Transcriptome Analyses of Resistant and Susceptible Near-Isogenic Wheat Lines following Inoculation with <i>Blumeria graminis</i> f. sp. <i>tritici</i> . <i>International Journal of Genomics</i> , 2017, 2017, 1-16.	0.8	9
5638	A comparative transcriptomic analysis of replicating and dormant liver stages of the relapsing malaria parasite <i>Plasmodium cynomolgi</i> . <i>ELife</i> , 2017, 6, .	2.8	56
5639	Bridging Chromosomal Architecture and Pathophysiology of <i>Streptococcus pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 350-361.	1.1	9
5640	Effects of feeding conditions on gene expression in chicken breast muscle. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	1
5641	Apigenin Impacts the Growth of the Gut Microbiota and Alters the Gene Expression of <i>Enterococcus</i> . <i>Molecules</i> , 2017, 22, 1292.	1.7	30
5642	Comprehensive Profiling of lincRNAs in Lung Adenocarcinoma of Never Smokers Reveals Their Roles in Cancer Development and Prognosis. <i>Genes</i> , 2017, 8, 321.	1.0	8
5643	A comparative study on genetic characteristics of two new varieties of <i>Pelodiscus sinensis</i> and their hybrid. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	2
5644	Variation and evolution of polyadenylation profiles in sauropsid mitochondrial mRNAs as deduced from the high-throughput RNA sequencing. <i>BMC Genomics</i> , 2017, 18, 665.	1.2	6

#	ARTICLE	IF	CITATIONS
5645	Dehydration induced transcriptomic responses in two Tibetan hulless barley ( <i>Hordeum vulgare</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	25
5646	UDP and NTF2 are the most consistently expressed genes in <i>Panax ginseng</i> roots at different growth stages. <i>Molecular Medicine Reports</i> , 2017, 15, 4382-4390.	1.1	1
5647	EUCANEXT: an integrated database for the exploration of genomic and transcriptomic data from <i>Eucalyptus</i> species. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	12
5648	Dual transcriptome of the immediate neutrophil and <i>Candida albicans</i> interplay. <i>BMC Genomics</i> , 2017, 18, 696.	1.2	45
5649	Detailed transcriptome analysis of the plant growth promoting <i>Paenibacillus riograndensis</i> SBR5 by using RNA-seq technology. <i>BMC Genomics</i> , 2017, 18, 846.	1.2	17
5650	<i>Trypanosoma cruzi</i> specific mRNA amplification by in vitro transcription improves parasite transcriptomics in host-parasite RNA mixtures. <i>BMC Genomics</i> , 2017, 18, 793.	1.2	5
5651	PPARD is an Inhibitor of Cartilage Growth in External Ears. <i>International Journal of Biological Sciences</i> , 2017, 13, 669-681.	2.6	19
5652	Isolation of ripening-related genes from ethylene/1-MCP treated papaya through RNA-seq. <i>BMC Genomics</i> , 2017, 18, 671.	1.2	33
5653	Time-dependent loss of mRNA transcripts from forensic stains. <i>Research and Reports in Forensic Medical Science</i> , 0, Volume 7, 1-12.	0.0	13
5654	First Insights into the Subterranean Crustacean Bathynellacea Transcriptome: Transcriptionally Reduced Opsin Repertoire and Evidence of Conserved Homeostasis Regulatory Mechanisms. <i>PLoS ONE</i> , 2017, 12, e0170424.	1.1	11
5655	Prediction of Poly(A) Sites by Poly(A) Read Mapping. <i>PLoS ONE</i> , 2017, 12, e0170914.	1.1	22
5656	Peptidomic and transcriptomic profiling of four distinct spider venoms. <i>PLoS ONE</i> , 2017, 12, e0172966.	1.1	25
5657	Gene expression profiling in Pekin duck embryonic breast muscle. <i>PLoS ONE</i> , 2017, 12, e0174612.	1.1	9
5658	Mobile Genome Express (MGE): A comprehensive automatic genetic analyses pipeline with a mobile device. <i>PLoS ONE</i> , 2017, 12, e0174696.	1.1	1
5659	Tracking disease progression by searching paths in a temporal network of biological processes. <i>PLoS ONE</i> , 2017, 12, e0176172.	1.1	6
5660	A comparison of per sample global scaling and per gene normalization methods for differential expression analysis of RNA-seq data. <i>PLoS ONE</i> , 2017, 12, e0176185.	1.1	60
5661	De novo assembly and comparative transcriptome analysis of the foot from Chinese green mussel ( <i>Perna viridis</i> ) in response to cadmium stimulation. <i>PLoS ONE</i> , 2017, 12, e0176677.	1.1	18
5662	The <i>Rhizoctonia solani</i> AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce ( <i>Lactuca sativa</i> L.). <i>PLoS ONE</i> , 2017, 12, e0177278.	1.1	28

#	ARTICLE	IF	CITATIONS
5663	Loss of prion protein induces a primed state of type I interferon-responsive genes. <i>PLoS ONE</i> , 2017, 12, e0179881.	1.1	22
5664	Deep RNA sequencing of pectoralis muscle transcriptomes during late-term embryonic to neonatal development in indigenous Chinese duck breeds. <i>PLoS ONE</i> , 2017, 12, e0180403.	1.1	10
5665	The integrated analysis of RNA-seq and microRNA-seq depicts miRNA-mRNA networks involved in Japanese flounder ( <i>Paralichthys olivaceus</i> ) albinism. <i>PLoS ONE</i> , 2017, 12, e0181761.	1.1	13
5666	Evaluation of changes to the <i>Rickettsia rickettsii</i> transcriptome during mammalian infection. <i>PLoS ONE</i> , 2017, 12, e0182290.	1.1	7
5667	Understanding the molecular mechanisms underlying the effects of light intensity on flavonoid production by RNA-seq analysis in <i>Epimedium pseudowushanense</i> B.L.Guo. <i>PLoS ONE</i> , 2017, 12, e0182348.	1.1	17
5668	A comparative transcriptomic analysis reveals the core genetic components of salt and osmotic stress responses in <i>Braya humilis</i> . <i>PLoS ONE</i> , 2017, 12, e0183778.	1.1	2
5669	Integrated analysis of mRNA and miRNA expression profiling in rice backcrossed progenies (BC2F12) with different plant height. <i>PLoS ONE</i> , 2017, 12, e0184106.	1.1	10
5670	Transcriptome analysis of the pectoral muscles of local chickens and commercial broilers using Ribo-Zero ribonucleic acid sequencing. <i>PLoS ONE</i> , 2017, 12, e0184115.	1.1	17
5671	Transcriptome analysis of Callery pear ( <i>Pyrus calleryana</i> ) reveals a comprehensive signalling network in response to <i>Alternaria alternata</i> . <i>PLoS ONE</i> , 2017, 12, e0184988.	1.1	16
5672	Global gene expression in cotton ( <i>Gossypium hirsutum</i> L.) leaves to waterlogging stress. <i>PLoS ONE</i> , 2017, 12, e0185075.	1.1	37
5673	Comparison of the transcriptomic analysis between two Chinese white pear ( <i>Pyrus bretschneideri</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.1	34
5674	Arginase expression modulates nitric oxide production in <i>Leishmania</i> ( <i>Leishmania</i> ) <i>amazonensis</i> . <i>PLoS ONE</i> , 2017, 12, e0187186.	1.1	43
5675	Differential transcriptome profiling of chilling stress response between shoots and rhizomes of <i>Oryza longistaminata</i> using RNA sequencing. <i>PLoS ONE</i> , 2017, 12, e0188625.	1.1	30
5676	Colorectal cancer stages transcriptome analysis. <i>PLoS ONE</i> , 2017, 12, e0188697.	1.1	29
5677	Effects of salinity on the cellular physiological responses of <i>Natrinema</i> sp. J7-2. <i>PLoS ONE</i> , 2017, 12, e0184974.	1.1	12
5678	The anti-tumorigenic activity of A2Mâ€™A lesson from the naked mole-rat. <i>PLoS ONE</i> , 2017, 12, e0189514.	1.1	36
5679	Profiling RNA-Seq at multiple resolutions markedly increases the number of causal eQTLs in autoimmune disease. <i>PLoS Genetics</i> , 2017, 13, e1007071.	1.5	23
5680	RNA-sequence analysis of gene expression from honeybees ( <i>Apis mellifera</i> ) infected with <i>Nosema ceranae</i> . <i>PLoS ONE</i> , 2017, 12, e0173438.	1.1	45



#	ARTICLE	IF	CITATIONS
5681	RNA-seq transcriptional profiling of <i>Leishmania amazonensis</i> reveals an arginase-dependent gene expression regulation. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006026.	1.3	36
5682	Transcriptome profiling analysis of senescent gingival fibroblasts in response to <i>Fusobacterium nucleatum</i> infection. <i>PLoS ONE</i> , 2017, 12, e0188755.	1.1	30
5683	RNA-Seq differential expression analysis: An extended review and a software tool. <i>PLoS ONE</i> , 2017, 12, e0190152.	1.1	451
5684	Transcriptomic analyses on muscle tissues of <i>Litopenaeus vannamei</i> provide the first profile insight into the response to low temperature stress. <i>PLoS ONE</i> , 2017, 12, e0178604.	1.1	39
5685	De novo leaf and root transcriptome analysis to identify putative genes involved in triterpenoid saponins biosynthesis in <i>Hedera helix</i> L. <i>PLoS ONE</i> , 2017, 12, e0182243.	1.1	17
5686	Transcriptomics technologies. <i>PLoS Computational Biology</i> , 2017, 13, e1005457.	1.5	677
5687	Transient In Vivo Resistance Mechanisms of <i>Burkholderia pseudomallei</i> to Ceftazidime and Molecular Markers for Monitoring Treatment Response. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005209.	1.3	14
5688	Investigation of the <i>Fusarium virguliforme</i> Transcriptomes Induced during Infection of Soybean Roots Suggests that Enzymes with Hydrolytic Activities Could Play a Major Role in Root Necrosis. <i>PLoS ONE</i> , 2017, 12, e0169963.	1.1	11
5689	Genome-wide exonic small interference RNA-mediated gene silencing regulates sexual reproduction in the homothallic fungus <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2017, 13, e1006595.	1.5	84
5690	Differential Sensitivity of Target Genes to Translational Repression by miR-17~92. <i>PLoS Genetics</i> , 2017, 13, e1006623.	1.5	31
5691	Adaptation of A-to-I RNA editing in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2017, 13, e1006648.	1.5	63
5692	Termination factor Rho: From the control of pervasive transcription to cell fate determination in <i>Bacillus subtilis</i> . <i>PLoS Genetics</i> , 2017, 13, e1006909.	1.5	56
5693	Development of a tissue-specific ribosome profiling approach in <i>Drosophila</i> enables genome-wide evaluation of translational adaptations. <i>PLoS Genetics</i> , 2017, 13, e1007117.	1.5	56
5694	Molecular characterization of tsetseâ€™s proboscis and its response to <i>Trypanosoma congolense</i> infection. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006057.	1.3	8
5695	Identification and analysis of glutathione S-transferase gene family in sweet potato reveal divergent GST-mediated networks in aboveground and underground tissues in response to abiotic stresses. <i>BMC Plant Biology</i> , 2017, 17, 225.	1.6	84
5696	Genome-wide analysis of miRNAs in <i>Carya cathayensis</i> . <i>BMC Plant Biology</i> , 2017, 17, 228.	1.6	11
5697	De novo assembly and comparative analysis of the transcriptome of embryogenic callus formation in bread wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 244.	1.6	23
5698	LesR is a novel upstream regulator that controls downstream Clp expression to modulate antibiotic HSAF biosynthesis and cell aggregation in <i>Lyso bacter</i> enzymogenes OH11. <i>Microbial Cell Factories</i> , 2017, 16, 202.	1.9	9

#	ARTICLE	IF	CITATIONS
5699	Automated identification of reference genes based on RNA-seq data. <i>BioMedical Engineering OnLine</i> , 2017, 16, 65.	1.3	26
5700	Tissue transglutaminase in astrocytes is enhanced by inflammatory mediators and is involved in the formation of fibronectin fibril-like structures. <i>Journal of Neuroinflammation</i> , 2017, 14, 260.	3.1	14
5701	Selection and validation of reference genes for RT-qPCR analysis in potato under abiotic stress. <i>Plant Methods</i> , 2017, 13, 85.	1.9	104
5702	RNA-sequence data normalization through in silico prediction of reference genes: the bacterial response to DNA damage as case study. <i>BioData Mining</i> , 2017, 10, 30.	2.2	15
5703	Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific <i>Arabidopsis</i> hybrid. <i>Genome Biology</i> , 2017, 18, 157.	3.8	86
5704	Sialotranscriptomics of <i>Rhipicephalus zambeziensis</i> reveals intricate expression profiles of secretory proteins and suggests tight temporal transcriptional regulation during blood-feeding. <i>Parasites and Vectors</i> , 2017, 10, 384.	1.0	28
5705	Transcriptomic analysis reveals the key immune-related signalling pathways of <i>Sebastiscus marmoratus</i> in response to infection with the parasitic ciliate <i>Cryptocaryon irritans</i> . <i>Parasites and Vectors</i> , 2017, 10, 576.	1.0	29
5706	Tsetse fly ( <i>Glossina pallidipes</i> ) midgut responses to <i>Trypanosoma brucei</i> challenge. <i>Parasites and Vectors</i> , 2017, 10, 614.	1.0	8
5707	The effect of Nipped-B-like (Nipbl) haploinsufficiency on genome-wide cohesin binding and target gene expression: modeling Cornelia de Lange syndrome. <i>Clinical Epigenetics</i> , 2017, 9, 89.	1.8	41
5708	Perilipin-2 modulates dietary fat-induced microbial global gene expression profiles in the mouse intestine. <i>Microbiome</i> , 2017, 5, 117.	4.9	17
5709	Whole plastid transcriptomes reveal abundant RNA editing sites and differential editing status in <i>Phalaenopsis aphrodite</i> subsp. <i>formosana</i> . , 2017, 58, 38.		34
5710	Comparative Transcriptome and DNA methylation analyses of the molecular mechanisms underlying skin color variations in Crucian carp ( <i>Carassius carassius</i> L.). <i>BMC Genetics</i> , 2017, 18, 95.	2.7	43
5711	Genome-wide identification and expression analysis of calmodulin-like (CML) genes in Chinese cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> ). <i>BMC Genomics</i> , 2017, 18, 842.	1.2	36
5712	Metabolic pathways and genes identified by RNA-seq analysis of barley near-isogenic lines differing by allelic state of the Black lemma and pericarp (Blp) gene. <i>BMC Plant Biology</i> , 2017, 17, 182.	1.6	22
5713	Differential expression of NBS-LRR-encoding genes in the root transcriptomes of two <i>Solanum phureja</i> genotypes with contrasting resistance to <i>Globodera rostochiensis</i> . <i>BMC Plant Biology</i> , 2017, 17, 251.	1.6	15
5714	2,4,6-Trinitrotoluene Induces Apoptosis via ROS-Regulated Mitochondrial Dysfunction and Endoplasmic Reticulum Stress in HepG2 and Hep3B Cells. <i>Scientific Reports</i> , 2017, 7, 8148.	1.6	27
5715	A broad range quorum sensing inhibitor working through sRNA inhibition. <i>Scientific Reports</i> , 2017, 7, 9857.	1.6	60
5716	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017, 18, 437.	1.2	45

#	ARTICLE	IF	CITATIONS
5717	LSTrAP: efficiently combining RNA sequencing data into co-expression networks. BMC Bioinformatics, 2017, 18, 444.	1.2	35
5718	BoolFilter: an R package for estimation and identification of partially-observed Boolean dynamical systems. BMC Bioinformatics, 2017, 18, 519.	1.2	17
5719	Non-SMC elements 1 and 3 are required for early embryo and seedling development in Arabidopsis. Journal of Experimental Botany, 2017, 68, 1039-1054.	2.4	58
5720	ARSDA: A New Approach for Storing, Transmitting and Analyzing Transcriptomic Data. G3: Genes, Genomes, Genetics, 2017, 7, 3839-3848.	0.8	16
5721	Venomics of Remipede Crustaceans Reveals Novel Peptide Diversity and Illuminates the Venom's Biological Role. Toxins, 2017, 9, 234.	1.5	27
5722	Transient inflammatory response mediated by interleukin-1 $\beta$ is required for proper regeneration in zebrafish fin fold. ELife, 2017, 6, .	2.8	112
5723	Sequencing and de novo assembly of the Asian gypsy moth transcriptome using the Illumina platform. Genetics and Molecular Biology, 2017, 40, 160-167.	0.6	2
5724	The Model-Based Study of the Effectiveness of Reporting Lists of Small Feature Sets Using RNA-Seq Data. Cancer Informatics, 2017, 16, 117693511771053.	0.9	1
5725	Toll-like receptor 3 as an immunotherapeutic target for KRAS mutated colorectal cancer. Oncotarget, 2017, 8, 35138-35153.	0.8	22
5726	Molecular Characterization of Copepod Photoreception. Biological Bulletin, 2017, 233, 96-110.	0.7	14
5727	Analysis of the Panax ginseng stem/leaf transcriptome and gene expression during the leaf expansion period. Molecular Medicine Reports, 2017, 16, 6396-6404.	1.1	5
5728	Comparative transcriptome and potential antiviral signaling pathways analysis of the gills in the red swamp crayfish, Procambarus clarkii infected with White Spot Syndrome Virus (WSSV). Genetics and Molecular Biology, 2017, 40, 168-180.	0.6	17
5729	Therapeutic Approaches and Role of ncRNAs in Cardiovascular Disorders and Insulin Resistance. BioMed Research International, 2017, 2017, 1-10.	0.9	14
5730	REGULAÇÃO GÊNICA DA VIA AMPK PELO EXERCÍCIO FÍSICO: REVISÃO SISTEMÁTICA E ANÁLISE IN SILICO. Revista Brasileira De Medicina Do Esporte, 2017, 23, 328-334.	0.1	3
5731	Elucidation of the molecular responses of a cucumber segment substitution line carrying Pm5.1 and its recurrent parent triggered by powdery mildew by comparative transcriptome profiling. BMC Genomics, 2017, 18, 21.	1.2	47
5732	Transcriptomics analysis of the flowering regulatory genes involved in the herbicide resistance of Asia minor bluegrass (Polypogon fugax). BMC Genomics, 2017, 18, 953.	1.2	10
5733	High-Throughput RNA-Seq Data Analysis of the Single Nucleotide Polymorphisms (SNPs) and Zygomorphic Flower Development in Pea (Pisum sativum L.). International Journal of Molecular Sciences, 2017, 18, 2710.	1.8	9
5734	Transcriptomics, metabolomics and histology indicate that high-carbohydrate diet negatively affects the liver health of blunt snout bream (Megalobrama amblycephala). BMC Genomics, 2017, 18, 856.	1.2	77

#	ARTICLE	IF	CITATIONS
5736	Transcriptomic profiling of genes in matured dimorphic seeds of euhalophyte Suaeda salsa. BMC Genomics, 2017, 18, 727.	1.2	27
5737	Amino Acid Changes during Energy Storage Compounds Accumulation of Microalgae under the Nitrogen Depletion. , 2017, , .		6
5738	Extending Immunological Profiling in the Gilthead Sea Bream, Sparus aurata, by Enriched cDNA Library Analysis, Microarray Design and Initial Studies upon the Inflammatory Response to PAMPs. International Journal of Molecular Sciences, 2017, 18, 317.	1.8	5
5739	Comparative Morphology, Transcription, and Proteomics Study Revealing the Key Molecular Mechanism of Camphor on the Potato Tuber Sprouting Effect. International Journal of Molecular Sciences, 2017, 18, 2280.	1.8	25
5740	Application of Next-generation Sequencing in Clinical Molecular Diagnostics. Brazilian Archives of Biology and Technology, 2017, 60, .	0.5	1
5741	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers1. Journal of Animal Science, 2017, 95, 599-615.	0.2	27
5742	RNA-Seq Validation of RNAi Identifies Additional Gene Connectivity in Tribolium castaneum (Coleoptera: Tenebrionidae). Journal of Insect Science, 2017, 17, .	0.6	6
5743	Association of variation in the sugarcane transcriptome with sugar content. BMC Genomics, 2017, 18, 909.	1.2	41
5744	Identification of Candidate Genes Responsible for Stem Pith Production Using Expression Analysis in Solidâ€Stemmed Wheat. Plant Genome, 2017, 10, plantgenome2017.02.0008.	1.6	8
5745	Investigating right ovary degeneration in chick embryos by transcriptome sequencing. Journal of Reproduction and Development, 2017, 63, 295-303.	0.5	9
5746	In Silico identification and annotation of non-coding RNAs by RNA-seq and De Novo assembly of the transcriptome of Tomato Fruits. PLoS ONE, 2017, 12, e0171504.	1.1	21
5747	TRIM28 multi-domain protein regulates cancer stem cell population in breast tumor development. Oncotarget, 2017, 8, 863-882.	0.8	49
5748	Transcriptome analysis for the restrained stem development of the wheat mutant dms. Ciencia Rural, 2017, 47, .	0.3	0
5749	THE ROLE OF TRANSCRIPTOMICS: PHYSIOLOGICAL EQUIVALENCE BASED ON GENE EXPRESSION PROFILES. Reviews in Agricultural Science, 2017, 5, 21-35.	0.9	1
5750	Omicseq: a web-based search engine for exploring omics datasets. Nucleic Acids Research, 2017, 45, W445-W452.	6.5	11
5751	<i>ERCC6L</i>, a DNA helicase, is involved in cell proliferation and associated with survival and progress in breast and kidney cancers. Oncotarget, 2017, 8, 42116-42124.	0.8	43
5752	Nucleosome Positioning of Intronless Genes in the Human Genome. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1111-1121.	1.9	3
5753	Examining De Novo Transcriptome Assemblies via a Quality Assessment Pipeline. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 494-505.	1.9	4

#	ARTICLE	IF	CITATIONS
5754	Optimal Fault Detection and Diagnosis in Transcriptional Circuits Using Next-Generation Sequencing. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 516-525.	1.9	16
5755	Morphophysiological and transcriptome analysis reveals a multiline defense system enabling cyanobacterium <i>Leptolyngbya</i> strain JSC-1 to withstand iron induced oxidative stress. Chemosphere, 2018, 200, 93-105.	4.2	12
5756	Role of the inositol pyrophosphate multikinase Kcs1 in <i>Cryptococcus</i> inositol metabolism. Fungal Genetics and Biology, 2018, 113, 42-51.	0.9	5
5757	Characterization of metabolic network of oxalic acid biosynthesis through RNA seq data analysis of developing spikes of finger millet ( <i>Eleusine coracana</i> ): Deciphering the role of key genes involved in oxalate formation in relation to grain calcium accumulation. Gene, 2018, 649, 40-49.	1.0	17
5758	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. Immunity, 2018, 48, 227-242.e8.	6.6	188
5759	OsDSSR1, a novel small peptide, enhances drought tolerance in transgenic rice. Plant Science, 2018, 270, 85-96.	1.7	22
5760	Transcriptomic and metabolomic responses induced in the livers of growing pigs by a short-term intravenous infusion of sodium butyrate. Animal, 2018, 12, 2318-2326.	1.3	11
5761	Patient-derived organoids model treatment response of metastatic gastrointestinal cancers. Science, 2018, 359, 920-926.	6.0	1,199
5762	De Novo Transcriptome Assembly of <i>Isatis indigotica</i> at Reproductive Stages and Identification of Candidate Genes Associated with Flowering Pathways. Journal of the American Society for Horticultural Science, 2018, 143, 56-66.	0.5	3
5763	Molecular identification of four novel cytochrome P450 genes related to the development of resistance of <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae) to chlorantraniliprole. Pest Management Science, 2018, 74, 1938-1952.	1.7	50
5764	Comparative transcriptome profiling and characterization of gene expression for ovarian differentiation under RU486 treatment. General and Comparative Endocrinology, 2018, 261, 166-173.	0.8	5
5765	Obligatory Metabolism of Angiotensin II to Angiotensin III for Zona Glomerulosa Cell-Mediated Relaxations of Bovine Adrenal Cortical Arteries. Endocrinology, 2018, 159, 238-247.	1.4	4
5766	Characterization of Spleen Transcriptome of <i>Schizothorax prenanti</i> during <i>Aeromonas hydrophila</i> Infection. Marine Biotechnology, 2018, 20, 246-256.	1.1	34
5767	Transcriptomic analyses of tributyltin-induced sexual dimorphisms in rare minnow ( <i>Gobiocypris</i> ) Tj ETQq1 1 0.7843]4 rgBT /Qverlock 10	2.9	7
5768	Improving the value of public RNA-seq expression data by phenotype prediction. Nucleic Acids Research, 2018, 46, e54-e54.	6.5	49
5769	Capturing the "ome": the expanding molecular toolbox for RNA and DNA library construction. Nucleic Acids Research, 2018, 46, 2701-2721.	6.5	22
5770	Culture-Facilitated Comparative Genomics of the Facultative Symbiont <i>Hamiltonella defensa</i> . Genome Biology and Evolution, 2018, 10, 786-802.	1.1	37
5771	Comparative transcriptome discovery and elucidation of the mechanism of long noncoding RNAs during vernalization in <i>Brassica rapa</i> . Plant Growth Regulation, 2018, 85, 27-39.	1.8	19

#	ARTICLE	IF	CITATIONS
5772	Combinatory use of distinct single-cell RNA-seq analytical platforms reveals the heterogeneous transcriptome response. <i>Scientific Reports</i> , 2018, 8, 3482.	1.6	19
5773	Recognition of the long range enhancer-promoter interactions by further adding DNA structure properties and transcription factor binding motifs in human cell lines. <i>Journal of Theoretical Biology</i> , 2018, 445, 136-150.	0.8	8
5774	Integrative omics for health and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 299-310.	7.7	676
5775	Comparative transcriptomics of multidrug-resistant <i>Acinetobacter baumannii</i> in response to antibiotic treatments. <i>Scientific Reports</i> , 2018, 8, 3515.	1.6	53
5776	Transcriptome-sequencing analyses reveal putative genes related to flower color variation in Chinese <i>Rosa rugosa</i> . <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	10
5777	Identification of "Xinlimei"™ radish candidate genes associated with anthocyanin biosynthesis based on a transcriptome analysis. <i>Gene</i> , 2018, 657, 81-91.	1.0	24
5778	Transcriptome analysis of colouration-related genes in two white-fleshed nectarine varieties and their yellow-fleshed mutants. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 899-907.	0.5	4
5779	Genome-scale biological models for industrial microbial systems. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3439-3451.	1.7	14
5780	Understanding the high l-valine production in <i>Corynebacterium glutamicum</i> VWB-1 using transcriptomics and proteomics. <i>Scientific Reports</i> , 2018, 8, 3632.	1.6	34
5781	Heme degradation enzyme biliverdin IX <sup>α</sup> reductase is required for stem cell glutamine metabolism. <i>Biochemical Journal</i> , 2018, 475, 1211-1223.	1.7	6
5782	Unraveling a crosstalk regulatory network of temporal aroma accumulation in tea plant ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Botany, 2018, 149, 81-94.	2.0	89
5783	Comparative transcriptomic analysis of white and red Chinese bayberry ( <i>Myrica rubra</i> ) fruits reveals flavonoid biosynthesis regulation. <i>Scientia Horticulturae</i> , 2018, 235, 9-20.	1.7	19
5784	Integrative analysis of transcriptomics and metabolomics profiling on flesh quality of large yellow croaker <i>Larimichthys crocea</i> fed a diet with hydroxyproline supplementation. <i>British Journal of Nutrition</i> , 2018, 119, 359-367.	1.2	23
5785	Measurement of metabolite variations and analysis of related gene expression in Chinese liquorice ( <i>Glycyrrhiza uralensis</i> ) plants under UV-B irradiation. <i>Scientific Reports</i> , 2018, 8, 6144.	1.6	39
5786	Introduction to Single-Cell RNA Sequencing. <i>Current Protocols in Molecular Biology</i> , 2018, 122, e57.	2.9	115
5787	GhWIP2, a WIP zinc finger protein, suppresses cell expansion in <i>Gerbera hybrida</i> by mediating crosstalk between gibberellin, abscisic acid, and auxin. <i>New Phytologist</i> , 2018, 219, 728-742.	3.5	29
5788	Characterization of Human Salivary Extracellular RNA by Next-generation Sequencing. <i>Clinical Chemistry</i> , 2018, 64, 1085-1095.	1.5	33
5789	Real-time Analysis of Transcription Factor Binding, Transcription, Translation, and Turnover to Display Global Events During Cellular Activation. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	1

#	ARTICLE	IF	CITATIONS
5790	Functional characterization of transposon-tagged abiotic stress-responsive rice genes and their molecular polymorphisms among various stress-tolerant genotypes. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	0
5791	Regulation of Large Number of Weak Targets—New Insights from Twin-microRNAs. <i>Genome Biology and Evolution</i> , 2018, 10, 1255-1264.	1.1	13
5792	A 360° view of circular RNAs: From biogenesis to functions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1478.	3.2	356
5793	RNA localization regulates diverse and dynamic cellular processes. <i>Traffic</i> , 2018, 19, 496-502.	1.3	61
5794	Mechanistic Investigations of Diarrhea Toxicity Induced by Anti-HER2/3 Combination Therapy. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1464-1474.	1.9	18
5795	Transcriptome analysis of <i>Hevea brasiliensis</i> in response to exogenous methyl jasmonate provides novel insights into regulation of jasmonate-elicited rubber biosynthesis. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 349-358.	1.4	20
5796	Fish red blood cells express immune genes and responses. <i>Aquaculture and Fisheries</i> , 2018, 3, 14-21.	1.2	63
5797	Transcriptomic data of pre-meiotic stage of floret development in apomictic and sexual types of guinea grass ( <i>Panicum maximum</i> Jacq.). <i>Data in Brief</i> , 2018, 18, 590-593.	0.5	15
5798	High-throughput sequencing for algal systematics. <i>European Journal of Phycology</i> , 2018, 53, 256-272.	0.9	33
5799	The <i>RNA</i> binding protein Hfq is important for ribosome biogenesis and affects translation fidelity. <i>EMBO Journal</i> , 2018, 37, .	3.5	73
5800	Predicting essential proteins based on RNA-Seq, subcellular localization and GO annotation datasets. <i>Knowledge-Based Systems</i> , 2018, 151, 136-148.	4.0	58
5801	Identification and function of FAR protein family genes from a transcriptome analysis of <i>Aphelenchoides besseyi</i> . <i>Bioinformatics</i> , 2018, 34, 2936-2943.	1.8	10
5802	MicroRNA networks associated with active systemic juvenile idiopathic arthritis regulate CD163 expression and anti-inflammatory functions in macrophages through two distinct mechanisms. <i>Journal of Leukocyte Biology</i> , 2018, 103, 71-85.	1.5	19
5803	Gonadal Transcriptome Analysis of Pacific Abalone <i>Haliotis discus discus</i> : Identification of Genes Involved in Germ Cell Development. <i>Marine Biotechnology</i> , 2018, 20, 467-480.	1.1	31
5804	Cis-regulated additively expressed genes play a fundamental role in the formation of triploid loquat ( <i>Eriobotrya japonica</i> (Thunb.) Lindl.) Heterosis. <i>Molecular Genetics and Genomics</i> , 2018, 293, 967-981.	1.0	4
5805	Transcriptome analysis of <i>Brassica juncea</i> var. <i>tumida</i> Tsen responses to <i>Plasmodiophora brassicae</i> primed by the biocontrol strain <i>Zhihengliuella aestuarii</i> . <i>Functional and Integrative Genomics</i> , 2018, 18, 301-314.	1.4	31
5806	The gene regulatory program of <i>Acroboloides nanus</i> reveals conservation of phylum-specific expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4459-4464.	3.3	20
5807	A Beginner's Guide to Analysis of RNA Sequencing Data. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 145-157.	1.4	78

#	ARTICLE	IF	CITATIONS
5808	Distinct transcriptomic and exomic abnormalities within myelodysplastic syndrome marrow cells. <i>Leukemia and Lymphoma</i> , 2018, 59, 2952-2962.	0.6	16
5809	Patterns of thaumarchaeal gene expression in culture and diverse marine environments. <i>Environmental Microbiology</i> , 2018, 20, 2112-2124.	1.8	92
5810	Gene expression during different periods of the handling-stress response in <i>Pampus argenteus</i> . <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1349-1359.	0.6	3
5811	Strand-specific RNA-seq analysis of the <i>Acidithiobacillus ferrooxidans</i> transcriptome in response to magnesium stress. <i>Archives of Microbiology</i> , 2018, 200, 1025-1035.	1.0	9
5812	Utility of pooled sequencing for association mapping in nonmodel organisms. <i>Molecular Ecology Resources</i> , 2018, 18, 825-837.	2.2	43
5813	Distinct gene expression pathways in islets from individuals with short- and long-duration type 1 diabetes. <i>Diabetes, Obesity and Metabolism</i> , 2018, 20, 1859-1867.	2.2	31
5814	Widespread changes in transcriptome profile of human mesenchymal stem cells induced by two-dimensional nanosilicates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3905-E3913.	3.3	119
5815	Effect of dietary chitosan oligosaccharide supplementation on the pig ovary transcriptome. <i>RSC Advances</i> , 2018, 8, 13266-13273.	1.7	6
5816	QStatin, a Selective Inhibitor of Quorum Sensing in <i>Vibrio</i> Species. <i>MBio</i> , 2018, 9, .	1.8	44
5817	De novo transcriptome assembly and analysis of differential gene expression following peptidoglycan (PGN) challenge in <i>Antheraea pernyi</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 112, 1199-1207.	3.6	8
5818	Transcriptome analysis reveals carbohydrate-mediated liver immune responses in <i>Epinephelus akaara</i> . <i>Scientific Reports</i> , 2018, 8, 639.	1.6	29
5819	Integrated transcriptomic and proteomic analyses reveal potential mechanisms linking thermal stress and depressed disease resistance in the turbot <i>Scophthalmus maximus</i> . <i>Scientific Reports</i> , 2018, 8, 1896.	1.6	17
5820	Identification of cancer-related potential biomarkers based on lncRNA-pseudogene-mRNA competitive networks. <i>FEBS Letters</i> , 2018, 592, 973-986.	1.3	9
5821	The genome sequence and transcriptome of <i>Potentilla micrantha</i> and their comparison to <i>Fragaria vesca</i> (the woodland strawberry). <i>GigaScience</i> , 2018, 7, 1-14.	3.3	37
5822	Age-Associated Decline in Thymic B Cell Expression of Aire and Aire-Dependent Self-Antigens. <i>Cell Reports</i> , 2018, 22, 1276-1287.	2.9	51
5823	Expression of homing endonuclease gene and insertion-like element in sea anemone mitochondrial genomes: Lesson learned from <i>Anemonia viridis</i> . <i>Gene</i> , 2018, 652, 78-86.	1.0	15
5824	RNA-Seq Analysis of the Transcriptome of Leaf Senescence in Tobacco. <i>Methods in Molecular Biology</i> , 2018, 1744, 331-337.	0.4	17
5825	Lose it or keep it: (how bivalves can provide) insights into mitochondrial inheritance mechanisms. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2018, 330, 41-51.	0.6	12



#	ARTICLE	IF	CITATIONS
5827	Analysis of digital gene expression profiling in the gonad of male silkworms ( <i>Bombyx mori</i> ) under fluoride stress. <i>Ecotoxicology and Environmental Safety</i> , 2018, 153, 127-134.	2.9	17
5828	An unusual strategy of stomatal control in the desert shrub <i>Ammopiptanthus mongolicus</i> . <i>Plant Physiology and Biochemistry</i> , 2018, 125, 13-26.	2.8	7
5829	Transcriptional and splicing dysregulation in the prefrontal cortex in valproic acid rat model of autism. <i>Reproductive Toxicology</i> , 2018, 77, 53-61.	1.3	38
5830	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490.	5.8	198
5831	Comparative Analysis of Differential Gene Expression Profiling of Sex-Bias Fat Body of <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) Identifying a New Vitellogenin Gene. <i>Annals of the Entomological Society of America</i> , 2018, 111, 43-54.	1.3	11
5832	Global transcriptome analysis identifies weight regain-induced activation of adaptive immune responses in white adipose tissue of mice. <i>International Journal of Obesity</i> , 2018, 42, 755-764.	1.6	14
5833	AmrZ is a major determinant of c-di-GMP levels in <i>Pseudomonas fluorescens</i> F113. <i>Scientific Reports</i> , 2018, 8, 1979.	1.6	27
5834	Transcriptomic insight into pathogenicity-associated factors of <i>Conidiobolus obscurus</i> , an obligate aphid pathogenic fungus belonging to Entomophthoromycota. <i>Pest Management Science</i> , 2018, 74, 1677-1686.	1.7	12
5835	Quantitative mRNA Imaging with Dual Channel qFIT Probes to Monitor Distribution and Degree of Hybridization. <i>ACS Chemical Biology</i> , 2018, 13, 742-749.	1.6	15
5836	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	2.8	133
5837	Advances in Transcriptomics of Plants. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, 164, 161-185.	0.6	18
5838	Global and targeted approaches to single-cell transcriptome characterization. <i>Briefings in Functional Genomics</i> , 2018, 17, 209-219.	1.3	28
5839	Prenatal Exposure to Bisphenol A Disrupts Naturally Occurring Bimodal DNA Methylation at Proximal Promoter of <i>fggy</i> , an Obesity-Relevant Gene Encoding a Carbohydrate Kinase, in Gonadal White Adipose Tissues of CD-1 Mice. <i>Endocrinology</i> , 2018, 159, 779-794.	1.4	29
5840	RNentropy: an entropy-based tool for the detection of significant variation of gene expression across multiple RNA-Seq experiments. <i>Nucleic Acids Research</i> , 2018, 46, e46-e46.	6.5	30
5841	Genome-wide and expression profiling analyses suggest the main cytochrome P450 genes related to pyrethroid resistance in the malaria vector, <i>Anopheles sinensis</i> (Diptera Culicidae). <i>Pest Management Science</i> , 2018, 74, 1810-1820.	1.7	27
5842	Genetic characterization and modification of a bioethanol-producing yeast strain. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2213-2223.	1.7	5
5843	Blood transcriptomics of captive forest musk deer ( <i>Moschus berezovskii</i> ) and possible associations with the immune response to abscesses. <i>Scientific Reports</i> , 2018, 8, 599.	1.6	17
5844	A Myc enhancer cluster regulates normal and leukaemic haematopoietic stem cell hierarchies. <i>Nature</i> , 2018, 553, 515-520.	13.7	256

#	ARTICLE	IF	CITATIONS
5845	Genome-wide comparative analysis of papain-like cysteine protease family genes in castor bean and physic nut. <i>Scientific Reports</i> , 2018, 8, 331.	1.6	28
5846	Brain of the blind: transcriptomics of the golden-line cavefish brain. <i>Environmental Epigenetics</i> , 2018, 64, 765-773.	0.9	8
5847	Genomic and transcriptomic analysis of the Asian honeybee <i>Apis cerana</i> provides novel insights into honeybee biology. <i>Scientific Reports</i> , 2018, 8, 822.	1.6	68
5848	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	21
5849	Transcriptome-wide identification and functional prediction of novel and flowering-related circular RNAs from trifoliolate orange ( <i>Poncirus trifoliata</i> L. Raf.). <i>Planta</i> , 2018, 247, 1191-1202.	1.6	32
5850	Hyperactive gp130/STAT3-driven gastric tumorigenesis promotes submucosal tertiary lymphoid structure development. <i>International Journal of Cancer</i> , 2018, 143, 167-178.	2.3	43
5851	Octopus-toolkit: a workflow to automate mining of public epigenomic and transcriptomic next-generation sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, e53-e53.	6.5	61
5852	Stress-induced pyruvate accumulation contributes to cross protection in a fungus. <i>Environmental Microbiology</i> , 2018, 20, 1158-1169.	1.8	22
5853	Effect of high night temperature on storage lipids and transcriptome changes in developing seeds of oilseed rape. <i>Journal of Experimental Botany</i> , 2018, 69, 1721-1733.	2.4	30
5854	Brain Transcriptome Databases: A User's Guide. <i>Journal of Neuroscience</i> , 2018, 38, 2399-2412.	1.7	68
5855	RNA-seq analysis of the transcriptome of the liver of cynomolgus monkeys with type 2 diabetes. <i>Gene</i> , 2018, 651, 118-125.	1.0	13
5856	Leukemia-propagating cells demonstrate distinctive gene expression profiles compared with other cell fractions from patients with de novo Philadelphia chromosome-positive ALL. <i>Annals of Hematology</i> , 2018, 97, 799-811.	0.8	0
5857	Transcriptomic and gene expression changes in response to postharvest surface pitting in 'Lingwu Long' jujube fruit. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 59-70.	0.7	9
5858	HpaP, a novel regulatory protein with ATPase and phosphatase activity, contributes to full virulence in <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Environmental Microbiology</i> , 2018, 20, 1389-1404.	1.8	16
5859	Defective XRN3-mediated transcription termination in <i>Arabidopsis</i> affects the expression of protein-coding genes. <i>Plant Journal</i> , 2018, 93, 1017-1031.	2.8	31
5860	Identification of the genes in tea leafhopper, <i>Empoasca onukii</i> (Hemiptera: Cicadellidae), that encode odorant-binding proteins and chemosensory proteins using transcriptome analyses of insect heads. <i>Applied Entomology and Zoology</i> , 2018, 53, 93-105.	0.6	15
5861	Examination of gene repertoires and physiological responses to iron and light limitation in Southern Ocean diatoms. <i>Polar Biology</i> , 2018, 41, 679-696.	0.5	28
5862	HtrA1 Mediated Intracellular Effects on Tubulin Using a Polarized RPE Disease Model. <i>EBioMedicine</i> , 2018, 27, 258-274.	2.7	17

#	ARTICLE	IF	CITATIONS
5863	RNA-Seq transcriptomic analysis of the <i>Morus alba</i> L. leaves exposed to high-level UVB with or without dark treatment. <i>Gene</i> , 2018, 645, 60-68.	1.0	18
5864	Physiological and transcriptomic analyses of a yellow-green mutant with high photosynthetic efficiency in wheat ( <i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2018, 18, 175-194.	1.4	21
5865	Comparative transcriptomic analysis of shrimp hemocytes in response to acute hepatopancreas necrosis disease (AHPND) causing <i>Vibrio parahaemolyticus</i> infection. <i>Fish and Shellfish Immunology</i> , 2018, 74, 10-18.	1.6	47
5866	Transcriptional landscapes of Axolotl ( <i>Ambystoma mexicanum</i> ). <i>Developmental Biology</i> , 2018, 433, 227-239.	0.9	31
5867	Cancer transcriptome profiling at the juncture of clinical translation. <i>Nature Reviews Genetics</i> , 2018, 19, 93-109.	7.7	202
5868	Metallothionein I as a direct link between therapeutic hematopoietic stem/progenitor cells and cerebral protection in stroke. <i>FASEB Journal</i> , 2018, 32, 2381-2394.	0.2	9
5869	Transcriptome analysis of $\hat{m}ig1\hat{m}ig2$ mutant reveals their roles in methanol catabolism, peroxisome biogenesis and autophagy in methylotrophic yeast <i>Pichia pastoris</i> . <i>Genes and Genomics</i> , 2018, 40, 399-412.	0.5	15
5870	Bothrops jararaca accessory venom gland is an ancillary source of toxins to the snake. <i>Journal of Proteomics</i> , 2018, 177, 137-147.	1.2	13
5871	Transcriptome analysis of bovine lymphocytes stimulated by <i>Atractylodis macrocephalae</i> Koidz. polysaccharides in vitro. <i>Veterinary Immunology and Immunopathology</i> , 2018, 196, 30-34.	0.5	21
5872	Selected microRNA-192 mutant indicates association with several function genes in bovine cells. <i>Genes and Genomics</i> , 2018, 40, 361-371.	0.5	0
5873	Transcription profiling and identification of infection-related genes in <i>Phytophthora cactorum</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 541-555.	1.0	23
5874	A Workflow for <i>In Vivo</i> Evaluation of Candidate Inputs and Outputs for Cell Classifier Gene Circuits. <i>ACS Synthetic Biology</i> , 2018, 7, 474-489.	1.9	12
5875	Comparative transcriptome analysis of <i>Anguilla japonica</i> livers following exposure to methylene blue. <i>Aquaculture Research</i> , 2018, 49, 1232-1241.	0.9	9
5876	The Role of Nucleosome Positioning in Genome Function and Evolution. , 2018, , 41-79.		2
5877	Identification of differentially expressed genes in longissimus dorsi muscle between Wei and Yorkshire pigs using RNA sequencing. <i>Genes and Genomics</i> , 2018, 40, 413-421.	0.5	43
5878	Transcriptome analysis of <i>Cyrtotrachelus buqueti</i> in two cities in China. <i>Gene</i> , 2018, 647, 1-12.	1.0	10
5879	Circular RNAs. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	2
5880	Transcriptome sequencing and de novo assembly in arecanut, <i>Areca catechu</i> L elucidates the secondary metabolite pathway genes. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2018, 17, 63-69.	2.1	14

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5881	Single-Molecule Fluorescence In Situ Hybridization (FISH) of Circular RNA CDR1as. <i>Methods in Molecular Biology</i> , 2018, 1724, 77-96.	0.4	26
5882	Transcriptomes of Fruit Cavity Revealed by De Novo Sequence Analysis in Nai Plum ( <i>Prunus salicina</i> ). <i>Journal of Plant Growth Regulation</i> , 2018, 37, 730-744.	2.8	3
5883	Transcriptomic profiling of developing fiber in levant cotton ( <i>Gossypium herbaceum</i> L.). <i>Functional and Integrative Genomics</i> , 2018, 18, 211-223.	1.4	10
5884	Analyzing the interactions of mRNAs, miRNAs, lncRNAs and circRNAs to predict competing endogenous RNA networks in glioblastoma. <i>Journal of Neuro-Oncology</i> , 2018, 137, 493-502.	1.4	67
5885	Whole transcriptome analysis reveals potential novel mechanisms of low-level linezolid resistance in <i>Enterococcus faecalis</i> . <i>Gene</i> , 2018, 647, 143-149.	1.0	22
5886	Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice. <i>Nature Genetics</i> , 2018, 50, 278-284.	9.4	453
5887	Statistical analysis of non-coding RNA data. <i>Cancer Letters</i> , 2018, 417, 161-167.	3.2	18
5888	DART: a fast and accurate RNA-seq mapper with a partitioning strategy. <i>Bioinformatics</i> , 2018, 34, 190-197.	1.8	16
5889	Transcriptome changes induced by arbuscular mycorrhizal fungi in sunflower ( <i>Helianthus annuus</i> L.) roots. <i>Scientific Reports</i> , 2018, 8, 4.	1.6	170
5891	ASElux: an ultra-fast and accurate allelic reads counter. <i>Bioinformatics</i> , 2018, 34, 1313-1320.	1.8	13
5892	Comparative genome and transcriptome analyses reveal adaptations to opportunistic infections in woody plant degrading pathogens of Botryosphaeriaceae. <i>DNA Research</i> , 2018, 25, 87-102.	1.5	60
5893	Selecting between-sample RNA-Seq normalization methods from the perspective of their assumptions. <i>Briefings in Bioinformatics</i> , 2018, 19, 776-792.	3.2	221
5894	Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. <i>Nucleic Acids Research</i> , 2018, 46, D221-D228.	6.5	97
5895	TranslatomeDB: a comprehensive database and cloud-based analysis platform for translatome sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, D206-D212.	6.5	36
5896	Ontological function annotation of long non-coding RNAs through hierarchical multi-label classification. <i>Bioinformatics</i> , 2018, 34, 1750-1757.	1.8	48
5897	An Evolutionary Landscape of A-to-I RNA Editome across Metazoan Species. <i>Genome Biology and Evolution</i> , 2018, 10, 521-537.	1.1	22
5898	The Expanding Landscape of Alternative Splicing Variation in Human Populations. <i>American Journal of Human Genetics</i> , 2018, 102, 11-26.	2.6	290
5899	N6-Methyladenosines Modulate A-to-I RNA Editing. <i>Molecular Cell</i> , 2018, 69, 126-135.e6.	4.5	108

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5900	Development of a new comprehensive and reliable endometrial receptivity map (ER Map/ER Grade) based on RT-qPCR gene expression analysis. <i>Human Reproduction</i> , 2018, 33, 220-228.	0.4	80
5901	Silhouette Scores for Arbitrary Defined Groups in Gene Expression Data and Insights into Differential Expression Results. <i>Biological Procedures Online</i> , 2018, 20, 5.	1.4	27
5902	High-throughput detection of RNA processing in bacteria. <i>BMC Genomics</i> , 2018, 19, 223.	1.2	33
5903	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. <i>BMC Genomics</i> , 2018, 19, 236.	1.2	19
5904	Robust Sub-nanomolar Library Preparation for High Throughput Next Generation Sequencing. <i>BMC Genomics</i> , 2018, 19, 326.	1.2	16
5905	Deciphering lignocellulose deconstruction by the white rot fungus <i>Irpex lacteus</i> based on genomic and transcriptomic analyses. <i>Biotechnology for Biofuels</i> , 2018, 11, 58.	6.2	38
5906	Gene regulatory network state estimation from arbitrary correlated measurements. <i>Eurasip Journal on Advances in Signal Processing</i> , 2018, 2018, .	1.0	15
5907	Genomic methylation and transcriptomic profiling provides insights into heading depression in inbred <i>Brassica rapa L. ssp. pekinensis</i> . <i>Gene</i> , 2018, 665, 119-126.	1.0	5
5908	Comparative transcriptomic analysis reveals the mechanism of leech environmental adaptation. <i>Gene</i> , 2018, 664, 70-77.	1.0	10
5909	De novo assembly of <i>Schizothorax waltoni</i> transcriptome to identify immune-related genes and microsatellite markers. <i>RSC Advances</i> , 2018, 8, 13945-13953.	1.7	4
5910	Enhanced JBrowse plugins for epigenomics data visualization. <i>BMC Bioinformatics</i> , 2018, 19, 159.	1.2	20
5911	Transcriptome profiling of two maize inbreds with distinct responses to <i>Gibberella ear rot</i> disease to identify candidate resistance genes. <i>BMC Genomics</i> , 2018, 19, 131.	1.2	43
5912	Finite-size effects in transcript sequencing count distribution: its power-law correction necessarily precedes downstream normalization and comparative analysis. <i>Biology Direct</i> , 2018, 13, 2.	1.9	1
5913	Identification of <i>Rehmannia glutinosa L.</i> NB-ARC family proteins and their typical changes under consecutive monoculture stress. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	4
5914	Using an Open-Source Microcontroller and a Dye-Sensitized Solar Cell To Guide Students from Basic Principles to a Practical Application. <i>Journal of Chemical Education</i> , 2018, 95, 1173-1178.	1.1	10
5915	Assessment of Embryo-Induced Transcriptomic Changes in Hamster Uterus Using RNA-Seq. <i>Cellular Physiology and Biochemistry</i> , 2018, 46, 1868-1878.	1.1	11
5916	Very Low Abundance Single-Cell Transcript Quantification with 5-Plex ddPCR™ Assays. <i>Methods in Molecular Biology</i> , 2018, 1768, 423-444.	0.4	0
5917	De novo transcriptome assembly and identification of salt-responsive genes in sugar beet M14. <i>Computational Biology and Chemistry</i> , 2018, 75, 1-10.	1.1	21

#	ARTICLE	IF	CITATIONS
5918	Transcriptome profiling analysis revealed co-regulation of multiple pathways in jujube during infection by <i>Candidatus Phytoplasma ziziphi</i> . <i>Gene</i> , 2018, 665, 82-95.	1.0	31
5919	Elucidation of the Mechanisms of Long-Distance mRNA Movement in a <i>Nicotiana benthamiana</i> /Tomato Heterograft System. <i>Plant Physiology</i> , 2018, 177, 745-758.	2.3	72
5920	Transcriptome analysis reveals hybridization-induced genome shock in an interspecific <i>F<sub>1</sub></i> hybrid from <i>Camellia</i> . <i>Genome</i> , 2018, 61, 477-485.	0.9	7
5921	<i>Aspergillus flavus</i> GPI-anchored protein-encoding <i>ecm33</i> has a role in growth, development, aflatoxin biosynthesis, and maize infection. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 5209-5220.	1.7	27
5922	Nickel-induced global gene expressions in red maple ( <i>Acer rubrum</i> ): Effect of nickel concentrations. <i>Plant Gene</i> , 2018, 14, 29-36.	1.4	8
5923	Comparative Transcriptomics in Two Bivalve Species Offers Different Perspectives on the Evolution of Sex-Biased Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 1389-1402.	1.1	17
5924	Transcriptional profiling of the CAM plant <i>Agave salmiana</i> reveals conservation of a genetic program for regeneration. <i>Developmental Biology</i> , 2018, 442, 28-39.	0.9	17
5925	Identification of diverse target RNAs that are functionally regulated by human Pumilio proteins. <i>Nucleic Acids Research</i> , 2018, 46, 362-386.	6.5	80
5926	MSIQ: Joint modeling of multiple RNA-seq samples for accurate isoform quantification. <i>Annals of Applied Statistics</i> , 2018, 12, 510-539.	0.5	5
5927	The bZIP transcriptional factor activator protein-1 regulates <i>Metarhizium rileyi</i> morphology and mediates microsclerotia formation. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 4577-4588.	1.7	15
5928	trans-10,cis-12 conjugated linoleic acid alters lipid metabolism of goat mammary epithelial cells by regulation of de novo synthesis and the AMPK signaling pathway. <i>Journal of Dairy Science</i> , 2018, 101, 5571-5581.	1.4	18
5929	Deep sequencing-based characterization of transcriptome of <i>Pyrus ussuriensis</i> in response to cold stress. <i>Gene</i> , 2018, 661, 109-118.	1.0	30
5930	Missing data and technical variability in single-cell RNA-sequencing experiments. <i>Biostatistics</i> , 2018, 19, 562-578.	0.9	388
5931	Identification of DFR as a promoter of anthocyanin accumulation in poinsettia ( <i>Euphorbia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T5 158-165.	1.7	18
5932	A transcriptional factor B paralog functions as an activator to DNA damage-responsive expression in archaea. <i>Nucleic Acids Research</i> , 2018, 46, 7085-7096.	6.5	32
5933	Complementary transcriptome and proteome profiling in cabbage buds of a recessive male sterile mutant provides new insights into male reproductive development. <i>Journal of Proteomics</i> , 2018, 179, 80-91.	1.2	24
5934	Tagmentation on Microbeads: Restore Long-Range DNA Sequence Information Using Next Generation Sequencing with Library Prepared by Surface-Immobilized Transposomes. <i>ACS Applied Materials &amp; Interfaces</i> , 2018, 10, 11539-11545.	4.0	8
5935	Identification of an Unfavorable Immune Signature in Advanced Lung Tumors from Nrf2-Deficient Mice. <i>Antioxidants and Redox Signaling</i> , 2018, 29, 1535-1552.	2.5	31

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5936	The long noncoding RNA landscape in cardiovascular disease. <i>Current Opinion in Cardiology</i> , 2018, 33, 282-289.	0.8	21
5937	Salicylic acid-induced flavonoid accumulation in <i>Ginkgo biloba</i> leaves is dependent on red and far-red light. <i>Industrial Crops and Products</i> , 2018, 118, 102-110.	2.5	35
5938	ESR2 regulates granulosa cell genes essential for follicle maturation and ovulation. <i>Molecular and Cellular Endocrinology</i> , 2018, 474, 214-226.	1.6	63
5939	Geospatial distribution of viromes in tropical freshwater ecosystems. <i>Water Research</i> , 2018, 137, 220-232.	5.3	33
5940	Genome-wide gene expression profiles in response to downy mildew in Chinese cabbage ( <i>Brassica rapa</i> ) Tj ETQq0 0.0 r gBT /Overlock 10	0.8	10
5941	Genome-wide characterization of the basic leucine zipper transcription factors in <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	17
5942	Serum biochemistry, histology and transcriptomic profile analysis reflect liver inflammation and damage following dietary histamine supplementation in yellow catfish ( <i>Pelteobagrus fulvidraco</i> ). <i>Fish and Shellfish Immunology</i> , 2018, 77, 83-90.	1.6	30
5943	Continuous Variation within Cell Types of the Nervous System. <i>Trends in Neurosciences</i> , 2018, 41, 337-348.	4.2	66
5944	Genome-wide differential expression profiling in wild and cultivar genotypes of cardamom reveals regulation of key pathways in plant growth and development. <i>Agri Gene</i> , 2018, 8, 18-27.	1.9	2
5945	Functional characteristics of phenolic compounds accumulated in young leaves of two subtropical forest tree species of different successional stages. <i>Tree Physiology</i> , 2018, 38, 1486-1501.	1.4	29
5946	Molecular characterization and evolution of a chemosensory receptor gene family in three notorious rice planthoppers, <i>Nilaparvata lugens</i> , <i>Sogatella furcifera</i> and <i>Laodelphax striatellus</i> , based on genome and transcriptome analyses. <i>Pest Management Science</i> , 2018, 74, 2156-2167.	1.7	54
5947	Profiling of glucose-induced transcription in <i>Sulfolobus acidocaldarius</i> DSM 639. <i>Genes and Genomics</i> , 2018, 40, 1157-1167.	0.5	3
5948	Deep Sequencing Reveals New Insights Into the Transcriptomic Response to Uva Radiation in the Heads of <i>Drosophila melanogaster</i> Meigen, 1830 (Diptera: Drosophilidae). <i>Proceedings of the Entomological Society of Washington</i> , 2018, 120, 211-226.	0.0	0
5949	Transcriptome analysis of Pacific white shrimp ( <i>Litopenaeus vannamei</i> ) challenged by <i>Vibrio parahaemolyticus</i> reveals unique immune-related genes. <i>Fish and Shellfish Immunology</i> , 2018, 77, 164-174.	1.6	82
5950	Polyamines Regulate Strawberry Fruit Ripening by Abscisic Acid, Auxin, and Ethylene. <i>Plant Physiology</i> , 2018, 177, 339-351.	2.3	129
5951	Improved Ribo-seq enables identification of cryptic translation events. <i>Nature Methods</i> , 2018, 15, 363-366.	9.0	153
5952	Loss and gain of N-linked glycosylation sequons due to single-nucleotide variation in cancer. <i>Scientific Reports</i> , 2018, 8, 4322.	1.6	15
5953	Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus <i>Sonneratia</i> . <i>Scientific Reports</i> , 2018, 8, 4425.	1.6	5

#	ARTICLE	IF	CITATIONS
5954	Reconstructing a metazoan genetic pathway with transcriptome-wide epistasis measurements. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2930-E2939.	3.3	21
5955	Translational profiling of B cells infected with the Epstein-Barr virus reveals 5' leader ribosome recruitment through upstream open reading frames. Nucleic Acids Research, 2018, 46, 2802-2819.	6.5	29
5956	Transcriptome analysis in the beet webworm, <i>Spoladea recurvalis</i> (Lepidoptera: Crambidae). Insect Science, 2018, 25, 33-44.	1.5	11
5957	The association of hormone signalling genes, transcription and changes in shoot anatomy during moso bamboo growth. Plant Biotechnology Journal, 2018, 16, 72-85.	4.1	87
5958	Next generation sequencing analysis of soy glyceollins and 17- $\beta$ estradiol: Effects on transcript abundance in the female mouse brain. Molecular and Cellular Endocrinology, 2018, 471, 15-21.	1.6	8
5959	Comparative analysis of the <i>Monochamus alternatus</i> immune system. Insect Science, 2018, 25, 581-603.	1.5	15
5960	Expression of lima bean terpene synthases in rice enhances recruitment of a beneficial enemy of a major rice pest. Plant, Cell and Environment, 2018, 41, 111-120.	2.8	36
5961	CASH: a constructing comprehensive splice site method for detecting alternative splicing events. Briefings in Bioinformatics, 2018, 19, 905-917.	3.2	47
5962	High throughput sequencing reveals <i>Drosophila suzukii</i> responses to insecticides. Insect Science, 2018, 25, 928-945.	1.5	11
5963	<i>RESISTANCE TO POWDERY MILDEW</i> boosts pattern-triggered immunity against multiple pathogens in Arabidopsis and rice. Plant Biotechnology Journal, 2018, 16, 428-441.	4.1	39
5964	<i>Verticillium dahliae</i> transcription factor VdFTF1 regulates the expression of multiple secreted virulence factors and is required for full virulence in cotton. Molecular Plant Pathology, 2018, 19, 841-857.	2.0	51
5965	High-throughput sequencing provides an insight into the hepatotoxicity mechanism of MC-LR in HepG2 cells. Toxin Reviews, 2018, 37, 1-10.	1.5	6
5966	Integrated transcriptomic and metabolomic analysis reveals adaptive changes of hibernating retinas. Journal of Cellular Physiology, 2018, 233, 1434-1445.	2.0	20
5967	New insight into foregut functions of xenobiotic detoxification in the cockroach <i>Periplaneta americana</i> . Insect Science, 2018, 25, 978-990.	1.5	7
5968	BET protein proteolysis targeting chimera (PROTAC) exerts potent lethal activity against mantle cell lymphoma cells. Leukemia, 2018, 32, 343-352.	3.3	127
5969	Comparative analysis of fruit volatiles and related gene expression between the wild strawberry <i>Fragaria pentaphylla</i> and cultivated <i>Fragaria</i> — <i>Ananassa</i> . European Food Research and Technology, 2018, 244, 57-72.	1.6	20
5970	Genome-wide identification and characterization of phospholipase C gene family in cotton ( <i>Gossypium</i> ) Tj ETQq0 0,0 rgBT /Oyerlock 10	2.3	26
5971	Identification of carboxylesterase genes associated with pyrethroid resistance in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). Pest Management Science, 2018, 74, 159-169.	1.7	26



#	ARTICLE	IF	CITATIONS
5972	Profiling of secondary metabolite gene clusters regulated by LaeA in <i>Aspergillus niger</i> FGSC A1279 based on genome sequencing and transcriptome analysis. <i>Research in Microbiology</i> , 2018, 169, 67-77.	1.0	40
5973	Development and Evolution through the Lens of Global Gene Regulation. <i>Trends in Genetics</i> , 2018, 34, 11-20.	2.9	20
5974	Wheat functional genomics in the era of next generation sequencing: An update. <i>Crop Journal</i> , 2018, 6, 7-14.	2.3	35
5975	A brief review of single-cell transcriptomic technologies. <i>Briefings in Functional Genomics</i> , 2018, 17, 64-76.	1.3	46
5976	Sparselso: a novel Bayesian approach to identify alternatively spliced isoforms from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 56-63.	1.8	7
5977	Controlling the false-discovery rate by procedures adapted to the length bias of RNA-Seq. <i>Journal of the Korean Statistical Society</i> , 2018, 47, 13-23.	0.3	4
5978	Effects of recombinant <i>Agrocybe aegerita</i> lectin as an immunoadjuvant on immune responses. <i>Immunopharmacology and Immunotoxicology</i> , 2018, 40, 6-12.	1.1	4
5979	Global transcriptional responses of denitrifying bacteria to functionalized single-walled carbon nanotubes revealed by weighted gene-coexpression network analysis. <i>Science of the Total Environment</i> , 2018, 613-614, 1240-1249.	3.9	26
5980	Transcriptomic analysis of <i>Ehrlichia ruminantium</i> during the developmental stages in bovine and tick cell culture. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 126-134.	1.1	10
5981	Comprehensive analysis of transcriptional and proteomic profiling reveals silver nanoparticles-induced toxicity to bacterial denitrification. <i>Journal of Hazardous Materials</i> , 2018, 344, 291-298.	6.5	58
5983	Differential gene regulatory networks in development and disease. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 1013-1025.	2.4	78
5984	Transcriptome Alterations in Posttraumatic Stress Disorder. <i>Biological Psychiatry</i> , 2018, 83, 840-848.	0.7	36
5985	Three <i>AtCesA6</i> -like members enhance biomass production by distinctively promoting cell growth in <i>Arabidopsis</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 976-988.	4.1	49
5986	G protein-coupled receptor GPR55 promotes colorectal cancer and has opposing effects to cannabinoid receptor 1. <i>International Journal of Cancer</i> , 2018, 142, 121-132.	2.3	49
5987	The potassium channel <i>FaTPK1</i> plays a critical role in fruit quality formation in strawberry ( <i>Fragaria</i> – <i>ananassa</i> ). <i>Plant Biotechnology Journal</i> , 2018, 16, 737-748.	4.1	25
5988	Transcriptomic profile reveals molecular events associated to focal adhesion and invasion in canine mammary gland tumour cell lines. <i>Veterinary and Comparative Oncology</i> , 2018, 16, E89-E98.	0.8	7
5989	Genome-wide analysis of gene expression profile in the respiratory tree of sea cucumber ( <i>Apostichopus japonicus</i> ) in response to hypoxia conditions. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2018, 98, 2039-2048.	0.4	6
5990	Transcriptome analysis of <i>Rana chensinensis</i> liver under trichlorfon stress. <i>Ecotoxicology and Environmental Safety</i> , 2018, 147, 487-493.	2.9	21

#	ARTICLE	IF	CITATIONS
5991	A <i>HDZIP III</i> gene, <i>PtrHB4</i> , is required for interfascicular cambium development in <i>Populus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 808-817.	4.1	50
5992	Specific interferon tau gene-regulation networks in bovine endometrial luminal epithelial cells. <i>Theriogenology</i> , 2018, 105, 51-60.	0.9	18
5993	Development of a set of PCR markers specific to <i>Aegilops longissima</i> chromosome arms and application in breeding a translocation line. <i>Theoretical and Applied Genetics</i> , 2018, 131, 13-25.	1.8	24
5994	Transcriptome analysis revealed glucose application affects plant hormone signal transduction pathway in "Red Globe" grape plantlets. <i>Plant Growth Regulation</i> , 2018, 84, 45-56.	1.8	18
5995	A multiple near isogenic line (multi-NIL) RNA-seq approach to identify candidate genes underpinning QTL. <i>Theoretical and Applied Genetics</i> , 2018, 131, 613-624.	1.8	30
5996	Regulation of pregnane-X-receptor and microRNAs on detoxification-related genes expressions in <i>Mugilogobius abei</i> under the exposure to diclofenac. <i>Environmental Pollution</i> , 2018, 233, 395-406.	3.7	19
5997	miRNAome, mRNAome and degradome analysis of Tibetan minipigs anterior pituitary. <i>General and Comparative Endocrinology</i> , 2018, 259, 104-114.	0.8	4
5998	Examining tRNA 3'-ends in <i>Escherichia coli</i> : teamwork between CCA-adding enzyme, RNase T, and RNase R. <i>Rna</i> , 2018, 24, 361-370.	1.6	20
5999	Post-genomic behavioral genetics: From revolution to routine. <i>Genes, Brain and Behavior</i> , 2018, 17, e12441.	1.1	17
6000	Phylogenomic detection and functional prediction of genes potentially important for plant meiosis. <i>Gene</i> , 2018, 643, 83-97.	1.0	4
6001	Cell-Type Transcriptomes of the Multicellular Green Alga <i>Volvox carteri</i> Yield Insights into the Evolutionary Origins of Germ and Somatic Differentiation Programs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 531-550.	0.8	29
6002	An ALOX12-HETE-GPR31 signaling axis is a key mediator of hepatic ischemia-reperfusion injury. <i>Nature Medicine</i> , 2018, 24, 73-83.	15.2	155
6003	Technical challenges of working with extracellular vesicles. <i>Nanoscale</i> , 2018, 10, 881-906.	2.8	366
6004	Orthogonality and Burdens of Heterologous AND Gate Gene Circuits in <i>E. coli</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 553-564.	1.9	49
6005	Polysaccharide Peptide-Induced Virus Resistance Depends on Ca <sup>2+</sup> Influx by Increasing the Salicylic Acid Content and Upregulating the Leucine-Rich Repeat Gene in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 516-524.	1.4	3
6006	Transcriptome analysis reveals a positive role for nerve growth factor in retinol metabolism in primary rat hepatocytes. <i>Cytokine</i> , 2018, 107, 74-78.	1.4	6
6007	Transcriptome sequencing of <i>Paeonia suffruticosa</i> "Shima Nishiki"™ to identify differentially expressed genes mediating double-color formation. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 114-124.	2.8	23
6008	Microscopic cuticle structure comparison of pupal melanic and wild strain of <i>Spodoptera exigua</i> and their gene expression profiles in three time points. <i>Microbial Pathogenesis</i> , 2018, 114, 483-493.	1.3	1

#	ARTICLE	IF	CITATIONS
6009	Sox9 Functions as a Master Regulator of Antler Growth by Controlling Multiple Cell Lineages. <i>DNA and Cell Biology</i> , 2018, 37, 15-22.	0.9	16
6010	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018, 28, 231-242.	2.4	64
6011	Comparative transcriptome analysis provides insights of anti-insect molecular mechanism of <i>Cassia obtusifolia</i> trypsin inhibitor against <i>Pieris rapae</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2018, 97, e21427.	0.6	7
6012	The Wnt/ $\beta$ -catenin pathway contributes to the regulation of adipocyte development induced by docosahexaenoic acid in grass carp, <i>Ctenopharyngodon idellus</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2018, 216, 18-24.	0.7	6
6013	Direct and indirect approaches to identify drug modes of action. <i>IUBMB Life</i> , 2018, 70, 9-22.	1.5	33
6014	Enhanced protection of C57 BL/6 vs Balb/c mice to melanoma liver metastasis is mediated by NK cells. <i>Oncot Immunology</i> , 2018, 7, e1409929.	2.1	26
6015	Transcriptome analysis provides insights into the immune responsive pathways and genes in the head kidney of tiger grouper ( <i>Epinephelus fuscoguttatus</i> ) fed with <i>Spatholobus suberectus</i> , <i>Phellodendron amurense</i> , or <i>Eclipta prostrata</i> . <i>Fish and Shellfish Immunology</i> , 2018, 73, 100-111.	1.6	18
6016	Identification of tomato miRNAs responsive to root colonization by endophytic <i>Pochonia chlamydosporia</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 907-919.	1.7	19
6017	Application of next generation semiconductor based sequencing for species identification in dairy products. <i>Food Chemistry</i> , 2018, 246, 90-98.	4.2	42
6018	Comparative transcriptomic insights into the mechanisms of electron transfer in <i>Geobacter</i> co-cultures with activated carbon and magnetite. <i>Science China Life Sciences</i> , 2018, 61, 787-798.	2.3	12
6019	RNA-Seq-derived identification of differential transcription in the eggplant ( <i>Solanum melongena</i> ) following inoculation with bacterial wilt. <i>Gene</i> , 2018, 644, 137-147.	1.0	9
6020	Systems Biology. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	0
6021	Prominent alterations of wild barley leaf transcriptome in response to individual and combined drought acclimation and heat shock conditions. <i>Physiologia Plantarum</i> , 2018, 163, 18-29.	2.6	16
6022	Pectin methylesterase inhibitor (PMEI) family can be related to male sterility in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Molecular Genetics and Genomics</i> , 2018, 293, 343-357.	1.0	21
6023	Comparative analysis of ovarian transcriptomes between prolific and non-prolific goat breeds via high-throughput sequencing. <i>Reproduction in Domestic Animals</i> , 2018, 53, 344-351.	0.6	9
6024	RNA-Seq analysis reveals the distinctive adaxial-abaxial polarity in the asymmetric one-theca stamen of <i>Canna indica</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 391-400.	1.0	12
6025	An integrated metabolic consequence of <i>Hepatospora eriocheir</i> infection in the Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Fish and Shellfish Immunology</i> , 2018, 72, 443-451.	1.6	27
6026	Ectopic expression of <i>Arabidopsis</i> broad-spectrum resistance gene <i>RPW8.2</i> improves the resistance to powdery mildew in grapevine ( <i>Vitis vinifera</i> ). <i>Plant Science</i> , 2018, 267, 20-31.	1.7	28

#	ARTICLE	IF	CITATIONS
6027	Characterization of a glycine-rich protein from <i>Rhipicephalus microplus</i> : tissue expression, gene silencing and immune recognition. <i>Parasitology</i> , 2018, 145, 927-938.	0.7	9
6028	Transcriptomic analysis reveals olfactory-related genes expression in large yellow croaker ( <i>Larimichthys crocea</i> ) regulated by taurine: May be a good phagostimulant for all-plant protein diets. <i>Aquaculture Research</i> , 2018, 49, 1095-1104.	0.9	7
6029	RNA-Seq of <i>Agropyron mongolicum</i> Keng in response to drought stress. <i>Grassland Science</i> , 2018, 64, 3-15.	0.6	4
6030	<i>Sulfolobus acidocaldarius</i> Transports Pentoses via a Carbohydrate Uptake Transporter 2 (CUT2)-Type ABC Transporter and Metabolizes Them through the Aldolase-Independent Weimberg Pathway. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	30
6031	RNA-Seq Analysis of Antibiotic-Producing <i>Bacillus subtilis</i> SC-8 Reveals a Role for Small Peptides in Controlling PapR Signaling. <i>Applied Biochemistry and Biotechnology</i> , 2018, 185, 359-369.	1.4	2
6032	Transcriptome analysis and discovery of genes involved in immune pathways from coelomocytes of <i>Onchidium struma</i> after bacterial challenge. <i>Fish and Shellfish Immunology</i> , 2018, 72, 528-543.	1.6	14
6033	Comparative genomics and transcriptome analysis of <i>Lactobacillus rhamnosus</i> ATCC 11443 and the mutant strain SCT-10-10-60 with enhanced l-lactic acid production capacity. <i>Molecular Genetics and Genomics</i> , 2018, 293, 265-276.	1.0	4
6034	Stilbenoid prenyltransferases define key steps in the diversification of peanut phytoalexins. <i>Journal of Biological Chemistry</i> , 2018, 293, 28-46.	1.6	36
6035	Differential gene expression in the intestine of sea cucumber ( <i>Apostichopus japonicus</i> ) under low and high salinity conditions. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 25, 34-41.	0.4	12
6036	A Method for Cross-Species Visualization and Analysis of RNA-Sequence Data. <i>Methods in Molecular Biology</i> , 2018, 1702, 291-305.	0.4	3
6037	Transcriptome analysis of gene expression patterns during embryonic development in golden cuttlefish ( <i>Sepia esculenta</i> ). <i>Genes and Genomics</i> , 2018, 40, 253-263.	0.5	12
6038	Transcriptome Scale characterization of salt responsive bean TCP transcription factors. <i>Gene</i> , 2018, 642, 64-73.	1.0	24
6039	MAT2A promotes porcine adipogenesis by mediating H3K27me3 at Wnt10b locus and repressing Wnt/ $\beta$ -catenin signaling. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2018, 1863, 132-142.	1.2	18
6040	A Bayesian model selection approach for identifying differentially expressed transcripts from RNA sequencing data. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2018, 67, 3-23.	0.5	6
6041	BNP-Seq: Bayesian Nonparametric Differential Expression Analysis of Sequencing Count Data. <i>Journal of the American Statistical Association</i> , 2018, 113, 81-94.	1.8	18
6042	Single-cell RNA sequencing to explore immune cell heterogeneity. <i>Nature Reviews Immunology</i> , 2018, 18, 35-45.	10.6	1,085
6043	Multiple System Atrophy: Many Lessons from the Transcriptome. <i>Neuroscientist</i> , 2018, 24, 294-307.	2.6	7
6044	Clustering of RNA-Seq samples: Comparison study on cancer data. <i>Methods</i> , 2018, 132, 42-49.	1.9	22

#	ARTICLE	IF	CITATIONS
6045	Transcriptome profiling analysis of <i>Mactra veneriformis</i> by deep sequencing after exposure to 2,2,4,4-tetrabromodiphenyl ether. <i>Journal of Oceanology and Limnology</i> , 2018, 36, 490-507.	0.6	4
6046	Computational approaches for the systematic analysis of aging-associated molecular alterations. <i>Drug Discovery Today: Disease Models</i> , 2018, 27, 51-59.	1.2	1
6047	Mining Gene Families in the Castor Bean Genome. <i>Compendium of Plant Genomes</i> , 2018, , 135-173.	0.3	4
6048	A Unified Model for Robust Differential Expression Analysis of RNA-Seq Data. , 2018, , .		0
6049	iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2018, 19, 534.	1.2	803
6050	Identifying Candidate Diseases-related Metabolites Based on Disease Similarity. , 2018, , .		3
6051	Genome-wide Transcriptional Response during the Shift to N <sub>2</sub> -fixing Conditions in <i>Heliobacterium modesticaldum</i> . <i>Journal of Proteomics and Bioinformatics</i> , 2018, 11, .	0.4	11
6052	Transcriptomic analysis reveals that enterovirus F strain SWUN-AB001 infection activates JNK/SAPK and p38 MAPK signaling pathways in MDBK cells. <i>BMC Veterinary Research</i> , 2018, 14, 395.	0.7	2
6053	<i>Cscs</i> encoding chorismate synthase is a candidate gene for leaf variegation mutation in cucumber. <i>Breeding Science</i> , 2018, 68, 571-581.	0.9	19
6054	Survival, Virulent Characteristics, and Transcriptomic Analyses of the Pathogenic <i>Vibrio anguillarum</i> Under Starvation Stress. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 389.	1.8	21
6055	How <i>Quercus ilex</i> L. saplings face combined salt and ozone stress: a transcriptome analysis. <i>BMC Genomics</i> , 2018, 19, 872.	1.2	15
6056	Transcriptomics: Quantifying Non-Uniform Read Distribution Using MapReduce. <i>International Journal of Foundations of Computer Science</i> , 2018, 29, 1355-1372.	0.8	3
6057	PAXgene-fixed paraffin-embedded sample is applicable to laser capture microdissection with well-balanced RNA quality and tissue morphology. <i>Journal of Toxicologic Pathology</i> , 2018, 31, 213-220.	0.3	2
6058	A comprehensive review of computational prediction of genome-wide features. <i>Briefings in Bioinformatics</i> , 2020, 21, 120-134.	3.2	12
6059	Transcriptional and Small RNA Responses of the White Mold Fungus <i>Sclerotinia sclerotiorum</i> to Infection by a Virulence-Attenuating Hypovirus. <i>Viruses</i> , 2018, 10, 713.	1.5	35
6060	Transcriptome Analysis and Functional Identification of Xa13 and Pi&eta Orthologs in <i>Oryza granulata</i> . <i>Plant Genome</i> , 2018, 11, 170097.	1.6	2
6061	Nucleic Acids: RNA Identification and Quantification Via Next-Generation Sequencing. , 2018, , .		0
6062	Transcriptomes of early developing tassels under drought stress reveal differential expression of genes related to drought tolerance in maize. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1276-1288.	1.7	17

#	ARTICLE	IF	CITATIONS
6063	Identification of the Genetic Variation and Gene Exchange between Citrus Trifoliata and Citrus Clementina. <i>Biomolecules</i> , 2018, 8, 182.	1.8	4
6065	Genetic analysis for the grain number heterosis of a super-hybrid rice WFYT025 combination using RNA-Seq. <i>Rice</i> , 2018, 11, 37.	1.7	39
6066	A mitochondrial phosphate transporter, McPht gene, confers an acclimation regulation of the transgenic rice to phosphorus deficiency. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1932-1945.	1.7	3
6067	Transcriptomic Profiling of the Immune Response to Crowding Stress in Juvenile Turbot ( <i>Scophthalmus maximus</i> ). <i>Journal of Clinical &amp; Cellular Immunology</i> , 2018, 09, .	1.5	0
6068	Transcriptome analysis of hsp18.3 functions and regulatory systems using RNA-sequencing in the red flour beetle, <i>Tribolium castaneum</i> . <i>Journal of Integrative Agriculture</i> , 2018, 17, 1040-1056.	1.7	5
6069	Optimal Control of Gene Regulatory Networks with Unknown Cost Function. , 2018, , .		13
6070	Proto-oncogenes in a eukaryotic unicellular organism play essential roles in plasmodial growth in host cells. <i>BMC Genomics</i> , 2018, 19, 881.	1.2	6
6071	OBSOLETE: Transcriptomics in Cardiovascular Medicine. , 2018, , .		0
6072	Cystic fibrosis-related diabetes is caused by islet loss and inflammation. <i>JCI Insight</i> , 2018, 3, .	2.3	127
6073	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	0.8	16
6074	A Simple Guideline to Assess the Characteristics of RNA-Seq Data. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	32
6075	Brain Theranostics and Radiotheranostics: Exosomes and Graphenes In Vivo as Novel Brain Theranostics. <i>Nuclear Medicine and Molecular Imaging</i> , 2018, 52, 407-419.	0.6	8
6076	Proteogenomic Analyses of Cellular Lysates Using a Phenol-Guanidinium Thiocyanate Reagent. <i>Journal of Proteome Research</i> , 2019, 18, 301-308.	1.8	13
6077	Insights into the seasonal adaptive mechanisms of Chinese alligators ( <i>Alligator sinensis</i> ) from transcriptomic analyses. <i>Australian Journal of Zoology</i> , 2018, 66, 93.	0.6	9
6078	Deblender: a semi-/unsupervised multi-operational computational method for complete deconvolution of expression data from heterogeneous samples. <i>BMC Bioinformatics</i> , 2018, 19, 408.	1.2	12
6079	Dynamic Changes in the Global MicroRNAome and Transcriptome Identify Key Nodes Associated With Ovarian Development in Chickens. <i>Frontiers in Genetics</i> , 2018, 9, 491.	1.1	16
6080	Differential expression of mRNA-miRNAs related to intramuscular fat content in the longissimus dorsi in Xinjiang brown cattle. <i>PLoS ONE</i> , 2018, 13, e0206757.	1.1	12
6081	DREAMSeq: An Improved Method for Analyzing Differentially Expressed Genes in RNA-seq Data. <i>Frontiers in Genetics</i> , 2018, 9, 588.	1.1	10

#	ARTICLE	IF	CITATIONS
6082	Symbiotic microbes affect the expression of male reproductive genes in <i>Glossina m. morsitans</i> . <i>BMC Microbiology</i> , 2018, 18, 169.	1.3	9
6083	Transcriptomes Divergence of <i>Ricotia lunaria</i> Between the Two Micro-Climatic Divergent Slopes at "Evolution Canyon", Israel. <i>Frontiers in Genetics</i> , 2018, 9, 506.	1.1	12
6084	Characterization of drought stress-responsive root transcriptome of faba bean ( <i>Vicia faba</i> L.) using RNA sequencing. <i>3 Biotech</i> , 2018, 8, 502.	1.1	15
6085	Enrichment of Autophagy and Proteasome Pathways in Breast Muscle of Feed Efficient Pedigree Male Broilers. <i>Frontiers in Physiology</i> , 2018, 9, 1342.	1.3	13
6086	Identification of Genes that Control Silk Yield by RNA Sequencing Analysis of Silkworm ( <i>Bombyx mori</i> ) Strains of Variable Silk Yield. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3718.	1.8	27
6087	Transcriptomic Profiling of <i>Lathyrus sativus</i> L. Metabolism of $\hat{I}^2$ -ODAP, a Neuroexcitatory Amino Acid Associated with Neurodegenerative Lower Limb Paralysis. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 832-843.	1.0	15
6088	Nucleolar Relocalization of RBM14 by Influenza A Virus NS1 Protein. <i>MSphere</i> , 2018, 3, .	1.3	8
6089	Elucidating the Interaction of CF Airway Epithelial Cells and Rhinovirus: Using the Host-Pathogen Relationship to Identify Future Therapeutic Strategies. <i>Frontiers in Pharmacology</i> , 2018, 9, 1270.	1.6	3
6090	Novel Factors of Viral Origin Inhibit TOR Pathway Gene Expression. <i>Frontiers in Physiology</i> , 2018, 9, 1678.	1.3	11
6091	Transcriptome analyses of reprogrammed feather / scale chimeric explants revealed co-expressed epithelial gene networks during organ specification. <i>BMC Genomics</i> , 2018, 19, 780.	1.2	7
6092	Improved xylose tolerance and 2,3-butanediol production of <i>Klebsiella pneumoniae</i> by directed evolution of rpoD and the mechanisms revealed by transcriptomics. <i>Biotechnology for Biofuels</i> , 2018, 11, 307.	6.2	18
6093	Temperature and photoperiod changes affect cucumber sex expression by different epigenetic regulations. <i>BMC Plant Biology</i> , 2018, 18, 268.	1.6	35
6094	Transcriptomics Study on <i>Staphylococcus aureus</i> Biofilm Under Low Concentration of Ampicillin. <i>Frontiers in Microbiology</i> , 2018, 9, 2413.	1.5	51
6095	CMV2b-Dependent Regulation of Host Defense Pathways in the Context of Viral Infection. <i>Viruses</i> , 2018, 10, 618.	1.5	14
6096	Integrative Analysis of Transcriptomic and Methylomic Data in Photoperiod-Dependent Regulation of Cucumber Sex Expression. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3981-3991.	0.8	3
6097	Dorsal Root Ganglia Coactivator-associated Arginine Methyltransferase 1 Contributes to Peripheral Nerve Injury-induced Pain Hypersensitivities. <i>Neuroscience</i> , 2018, 394, 232-242.	1.1	9
6098	Comparative Transcriptional Profiling and Physiological Responses of Two Contrasting Oat Genotypes under Salt Stress. <i>Scientific Reports</i> , 2018, 8, 16248.	1.6	25
6099	Transcriptome Analysis of Newly Emerged Honeybees Exposure to Sublethal Carbendazim During Larval Stage. <i>Frontiers in Genetics</i> , 2018, 9, 426.	1.1	15

#	ARTICLE	IF	CITATIONS
6100	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. <i>PLoS Genetics</i> , 2018, 14, e1007735.	1.5	46
6101	Comparative Transcriptome and iTRAQ Proteome Analyses Reveal the Mechanisms of Diapause in <i>Aphidius gifuensis</i> Ashmead (Hymenoptera: Aphidiidae). <i>Frontiers in Physiology</i> , 2018, 9, 1697.	1.3	32
6102	The Clinical Application of RNA Sequencing in Genetic Diagnosis of Mendelian Disorders. <i>Advances in Molecular Pathology</i> , 2018, 1, 27-36.	0.2	1
6103	Identification of cytochrome P450 monooxygenase genes and their expression in response to high temperature in the alligatorweed flea beetle <i>Agasicles hygrophila</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018, 8, 17847.	1.6	22
6104	Multiparameter Responses to Tedizolid Monotherapy and Moxifloxacin Combination Therapy Models of Children With Intracellular Tuberculosis. <i>Clinical Infectious Diseases</i> , 2018, 67, S342-S348.	2.9	18
6105	Comparative transcriptome analysis reveals that photosynthesis contributes to drought tolerance of <i>Nostoc flagelliforme</i> (Nostocales, Cyanobacteria). <i>Phycologia</i> , 2018, 57, 113-120.	0.6	15
6106	Genomic and in-situ Transcriptomic Characterization of the Candidate Phylum NPL-UPL2 From Highly Alkaline Highly Reducing Serpentinized Groundwater. <i>Frontiers in Microbiology</i> , 2018, 9, 3141.	1.5	31
6107	Functional analysis of the role of CcpA in <i>Lactobacillus plantarum</i> grown on fructooligosaccharides or glucose: a transcriptomic perspective. <i>Microbial Cell Factories</i> , 2018, 17, 201.	1.9	29
6108	Transcriptome analysis of the typical freshwater rhodophytes <i>Sheathia arcuata</i> grown under different light intensities. <i>PLoS ONE</i> , 2018, 13, e0197729.	1.1	12
6109	Transcriptional analysis of viral mRNAs reveals common transcription patterns in cells infected by five different filoviruses. <i>PLoS ONE</i> , 2018, 13, e0201827.	1.1	22
6110	The Use of Targeted Next Generation Sequencing to Explore Candidate Regulators of TGF- $\beta$ 1's Impact on Kidney Cells. <i>Frontiers in Physiology</i> , 2018, 9, 1755.	1.3	8
6111	Predicting Tumor Growth and Ligand Dependence from mRNA by Combining Machine Learning with Mechanistic Modeling. <i>Methods in Pharmacology and Toxicology</i> , 2018, , 1.	0.1	0
6112	Identification of a phosphine resistance mechanism in <i>Rhyzopertha dominica</i> based on transcriptome analysis. <i>Journal of Asia-Pacific Entomology</i> , 2018, 21, 1450-1456.	0.4	12
6113	Copy number variation in the MSR3 gene enlarges porcine ear size through a mechanism involving miR-584-5p. <i>Genetics Selection Evolution</i> , 2018, 50, 72.	1.2	37
6114	Inflammation and transcriptional responses of peripheral blood mononuclear cells in classic ataxia telangiectasia. <i>PLoS ONE</i> , 2018, 13, e0209496.	1.1	20
6115	Transcriptome profile in bursa of Fabricius reveals potential mode for stress-influenced immune function in chicken stress model. <i>BMC Genomics</i> , 2018, 19, 918.	1.2	25
6116	Anthocyanin accumulation correlates with hormones in the fruit skin of 'Red Delicious' and its four generation bud sport mutants. <i>BMC Plant Biology</i> , 2018, 18, 363.	1.6	55
6117	Integration of transcriptome and proteome analyses reveal molecular mechanisms for formation of replant disease in <i>Nelumbo nucifera</i> . <i>RSC Advances</i> , 2018, 8, 32574-32587.	1.7	10



#	ARTICLE	IF	CITATIONS
6118	A graph based model for multiple biological data sources integration. , 2018, , .		3
6119	Systemic functional enrichment and ceRNA network identification following peripheral nerve injury. <i>Molecular Brain</i> , 2018, 11, 73.	1.3	15
6120	Transcriptome Analysis of Phycocyanin-Mediated Inhibitory Functions on Non-Small Cell Lung Cancer A549 Cell Growth. <i>Marine Drugs</i> , 2018, 16, 511.	2.2	26
6121	Comparative transcriptome and metabolome analysis suggests bottlenecks that limit seed and oil yields in transgenic <i>Camelina sativa</i> expressing diacylglycerol acyltransferase 1 and glycerol-3-phosphate dehydrogenase. <i>Biotechnology for Biofuels</i> , 2018, 11, 335.	6.2	12
6122	Transcriptomic and proteomic analyses of drought responsive genes and proteins in <i>Agropyron mongolicum</i> Keng. <i>Current Plant Biology</i> , 2018, 14, 19-29.	2.3	12
6123	Revealing transcription factor and histone modification co-localization and dynamics across cell lines by integrating ChIP-seq and RNA-seq data. <i>BMC Genomics</i> , 2018, 19, 914.	1.2	17
6124	Discerning novel splice junctions derived from RNA-seq alignment: a deep learning approach. <i>BMC Genomics</i> , 2018, 19, 971.	1.2	26
6125	De novo transcriptome assembly of brackish water flea <i>Diaphanosoma celebensis</i> based on short-term cadmium and benzo[a]pyrene exposure experiments. <i>Hereditas</i> , 2018, 155, 36.	0.5	22
6126	Comparative transcriptome analysis provides insights into dwarfism in cherry tomato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Qverlock <sub>7,10</sub> Tf 50 4.	1.1	11
6127	Transcriptional Landscape of a blaKPC-2 Plasmid and Response to Imipenem Exposure in <i>Escherichia coli</i> TOP10. <i>Frontiers in Microbiology</i> , 2018, 9, 2929.	1.5	12
6128	Global Expression Profiling Identifies a Novel Hyaluronan Synthases 2 Gene in the Pathogenesis of Lower Extremity Varicose Veins. <i>Journal of Clinical Medicine</i> , 2018, 7, 537.	1.0	5
6129	Identification of the major diacylglycerol acyltransferase mRNA in mouse adipocytes and macrophages. <i>BMC Biochemistry</i> , 2018, 19, 11.	4.4	6
6130	Novel miRNA-25 inhibits AMPD2 in peripheral blood mononuclear cells of patients with systemic lupus erythematosus and represents a promising novel biomarker. <i>Journal of Translational Medicine</i> , 2018, 16, 370.	1.8	52
6131	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	6.0	516
6132	Spatiotemporal transcriptomic divergence across human and macaque brain development. <i>Science</i> , 2018, 362, .	6.0	279
6133	Comparative cochlear transcriptomics of echolocating bats provides new insights into different nervous activities of CF bat species. <i>Scientific Reports</i> , 2018, 8, 15934.	1.6	9
6134	Reconstruction and analysis of carbon metabolic pathway of <i>Ketogulonicigenium vulgare</i> SPU B805 by genome and transcriptome. <i>Scientific Reports</i> , 2018, 8, 17838.	1.6	8
6135	Transcriptomic Responses to Different Cry1Ac Selection Stresses in <i>Helicoverpa armigera</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1653.	1.3	24

#	ARTICLE	IF	CITATIONS
6136	RNA Sequencing Provides Insights into the Regulation of Solanesol Biosynthesis in <i>Nicotiana tabacum</i> Induced by Moderately High Temperature. <i>Biomolecules</i> , 2018, 8, 165.	1.8	4
6137	Combination of transcriptome sequencing and iTRAQ proteome reveals the molecular mechanisms determining petal shape in herbaceous peony ( <i>Paeonia lactiflora</i> Pall.). <i>Bioscience Reports</i> , 2018, 38, .	1.1	15
6138	Comparative transcriptomics between high and low rubber producing <i>Taraxacum kok-saghyz</i> R. plants. <i>BMC Genomics</i> , 2018, 19, 875.	1.2	13
6139	Analysis of the transcriptome data in <i>Litopenaeus vannamei</i> reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. <i>PLoS ONE</i> , 2018, 13, e0207771.	1.1	20
6141	Chain organization of human interphase chromosome determines the spatiotemporal dynamics of chromatin loci. <i>PLoS Computational Biology</i> , 2018, 14, e1006617.	1.5	71
6142	Temporal changes in the viromes of Swedish <i>Varroa</i> -resistant and <i>Varroa</i> -susceptible honeybee populations. <i>PLoS ONE</i> , 2018, 13, e0206938.	1.1	26
6143	ISODb: A Comprehensive Database of Full-Length Isoforms Generated by Iso-Seq. <i>International Journal of Genomics</i> , 2018, 2018, 1-6.	0.8	8
6144	Comparative transcriptomics identifies genes differentially expressed in the intestine of a new fast-growing strain of common carp with higher unsaturated fatty acid content in muscle. <i>PLoS ONE</i> , 2018, 13, e0206615.	1.1	14
6145	RNA Sequencing for Gene Expression Profiles in a Rat Model of Middle Cerebral Artery Occlusion. <i>BioMed Research International</i> , 2018, 2018, 1-14.	0.9	8
6146	Hairy Roots. , 2018, , .		20
6147	Effects of 5-Azacytidine on Growth and Hypocrellin Production of <i>Shiraia bambusicola</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2508.	1.5	16
6148	Electron and Proton Flux for Carbon Dioxide Reduction in <i>Methanosarcina barkeri</i> During Direct Interspecies Electron Transfer. <i>Frontiers in Microbiology</i> , 2018, 9, 3109.	1.5	75
6149	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018, 34, 996-1011.e8.	7.7	190
6150	Transcriptomics reveal the molecular underpinnings of chemosensory proteins in <i>Chlorops oryzae</i> . <i>BMC Genomics</i> , 2018, 19, 890.	1.2	19
6151	Comparison of Olfactory Genes in Two <i>Ectropis</i> Species: Emphasis on Candidates Involved in the Detection of Type-II Sex Pheromones. <i>Frontiers in Physiology</i> , 2018, 9, 1602.	1.3	5
6152	Transcriptome analysis reveals the molecular response to cadmium toxicity in <i>P. pseudoannulata</i> . <i>Environmental Science and Pollution Research</i> , 2018, 25, 34294-34305.	2.7	15
6153	Transcriptomic analysis reveals the effect of the exopolysaccharide of <i>Psychrobacter</i> sp. B-3 on gene expression in RAW264.7 macrophage cells. <i>Acta Oceanologica Sinica</i> , 2018, 37, 46-53.	0.4	7
6154	NagRBt Is a Pleiotropic and Dual Transcriptional Regulator in <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1899.	1.5	4

#	ARTICLE	IF	CITATIONS
6155	Characterizing the Role of Exoribonucleases in the Control of Microbial Gene Expression: Differential RNA-Seq. <i>Methods in Enzymology</i> , 2018, 612, 1-24.	0.4	3
6156	ProteomeGenerator: A Framework for Comprehensive Proteomics Based on de Novo Transcriptome Assembly and High-Accuracy Peptide Mass Spectral Matching. <i>Journal of Proteome Research</i> , 2018, 17, 3681-3692.	1.8	24
6157	Adaptive transcription-splicing resynchronization upon losing an essential splicing factor. <i>Nature Ecology and Evolution</i> , 2018, 2, 1818-1823.	3.4	4
6158	Modeling and analysis of RNA-seq data: a review from a statistical perspective. <i>Quantitative Biology</i> , 2018, 6, 195-209.	0.3	49
6159	Microfluidic and Paper-Based Devices for Disease Detection and Diagnostic Research. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2731.	1.8	49
6160	Analyses of gene expression profiles in the rat dorsal horn of the spinal cord using RNA sequencing in chronic constriction injury rats. <i>Journal of Neuroinflammation</i> , 2018, 15, 280.	3.1	26
6161	Hemocytes transcriptome profile of the Chinese mitten crab ( <i>Eriocheir sinensis</i> ). <i>Aquaculture and Fisheries</i> , 2018, 3, 191-195.	1.2	0
6162	Primary transcripts: From the discovery of RNA processing to current concepts of gene expression Review. <i>Experimental Cell Research</i> , 2018, 373, 1-33.	1.2	25
6163	Transcriptomic evidence of adaptive tolerance to high environmental ammonia in mudskippers. <i>Genomics</i> , 2018, 110, 404-413.	1.3	21
6164	Curcumin downregulates expression of opioid-related nociceptin receptor gene (OPRL1) in isolated neuroglia cells. <i>Phytomedicine</i> , 2018, 50, 285-299.	2.3	29
6165	Novel molecular mechanisms for the adaptogenic effects of herbal extracts on isolated brain cells using systems biology. <i>Phytomedicine</i> , 2018, 50, 257-284.	2.3	77
6166	Waves of chromatin modifications in mouse dendritic cells in response to LPS stimulation. <i>Genome Biology</i> , 2018, 19, 138.	3.8	19
6167	Blue Light Regulates Secondary Cell Wall Thickening via MYC2/MYC4 Activation of the <i>NST1</i> -Directed Transcriptional Network in Arabidopsis. <i>Plant Cell</i> , 2018, 30, 2512-2528.	3.1	59
6168	Integrated genomic analyses in PDX model reveal a cyclin-dependent kinase inhibitor Palbociclib as a novel candidate drug for nasopharyngeal carcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 233.	3.5	23
6169	A comparative analysis of library prep approaches for sequencing low input translome samples. <i>BMC Genomics</i> , 2018, 19, 696.	1.2	66
6170	A Genomic Variation Map Provides Insights into the Genetic Basis of Spring Chinese Cabbage ( <i>Brassica</i> ) Tj ETQq1 1,0,784314 rgBT /Ove	3.9	63
6171	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> intestines under the white spot syndrome virus and poly (I:C) challenges. <i>PLoS ONE</i> , 2018, 13, e0204626.	1.1	12
6172	Identifying novel candidate biomarkers of RCC based on WGCNA analysis. <i>Personalized Medicine</i> , 2018, 15, 381-394.	0.8	12

#	ARTICLE	IF	CITATIONS
6173	HSRA: Hadoop-based spliced read aligner for RNA sequencing data. PLoS ONE, 2018, 13, e0201483.	1.1	12
6174	Genotypic response of pollen germination in Dura, Pisifera and Tenera oil palm ( <i>Elaeis guineensis</i> ) Tj ETQq1 1 0.784314 rgBT 1 Overloc	0.6	1
6175	Genomic approaches for studying crop evolution. Genome Biology, 2018, 19, 140.	3.8	54
6176	Transcriptome and gene expression analysis of docosahexaenoic acid producer <i>Schizochytrium</i> sp. under different oxygen supply conditions. Biotechnology for Biofuels, 2018, 11, 249.	6.2	44
6177	Transcriptome reprogramming of resistant and susceptible peach genotypes during <i>Xanthomonas arboricola</i> pv. <i>pruni</i> early leaf infection. PLoS ONE, 2018, 13, e0196590.	1.1	13
6178	Core non-coding RNAs of <i>Piscirickettsia salmonis</i> . PLoS ONE, 2018, 13, e0197206.	1.1	7
6179	Development and Characterization of Novel Genic-SSR Markers in Apple-Juniper Rust Pathogen <i>Gymnosporangium yamadae</i> (Pucciniales: Pucciniaceae) Using Next-Generation Sequencing. International Journal of Molecular Sciences, 2018, 19, 1178.	1.8	10
6180	Intracellular RNA-tracking methods. Open Biology, 2018, 8, 180104.	1.5	28
6181	Transcriptome profiling analysis characterized the gene expression patterns responded to combined drought and heat stresses in soybean. Computational Biology and Chemistry, 2018, 77, 413-429.	1.1	46
6182	Comparative RNA-Seq Analysis of High- and Low-Oil Yellow Horn During Embryonic Development. International Journal of Molecular Sciences, 2018, 19, 3071.	1.8	19
6183	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. Methods in Molecular Biology, 2018, 1849, 227-242.	0.4	23
6184	Differential gene expression analyses related to fruit yield of <i>Jatropha curcas</i> L. using RNA-seq. Biotechnology and Biotechnological Equipment, 2018, 32, 1126-1133.	0.5	0
6185	Genome-Wide Identification and Characterization of wALOG Family Genes Involved in Branch Meristem Development of Branching Head Wheat. Genes, 2018, 9, 510.	1.0	8
6186	Transcriptome Profiling Reveals Transcriptional Regulation by DNA Methyltransferase Inhibitor 5-Aza-2-Deoxycytidine Enhancing Red Pigmentation in Bagged 'Granny Smith' Apples ( <i>Malus domestica</i> ). International Journal of Molecular Sciences, 2018, 19, 3133.	1.8	19
6187	New Insight into the Molecular Mechanism of the FUT2 Regulating <i>Escherichia coli</i> F18 Resistance in Weaned Piglets. International Journal of Molecular Sciences, 2018, 19, 3301.	1.8	18
6188	Mapping Molecular Datasets Back to the Brain Regions They are Extracted from: Remembering the Native Countries of Hypothalamic Expatriates and Refugees. Advances in Neurobiology, 2018, 21, 101-193.	1.3	10
6189	Comparative transcriptome reveals circadian and hormonal control of adventitious rooting in mulberry hardwood cuttings. Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	15
6190	Genome-wide identification of AP2/ERF superfamily genes and their expression during fruit ripening of Chinese jujube. Scientific Reports, 2018, 8, 15612.	1.6	67

#	ARTICLE	IF	CITATIONS
6191	Transcriptomic analysis reveals critical genes for the hair follicle of Inner Mongolia cashmere goat from catagen to telogen. <i>PLoS ONE</i> , 2018, 13, e0204404.	1.1	25
6192	OsWRKY67 positively regulates blast and bacteria blight resistance by direct activation of PR genes in rice. <i>BMC Plant Biology</i> , 2018, 18, 257.	1.6	48
6193	DNA replication and repair kinetics of Alu, LINE-1 and satellite III genomic repetitive elements. <i>Epigenetics and Chromatin</i> , 2018, 11, 61.	1.8	18
6194	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. <i>Frontiers in Plant Science</i> , 2018, 9, 1376.	1.7	10
6195	Identifying deer antler uhrf1 proliferation and s100a10 mineralization genes using comparative RNA-seq. <i>Stem Cell Research and Therapy</i> , 2018, 9, 292.	2.4	17
6196	Comparison of normalization approaches for gene expression studies completed with high-throughput sequencing. <i>PLoS ONE</i> , 2018, 13, e0206312.	1.1	60
6197	Single Cell Gene Expression to Understand the Dynamic Architecture of the Heart. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 167.	1.1	16
6198	Selection and validation of suitable reference genes for qPCR gene expression analysis in goats and sheep under Peste des petits ruminants virus (PPRV), lineage IV infection. <i>Scientific Reports</i> , 2018, 8, 15969.	1.6	19
6199	Tumor-immune profiling of murine syngeneic tumor models as a framework to guide mechanistic studies and predict therapy response in distinct tumor microenvironments. <i>PLoS ONE</i> , 2018, 13, e0206223.	1.1	149
6200	mRNA-seq whole transcriptome profiling of fresh frozen versus archived fixed tissues. <i>BMC Genomics</i> , 2018, 19, 419.	1.2	38
6201	Combining DNA methylation and RNA sequencing data of cancer for supervised knowledge extraction. <i>BioData Mining</i> , 2018, 11, 22.	2.2	24
6202	Barcoded solid-phase RNA capture for Spatial Transcriptomics profiling in mammalian tissue sections. <i>Nature Protocols</i> , 2018, 13, 2501-2534.	5.5	144
6203	E-cadherin loss induces targetable autocrine activation of growth factor signalling in lobular breast cancer. <i>Scientific Reports</i> , 2018, 8, 15454.	1.6	55
6204	Non-target site-based resistance to tribenuron-methyl and essential involved genes in <i>Myosoton aquaticum</i> (L.). <i>BMC Plant Biology</i> , 2018, 18, 225.	1.6	37
6205	Identification of water use efficiency related genes in Garnem™ almond-peach rootstock using time-course transcriptome analysis. <i>PLoS ONE</i> , 2018, 13, e0205493.	1.1	24
6206	A Bayesian hierarchical model for analyzing methylated RNA immunoprecipitation sequencing data. <i>Quantitative Biology</i> , 2018, 6, 275-286.	0.3	5
6207	Characterization of sugar metabolism in the stem of Tachisuzuka, a whole-crop silage rice cultivar with high sugar content in the stem. <i>Plant Production Science</i> , 2018, 21, 233-243.	0.9	2
6208	Identification of differentially expressed immunity-related genes in <i>Monoctonus alternatus</i> Hope (Coleoptera: Cerambycidae) larvae parasitized by <i>Dastarcus helophoroides</i> (Fairmaire) (Coleoptera: Bothriideridae). <i>Entomological Research</i> , 2018, 48, 248-261.	0.6	1

#	ARTICLE	IF	CITATIONS
6209	Global Transcriptome Analysis During Adipogenic Differentiation and Involvement of Transthyretin Gene in Adipogenesis in Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 463.	1.1	25
6210	Molecular role of cytokinin in bud activation and outgrowth in apple branching based on transcriptomic analysis. <i>Plant Molecular Biology</i> , 2018, 98, 261-274.	2.0	23
6211	Expression of genes in the potential regulatory pathways controlling alternate bearing in "Fuji"™ ( <i>Malus domestica</i> Borkh.) apple trees during flower induction. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 579-589.	2.8	15
6212	Regulation of the G $\beta$ -cAMP/PKA signaling pathway in cellulose utilization of <i>Chaetomium globosum</i> . <i>Microbial Cell Factories</i> , 2018, 17, 160.	1.9	13
6213	acI Actinobacteria Assemble a Functional Actinorhodopsin with Natively Synthesized Retinal. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
6214	CamurWeb: a classification software and a large knowledge base for gene expression data of cancer. <i>BMC Bioinformatics</i> , 2018, 19, 354.	1.2	9
6215	Single-cell RNA sequencing reveals gene expression signatures of breast cancer-associated endothelial cells. <i>Oncotarget</i> , 2018, 9, 10945-10961.	0.8	45
6216	The Wheat MYB Transcription Factor TaMYB31 Is Involved in Drought Stress Responses in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1426.	1.7	87
6217	Maternal Melatonin Therapy Attenuates Methyl-Donor Diet-Induced Programmed Hypertension in Male Adult Rat Offspring. <i>Nutrients</i> , 2018, 10, 1407.	1.7	31
6218	Extracellular Matrix Components in Bivalvia: Shell and ECM Components in Developmental and Adult Tissues. <i>Fisheries and Aquaculture Journal</i> , 2018, 09, .	0.2	4
6220	Integrative Analysis of Three RNA Sequencing Methods Identifies Mutually Exclusive Exons of MADS-Box Isoforms During Early Bud Development in <i>Picea abies</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1625.	1.7	10
6221	Overexpression of <i>Lilium formosanum</i> MADS-box (LFMADS) Causing Floral Defects While Promoting Flowering in <i>Arabidopsis thaliana</i> , Whereas Only Affecting Floral Transition Time in <i>Nicotiana tabacum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2217.	1.8	15
6222	De novo transcriptome based on next-generation sequencing reveals candidate genes with sex-specific expression in <i>Arapaima gigas</i> (Schinz, 1822), an ancient Amazonian freshwater fish. <i>PLoS ONE</i> , 2018, 13, e0206379.	1.1	13
6223	Quality control implementation for universal characterization of DNA and RNA viruses in clinical respiratory samples using single metagenomic next-generation sequencing workflow. <i>BMC Infectious Diseases</i> , 2018, 18, 537.	1.3	44
6224	Transcriptome Profiles Reveal the Crucial Roles of Auxin and Cytokinin in the "Shoot Branching" of <i>Cremastra appendiculata</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3354.	1.8	14
6225	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. <i>Scientific Reports</i> , 2018, 8, 15338.	1.6	45
6226	Transcriptome analysis reveals crucial genes involved in the biosynthesis of nervonic acid in woody <i>Malania oleifera</i> oilseeds. <i>BMC Plant Biology</i> , 2018, 18, 247.	1.6	31
6227	Long non-coding RNA ChRO1 facilitates ATRX/DAXX-dependent H3.3 deposition for transcription-associated heterochromatin reorganization. <i>Nucleic Acids Research</i> , 2018, 46, 11759-11775.	6.5	37

#	ARTICLE	IF	CITATIONS
6228	RNA-Seq analysis of differentially expressed genes relevant to innate and adaptive immunity in cecropin P1 transgenic rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>BMC Genomics</i> , 2018, 19, 760.	1.2	13
6229	Multiple Regulatory Networks Are Activated during Cold Stress in <i>Medicago sativa</i> L.. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3169.	1.8	27
6230	Comparative transcriptome analysis two genotypes of <i>Acer truncatum</i> Bunge seeds reveals candidate genes that influences seed VLCFAs accumulation. <i>Scientific Reports</i> , 2018, 8, 15504.	1.6	20
6231	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	14
6232	Genetic characterization of norovirus GII.4 variants circulating in Canada using a metagenomic technique. <i>BMC Infectious Diseases</i> , 2018, 18, 521.	1.3	23
6233	Insights into the correlation between Physiological changes in and seed development of tartary buckwheat ( <i>Fagopyrum tataricum</i> Gaertn.). <i>BMC Genomics</i> , 2018, 19, 648.	1.2	62
6234	Detection of copy number variants and loss of heterozygosity from impure tumor samples using whole exome sequencing data. <i>Oncology Letters</i> , 2018, 16, 4713-4720.	0.8	2
6235	Endochondral ossification in hindlimbs during <i>bufo gargarizans</i> metamorphosis: A model of studying skeletal development in vertebrates. <i>Developmental Dynamics</i> , 2018, 247, 1121-1134.	0.8	13
6236	lncSLdb: a resource for long non-coding RNA subcellular localization. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-6.	1.4	40
6237	Long non-coding RNA AB007962 is downregulated in gastric cancer and associated with poor prognosis. <i>Oncology Letters</i> , 2018, 16, 4621-4627.	0.8	3
6238	A Chromatin Basis for Cell Lineage and Disease Risk in the Human Pancreas. <i>Cell Systems</i> , 2018, 7, 310-322.e4.	2.9	38
6239	Comparison of diploid and triploid <i>Carassius auratus</i> provides insights into adaptation to environmental change. <i>Science China Life Sciences</i> , 2018, 61, 1407-1419.	2.3	9
6240	Comparative transcriptome analysis of <i>Paphia undulata</i> with different foot colors. <i>Marine Genomics</i> , 2018, 42, 25-31.	0.4	1
6241	Chloroplast Damage Induced by the Inhibition of Fatty Acid Synthesis Triggers Autophagy in <i>Chlamydomonas</i> . <i>Plant Physiology</i> , 2018, 178, 1112-1129.	2.3	42
6242	Transcriptomic Insights Into the Growth Phase- and Sugar-Associated Changes in the Exopolysaccharide Production of a High EPS-Producing <i>Streptococcus thermophilus</i> ASCC 1275. <i>Frontiers in Microbiology</i> , 2018, 9, 1919.	1.5	48
6243	Overcoming chemoresistance in pancreatic cancer cells: role of the bitter taste receptor T2R10. <i>Journal of Cancer</i> , 2018, 9, 711-725.	1.2	32
6244	The acute transcriptomic response of coral-algae interactions to pH fluctuation. <i>Marine Genomics</i> , 2018, 42, 32-40.	0.4	9
6245	Characterization of a novel regulatory pathway for mannitol metabolism and its coordination with biofilm formation in <i>Mycobacterium smegmatis</i> . <i>Journal of Genetics and Genomics</i> , 2018, 45, 477-488.	1.7	2

#	ARTICLE	IF	CITATIONS
6246	RNA sequencing-based transcriptome analysis of mature strawberry fruit infected by necrotrophic fungal pathogen <i>Botrytis cinerea</i> . <i>Physiological and Molecular Plant Pathology</i> , 2018, 104, 77-85.	1.3	35
6247	Venom gland transcriptomics and microRNA profiling of juvenile and adult yellow-bellied sea snake, <i>Hydrophis platurus</i> , from Playa del Coco (Guanacaste, Costa Rica). <i>Toxicon</i> , 2018, 153, 96-105.	0.8	14
6248	Epigenetic Regulation of Skin Development and Regeneration. <i>Pancreatic Islet Biology</i> , 2018, , .	0.1	0
6249	Enhancer-Promoter Interactions and Their Role in the Control of Epidermal Differentiation. <i>Contributions To Management Science</i> , 2018, , 231-262.	0.4	0
6250	De novo transcriptome analysis of the egg parasitoid <i>Trichogramma chilonis</i> Ishii (Hymenoptera: Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	0.4	3
6251	Plant Genetics and Molecular Biology. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2018, , .	0.6	6
6252	Targeting LRP8 inhibits breast cancer stem cells in triple-negative breast cancer. <i>Cancer Letters</i> , 2018, 438, 165-173.	3.2	28
6253	Timing and Order of the Molecular Events Marking the Onset of Berry Ripening in Grapevine. <i>Plant Physiology</i> , 2018, 178, 1187-1206.	2.3	84
6254	Lignocellulose degradation at the holobiont level: teamwork in a keystone soil invertebrate. <i>Microbiome</i> , 2018, 6, 162.	4.9	70
6256	De novo sequencing of the <i>Freesia hybrida</i> petal transcriptome to discover putative anthocyanin biosynthetic genes and develop EST-SSR markers. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	6
6257	A whole-transcriptome approach to evaluate reference genes for quantitative diurnal gene expression studies under natural field conditions in <i>Tamarix ramosissima</i> leaves. <i>Electronic Journal of Biotechnology</i> , 2018, 35, 48-56.	1.2	3
6258	Transient T-bet expression functionally specifies a distinct T follicular helper subset. <i>Journal of Experimental Medicine</i> , 2018, 215, 2705-2714.	4.2	68
6259	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. <i>BMC Genomics</i> , 2018, 19, 351.	1.2	49
6260	Transcriptome Analysis of Acute Phase Liver Graft Injury in Liver Transplantation. <i>Biomedicines</i> , 2018, 6, 41.	1.4	5
6261	Transcriptional Insights into the Sugarcane-Sorghum mosaic virus Interaction. <i>Tropical Plant Biology</i> , 2018, 11, 163-176.	1.0	25
6262	The Systems Biology of Single-Cell Aging. <i>IScience</i> , 2018, 7, 154-169.	1.9	22
6263	Single cell transcriptome analysis of MCF-7 reveals consistently and inconsistently expressed gene groups each associated with distinct cellular localization and functions. <i>PLoS ONE</i> , 2018, 13, e0199471.	1.1	7
6264	Hfq, a RNA Chaperone, Contributes to Virulence by Regulating Plant Cell Wall-Degrading Enzyme Production, Type VI Secretion System Expression, Bacterial Competition, and Suppressing Host Defense Response in <i>Pectobacterium carotovorum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 1166-1178.	1.4	39



#	ARTICLE	IF	CITATIONS
6265	Dose-dependent transcriptomic responses of zebrafish leutheroembryos to Bisphenol A. <i>Environmental Pollution</i> , 2018, 243, 988-997.	3.7	30
6266	Improving nanopore read accuracy with the R2C2 method enables the sequencing of highly multiplexed full-length single-cell cDNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9726-9731.	3.3	180
6267	Global Analysis of Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus Gene Expression in the Midgut of the Lepidopteran Host <i>Trichoplusia ni</i> . <i>Journal of Virology</i> , 2018, 92, .	1.5	21
6268	Transcriptional response of honey bee ( <i>Apis mellifera</i> ) to differential nutritional status and <i>Nosema</i> infection. <i>BMC Genomics</i> , 2018, 19, 628.	1.2	31
6269	Quantitative single-cell transcriptomics. <i>Briefings in Functional Genomics</i> , 2018, 17, 220-232.	1.3	50
6270	Expression of Granulysin, Perforin and Granzymes in Human Milk over Lactation and in the Case of Maternal Infection. <i>Nutrients</i> , 2018, 10, 1230.	1.7	27
6271	Research Article Preliminary analysis on the developmental transcriptomes of swallowtail butterfly <i>Papilio polytes</i> (Lepidoptera: Papilioidae). <i>Genetics and Molecular Research</i> , 2018, 17, .	0.3	0
6272	Cellular and molecular characteristics of pollen abortion in chrysanthemum cv. Kingfisher. <i>Plant Molecular Biology</i> , 2018, 98, 233-247.	2.0	8
6273	Comparative Transcriptome Analysis Revealed the Tissue-Specific Accumulations of Taxanes among Three Experimental Lines of <i>Taxus yunnanensis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 10410-10420.	2.4	14
6274	Comparative transcriptome analysis between the short-term stress and long-term adaptation of the <i>Ruditapes philippinarum</i> in response to benzo[a]pyrene. <i>Aquatic Toxicology</i> , 2018, 204, 59-69.	1.9	12
6275	Comparative transcriptome analysis of hESC- and iPSC-derived corneal endothelial cells. <i>Experimental Eye Research</i> , 2018, 176, 252-257.	1.2	16
6276	Comparative transcriptome analysis to identify putative genes involved in thymol biosynthesis pathway in medicinal plant <i>Trachyspermum ammi</i> L.. <i>Scientific Reports</i> , 2018, 8, 13405.	1.6	24
6277	Transcriptome analysis of differentially expressed unigenes involved in flavonoid biosynthesis during flower development of <i>Chrysanthemum morifolium</i> "Chuju". <i>Scientific Reports</i> , 2018, 8, 13414.	1.6	43
6278	Comparative genomics and transcriptomics of <i>Chrysolophus</i> provide insights into the evolution of complex plumage colouration. <i>GigaScience</i> , 2018, 7, .	3.3	14
6279	Pre- and post-puberty expression of genes and proteins in the uterus of <i>Bos indicus</i> heifers: the luteal phase effect post-puberty. <i>Animal Genetics</i> , 2018, 49, 539-549.	0.6	20
6280	RpfC regulates the expression of the key regulator hrpX of the hrp/T3SS system in <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>BMC Microbiology</i> , 2018, 18, 103.	1.3	11
6281	Observations of extensive gene expression differences in the cerebellum and potential relevance to Alzheimer's disease. <i>BMC Research Notes</i> , 2018, 11, 646.	0.6	12
6282	Novel alternatively spliced isoforms of MEF2A and their mRNA expression patterns in pigs. <i>Journal of Genetics</i> , 2018, 97, 977-985.	0.4	1

#	ARTICLE	IF	CITATIONS
6283	Whole transcriptome sequence data of 5-FU sensitive and 5-FU resistant tumors generated in a mouse model of de novo carcinogenesis. <i>Data in Brief</i> , 2018, 20, 1602-1606.	0.5	1
6284	New insights into <i>Phakopsora pachyrhizi</i> infection based on transcriptome analysis in planta. <i>Genetics and Molecular Biology</i> , 2018, 41, 671-691.	0.6	4
6285	Gene expression profile of human lung in a relatively early stage of COPD with emphysema. <i>International Journal of COPD</i> , 2018, Volume 13, 2643-2655.	0.9	22
6286	WUS and PIN1-related genes undergo dynamic expressional change during organ regeneration in response to wounding in <i>Zoysia japonica</i> . <i>Molecular Biology Reports</i> , 2018, 45, 1733-1744.	1.0	2
6287	Umap and Bimap: quantifying genome and methylome mappability. <i>Nucleic Acids Research</i> , 2018, 46, e120.	6.5	94
6288	DECTp: Calling Differential Gene Expression Between Cancer and Normal Samples by Integrating Tumor Purity Information. <i>Frontiers in Genetics</i> , 2018, 9, 321.	1.1	8
6289	Epioncogene Networks: Identification of Epigenomic and Transcriptomic Cooperation by Multi-omics Integration of ChIP-Seq and RNA-Seq Data. <i>RNA Technologies</i> , 2018, , 129-151.	0.2	1
6290	Genomics as a service: A joint computing and networking perspective. <i>Computer Networks</i> , 2018, 145, 27-51.	3.2	8
6291	Microgravity-Induced Alterations of Inflammation-Related Mechanotransduction in Endothelial Cells on Board SJ-10 Satellite. <i>Frontiers in Physiology</i> , 2018, 9, 1025.	1.3	38
6292	Exploring the Mechanisms of Electroacupuncture-Induced Analgesia through RNA Sequencing of the Periaqueductal Gray. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2.	1.8	53
6293	Molecular and physiological responses in roots of two full-sib poplars uncover mechanisms that contribute to differences in partial submergence tolerance. <i>Scientific Reports</i> , 2018, 8, 12829.	1.6	16
6294	Transcriptome sequencing of the human pathogen <i>Corynebacterium diphtheriae</i> NCTC 13129 provides detailed insights into its transcriptional landscape and into DtxR-mediated transcriptional regulation. <i>BMC Genomics</i> , 2018, 19, 82.	1.2	26
6295	De novo assembly and annotation of <i>Hyalomma dromedarii</i> tick (Acari: Ixodidae) sialotranscriptome with regard to gender differences in gene expression. <i>Parasites and Vectors</i> , 2018, 11, 314.	1.0	21
6296	BdorOR88a Modulates the Responsiveness to Methyl Eugenol in Mature Males of <i>Bactrocera dorsalis</i> (Hendel). <i>Frontiers in Physiology</i> , 2018, 9, 987.	1.3	29
6297	Pmel and Tyrp1b Contribute to Melanophore Variation in Mexican Cavefish. , 2018, , 3-22.		2
6298	Transcriptome analysis and physiological responses of the potato plantlets in vitro under red, blue, and white light conditions. <i>3 Biotech</i> , 2018, 8, 394.	1.1	9
6299	Seasonal Gene Expression and the Ecophysiological Implications of Toxic <i>Microcystis aeruginosa</i> Blooms in Lake Taihu. <i>Environmental Science &amp; Technology</i> , 2018, 52, 11049-11059.	4.6	79
6300	Glucocorticoid receptor recruits to enhancers and drives activation by motif-directed binding. <i>Genome Research</i> , 2018, 28, 1272-1284.	2.4	102

#	ARTICLE	IF	CITATIONS
6301	Genome-Guided Transcriptomics, DNA-Protein Interactions, and Variant Calling. , 2018, , .		0
6302	MRTFA augments megakaryocyte maturation by enhancing the SRF regulatory axis. <i>Blood Advances</i> , 2018, 2, 2691-2703.	2.5	16
6303	Gfi1aa and Gfi1b set the pace for primitive erythroblast differentiation from hemangioblasts in the zebrafish embryo. <i>Blood Advances</i> , 2018, 2, 2589-2606.	2.5	12
6304	Compare and Contrast of Differential Gene Expression Software Packages of RNA-Seq. , 2018, , .		1
6305	Transcriptome sequencing analysis of two different genotypes of Asian pear reveals potential drought stress genes. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	9
6306	Application of Brachypodium genotypes to the analysis of type II resistance to Fusarium head blight (FHB). <i>Plant Science</i> , 2018, 272, 255-266.	1.7	4
6307	Bloom of a denitrifying methanotroph, <i>Candidatus</i> <i>Methylomirabilis limnetica</i> ™, in a deep stratified lake. <i>Environmental Microbiology</i> , 2018, 20, 2598-2614.	1.8	87
6308	Overexpression of VaWRKY14 increases drought tolerance in Arabidopsis by modulating the expression of stress-related genes. <i>Plant Cell Reports</i> , 2018, 37, 1159-1172.	2.8	54
6309	Inhalation of Hydrogen of Different Concentrations Ameliorates Spinal Cord Injury in Mice by Protecting Spinal Cord Neurons from Apoptosis, Oxidative Injury and Mitochondrial Structure Damages. <i>Cellular Physiology and Biochemistry</i> , 2018, 47, 176-190.	1.1	43
6310	KDM5B decommissions the H3K4 methylation landscape of self-renewal genes during trophoblast stem cell differentiation. <i>Biology Open</i> , 2018, 7, .	0.6	20
6311	Overview of Gene Expression Analysis: Transcriptomics. <i>Methods in Molecular Biology</i> , 2018, 1783, 1-6.	0.4	12
6312	Current and Future Methods for mRNA Analysis: A Drive Toward Single Molecule Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1783, 209-241.	0.4	46
6313	Analysis of CHIP-Seq and RNA-Seq Data with BioWardrobe. <i>Methods in Molecular Biology</i> , 2018, 1783, 343-360.	0.4	11
6314	RNA-Seq and Expression Arrays: Selection Guidelines for Genome-Wide Expression Profiling. <i>Methods in Molecular Biology</i> , 2018, 1783, 7-33.	0.4	8
6315	A Guide for Designing and Analyzing RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2018, 1783, 35-80.	0.4	23
6316	Melatonin attenuates osteosarcoma cell invasion by suppression of Cxcl12 motif chemokine ligand 24 through inhibition of the c-Jun N-terminal kinase pathway. <i>Journal of Pineal Research</i> , 2018, 65, e12507.	3.4	46
6317	Gene Expression Analysis. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
6318	Integrated analysis of hepatic mRNA and miRNA profiles identified molecular networks and potential biomarkers of NAFLD. <i>Scientific Reports</i> , 2018, 8, 7628.	1.6	34

#	ARTICLE	IF	CITATIONS
6319	The transcription factor Bhlhe40 is a switch of inflammatory versus antiinflammatory Th1 cell fate determination. <i>Journal of Experimental Medicine</i> , 2018, 215, 1813-1821.	4.2	115
6320	De novo assembly and annotation of the blood transcriptome of the southern giant petrel <i>Macronectes giganteus</i> from the South Shetland Islands, Antarctica. <i>Marine Genomics</i> , 2018, 42, 63-66.	0.4	2
6321	Probing the transcriptome of <i>Aconitum carmichaelii</i> reveals the candidate genes associated with the biosynthesis of the toxic aconitine-type C19-diterpenoid alkaloids. <i>Phytochemistry</i> , 2018, 152, 113-124.	1.4	20
6322	Transcriptome profile analysis reveals the ontogenesis of rooted chichi in <i>Ginkgo biloba</i> L. <i>Gene</i> , 2018, 669, 8-14.	1.0	7
6323	The two "œrules of speciation" in species with young sex chromosomes. <i>Molecular Ecology</i> , 2018, 27, 3799-3810.	2.0	25
6324	Transcriptomic Impacts of Rumen Epithelium Induced by Butyrate Infusion in Dairy Cattle in Dry Period. <i>Gene Regulation and Systems Biology</i> , 2018, 12, 117762501877479.	2.3	12
6325	Calreticulin and integrin alpha dissociation induces anti-inflammatory programming in animal models of inflammatory bowel disease. <i>Nature Communications</i> , 2018, 9, 1982.	5.8	28
6326	Occurrence of Traditional and Alternative Fecal Indicators in Tropical Urban Environments under Different Land Use Patterns. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	18
6327	Identification of genes involved in metabolism and signalling of abscisic acid and gibberellins during <i>Epimedium pseudowushanense</i> B.L.Guo seed morphophysiological dormancy. <i>Plant Cell Reports</i> , 2018, 37, 1061-1075.	2.8	9
6328	Broad distribution spectrum from Gaussian to power law appears in stochastic variations in RNA-seq data. <i>Scientific Reports</i> , 2018, 8, 8339.	1.6	8
6329	Differential gene expression in the body wall of the sea cucumber ( <i>Apostichopus japonicus</i> ) under strong lighting and dark conditions. <i>Acta Oceanologica Sinica</i> , 2018, 37, 54-66.	0.4	9
6330	Itraconazole targets cell cycle heterogeneity in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2018, 215, 1891-1912.	4.2	54
6331	HLA Typing. <i>Methods in Molecular Biology</i> , 2018, . .	0.4	4
6332	Transcriptomic profiling and identification of candidate genes in two <i>Phoebe bournei</i> ecotypes with contrasting cold stress responses. <i>Trees - Structure and Function</i> , 2018, 32, 1315-1333.	0.9	15
6333	RNA sequencing to predict response to TNF- $\alpha$ inhibitors reveals possible mechanism for nonresponse in smokers. <i>Expert Review of Clinical Immunology</i> , 2018, 14, 623-633.	1.3	5
6334	Transcriptomic response of <i>Ralstonia solanacearum</i> to antimicrobial <i>Pseudomonas fluorescens</i> SN15-2 metabolites. <i>Canadian Journal of Microbiology</i> , 2018, 64, 816-825.	0.8	10
6335	Comparative transcription profiling of two fermentation cultures of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 sampled in the growth and in the stationary phase. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6613-6625.	1.7	8
6336	Gene expression profiles of glomerular endothelial cells support their role in the glomerulopathy of $\Delta$ diabetic mice. <i>Kidney International</i> , 2018, 94, 326-345.	2.6	55

#	ARTICLE	IF	CITATIONS
6337	Comparative transcriptome analysis of rumen papillae in suckling and weaned Japanese Black calves using RNA sequencing. <i>Journal of Animal Science</i> , 2018, 96, 2226-2237.	0.2	31
6338	An intersection network based on combining SNP coassociation and RNA coexpression networks for feed utilization traits in Japanese Black cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 2553-2566.	0.2	11
6339	An Online Compendium of CHO RNA-seq Data Allows Identification of CHO Cell Line-specific Transcriptomic Signatures. <i>Biotechnology Journal</i> , 2018, 13, e1800070.	1.8	21
6340	The floral transcriptome of <i>Machilus yunnanensis</i> , a tree in the magnoliid family Lauraceae. <i>Computational Biology and Chemistry</i> , 2018, 77, 456-465.	1.1	1
6341	Transcriptome and Expression Profiling Analysis of Recalcitrant Tea ( <i>Camellia sinensis</i> L.) Seeds Sensitive to Dehydration. <i>International Journal of Genomics</i> , 2018, 2018, 1-11.	0.8	7
6342	Differentially regulated genes in <i>Esr2</i> -mutant rat granulosa cells. <i>Data in Brief</i> , 2018, 19, 1008-1011.	0.5	10
6343	The transcriptome of the rat subfornical organ is altered in response to early postnatal overnutrition. <i>IBRO Reports</i> , 2018, 5, 17-23.	0.3	7
6344	Transcriptome Analysis of the Thymus in Short-Term Calorie-Restricted Mice Using RNA-seq. <i>International Journal of Genomics</i> , 2018, 2018, 1-10.	0.8	5
6345	Combination of TP53 and AGR3 to distinguish ovarian high-grade serous carcinoma from low-grade serous carcinoma. <i>International Journal of Oncology</i> , 2018, 52, 2041-2050.	1.4	3
6346	Transcriptome Analysis Reveals Dynamic Gene Expression Profiles in Porcine Alveolar Macrophages in Response to the Chinese Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus. <i>BioMed Research International</i> , 2018, 2018, 1-23.	0.9	24
6347	IL-13 receptors as possible therapeutic targets in diffuse intrinsic pontine glioma. <i>PLoS ONE</i> , 2018, 13, e0193565.	1.1	18
6348	De novo assembly and annotation of <i>Didymium iridis</i> transcriptome and identification of stage-specific genes. <i>Biologia (Poland)</i> , 2018, 73, 393-402.	0.8	4
6349	Identification of candidate chemosensory receptors in the antennal transcriptome of the large black chafer <i>Holotrichia parallela</i> Motschulsky (Coleoptera: Scarabaeidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 28, 63-71.	0.4	17
6350	Transcriptome analysis of differentially expressed genes involved in selenium accumulation in tea plant ( <i>Camellia sinensis</i> ). <i>PLoS ONE</i> , 2018, 13, e0197506.	1.1	44
6351	Characterization of the glutathione S-transferase (GST) gene family in <i>Pyrus bretschneideri</i> and their expression pattern upon superficial scald development. <i>Plant Growth Regulation</i> , 2018, 86, 211-222.	1.8	36
6352	Differential Expression Profiling of Long Noncoding RNA and mRNA during Osteoblast Differentiation in Mouse. <i>International Journal of Genomics</i> , 2018, 2018, 1-13.	0.8	6
6353	Biological classification with RNA-seq data: Can alternatively spliced transcript expression enhance machine learning classifiers?. <i>Rna</i> , 2018, 24, 1119-1132.	1.6	34
6354	Genomics and Proteomics in Neuro-Oncology. , 2018, , 75-85.		0

#	ARTICLE	IF	CITATIONS
6355	De novo genome assembly of <i>Oryza granulata</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018, 1, 84.	2.0	24
6356	RNA-Seq analysis of differentially expressed genes in the grand jackknife clam <i>Solen grandis</i> under aerial exposure. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 28, 54-62.	0.4	3
6357	Comparative transcriptome analysis between interspecific hybridization (Huaren apricot $\hat{\text{A}}^{\text{TM}}$ — almond $\hat{\text{A}}^{\text{TM}}$ ), and intraspecific hybridization (Huaren apricot) during young fruit developmental stage. <i>Scientia Horticulturae</i> , 2018, 240, 397-404.	1.7	4
6358	Analysis of Temporal Changes in Growth and Gene Expression for Commensal Gut Microbes in Response to the Polyphenol Naringenin. <i>Microbiology Insights</i> , 2018, 11, 117863611877510.	0.9	16
6359	Transcriptomics in Cardiovascular Medicine. , 2018, , 558-571.		0
6360	Genome-Wide analysis of aluminum-activated malate transporter family genes in six rosaceae species, and expression analysis and functional characterization on malate accumulation in Chinese white pear. <i>Plant Science</i> , 2018, 274, 451-465.	1.7	26
6361	Genome-wide analysis of the spatiotemporal regulation of firing and dormant replication origins in human cells. <i>Nucleic Acids Research</i> , 2018, 46, 6683-6696.	6.5	60
6362	The Challenges and Opportunities in the Clinical Application of Noncoding RNAs: The Road Map for miRNAs and piRNAs in Cancer Diagnostics and Prognostics. <i>International Journal of Genomics</i> , 2018, 1-18.	0.8	34
6363	Transcriptome data of <i>Prorocentrum donghaiense</i> Lu under nitrogen and phosphorus limitation. <i>Data in Brief</i> , 2018, 18, 799-802.	0.5	1
6364	Transcriptomic analysis of <i>Momordica charantia</i> polysaccharide on streptozotocin-induced diabetic rats. <i>Gene</i> , 2018, 675, 208-216.	1.0	11
6365	Angiogenin and Osteoprotegerin are type II muscle specific myokines protecting pancreatic beta-cells against proinflammatory cytokines. <i>Scientific Reports</i> , 2018, 8, 10072.	1.6	29
6366	Identification of Biomarkers Based on Differentially Expressed Genes in Papillary Thyroid Carcinoma. <i>Scientific Reports</i> , 2018, 8, 9912.	1.6	39
6367	Comparative transcript profiling reveals the mechanism of female sterility associated with seedless Ponkan mandarin ( <i>Citrus reticulata</i> Blanco). <i>Genome</i> , 2018, 61, 595-604.	0.9	1
6368	Candidate Genes as Biomarkers in Lipopolysaccharide-Induced Acute Respiratory Distress Syndrome Based on mRNA Expression Profile by Next-Generation RNA-Seq Analysis. <i>BioMed Research International</i> , 2018, 2018, 1-9.	0.9	6
6369	G $\hat{\text{I}}^{\pm}$ -cAMP/PKA pathway positively regulates pigmentation, chaetoglobosin A biosynthesis and sexual development in <i>Chaetomium globosum</i> . <i>PLoS ONE</i> , 2018, 13, e0195553.	1.1	14
6370	Integrated microRNA and mRNA expression profiling reveals a complex network regulating pomegranate ( <i>Punica granatum</i> L.) seed hardness. <i>Scientific Reports</i> , 2018, 8, 9292.	1.6	20
6371	RNA sequencing, <i>de novo</i> assembly and differential analysis of the gill transcriptome of freshwater climbing perch <i>Anabas testudineus</i> after 6 days of seawater exposure. <i>Journal of Fish Biology</i> , 2018, 93, 215-228.	0.7	10
6372	Multitarget Effects of Danqi Pill on Global Gene Expression Changes in Myocardial Ischemia. <i>International Journal of Genomics</i> , 2018, 2018, 1-11.	0.8	8

#	ARTICLE	IF	CITATIONS
6373	Transcriptomic response to GABA-producing <i>Lactobacillus plantarum</i> CGMCC 1.2437T induced by L-MSG. <i>PLoS ONE</i> , 2018, 13, e0199021.	1.1	36
6374	FLO Genes Family and Transcription Factor MIG1 Regulate <i>Saccharomyces cerevisiae</i> Biofilm Formation During Immobilized Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 1860.	1.5	26
6375	Genome-Wide Analysis of CDPK Family in Foxtail Millet and Determination of SiCDPK24 Functions in Drought Stress. <i>Frontiers in Plant Science</i> , 2018, 9, 651.	1.7	52
6376	Oxidized fish oil injury stress in <i>Megalobrama amblycephala</i> : Evaluated by growth, intestinal physiology, and transcriptome-based PI3K-Akt/NF- $\kappa$ B/TCR inflammatory signaling. <i>Fish and Shellfish Immunology</i> , 2018, 81, 446-455.	1.6	67
6377	RNA-seq based monitoring of gene expression changes of viable but non-culturable state of <i>Vibrio cholerae</i> induced by cold seawater. <i>Environmental Microbiology Reports</i> , 2018, 10, 594-604.	1.0	48
6378	Production and transplantation of bioengineered lung into a large-animal model. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	85
6379	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 236.	1.2	105
6380	Temporal transcriptome profiling of developing seeds reveals a concerted gene regulation in relation to oil accumulation in <i>Pongamia</i> ( <i>Milletia pinnata</i> ). <i>BMC Plant Biology</i> , 2018, 18, 140.	1.6	11
6381	Ectopic Expression of a <i>Thellungiella salsuginea</i> Aquaporin Gene, TsPIP1;1, Increased the Salt Tolerance of Rice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2229.	1.8	23
6382	VRTN is Required for the Development of Thoracic Vertebrae in Mammals. <i>International Journal of Biological Sciences</i> , 2018, 14, 667-681.	2.6	50
6383	Identifying differentially expressed genes from cross-site integrated data based on relative expression orderings. <i>International Journal of Biological Sciences</i> , 2018, 14, 892-900.	2.6	37
6384	Foodomics Applications. <i>Comprehensive Analytical Chemistry</i> , 2018, , 643-685.	0.7	12
6385	Lossy Compression of Quality Scores in Differential Gene Expression: A First Assessment and Impact Analysis. , 2018, , .		1
6386	Comparative transcriptome profiling of genes and pathways involved in leaf-patterning of <i>Clivia miniata</i> var. <i>variegata</i> . <i>Gene</i> , 2018, 677, 280-288.	1.0	13
6387	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. <i>Scientific Reports</i> , 2018, 8, 11612.	1.6	91
6388	Transcriptome alteration in <i>Phytophthora infestans</i> in response to phenazine-1-carboxylic acid production by <i>Pseudomonas fluorescens</i> strain LBUM223. <i>BMC Genomics</i> , 2018, 19, 474.	1.2	21
6389	Disruption of <i>gul-1</i> decreased the culture viscosity and improved protein secretion in the filamentous fungus <i>Neurospora crassa</i> . <i>Microbial Cell Factories</i> , 2018, 17, 96.	1.9	22
6390	CaGdt1 plays a compensatory role for the calcium pump CaPmr1 in the regulation of calcium signaling and cell wall integrity signaling in <i>Candida albicans</i> . <i>Cell Communication and Signaling</i> , 2018, 16, 33.	2.7	24

#	ARTICLE	IF	CITATIONS
6391	Characterization of increased cuticular wax mutant and analysis of genes involved in wax biosynthesis in <i>Dianthus spiculifolius</i> . <i>Horticulture Research</i> , 2018, 5, 40.	2.9	21
6392	The Global Response of <i>Cronobacter sakazakii</i> Cells to Amino Acid Deficiency. <i>Frontiers in Microbiology</i> , 2018, 9, 1875.	1.5	8
6393	RNA-seq Analysis Reveals Gene Expression Profiling of Female Fertile and Sterile Ovules of <i>Pinus Tabulaeformis</i> Carr. during Free Nuclear Mitosis of the Female Gametophyte. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2246.	1.8	7
6394	Transcriptomic analysis of porcine PBMCs in response to <i>Actinobacillus pleuropneumoniae</i> reveals the dynamic changes of differentially expressed genes related to immuno-inflammatory responses. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 2371-2384.	0.7	3
6395	Inhibition of Protein Glycation by Tiger Milk Mushroom [ <i>Lignosus rhinocerus</i> (Cooke) Ryvarden] and Search for Potential Anti-diabetic Activity-Related Metabolic Pathways by Genomic and Transcriptomic Data Mining. <i>Frontiers in Pharmacology</i> , 2018, 9, 103.	1.6	17
6396	Actin Cytoskeleton Affects Schwann Cell Migration and Peripheral Nerve Regeneration. <i>Frontiers in Physiology</i> , 2018, 9, 23.	1.3	31
6397	Silencing the Odorant Binding Protein RferOBP1768 Reduces the Strong Preference of Palm Weevil for the Major Aggregation Pheromone Compound Ferrugineol. <i>Frontiers in Physiology</i> , 2018, 9, 252.	1.3	33
6398	The Molecular Mechanism Underlying Pro-apoptotic Role of Hemocytes Specific Transcriptional Factor Lhx9 in <i>Crassostrea hongkongensis</i> . <i>Frontiers in Physiology</i> , 2018, 9, 612.	1.3	10
6399	Characterization of Transcription Factor Gene OsDRAP1 Conferring Drought Tolerance in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 94.	1.7	63
6400	Optimization of an RNA-Seq Differential Gene Expression Analysis Depending on Biological Replicate Number and Library Size. <i>Frontiers in Plant Science</i> , 2018, 9, 108.	1.7	75
6401	SKL1 Is Essential for Chloroplast Development in Arabidopsis. <i>Frontiers in Plant Science</i> , 2018, 9, 179.	1.7	15
6402	<i>Panax notoginseng</i> Root Cell Death Caused by the Autotoxic Ginsenoside Rg1 Is Due to Over-Accumulation of ROS, as Revealed by Transcriptomic and Cellular Approaches. <i>Frontiers in Plant Science</i> , 2018, 9, 264.	1.7	34
6403	Identification of Rice Genes Associated With Enhanced Cold Tolerance by Comparative Transcriptome Analysis With Two Transgenic Rice Plants Overexpressing DaCBF4 or DaCBF7, Isolated From Antarctic Flowering Plant <i>Deschampsia antarctica</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 601.	1.7	36
6404	Asymmetric expression patterns reveal a strong maternal effect and dosage compensation in polyploid hybrid fish. <i>BMC Genomics</i> , 2018, 19, 517.	1.2	12
6405	Using Transcriptomes as Mutant Phenotypes Reveals Functional Regions of a Mediator Subunit in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2018, 210, 15-24.	1.2	5
6406	Comparative transcriptome analysis of <i>Poncirus trifoliata</i> identifies a core set of genes involved in arbuscular mycorrhizal symbiosis. <i>Journal of Experimental Botany</i> , 2018, 69, 5255-5264.	2.4	19
6407	Comparative metatranscriptomics reveals extracellular electron transfer pathways conferring microbial adaptivity to surface redox potential changes. <i>ISME Journal</i> , 2018, 12, 2844-2863.	4.4	68
6408	A head transcriptome provides insights into odorant binding proteins of the bamboo grasshopper. <i>Genes and Genomics</i> , 2018, 40, 991-1000.	0.5	14



#	ARTICLE	IF	CITATIONS
6409	Effect of UV irradiation on <i>Sulfolobus acidocaldarius</i> and involvement of the general transcription factor TFB3 in the early UV response. <i>Nucleic Acids Research</i> , 2018, 46, 7179-7192.	6.5	38
6410	MATHT: A web server for comprehensive transcriptome data analysis. <i>Journal of Theoretical Biology</i> , 2018, 455, 140-146.	0.8	2
6411	Comparative transcriptome analysis of field- and chamber-grown samples of <i>Colobanthus quitensis</i> (Kunth) Bartl, an Antarctic flowering plant. <i>Scientific Reports</i> , 2018, 8, 11049.	1.6	27
6412	Comparative transcriptomics reveals shared gene expression changes during independent evolutionary origins of stem and hypocotyl/root tubers in <i>Brassica</i> (Brassicaceae). <i>PLoS ONE</i> , 2018, 13, e0197166.	1.1	16
6413	Comparative Transcriptome Analysis for Understanding Predator-Induced Polyphenism in the Water Flea <i>Daphnia pulex</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2110.	1.8	20
6414	Transcriptome analysis and identification of genes related to terpenoid biosynthesis in <i>Cinnamomum camphora</i> . <i>BMC Genomics</i> , 2018, 19, 550.	1.2	88
6415	Gene set analysis methods: a systematic comparison. <i>BioData Mining</i> , 2018, 11, 8.	2.2	68
6416	Data Analysis in Transcriptomics and Metabolomics Clinical Applications. <i>Comprehensive Analytical Chemistry</i> , 2018, 82, 613-641.	0.7	0
6417	Berberine ameliorates blockade of autophagic flux in the liver by regulating cholesterol metabolism and inhibiting COX2-prostaglandin synthesis. <i>Cell Death and Disease</i> , 2018, 9, 824.	2.7	24
6418	Retinoic acid signaling promotes the cytoskeletal rearrangement of embryonic epicardial cells. <i>FASEB Journal</i> , 2018, 32, 3765-3781.	0.2	28
6419	Transcriptomic analysis reveals differentially expressed genes associated with wool length in rabbit. <i>Animal Genetics</i> , 2018, 49, 428-437.	0.6	6
6420	H4K20me3 co-localizes with activating histone modifications at transcriptionally dynamic regions in embryonic stem cells. <i>BMC Genomics</i> , 2018, 19, 514.	1.2	23
6421	Dietary supplementation with Essential-oils-cobalt for improving growth performance, meat quality and skin cell capacity of goats. <i>Scientific Reports</i> , 2018, 8, 11634.	1.6	21
6422	Limitations of alignment-free tools in total RNA-seq quantification. <i>BMC Genomics</i> , 2018, 19, 510.	1.2	64
6423	Expression profiling of <i>Trypanosoma congolense</i> genes during development in the tsetse fly vector <i>Glossina morsitans morsitans</i> . <i>Parasites and Vectors</i> , 2018, 11, 380.	1.0	15
6424	Transcriptomic Profiles of Senegalese Sole Infected With Nervous Necrosis Virus Reassortants Presenting Different Degree of Virulence. <i>Frontiers in Immunology</i> , 2018, 9, 1626.	2.2	25
6425	NFIX Circular RNA Promotes Glioma Progression by Regulating miR-34a-5p via Notch Signaling Pathway. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 225.	1.4	91
6426	Alternative Splicing of Differentiated Myeloid Cell Transcripts after Infection by <i>Anaplasma phagocytophilum</i> Impacts a Selective Group of Cellular Programs. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 14.	1.8	21

#	ARTICLE	IF	CITATIONS
6427	Genetic Separation of <i>Listeria monocytogenes</i> Causing Central Nervous System Infections in Animals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 20.	1.8	22
6428	Integration of Transcriptomic and Proteomic Approaches Reveals the Temperature-Dependent Virulence of <i>Pseudomonas plecoglossicida</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 207.	1.8	77
6429	STAT6, PBX2, and PBRM1 Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018, 9, 87.	1.1	34
6430	A Leveraged Signal-to-Noise Ratio (LSTNR) Method to Extract Differentially Expressed Genes and Multivariate Patterns of Expression From Noisy and Low-Replication RNAseq Data. <i>Frontiers in Genetics</i> , 2018, 9, 176.	1.1	13
6431	Deep Surveying of the Transcriptional and Alternative Splicing Signatures for Decidual CD8+ T Cells at the First Trimester of Human Healthy Pregnancy. <i>Frontiers in Immunology</i> , 2018, 9, 937.	2.2	20
6432	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2018, 8, 2708.	1.5	64
6433	c-di-GMP Regulates Various Phenotypes and Insecticidal Activity of Gram-Positive <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 45.	1.5	39
6434	Analyzing AbrB-Knockout Effects through Genome and Transcriptome Sequencing of <i>Bacillus licheniformis</i> DW2. <i>Frontiers in Microbiology</i> , 2018, 9, 307.	1.5	24
6435	Diversity and Contributions to Nitrogen Cycling and Carbon Fixation of Soil Salinity Shaped Microbial Communities in Tarim Basin. <i>Frontiers in Microbiology</i> , 2018, 9, 431.	1.5	89
6436	PHB Biosynthesis Counteracts Redox Stress in <i>Herbaspirillum seropedicae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 472.	1.5	44
6437	The F1Fo-ATP Synthase $\hat{I}^2$ Subunit Is Required for <i>Candida albicans</i> Pathogenicity Due to Its Role in Carbon Flexibility. <i>Frontiers in Microbiology</i> , 2018, 9, 1025.	1.5	26
6438	Comparative Methylome Analysis Reveals Perturbation of Host Epigenome in Chestnut Blight Fungus by a Hypovirus. <i>Frontiers in Microbiology</i> , 2018, 9, 1026.	1.5	13
6439	Avian Leukosis Virus Subgroup J Attenuates Type I Interferon Production Through Blocking $\hat{I}^B$ Phosphorylation. <i>Frontiers in Microbiology</i> , 2018, 9, 1089.	1.5	11
6440	Large-Scale Comparative Analysis of Eugenol-Induced/Repressed Genes Expression in <i>Aspergillus flavus</i> Using RNA-seq. <i>Frontiers in Microbiology</i> , 2018, 9, 1116.	1.5	59
6441	The Presence or Absence of Intestinal Microbiota Affects Lipid Deposition and Related Genes Expression in Zebrafish ( <i>Danio rerio</i> ). <i>Frontiers in Microbiology</i> , 2018, 9, 1124.	1.5	63
6442	Trehalose Contributes to Gamma-Linolenic Acid Accumulation in <i>Cunninghamella echinulata</i> Based on de Novo Transcriptomic and Lipidomic Analyses. <i>Frontiers in Microbiology</i> , 2018, 9, 1296.	1.5	12
6443	Integrated Multi-Omic Analysis of <i>Mycobacterium tuberculosis</i> H37Ra Redefines Virulence Attributes. <i>Frontiers in Microbiology</i> , 2018, 9, 1314.	1.5	16
6444	Olfactory Receptors as Biomarkers in Human Breast Carcinoma Tissues. <i>Frontiers in Oncology</i> , 2018, 8, 33.	1.3	52

#	ARTICLE	IF	CITATIONS
6445	Methanol metabolism in the acetogenic bacterium <i>Acetobacterium woodii</i> . <i>Environmental Microbiology</i> , 2018, 20, 4369-4384.	1.8	73
6446	Cationic liposomes induce cytotoxicity in HepG2 via regulation of lipid metabolism based on whole-transcriptome sequencing analysis. <i>BMC Pharmacology &amp; Toxicology</i> , 2018, 19, 43.	1.0	11
6447	Visual tuning in the flashlight fish <i>Anomalops katoptron</i> to detect blue, bioluminescent light. <i>PLoS ONE</i> , 2018, 13, e0198765.	1.1	16
6448	Genome-Wide Analysis of Gene and microRNA Expression in Diploid and Autotetraploid <i>Paulownia fortunei</i> (Seem) Hemsl. under Drought Stress by Transcriptome, microRNA, and Degradome Sequencing. <i>Forests</i> , 2018, 9, 88.	0.9	11
6449	Comparative Transcriptomics Analysis of Phytohormone-Related Genes and Alternative Splicing Events Related to Witches' Broom in <i>Paulownia</i> . <i>Forests</i> , 2018, 9, 318.	0.9	3
6450	Transcriptomic Studies of the Effect of nod Gene-Inducing Molecules in Rhizobia: Different Weapons, One Purpose. <i>Genes</i> , 2018, 9, 1.	1.0	120
6451	Transcriptomic Analysis of Flower Bud Differentiation in <i>Magnolia sinostellata</i> . <i>Genes</i> , 2018, 9, 212.	1.0	24
6452	Combining Targeted Metabolites Analysis and Transcriptomics to Reveal Chemical Composition Difference and Underlying Transcriptional Regulation in Maca ( <i>Lepidium Meyenii</i> Walp.) Ecotypes. <i>Genes</i> , 2018, 9, 335.	1.0	6
6453	Abrogation of glutathione peroxidase-1 drives EMT and chemoresistance in pancreatic cancer by activating ROS-mediated Akt/GSK3 $\beta$ /Snail signaling. <i>Oncogene</i> , 2018, 37, 5843-5857.	2.6	92
6454	De novo characterization of the <i>Baphicacanthus cusia</i> (Nees) Bremek transcriptome and analysis of candidate genes involved in indican biosynthesis and metabolism. <i>PLoS ONE</i> , 2018, 13, e0199788.	1.1	15
6455	Transcriptome-Wide Analysis Reveals the Origin of <i>Peloria</i> in Chinese <i>Cymbidium</i> ( <i>Cymbidium sinense</i> ). <i>Plant and Cell Physiology</i> , 2018, 59, 2064-2074.	1.5	14
6456	Gene expression analysis of porcine whole blood cells infected with foot-and-mouth disease virus using high-throughput sequencing technology. <i>PLoS ONE</i> , 2018, 13, e0200081.	1.1	8
6457	Identification of novel $\hat{N}p63\hat{\pm}$ -regulated miRNAs using an optimized small RNA-Seq analysis pipeline. <i>Scientific Reports</i> , 2018, 8, 10069.	1.6	5
6458	Nucleotide Substitution Models and Evolutionary Distances. , 2018, , 269-314.		3
6459	Evolutionary and expression analysis of CAMTA gene family in <i>Nicotiana tabacum</i> yielded insights into their origin, expansion and stress responses. <i>Scientific Reports</i> , 2018, 8, 10322.	1.6	22
6460	Natural Antisense Transcripts: Molecular Mechanisms and Implications in Breast Cancers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 123.	1.8	69
6461	Transcriptome Analysis of Kiwifruit in Response to <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 373.	1.8	30
6462	Transcriptomics Sequencing Provides Insights into Understanding the Mechanism of Grass Carp Reovirus Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 488.	1.8	36

#	ARTICLE	IF	CITATIONS
6463	Investigation of Differences in Fertility among Progenies from Self-Pollinated Chrysanthemum. <i>International Journal of Molecular Sciences</i> , 2018, 19, 832.	1.8	11
6464	Transcriptomic and GC-MS Metabolomic Analyses Reveal the Sink Strength Changes during <i>Petunia</i> Anther Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 955.	1.8	15
6465	Transcriptome Analysis Reveals Molecular Signatures of Luteoloside Accumulation in Senescing Leaves of <i>Lonicera macranthoides</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1012.	1.8	16
6466	Comparative Transcriptome Analysis of Waterlogging-Sensitive and Waterlogging-Tolerant <i>Chrysanthemum morifolium</i> Cultivars under Waterlogging Stress and Reoxygenation Conditions. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1455.	1.8	44
6467	Fatty Acid $\beta$ -Oxidation Is Essential in Leptin-Mediated Oocytes Maturation of Yellow Catfish <i>Pelteobagrus fulvidraco</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1457.	1.8	11
6468	Transcriptomics Investigation into the Mechanisms of Self-Incompatibility between Pin and Thrum Morphs of <i>Primula maximowiczii</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1840.	1.8	9
6469	Comparative Transcriptome Analysis Identifies Putative Genes Involved in Dioscin Biosynthesis in <i>Dioscorea zingiberensis</i> . <i>Molecules</i> , 2018, 23, 454.	1.7	27
6470	RNA-Seq as an Emerging Tool for Marine Dinoflagellate Transcriptome Analysis: Process and Challenges. <i>Processes</i> , 2018, 6, 5.	1.3	36
6471	Phenotypic Variation in Mojave Rattlesnake ( <i>Crotalus scutulatus</i> ) Venom Is Driven by Four Toxin Families. <i>Toxins</i> , 2018, 10, 135.	1.5	32
6472	Transcriptome Analysis of Epithelioma Papulosum Cyprini Cells Infected by Reovirus Isolated from Allogynogenetic Silver Crucian Carp. <i>Viruses</i> , 2018, 10, 135.	1.5	3
6473	Comprehensive multi-center assessment of small RNA-seq methods for quantitative miRNA profiling. <i>Nature Biotechnology</i> , 2018, 36, 746-757.	9.4	134
6474	Integration of proteomic and transcriptomic profiles reveals multiple levels of genetic regulation of salt tolerance in cotton. <i>BMC Plant Biology</i> , 2018, 18, 128.	1.6	42
6475	Transcriptome analyses reveal genes of alternative splicing associated with muscle development in chickens. <i>Gene</i> , 2018, 676, 146-155.	1.0	13
6476	Impact of miRNA-mRNA Profiling and Their Correlation on Medulloblastoma Tumorigenesis. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 12, 490-503.	2.3	36
6477	String Mathematics, BLAST, and FASTA. , 2018, , 1-31.		0
6478	Distance-Based Phylogenetic Methods. , 2018, , 343-379.		3
6479	Transcriptomics and RNA-Seq Data Analysis. , 2018, , 113-128.		0
6480	Bioinformatics and Translation Initiation. , 2018, , 173-195.		0

#	ARTICLE	IF	CITATIONS
6481	Bioinformatics and Translation Elongation. , 2018, , 197-238.		1
6482	Protein Isoelectric Point and Helicobacter pylori. , 2018, , 397-412.		0
6483	Fundamentals of Proteomics. , 2018, , 421-436.		0
6484	Large-scale de novo transcriptome analysis reveals specific gene expression and novel simple sequence repeats markers in salinized roots of the euhalophyte <i>Salicornia europaea</i> . <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	2
6485	Understanding the Diversity of <i>Penicillium</i> Using Next-Generation Sequencing. , 2018, , 19-43.		0
6486	Ectopic expression of a <i>Brassica rapa</i> AINTEGUMENTA gene (BrANT-1) increases organ size and stomatal density in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2018, 8, 10528.	1.6	7
6487	A novel FADS2 isoform identified in human milk fat globule suppresses FADS2 mediated $\Delta^6$ -desaturation of omega-3 fatty acids. <i>Prostaglandins Leukotrienes and Essential Fatty Acids</i> , 2018, 138, 52-59.	1.0	6
6488	LST1: A multifunctional gene encoded in the MHC class III region. <i>Immunobiology</i> , 2018, 223, 699-708.	0.8	7
6489	Culture of haploid blastocysts in FGF4 favors the derivation of epiblast stem cells with a primed epigenetic and transcriptional landscape. <i>Scientific Reports</i> , 2018, 8, 10775.	1.6	2
6490	Identification of candidate chemosensory genes in <i>Mythimna separata</i> by transcriptomic analysis. <i>BMC Genomics</i> , 2018, 19, 518.	1.2	34
6491	Systems analysis of phosphate-limitation-induced lipid accumulation by the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 148.	6.2	78
6492	Epigenetic changes of the thioredoxin system in the tx-j mouse model and in patients with Wilson disease. <i>Human Molecular Genetics</i> , 2018, 27, 3854-3869.	1.4	18
6493	Genome-wide analysis of H3K36me3 and its regulations to cancer-related genes expression in human cell lines. <i>BioSystems</i> , 2018, 171, 59-65.	0.9	13
6494	Advancing insights into stem cell niche complexities with next-generation technologies. <i>Current Opinion in Cell Biology</i> , 2018, 55, 87-95.	2.6	24
6495	Next-generation sequencing and prenatal 'omics: advanced diagnostics and new insights into human development. <i>Genetics in Medicine</i> , 2018, 20, 791-799.	1.1	25
6496	Direct Reprogramming of Spiral Ganglion Non-neuronal Cells into Neurons: Toward Ameliorating Sensorineural Hearing Loss by Gene Therapy. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 16.	1.8	36
6497	Evolutionary and expression analyses of soybean basic Leucine zipper transcription factor family. <i>BMC Genomics</i> , 2018, 19, 159.	1.2	75
6498	Combinatorial synthetic pathway fine-tuning and comparative transcriptomics for metabolic engineering of <i>Raoultella ornithinolytica</i> BF60 to efficiently synthesize 2,5-furandicarboxylic acid. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2148-2155.	1.7	36

#	ARTICLE	IF	CITATIONS
6499	Combined analysis and miRNA expression profiles of the flowering related genes in common wild rice ( <i>Oryza rufipogon</i> Griff.). <i>Genes and Genomics</i> , 2018, 40, 835-845.	0.5	5
6500	RUNX1 promotes cell growth in human T-cell acute lymphoblastic leukemia by transcriptional regulation of key target genes. <i>Experimental Hematology</i> , 2018, 64, 84-96.	0.2	8
6501	Transcriptome profiling reveals candidate cleft palate-related genes in cultured Chinese sturgeons ( <i>Acipenser sinensis</i> ). <i>Journal of Heredity</i> , 2018, 109, 107-115.	1.0	9
6502	Impact of Three Different Mutations in <i>Ehrlichia chaffeensis</i> in Altering the Global Gene Expression Patterns. <i>Scientific Reports</i> , 2018, 8, 6162.	1.6	8
6503	Differential levels of gene expression and molecular mechanisms between red maple ( <i>Acer rubrum</i> L.) and Norway spruce ( <i>Picea abies</i> (L.) Mill.). <i>Ecology and Evolution</i> , 2018, 8, 4876-4890.	0.8	8
6504	CsMYB36 is involved in the formation of yellow green peel in cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 1659-1669.	1.8	57
6505	Characterization of <i>Chiton ischnochiton hakodadensis</i> Foot Based on Transcriptome Sequencing. <i>Journal of Ocean University of China</i> , 2018, 17, 632-640.	0.6	3
6506	The aquatic animals' transcriptome resource for comparative functional analysis. <i>BMC Genomics</i> , 2018, 19, 103.	1.2	5
6507	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in <i>Aspergillus nidulans</i> . <i>BMC Genomics</i> , 2018, 19, 214.	1.2	11
6508	Decreased testosterone levels after castration leads to abdominal fat deposition in chickens. <i>BMC Genomics</i> , 2018, 19, 344.	1.2	20
6509	Transcriptome analysis of adipose tissues from two fat-tailed sheep breeds reveals key genes involved in fat deposition. <i>BMC Genomics</i> , 2018, 19, 338.	1.2	57
6510	Targeting TWIST1 through loss of function inhibits tumorigenicity of human glioblastoma. <i>Molecular Oncology</i> , 2018, 12, 1188-1202.	2.1	25
6511	Next generation sequencing for miRNA profile of spleen CD4 <sup>+</sup> T cells in the murine model of acute asthma. <i>Epigenomics</i> , 2018, 10, 1071-1083.	1.0	8
6512	Chronophin regulates active vitamin B6 levels and transcriptomic features of glioblastoma cell lines cultured under non-adherent, serum-free conditions. <i>BMC Cancer</i> , 2018, 18, 524.	1.1	6
6513	In-depth resistome analysis by targeted metagenomics. <i>Microbiome</i> , 2018, 6, 11.	4.9	115
6514	BTNET : boosted tree based gene regulatory network inference algorithm using time-course measurement data. <i>BMC Systems Biology</i> , 2018, 12, 20.	3.0	33
6515	Microbial effects of part-stream low-frequency ultrasonic pretreatment on sludge anaerobic digestion as revealed by high-throughput sequencing-based metagenomics and metatranscriptomics. <i>Biotechnology for Biofuels</i> , 2018, 11, 47.	6.2	26
6516	Transcriptome analysis of phosphorus stress responsiveness in the seedlings of Dongxiang wild rice ( <i>Oryza rufipogon</i> Griff.). <i>Biological Research</i> , 2018, 51, 7.	1.5	46

#	ARTICLE	IF	CITATIONS
6517	Integrated microRNA and mRNA sequencing analysis of age-related changes to mouse thymic epithelial cells. <i>IUBMB Life</i> , 2018, 70, 678-690.	1.5	15
6518	iPSC-derived neurons profiling reveals GABAergic circuit disruption and acetylated $\alpha$ -tubulin defect which improves after iHDAC6 treatment in Rett syndrome. <i>Experimental Cell Research</i> , 2018, 368, 225-235.	1.2	36
6519	Identification of candidate genes involved in the sugar metabolism and accumulation during pear fruit post-harvest ripening of "Red Clapp's Favorite" ( <i>Pyrus communis</i> L.) by transcriptome analysis. <i>Hereditas</i> , 2018, 155, 11.	0.5	11
6520	Transcriptome-based identification of genes related to resistance against <i>Botrytis elliptica</i> in <i>Lilium regale</i> . <i>Canadian Journal of Plant Science</i> , 2018, 98, 1058-1071.	0.3	17
6521	Developmental transcriptome analysis of floral transition in <i>Rosa odorata</i> var. <i>gigantea</i> . <i>Plant Molecular Biology</i> , 2018, 97, 113-130.	2.0	11
6522	SpliceDetector: a software for detection of alternative splicing events in human and model organisms directly from transcript IDs. <i>Scientific Reports</i> , 2018, 8, 5063.	1.6	7
6523	PIVOT: platform for interactive analysis and visualization of transcriptomics data. <i>BMC Bioinformatics</i> , 2018, 19, 6.	1.2	55
6524	Inference of Transcription Factor Regulation Patterns Using Gene Expression Covariation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Biophysics (Russian Federation)</i> , 2018, 63, 43-51.	0.2	0
6525	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 207-234.	2.8	108
6526	HLA and proteasome expression body map. <i>BMC Medical Genomics</i> , 2018, 11, 36.	0.7	95
6527	Transcriptome remodeling of <i>Pseudomonas putida</i> KT2440 during mcl-PHAs synthesis: effect of different carbon sources and response to nitrogen stress. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018, 45, 433-446.	1.4	26
6528	Identification of novel transcripts and peptides in developing murine lens. <i>Scientific Reports</i> , 2018, 8, 11162.	1.6	5
6529	Mapping podophyllotoxin biosynthesis and growth-related transcripts with high elevation in <i>Sinopodophyllum hexandrum</i> . <i>Industrial Crops and Products</i> , 2018, 124, 510-518.	2.5	23
6530	Complementary iTRAQ-based proteomic and RNA sequencing-based transcriptomic analyses reveal a complex network regulating pomegranate ( <i>Punica granatum</i> L.) fruit peel colour. <i>Scientific Reports</i> , 2018, 8, 12362.	1.6	31
6531	Techniques for studying mechanobiology. , 2018, , 1-53.		2
6532	Identification of H4K20me3- and H3K4me3-associated RNAs using CARIP-Seq expands the transcriptional and epigenetic networks of embryonic stem cells. <i>Journal of Biological Chemistry</i> , 2018, 293, 15120-15135.	1.6	7
6533	Trans-chalcone increases p53 activity via DNAJB1/HSP40 induction and CRM1 inhibition. <i>PLoS ONE</i> , 2018, 13, e0202263.	1.1	17
6534	An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2018, , 61-89.		0

#	ARTICLE	IF	CITATIONS
6535	Generalist and Specialist Mite Herbivores Induce Similar Defense Responses in Maize and Barley but Differ in Susceptibility to Benzoxazinoids. <i>Frontiers in Plant Science</i> , 2018, 9, 1222.	1.7	38
6536	Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2923-2940.	0.8	11
6537	RNA sequencing of kidney distal tubule cells reveals multiple mediators of chronic aldosterone action. <i>Physiological Genomics</i> , 2018, 50, 343-354.	1.0	20
6538	Heterologous Expression of a Novel <i>Zoysia japonica</i> C2H2 Zinc Finger Gene, ZJZFN1, Improved Salt Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1159.	1.7	34
6539	Epigenetic regulation of the circadian gene <i>Per1</i> contributes to age-related changes in hippocampal memory. <i>Nature Communications</i> , 2018, 9, 3323.	5.8	118
6540	Studying Smaller and Neglected Organisms in Modern Evolutionary Venomics Implementing RNASeq (Transcriptomics)â€”A Critical Guide. <i>Toxins</i> , 2018, 10, 292.	1.5	26
6541	Potential Survival and Pathogenesis of a Novel Strain, <i>Vibrio parahaemolyticus</i> FORC_022, Isolated From a Soy Sauce Marinated Crab by Genome and Transcriptome Analyses. <i>Frontiers in Microbiology</i> , 2018, 9, 1504.	1.5	5
6542	Long Non-Coding RNAs Guide the Fine-Tuning of Gene Regulation in B-Cell Development and Malignancy. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2475.	1.8	33
6543	Pleiotropic control of antibiotic biosynthesis, flagellar operon expression, biofilm formation, and carbon source utilization by RpoN in <i>Pseudomonas protegens</i> H78. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9719-9730.	1.7	17
6544	Transcriptomic analyses of <i>Chrysanthemum morifolium</i> Ramat under UV-B radiation treatment reveal variations in the metabolisms associated with bioactive components. <i>Industrial Crops and Products</i> , 2018, 124, 475-486.	2.5	17
6545	Enhanced Herbicide Metabolism and Metabolic Resistance Genes Identified in Tribenuron-Methyl Resistant <i>Myosoton aquaticum</i> L.. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 9850-9857.	2.4	33
6546	RNA sequencing and bioinformatics analysis of the long noncoding RNAâ€”mRNA network in colorectal cancer. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 9957-9966.	1.2	16
6547	Accurate Recycling of Parental Histones Reproduces the Histone Modification Landscape during DNA Replication. <i>Molecular Cell</i> , 2018, 72, 239-249.e5.	4.5	188
6548	Physiological characterization of the emergence from diapause: A transcriptomics approach. <i>Scientific Reports</i> , 2018, 8, 12577.	1.6	40
6549	Astaxanthin overproduction in yeast by strain engineering and new gene target uncovering. <i>Biotechnology for Biofuels</i> , 2018, 11, 230.	6.2	77
6550	Genomeâ€”scale analysis to identify prognostic markers and predict the survival of lung adenocarcinoma. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 8909-8921.	1.2	17
6551	Physiological and transcriptomic responses of reproductive stage soybean to drought stress. <i>Plant Cell Reports</i> , 2018, 37, 1611-1624.	2.8	44
6552	Auxin homeostasis and signaling alterations result in the aberrant phenotype in scl mutant of cotton ( <i>Gossypium hirsutum</i> L.). <i>Revista Brasileira De Botanica</i> , 2018, 41, 775-784.	0.5	0



#	ARTICLE	IF	CITATIONS
6553	Characterization of the hot pepper ( <i>Capsicum frutescens</i> ) fruit ripening regulated by ethylene and ABA. <i>BMC Plant Biology</i> , 2018, 18, 162.	1.6	52
6554	Single-cell RNAseq for the study of isoforms—how is that possible?. <i>Genome Biology</i> , 2018, 19, 110.	3.8	100
6555	Comparative Transcriptomic Analysis of Immune-Related Gene Expression in Duck Embryo Fibroblasts Following Duck Tembusu Virus Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2328.	1.8	31
6556	De novo transcriptome sequencing reveals candidate genes involved in orange shell coloration of bay scallop <i>Argopecten irradians</i> . <i>Journal of Oceanology and Limnology</i> , 2018, 36, 1408-1416.	0.6	10
6557	Differential expression of lncRNAs and predicted target genes in normal mouse melanocytes and B16 cells. <i>Experimental Dermatology</i> , 2018, 27, 1230-1236.	1.4	8
6558	ASAP - A Webserver for Immunoglobulin-Sequencing Analysis Pipeline. <i>Frontiers in Immunology</i> , 2018, 9, 1686.	2.2	17
6559	Transcriptome Analysis of JA Signal Transduction, Transcription Factors, and Monoterpene Biosynthesis Pathway in Response to Methyl Jasmonate Elicitation in <i>Mentha canadensis</i> L.. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2364.	1.8	22
6560	Network analysis reveals the co-expression of sugar and aroma genes in the Chinese white pear ( <i>Pyrus</i> ) Tj ETQq1 1 0,784314,rgBT /Over	1.0	
6561	The Synergistic Effect of Exogenous Glutamine and Rifampicin Against <i>Mycobacterium</i> Persisters. <i>Frontiers in Microbiology</i> , 2018, 9, 1625.	1.5	14
6562	Molecular evidence for an intrinsic circadian pacemaker in the cardiac ganglion of the American lobster, <i>Homarus americanus</i> - Is diel cycling of heartbeat frequency controlled by a peripheral clock system?. <i>Marine Genomics</i> , 2018, 41, 19-30.	0.4	30
6563	Hypermethylation of gene body CpG islands predicts high dosage of functional oncogenes in liver cancer. <i>Nature Communications</i> , 2018, 9, 3164.	5.8	134
6564	Biological roles of indole-3-acetic acid in <i>Acinetobacter baumannii</i> . <i>Microbiological Research</i> , 2018, 216, 30-39.	2.5	35
6565	Naturally-occurring canine invasive urothelial carcinoma harbors luminal and basal transcriptional subtypes found in human muscle invasive bladder cancer. <i>PLoS Genetics</i> , 2018, 14, e1007571.	1.5	33
6566	Single-cell RNA sequencing technologies and bioinformatics pipelines. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-14.	3.2	1,087
6567	Effect of deletion of a trichothecene toxin regulatory gene on the secondary metabolism transcriptome of the saprotrophic fungus <i>Trichoderma arundinaceum</i> . <i>Fungal Genetics and Biology</i> , 2018, 119, 29-46.	0.9	27
6568	Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. <i>Translational Psychiatry</i> , 2018, 8, 158.	2.4	15
6569	Extracting proteins involved in disease progression using temporally connected networks. <i>BMC Systems Biology</i> , 2018, 12, 78.	3.0	10
6570	Comparative performance of the BGISEQ-500 and Illumina HiSeq4000 sequencing platforms for transcriptome analysis in plants. <i>Plant Methods</i> , 2018, 14, 69.	1.9	128

#	ARTICLE	IF	CITATIONS
6571	Comparative Transcriptome Analysis Identifies Putative Genes Involved in Steroid Biosynthesis in <i>Euphorbia tirucalli</i> . <i>Genes</i> , 2018, 9, 38.	1.0	7
6572	Open questions: How many genes do we have?. <i>BMC Biology</i> , 2018, 16, 94.	1.7	127
6573	Specific expression pattern of IMP metabolism related-genes in chicken muscle between cage and free range conditions. <i>PLoS ONE</i> , 2018, 13, e0201736.	1.1	12
6574	Using Supervised Learning Methods for Gene Selection in RNA-Seq Case-Control Studies. <i>Frontiers in Genetics</i> , 2018, 9, 297.	1.1	36
6575	Comparative Transcriptome Profiling Reveals Defense-Related Genes against <i>Meloidogyne incognita</i> Invasion in Tobacco. <i>Molecules</i> , 2018, 23, 2081.	1.7	14
6576	In Silico Typing of Classical and Non-classical HLA Alleles from Standard RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2018, 1802, 177-191.	0.4	6
6577	Comprehensive transcriptional and functional analyses of HbGASA genes reveal their roles in fungal pathogen resistance in <i>Hevea brasiliensis</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	18
6578	Identification and expression analysis of chemosensory genes in the tea green leafhopper, <i>Empoasca onukii</i> Matsuda. <i>Journal of Applied Entomology</i> , 2018, 142, 828-846.	0.8	7
6579	Altered Wnt and NF- $\kappa$ B Signaling in Facet Joint Osteoarthritis: Insights from RNA Deep Sequencing. <i>Tohoku Journal of Experimental Medicine</i> , 2018, 245, 69-77.	0.5	20
6580	RNA-seq analysis of aberrantly expressed long non-coding RNAs and mRNAs in a mouse model of ventilator-induced lung injury. <i>Molecular Medicine Reports</i> , 2018, 18, 882-892.	1.1	9
6581	Evolution and Diversity of Pre-mRNA Splicing in Highly Reduced Nucleomorph Genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 1573-1583.	1.1	7
6582	Airway Microbiota Is Associated with Upregulation of the PI3K Pathway in Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1188-1198.	2.5	232
6583	Bayesian Analysis of RNA-Seq Data Using a Family of Negative Binomial Models. <i>Bayesian Analysis</i> , 2018, 13, 411-436.	1.6	5
6584	Evaluation of the protective efficacy of <i>Ornithodoros moubata</i> midgut membrane antigens selected using omics and in silico prediction algorithms. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1158-1172.	1.1	16
6585	Transcriptomics insights into the genetic regulation of root apical meristem exhaustion and determinate primary root growth in <i>Pachycereus pringlei</i> (Cactaceae). <i>Scientific Reports</i> , 2018, 8, 8529.	1.6	14
6586	The Human Transcriptome. , 2018, , 135-164.		4
6587	Construction of lentiviral RNAi vector of PPAR $\gamma$ 3 gene in cashmere goats and comparison with the transcriptome analysis of adipose cells treatments. <i>Small Ruminant Research</i> , 2018, 164, 87-93.	0.6	2
6588	Transcriptome analysis reveals GA induced apoptosis in HCT116 human colon cancer cells through calcium and p53 signal pathways. <i>RSC Advances</i> , 2018, 8, 12449-12458.	1.7	14

#	ARTICLE	IF	CITATIONS
6589	Fungal Transcriptomics. <i>Methods in Molecular Biology</i> , 2018, 1775, 83-92.	0.4	0
6590	Oil biosynthesis and transcriptome profiles in developing endosperm and oil characteristic analyses in <i>Paeonia ostii</i> var. <i>lishizhenii</i> . <i>Journal of Plant Physiology</i> , 2018, 228, 121-133.	1.6	18
6591	Characterization and Transcriptome Analysis of <i>Acinetobacter baumannii</i> Persister Cells. <i>Microbial Drug Resistance</i> , 2018, 24, 1466-1474.	0.9	31
6592	Optimal Bayesian Classification With Missing Values. <i>IEEE Transactions on Signal Processing</i> , 2018, 66, 4182-4192.	3.2	11
6593	Transcriptomics provides mechanistic indicators of fluoride toxicology on endochondral ossification in the hind limb of <i>Bufo gargarizans</i> . <i>Aquatic Toxicology</i> , 2018, 201, 138-150.	1.9	17
6594	RNA-Seq reveals large quantitative differences between the transcriptomes of outbreak and non-outbreak locusts. <i>Scientific Reports</i> , 2018, 8, 9207.	1.6	10
6595	Identification of chemosensory genes from the antennal transcriptome of Indian meal moth <i>Plodia interpunctella</i> . <i>PLoS ONE</i> , 2018, 13, e0189889.	1.1	41
6596	Transcriptome analysis during ripening of table grape berry cv. Thompson Seedless. <i>PLoS ONE</i> , 2018, 13, e0190087.	1.1	23
6597	Midgut transcriptomal response of the rice leaffolder, <i>Cnaphalocrocis medinalis</i> (Guenée) to Cry1C toxin. <i>PLoS ONE</i> , 2018, 13, e0191686.	1.1	16
6598	Proteomic endorsed transcriptomic profiles of venom glands from <i>Tityus obscurus</i> and <i>T. serrulatus</i> scorpions. <i>PLoS ONE</i> , 2018, 13, e0193739.	1.1	55
6599	Digital gene-expression profiling analysis of the fatty liver of Landes geese fed different supplemental oils. <i>Gene</i> , 2018, 673, 32-45.	1.0	11
6600	Iron targeted transcriptome study draws attention to novel redox protein candidates involved in ferrous iron oxidation in <i>Ferroplasma</i> sp. JA12. <i>Research in Microbiology</i> , 2018, 169, 618-627.	1.0	9
6601	Transcriptome analysis reveals the hawthorn response to the infection of apple chlorotic leaf spot virus. <i>Scientia Horticulturae</i> , 2018, 239, 171-180.	1.7	3
6602	RNA sequencing and differential expression reveals the effects of serial oestrus synchronisation on ovarian genes in dairy goats. <i>Reproduction, Fertility and Development</i> , 2018, 30, 1622.	0.1	4
6603	Hydrogen gas inhibits lung cancer progression through targeting SMC3. <i>Biomedicine and Pharmacotherapy</i> , 2018, 104, 788-797.	2.5	61
6604	Comparative transcriptome analysis of <i>Sogatella furcifera</i> (Horváth) exposed to different insecticides. <i>Scientific Reports</i> , 2018, 8, 8773.	1.6	57
6605	Transcriptome profiling of immune-responsive genes in the intestine of <i>Cynoglossus semilaevis</i> challenged with <i>Shewanella</i> algae. <i>Fish and Shellfish Immunology</i> , 2018, 80, 291-301.	1.6	13
6606	A transcriptionally and functionally distinct PD-1+ CD8+ T cell pool with predictive potential in non-small-cell lung cancer treated with PD-1 blockade. <i>Nature Medicine</i> , 2018, 24, 994-1004.	15.2	783

#	ARTICLE	IF	CITATIONS
6607	High-level extracellular protein expression in <i>Bacillus subtilis</i> by optimizing strong promoters based on the transcriptome of <i>Bacillus subtilis</i> and <i>Bacillus megaterium</i> . <i>Protein Expression and Purification</i> , 2018, 151, 72-77.	0.6	19
6608	The influence of transcript assembly on the proteogenomics discovery of microproteins. <i>PLoS ONE</i> , 2018, 13, e0194518.	1.1	19
6609	Microexon gene transcriptional profiles and evolution provide insights into blood processing by the <i>Schistosoma japonicum</i> esophagus. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006235.	1.3	14
6610	Genome-wide identification, expansion, and evolution analysis of homeobox genes and their expression profiles during root development in carrot. <i>Functional and Integrative Genomics</i> , 2018, 18, 685-700.	1.4	18
6611	Transcriptome analyses of sex differential gene expression in brains of rare minnow ( <i>Gobiocypris</i> ). <i>Trends in Ecology and Evolution</i> , 2019, 30, 107-115.	0.5	2
6612	Conservation and lineage-specific rearrangements in the GOBP/PBP gene complex of distantly related ditrysian Lepidoptera. <i>PLoS ONE</i> , 2018, 13, e0192762.	1.1	8
6613	Integrative transcriptomic and genomic analysis of odorant binding proteins and chemosensory proteins in aphids. <i>Insect Molecular Biology</i> , 2019, 28, 1-22.	1.0	45
6614	Examination of carbohydrate and lipid metabolic changes during <i>Haematococcus pluvialis</i> non-motile cell germination using transcriptome analysis. <i>Journal of Applied Phycology</i> , 2019, 31, 145-156.	1.5	9
6615	Computational approaches for high-throughput single-cell data analysis. <i>FEBS Journal</i> , 2019, 286, 1451-1467.	2.2	33
6616	<i>LcFIN2</i> , a novel chloroplast protein gene from sheepgrass, enhances tolerance to low temperature in <i>Arabidopsis</i> and rice. <i>Physiologia Plantarum</i> , 2019, 166, 628-645.	2.6	12
6617	<i>lrf3</i> from mandarin fish thymus initiates interferon transcription. <i>Fish Physiology and Biochemistry</i> , 2019, 45, 133-144.	0.9	8
6618	Transient activation of AMPK preceding left ventricular pressure overload reduces adverse remodeling and preserves left ventricular function. <i>FASEB Journal</i> , 2019, 33, 711-721.	0.2	10
6619	Comparative mRNA and miRNA expression in European mouflon ( <i>Ovis musimon</i> ) and sheep ( <i>Ovis aries</i> ) provides novel insights into the genetic mechanisms for female reproductive success. <i>Heredity</i> , 2019, 122, 172-186.	1.2	21
6620	Compositional and transcriptomic analysis associated with cuticle lipid production on rosette and inflorescence stem leaves in the extremophyte <i>Thellungiella salsuginea</i> . <i>Physiologia Plantarum</i> , 2019, 165, 584-603.	2.6	5
6621	De novo transcriptomics analysis revealed a global reprogramming towards dehydration and hyposalinity in <i>Bangia fuscopurpurea</i> gametophytes (Rhodophyta). <i>Journal of Applied Phycology</i> , 2019, 31, 637-651.	1.5	8
6622	Transcriptome profiles of isolated murine Achilles tendon proper and peritoneal-derived progenitor cells. <i>Journal of Orthopaedic Research</i> , 2019, 37, 1409-1418.	1.2	17
6623	Expression Clustering. , 2019, , 388-395.		1
6624	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		0

#	ARTICLE	IF	CITATIONS
6625	Transcriptome Informatics. , 2019, , 324-340.		8
6626	Transcriptomic Data Normalization. , 2019, , 364-371.		0
6627	Differential Expression From Microarray and RNA-seq Experiments. , 2019, , 372-387.		0
6628	Genome Annotation. , 2019, , 195-209.		3
6629	Characterization of Transcriptional Activities. , 2019, , 830-841.		0
6630	Molecular and cellular studies of PTSD: Postmortem transcriptome analysis and novel therapeutic targets. <i>Journal of Neuroscience Research</i> , 2019, 97, 292-299.	1.3	11
6631	Transcriptomic analysis of <i>Staphylococcus aureus</i> under the stress condition of antibacterial erythorbil laurate by RNA sequencing. <i>Food Control</i> , 2019, 96, 1-8.	2.8	33
6632	New lncRNA annotation reveals extensive functional divergence of the transcriptome in maize. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 394-405.	4.1	15
6633	Transcriptional Study Revealed That Boron Supplementation May Alter the Immune-Related Genes Through MAPK Signaling in Ostrich Chick Thymus. <i>Biological Trace Element Research</i> , 2019, 189, 209-223.	1.9	8
6634	Bioinformatic and biological avenues for understanding alcohol use disorder. <i>Alcohol</i> , 2019, 74, 65-71.	0.8	3
6635	Stable maintenance of the rudivirus SIRV3 in a carrier state in <i>Sulfolobus islandicus</i> despite activation of the CRISPR-Cas immune response by a second virus SMV1. <i>RNA Biology</i> , 2019, 16, 557-565.	1.5	12
6636	Environmental drivers and genomic architecture of trait differentiation in fire-adapted <i>Banksia attenuata</i> ecotypes. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 417-432.	4.1	10
6637	Alleviation by abscisic acid of Al toxicity in rice bean is not associated with citrate efflux but depends on ABI5-mediated signal transduction pathways. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 140-154.	4.1	38
6638	Next-generation sequencing technologies accelerate advances in T-cell therapy for cancer. <i>Briefings in Functional Genomics</i> , 2019, 18, 119-128.	1.3	4
6639	Physiological RNA dynamics in RNA-Seq analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1725-1733.	3.2	7
6640	Bosutinib, dasatinib, imatinib, nilotinib, and ponatinib differentially affect the vascular molecular pathways and functionality of human endothelial cells. <i>Leukemia and Lymphoma</i> , 2019, 60, 189-199.	0.6	43
6641	Adaptive mechanism of <i>Acidithiobacillus thiooxidans</i> CCTCC M 2012104 under stress during bioleaching of low-grade chalcopyrite based on physiological and comparative transcriptomic analysis. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1643-1656.	1.4	20
6642	Genome-wide characterization of the AP2/ERF gene family in radish ( <i>Raphanus sativus</i> L.): Unveiling evolution and patterns in response to abiotic stresses. <i>Gene</i> , 2019, 718, 144048.	1.0	39

#	ARTICLE	IF	CITATIONS
6643	Steroids originating from bacterial bile acid degradation affect <i>Caenorhabditis elegans</i> and indicate potential risks for the fauna of manured soils. <i>Scientific Reports</i> , 2019, 9, 11120.	1.6	17
6644	Comparative Analysis of the Liver and Spleen Transcriptomes between Holstein and Yunnan Humped Cattle. <i>Animals</i> , 2019, 9, 527.	1.0	3
6645	A homolog of the ALOG family controls corolla tube differentiation in <i>Torenia fournieri</i> . <i>Development (Cambridge)</i> , 2019, 146, .	1.2	7
6646	Time-dependent effects of <i>Pochonia chlamydosporia</i> endophytism on gene expression profiles of colonized tomato roots. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8511-8527.	1.7	14
6647	Linker histones are fine-scale chromatin architects modulating developmental decisions in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2019, 20, 157.	3.8	67
6648	Egg-laying and brooding stage-specific hormonal response and transcriptional regulation in pituitary of Muscovy duck ( <i>Cairina moschata</i> ). <i>Poultry Science</i> , 2019, 98, 5287-5296.	1.5	18
6649	Salivary Diagnostics. , 0, , .		2
6650	Comparative transcriptome analysis of male and female gonads reveals sex-biased genes in spotted scat ( <i>Scatophagus argus</i> ). <i>Fish Physiology and Biochemistry</i> , 2019, 45, 1963-1980.	0.9	37
6651	Multilayered Tuning of Dosage Compensation and Z-Chromosome Masculinization in the Wood White ( <i>Leptidea sinapis</i> ) Butterfly. <i>Genome Biology and Evolution</i> , 2019, 11, 2633-2652.	1.1	6
6652	Uncovering the Transcriptional Correlates of Hub Connectivity in Neural Networks. <i>Frontiers in Neural Circuits</i> , 2019, 13, 47.	1.4	20
6653	PropaNet: Time-Varying Condition-Specific Transcriptional Network Construction by Network Propagation. <i>Frontiers in Plant Science</i> , 2019, 10, 698.	1.7	6
6654	Integrative Systems Biology Resources and Approaches in Disease Analytics. , 0, , .		1
6655	Elucidation of Galactomannan Biosynthesis Pathway Genes through Transcriptome Sequencing of Seeds Collected at Different Developmental Stages of Commercially Important Indian Varieties of Cluster Bean ( <i>Cyamopsis tetragonoloba</i> L.). <i>Scientific Reports</i> , 2019, 9, 11539.	1.6	11
6656	Candidates for chemosensory genes identified in the Chinese citrus fly, <i>Bactrocera minax</i> , through a transcriptomic analysis. <i>BMC Genomics</i> , 2019, 20, 646.	1.2	20
6657	Transcriptome analysis of the molecular mechanism underlying immunity- and reproduction trade-off in <i>Locusta migratoria</i> infected by <i>Micrococcus luteus</i> . <i>PLoS ONE</i> , 2019, 14, e0211605.	1.1	4
6658	Transcriptome Analysis of Acid-Responsive Genes and Pathways Involved in Polyamine Regulation in Iron Walnut. <i>Genes</i> , 2019, 10, 605.	1.0	5
6659	Genome-Wide Identification of Long Non-Coding RNAs and Their Regulatory Networks Involved in <i>Apis mellifera ligustica</i> Response to <i>Nosema ceranae</i> Infection. <i>Insects</i> , 2019, 10, 245.	1.0	35
6660	Enhancing peptaibols production in the biocontrol fungus <i>Trichoderma longibrachiatum</i> SMF2 by elimination of a putative glucose sensor. <i>Biotechnology and Bioengineering</i> , 2019, 116, 3030-3040.	1.7	9

#	ARTICLE	IF	CITATIONS
6661	Systemic understanding of <i>Lactococcus lactis</i> response to acid stress using transcriptomics approaches. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1621-1629.	1.4	21
6662	Comparative transcriptomic analysis and structure prediction of novel <i>Newt</i> proteins. <i>PLoS ONE</i> , 2019, 14, e0220416.	1.1	13
6664	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834.	1.1	44
6665	Efficient two-dimensional Haar wavelet synopsis construction for the maximum absolute error measure. <i>VLDB Journal</i> , 2019, 28, 675-701.	2.7	1
6666	CKLF1 aggravates neointimal hyperplasia by inhibiting apoptosis of vascular smooth muscle cells through PI3K/AKT/NF- $\kappa$ B signaling. <i>Biomedicine and Pharmacotherapy</i> , 2019, 117, 108986.	2.5	6
6667	Differential Inhibition of Target Gene Expression by Human microRNAs. <i>Cells</i> , 2019, 8, 791.	1.8	14
6668	Development of an attenuated oral vaccine strain of tilapia Group B <i>Streptococci</i> serotype Ia by gene knockout technology. <i>Fish and Shellfish Immunology</i> , 2019, 93, 924-933.	1.6	6
6669	Transcriptome Analysis Reveals New Insights into MdBAK1-Mediated Plant Growth in <i>Malus domestica</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9757-9771.	2.4	9
6670	RNA sequencing: the teenage years. <i>Nature Reviews Genetics</i> , 2019, 20, 631-656.	7.7	1,192
6671	Comparative transcriptomics and weighted gene co-expression correlation network analysis (WGCNA) reveal potential regulation mechanism of carotenoid accumulation in <i>Chrysanthemum morifolium</i> . <i>Plant Physiology and Biochemistry</i> , 2019, 142, 415-428.	2.8	48
6672	Moving Just Enough Deep Sequencing Data to Get the Job Done. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221985635.	1.0	2
6673	The first transcriptome sequencing and analysis of the endangered plant species <i>Picea neveitchii</i> Mast. and potential EST-SSR markers development. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 967-973.	0.5	5
6674	On the Bias of Precision Estimation Under Separate Sampling. <i>Cancer Informatics</i> , 2019, 18, 117693511986082.	0.9	1
6675	Accurate Classification of Differential Expression Patterns in a Bayesian Framework With Robust Normalization for Multi-Group RNA-Seq Count Data. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221986081.	1.0	12
6676	Whole transcriptome analysis of chemically induced hepatocellular carcinoma using RNA sequencing analysis. <i>FEBS Open Bio</i> , 2019, 9, 1900-1908.	1.0	3
6677	Cell wall composition and transcriptomics in stem tissues of stinging nettle ( <i>Urtica dioica</i> L.): Spotlight on a neglected fibre crop. <i>Plant Direct</i> , 2019, 3, e00151.	0.8	28
6678	Transcriptome analysis of the effects of <i>Herichium erinaceus</i> polysaccharide on the lymphocyte homing in Muscovy duck reovirus-infected ducklings. <i>International Journal of Biological Macromolecules</i> , 2019, 140, 697-708.	3.6	10
6679	Morphological characterization and transcriptome analysis of pistillate flowering in pecan ( <i>Carya</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc 15	1.7	15

#	ARTICLE	IF	CITATIONS
6680	Transcriptional characterisation of the <i>Exaiptasia pallida</i> pedal disc. <i>BMC Genomics</i> , 2019, 20, 581.	1.2	10
6681	Gene expression in <i>Tribolium castaneum</i> life stages: Identifying a species-specific target for pest control applications. <i>PeerJ</i> , 2019, 7, e6946.	0.9	25
6682	De novo transcriptome sequencing and identification of genes related to salt and PEG stress in <i>Tetraena mongolica</i> Maxim. <i>Trees - Structure and Function</i> , 2019, 33, 1639-1656.	0.9	8
6683	Multi-omic analyses of exogenous nutrient bag decomposition by the black morel <i>Morchella importuna</i> reveal sustained carbon acquisition and transferring. <i>Environmental Microbiology</i> , 2019, 21, 3909-3926.	1.8	54
6684	De novo Assembly and Characterization of the Floral Transcriptomes of Two Varieties of <i>Melastoma malabathricum</i> . <i>Frontiers in Genetics</i> , 2019, 10, 521.	1.1	4
6685	Transcriptomic Profiling of Duodenal Epithelium Reveals Temporally Dynamic Impacts of Direct Duodenal Starch-Infusion During Dry Period of Dairy Cattle. <i>Frontiers in Veterinary Science</i> , 2019, 6, 214.	0.9	2
6686	Growth and Transcriptional Changes in Poplar Under Different Nitrogen Sources. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 291-302.	1.0	4
6687	BALLI: Bartlett-adjusted likelihood-based linear model approach for identifying differentially expressed genes with RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 540.	1.2	3
6688	AraPPINet: An Updated Interactome for the Analysis of Hormone Signaling Crosstalk in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 870.	1.7	12
6689	Cloudy with a Chance of Insights: Context Dependent Gene Regulation and Implications for Evolutionary Studies. <i>Genes</i> , 2019, 10, 492.	1.0	21
6690	De novo sequencing of tree peony ( <i>Paeonia suffruticosa</i> ) transcriptome to identify critical genes involved in flowering and floral organ development. <i>BMC Genomics</i> , 2019, 20, 572.	1.2	23
6691	Independent modulation of individual genomic component transcription and a cis-acting element related to high transcriptional activity in a multipartite DNA virus. <i>BMC Genomics</i> , 2019, 20, 573.	1.2	17
6692	Systematic evaluation of RNA-Seq preparation protocol performance. <i>BMC Genomics</i> , 2019, 20, 571.	1.2	38
6693	Epithelial-mesenchymal transition markers screened in a cell-based model and validated in lung adenocarcinoma. <i>BMC Cancer</i> , 2019, 19, 680.	1.1	31
6694	Differential Gene Expression Analysis of RNA-seq Data Using Machine Learning for Cancer Research. <i>Learning and Analytics in Intelligent Systems</i> , 2019, , 27-65.	0.5	5
6695	<i>Musa balbisiana</i> genome reveals subgenome evolution and functional divergence. <i>Nature Plants</i> , 2019, 5, 810-821.	4.7	132
6696	Co-expression analysis reveals dysregulated miRNAs and miRNA-mRNA interactions in the development of contrast-induced acute kidney injury. <i>PLoS ONE</i> , 2019, 14, e0218574.	1.1	9
6697	Transcriptomics: Genome-Wide Expression Analysis in Livestock Research. , 2019, , 373-385.		1



#	ARTICLE	IF	CITATIONS
6698	RNA Splicing Analysis: From In Vitro Testing to Single-Cell Imaging. <i>CheM</i> , 2019, 5, 2571-2592.	5.8	41
6700	Epigenetic Regulation at the Interplay Between Gut Microbiota and Host Metabolism. <i>Frontiers in Genetics</i> , 2019, 10, 638.	1.1	116
6701	Getting the Entire Message: Progress in Isoform Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 709.	1.1	39
6702	Genomewide identification and analysis of heat shock proteins 70/110 to reveal their potential functions in Chinese soft-shelled turtle <i>Pelodiscus sinensis</i> . <i>Ecology and Evolution</i> , 2019, 9, 6968-6985.	0.8	5
6703	Mechanisms of Progression of Myeloid Preleukemia to Transformed Myeloid Leukemia in Children with Down Syndrome. <i>Cancer Cell</i> , 2019, 36, 123-138.e10.	7.7	93
6704	De novo assembly of the <i>Platyclus orientalis</i> (L.) Franco transcriptome provides insight into the development and pollination mechanism of female cone based on RNA-Seq data. <i>Scientific Reports</i> , 2019, 9, 10191.	1.6	4
6705	Modelling RNA-Seq data with a zero-inflated mixture Poisson linear model. <i>Genetic Epidemiology</i> , 2019, 43, 786-799.	0.6	4
6706	FadP affects the virulence of <i>Ralstonia pseudosolanacearum</i> by altering nitrogen metabolism processes and reducing motility, cellulase, and extracellular polysaccharide production. <i>Journal of Plant Pathology</i> , 2019, 101, 1085-1098.	0.6	0
6707	Non-cell autonomous mechanism of Parkinson's disease pathology caused by G2019S LRRK2 mutation in Ashkenazi Jewish patient: Single cell analysis. <i>Brain Research</i> , 2019, 1722, 146342.	1.1	8
6708	The anti-aflatoxigenic mechanism of cinnamaldehyde in <i>Aspergillus flavus</i> . <i>Scientific Reports</i> , 2019, 9, 10499.	1.6	61
6709	Identifying the growth associating genes of <i>Nannochloropsis oceanica</i> by bulked mutant analysis (BMA) and RNA sequencing (BMR-seq). <i>Journal of Applied Phycology</i> , 2019, 31, 3677-3690.	1.5	6
6710	oqxAB-Positive IncHI2 Plasmid pHXY0908 Increase <i>Salmonella enterica</i> Serotype Typhimurium Strains Tolerance to Ciprofloxacin. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 242.	1.8	10
6711	Global Transcriptome Profiling of Multiple Porcine Organs Reveals <i>Toxoplasma gondii</i> -Induced Transcriptional Landscapes. <i>Frontiers in Immunology</i> , 2019, 10, 1531.	2.2	9
6712	Transcriptomic Responses to Water Deficit and Nematode Infection in Mycorrhizal Tomato Roots. <i>Frontiers in Microbiology</i> , 2019, 10, 1807.	1.5	39
6713	Marine Metagenomics. , 2019, , .		1
6714	Differentially expressed genes during berry ripening in de novo RNA assembly of <i>Vitis flexuosa</i> fruits. <i>Horticulture Environment and Biotechnology</i> , 2019, 60, 531-553.	0.7	4
6715	The Role of Long Noncoding RNAs in Gene Expression Regulation. , 0, , .		26
6716	Heterogeneous Loop Model to Infer 3D Chromosome Structures from Hi-C. <i>Biophysical Journal</i> , 2019, 117, 613-625.	0.2	20

#	ARTICLE	IF	CITATIONS
6717	Histone Deacetylase HDT1 is Involved in Stem Vascular Development in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3452.	1.8	6
6718	Methods for the analysis of transcriptome dynamics. <i>Toxicology Research</i> , 2019, 8, 597-612.	0.9	6
6719	Comparative transcriptomics suggest unique molecular adaptations within tardigrade lineages. <i>BMC Genomics</i> , 2019, 20, 607.	1.2	68
6720	An <i>eFP-seq Browser</i> ™ for visualizing and exploring <i>RNA-seq</i> sequencing data. <i>Plant Journal</i> , 2019, 100, 641-654.	2.8	41
6721	Comparison of the RNA Content of Extracellular Vesicles Derived from <i>Paracoccidioides brasiliensis</i> and <i>Paracoccidioides lutzii</i> . <i>Cells</i> , 2019, 8, 765.	1.8	54
6722	Dissecting Adaptation Mechanisms to Contrasting Solar Irradiance in the Mediterranean Shrub <i>Cistus incanus</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3599.	1.8	7
6723	Transcriptomic response to changing ambient phosphorus in the marine dinoflagellate <i>Prorocentrum donghaiense</i> . <i>Science of the Total Environment</i> , 2019, 692, 1037-1047.	3.9	36
6724	Magic-BLAST, an accurate RNA-seq aligner for long and short reads. <i>BMC Bioinformatics</i> , 2019, 20, 405.	1.2	216
6725	Comparative Analysis of the Characteristics of Triterpenoid Transcriptome from Different Strains of <i>Wolfiporia cocos</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3703.	1.8	7
6726	The relationship between cuticular lipids and associated gene expression in above ground organs of <i>Thellungiella salsugineum</i> (Pall.) Al-Shehbaz & Warwick. <i>Plant Science</i> , 2019, 287, 110200.	1.7	4
6727	mRNAs expression profiles of high glucose-induced memory in human umbilical vein endothelial cells. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 2019, Volume 12, 1249-1261.	1.1	5
6728	New Aquaculture Technology Based on Host-Symbiotic Co-metabolism. , 2019, , 189-228.		0
6729	De novo transcriptome analysis of lettuce ( <i>Lactuca sativa</i> L.) and the identification of structural genes involved in anthocyanin biosynthesis in response to UV-B radiation. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	7
6730	TuBA: Tunable biclustering algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. <i>GigaScience</i> , 2019, 8, .	3.3	6
6731	Integrated transcriptomic and phytochemical analyses provide insights into characteristic metabolites variation in leaves of 1-year-old grafted tea ( <i>Camellia sinensis</i> ). <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	6
6732	Ozone ultrafine bubble water induces the cellular signaling involved in oxidative stress responses in human periodontal ligament fibroblasts. <i>Science and Technology of Advanced Materials</i> , 2019, 20, 590-599.	2.8	14
6733	Transcriptomic analysis of early B-cell development in the chicken embryo. <i>Poultry Science</i> , 2019, 98, 5342-5354.	1.5	11
6734	Gene expression profiles of the small intestine of village chickens from an <i>Ascaridia galli</i> infested environment. <i>Veterinary Parasitology: X</i> , 2019, 276, 100012.	2.7	4

#	ARTICLE	IF	CITATIONS
6735	Genetic basis and timing of a major mating system shift in <i>Capsella</i> . <i>New Phytologist</i> , 2019, 224, 505-517.	3.5	23
6736	Molecular and biological properties of two putative new cytorhabdoviruses infecting <i>Trifolium pratense</i> . <i>Plant Pathology</i> , 2019, 68, 1276-1286.	1.2	9
6737	pcaExplorer: an R/Bioconductor package for interacting with RNA-seq principal components. <i>BMC Bioinformatics</i> , 2019, 20, 331.	1.2	178
6738	Transgenic RXLR Effector PITG_15718.2 Suppresses Immunity and Reduces Vegetative Growth in Potato. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3031.	1.8	15
6739	Magnesium Deficiency Induced Global Transcriptome Change in <i>Citrus sinensis</i> Leaves Revealed by RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3129.	1.8	28
6740	De novo transcriptome analysis of needles of <i>Thuja dolabrata</i> var. <i>hondae</i> . <i>Plant Biotechnology</i> , 2019, 36, 113-118.	0.5	3
6741	De novo transcriptome analysis of Tibetan medicinal plant <i>Dysphania schraderiana</i> . <i>Genetics and Molecular Biology</i> , 2019, 42, 480-487.	0.6	8
6742	Single-cell RNA-seq variant analysis for exploration of genetic heterogeneity in cancer. <i>Scientific Reports</i> , 2019, 9, 9524.	1.6	19
6743	Digital gene expression analyses of mammary glands from meat ewes naturally infected with clinical mastitis. <i>Royal Society Open Science</i> , 2019, 6, 181604.	1.1	8
6744	Heterologous Expression of the DREB Transcription Factor AhDREB in <i>Populus tomentosa</i> Carrière Confers Tolerance to Salt without Growth Reduction under Greenhouse Conditions. <i>Forests</i> , 2019, 10, 214.	0.9	2
6745	Considering smoking status, coexpression network analysis of non-small cell lung cancer at different cancer stages, exhibits important genes and pathways. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 19172-19185.	1.2	5
6746	De novo assembly and transcriptome analysis of differentially expressed genes relevant to variegation in hawthorn flowers. <i>Plant Biotechnology Reports</i> , 2019, 13, 579-590.	0.9	2
6747	Comparative analysis of biocontrol agent <i>Trichoderma asperellum</i> ACCC30536 transcriptome during its interaction with <i>Populus davidiana</i> – <i>P. alba</i> var. <i>pyramidalis</i> . <i>Microbiological Research</i> , 2019, 227, 126294.	2.5	15
6748	Comparative transcriptome analysis reveals important roles of nonadditive genes in maize hybrid Anong 591 under heat stress. <i>BMC Plant Biology</i> , 2019, 19, 273.	1.6	43
6749	Evaluation of Graphene Oxide Induced Cellular Toxicity and Transcriptome Analysis in Human Embryonic Kidney Cells. <i>Nanomaterials</i> , 2019, 9, 969.	1.9	65
6750	SRAssembler: Selective Recursive local Assembly of homologous genomic regions. <i>BMC Bioinformatics</i> , 2019, 20, 371.	1.2	8
6751	Systems Genetics for Evolutionary Studies. <i>Methods in Molecular Biology</i> , 2019, 1910, 635-652.	0.4	1
6752	Verification and Improvement of the Capability of ENSEMBLES to Predict the Winter Arctic Oscillation. <i>Earth and Space Science</i> , 2019, 6, 1887-1899.	1.1	6

#	ARTICLE	IF	CITATIONS
6753	CoCo: RNA-seq read assignment correction for nested genes and multimapped reads. <i>Bioinformatics</i> , 2019, 35, 5039-5047.	1.8	28
6754	Alternating EM algorithm for a bilinear model in isoform quantification from RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 805-812.	1.8	8
6755	Genome-Wide Identification of Direct Targets of the TTG1-bHLH-MYB Complex in Regulating Trichome Formation and Flavonoid Accumulation in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5014.	1.8	25
6757	Comparative analysis of eddy current pulsed thermography and long pulse thermography for damage detection in metals and composites. <i>NDT and E International</i> , 2019, 107, 102155.	1.7	49
6758	RNA-Seq analysis of ileocecal valve and peripheral blood from Holstein cattle infected with <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> revealed dysregulation of the CXCL8/IL8 signaling pathway. <i>Scientific Reports</i> , 2019, 9, 14845.	1.6	38
6759	Identification and Validation of Candidate Genes Involved in Fatty Acid Content in Oil Palm by Genome-Wide Association Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1263.	1.7	24
6760	Differentiation of Long Non-Coding RNA and mRNA Expression Profiles in Male and Female <i>Aedes albopictus</i> . <i>Frontiers in Genetics</i> , 2019, 10, 975.	1.1	16
6761	Anticancer Effect and Mechanism of Hydroxygenkwanin in Oral Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2019, 9, 911.	1.3	13
6762	Transcriptional landscape and clinical utility of enhancer RNAs for eRNA-targeted therapy in cancer. <i>Nature Communications</i> , 2019, 10, 4562.	5.8	165
6763	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019, 102, 9043-9059.	1.4	32
6764	Hepatic Transcriptomics Reveals that Lipogenesis Is a Key Signaling Pathway in Isocitrate Dehydrogenase 2 Deficient Mice. <i>Genes</i> , 2019, 10, 728.	1.0	1
6765	Informing disease modelling with brain-relevant functional genomic annotations. <i>Brain</i> , 2019, 142, 3694-3712.	3.7	8
6766	Transcriptome Profile Analysis of Mammary Gland Tissue from Two Breeds of Lactating Sheep. <i>Genes</i> , 2019, 10, 781.	1.0	12
6767	Chemical and Transcriptomic Analysis of Cuticle Lipids under Cold Stress in <i>Thellungiella salsuginea</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 4519.	1.8	19
6768	Complex and dynamic transcriptional changes allow the helminth <i>Fasciola gigantica</i> to adjust to its intermediate snail and definitive mammalian hosts. <i>BMC Genomics</i> , 2019, 20, 729.	1.2	26
6769	Transcriptomic analysis of <i>Eruca vesicaria</i> subs. <i>sativa</i> lines with contrasting tolerance to polyethylene glycol-simulated drought stress. <i>BMC Plant Biology</i> , 2019, 19, 419.	1.6	20
6770	Transcriptional changes during tomato ripening and influence of brackish water irrigation on fruit transcriptome and sugar content. <i>Plant Physiology and Biochemistry</i> , 2019, 145, 21-33.	2.8	13
6771	Transcriptome Profiling of the Salt-Stress Response in the Halophytic Green Alga <i>Dunaliella salina</i> . <i>Plant Molecular Biology Reporter</i> , 2019, 37, 421-435.	1.0	13

#	ARTICLE	IF	CITATIONS
6772	High-resolution imaging algorithm based on temporal focal characteristic of time-reversed signal. <i>Systems Science and Control Engineering</i> , 2019, 7, 198-209.	1.8	0
6773	Detection of Belt Longitudinal Rip based on Canny Operator. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 252, 022002.	0.2	0
6774	Autopolyploidization in switchgrass alters phenotype and flowering time via epigenetic and transcription regulation. <i>Journal of Experimental Botany</i> , 2019, 70, 5673-5686.	2.4	22
6775	Transcriptome analysis reveals that barnyard grass exudates increase the allelopathic potential of allelopathic and non-allelopathic rice ( <i>Oryza sativa</i> ) accessions. <i>Rice</i> , 2019, 12, 30.	1.7	14
6776	AMBRA1-mediated autophagy and apoptosis associated with an epithelial-mesenchymal transition in the development of cleft palate induced by all-trans retinoic acid. <i>Annals of Translational Medicine</i> , 2019, 7, 128-128.	0.7	10
6777	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
6778	Dynamic transcriptome sequencing and analysis during early development in the bighead carp ( <i>Hypophthalmichthys nobilis</i> ). <i>BMC Genomics</i> , 2019, 20, 781.	1.2	13
6779	RNA-Seq Perspectives to Improve Clinical Diagnosis. <i>Frontiers in Genetics</i> , 2019, 10, 1152.	1.1	72
6780	The Discrepancy of Fatty Acid Composition of Astaxanthin Esters and Total Fatty Acids in Photoautotrophic and Heterotrophic <i>Chlorella zofingiensis</i> . <i>JAOCS, Journal of the American Oil Chemists' Society</i> , 2019, 96, 891-901.	0.8	8
6781	Disruption of a putative mitochondrial oxaloacetate shuttle protein in <i>Aspergillus carbonarius</i> results in secretion of malic acid at the expense of citric acid production. <i>BMC Biotechnology</i> , 2019, 19, 72.	1.7	11
6782	Integrated mRNA and small RNA sequencing reveals microRNA regulatory network associated with internode elongation in sugarcane ( <i>Saccharum officinarum</i> L.). <i>BMC Genomics</i> , 2019, 20, 817.	1.2	25
6783	Cell-Free DNA Methylation Profiling Analysis Technologies and Bioinformatics. <i>Cancers</i> , 2019, 11, 1741.	1.7	37
6784	A systemic study of indoxacarb resistance in <i>Spodoptera litura</i> revealed complex expression profiles and regulatory mechanism. <i>Scientific Reports</i> , 2019, 9, 14997.	1.6	42
6785	Omics Approaches to Understanding Muscle Biology. , 2019, , .		3
6786	Recurrent functional misinterpretation of RNA-seq data caused by sample-specific gene length bias. <i>PLoS Biology</i> , 2019, 17, e3000481.	2.6	53
6787	Transcriptomic analysis reveals flavonoid biosynthesis of <i>Syringa oblata</i> Lindl. in response to different light intensity. <i>BMC Plant Biology</i> , 2019, 19, 487.	1.6	21
6788	Lignin degradation potential and draft genome sequence of <i>Trametes trogii</i> S0301. <i>Biotechnology for Biofuels</i> , 2019, 12, 256.	6.2	16
6789	Selection of reference genes for normalization of cranberry ( <i>Vaccinium macrocarpon</i> Ait.) gene expression under different experimental conditions. <i>PLoS ONE</i> , 2019, 14, e0224798.	1.1	12

#	ARTICLE	IF	CITATIONS
6790	A Novel Nitrite-Base Aerobic Denitrifying Bacterium <i>Acinetobacter</i> sp. YTO3 and Its Transcriptome Analysis. <i>Frontiers in Microbiology</i> , 2019, 10, 2580.	1.5	17
6791	Identification of gene specific cis-regulatory elements during differentiation of mouse embryonic stem cells: An integrative approach using high-throughput datasets. <i>PLoS Computational Biology</i> , 2019, 15, e1007337.	1.5	18
6792	AIDE: annotation-assisted isoform discovery with high precision. <i>Genome Research</i> , 2019, 29, 2056-2072.	2.4	10
6793	Transcriptome analysis reveals a positive effect of brassinosteroids on the photosynthetic capacity of wucau under low temperature. <i>BMC Genomics</i> , 2019, 20, 810.	1.2	29
6794	Sex- and tissue-specific transcriptome analyses and expression profiling of olfactory-related genes in <i>Ceracris nigricornis</i> Walker (Orthoptera: Acrididae). <i>BMC Genomics</i> , 2019, 20, 808.	1.2	12
6795	Insight into transketolase of <i>Pyropia haitanensis</i> under desiccation stress based on integrative analysis of omics and transformation. <i>BMC Plant Biology</i> , 2019, 19, 475.	1.6	17
6796	Genome-wide expression profiling in colorectal cancer focusing on lncRNAs in the adenoma-carcinoma transition. <i>BMC Cancer</i> , 2019, 19, 1059.	1.1	36
6798	Identification of Single Nucleotide Polymorphism in Red Clover ( <i>Trifolium pratense</i> L.) Using Targeted Genomic Amplicon Sequencing and RNA-seq. <i>Frontiers in Plant Science</i> , 2019, 10, 1257.	1.7	8
6799	Growing Human Dermal Fibroblasts as Spheroids Renders Them Susceptible for Early Expression of Pluripotency Genes. <i>Advanced Biology</i> , 2019, 3, 1900094.	3.0	9
6800	Transcriptome profiling of maternal stress-induced wing dimorphism in pea aphids. <i>Ecology and Evolution</i> , 2019, 9, 11848-11862.	0.8	8
6801	Culm transcriptome sequencing of <i>Badila</i> ( <i>Saccharum officinarum</i> L.) and analysis of major genes involved in sucrose accumulation. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 455-465.	2.8	12
6802	Predicting Essential Proteins Based on Second-Order Neighborhood Information and Information Entropy. <i>IEEE Access</i> , 2019, 7, 136012-136022.	2.6	6
6803	Changes in gene expression and metabolic profile of drupes of <i>Olea europaea</i> L. cv Carolea in relation to maturation stage and cultivation area. <i>BMC Plant Biology</i> , 2019, 19, 428.	1.6	21
6804	SLUG Directs the Precursor State of Human Brain Tumor Stem Cells. <i>Cancers</i> , 2019, 11, 1635.	1.7	13
6805	Candidate genes in red pigment biosynthesis of a red-fleshed radish cultivar ( <i>Raphanus sativus</i> L.) as revealed by transcriptome analysis. <i>Biochemical Systematics and Ecology</i> , 2019, 86, 103933.	0.6	3
6806	Integrated analysis of transcriptomic and proteomic data from tree peony ( <i>P. ostii</i> ) seeds reveals key developmental stages and candidate genes related to oil biosynthesis and fatty acid metabolism. <i>Horticulture Research</i> , 2019, 6, 111.	2.9	68
6807	Adaptation of the Alphaproteobacterium <i>Rhodobacter sphaeroides</i> to stationary phase. <i>Environmental Microbiology</i> , 2019, 21, 4425-4445.	1.8	12
6808	Long non-coding RNA GAPLINC promotes angiogenesis by regulating miR-211 under hypoxia in human umbilical vein endothelial cells. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 8090-8100.	1.6	13

#	ARTICLE	IF	CITATIONS
6809	Comparative transcriptome and metabolome analyses provide new insights into the molecular mechanisms underlying taproot thickening in <i>Panax notoginseng</i> . <i>BMC Plant Biology</i> , 2019, 19, 451.	1.6	24
6810	Maternal transcripts in good and poor quality eggs from Japanese eel, <i>Anguilla japonica</i> their identification by large-scale quantitative analysis. <i>Molecular Reproduction and Development</i> , 2019, 86, 1846-1864.	1.0	8
6811	Deletion of Gcw13 represses autophagy in <i>Pichia pastoris</i> cells grown in methanol medium with sufficient amino acids. <i>Biotechnology Letters</i> , 2019, 41, 1423-1431.	1.1	1
6812	The differences of gonadal hormones and uterine transcriptome during shell calcification of hens laying hard or weak-shelled eggs. <i>BMC Genomics</i> , 2019, 20, 707.	1.2	11
6813	Transcriptome changes reveal the genetic mechanisms of the reproductive plasticity of workers in lower termites. <i>BMC Genomics</i> , 2019, 20, 702.	1.2	17
6814	Gene Cascade Finder: A tool for identification of gene cascades and its application in <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2019, 14, e0215187.	1.1	5
6815	Plasma extracellular vesicle-packaged microRNAs as candidate diagnostic biomarkers for early-stage breast cancer. <i>Molecular Medicine Reports</i> , 2019, 20, 3991-4002.	1.1	17
6816	Transcriptomic Revelation of Phenolic Compounds Involved in Aluminum Toxicity Responses in Roots of <i>Cunninghamia lanceolata</i> (Lamb.) Hook. <i>Genes</i> , 2019, 10, 835.	1.0	11
6817	Research on the mechanism and testing technology of dynamic compaction of high-filled gravel soil roadbed. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 304, 032097.	0.2	0
6818	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019, 29, 1900-1909.	2.4	21
6819	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	28
6820	Efficient Mining of Variants From Trios for Ventricular Septal Defect Association Study. <i>Frontiers in Genetics</i> , 2019, 10, 670.	1.1	0
6821	Profiling allele-specific gene expression in brains from individuals with autism spectrum disorder reveals preferential minor allele usage. <i>Nature Neuroscience</i> , 2019, 22, 1521-1532.	7.1	28
6822	Towards an Analysis of Post-Transcriptional Gene Regulation in Psoriasis via microRNAs using Machine Learning Algorithms. , 2019, , .		0
6823	Comparative multi-omics systems analysis reveal the glycolysis / gluconeogenesis signal pathway play an important role in virulence attenuation in fish-derived GBS YM001. <i>PLoS ONE</i> , 2019, 14, e0221634.	1.1	3
6824	Nonallelic homologous recombination events responsible for copy number variation within an RNA silencing locus. <i>Plant Direct</i> , 2019, 3, e00162.	0.8	14
6825	Transcriptome analysis to understand the effects of the toxoflavin and tropolone produced by phytopathogenic <i>Burkholderia</i> on <i>Escherichia coli</i> . <i>Journal of Microbiology</i> , 2019, 57, 781-794.	1.3	8
6826	Deciphering links between bacterial interactions and spatial organization in multispecies biofilms. <i>ISME Journal</i> , 2019, 13, 3054-3066.	4.4	59

#	ARTICLE	IF	CITATIONS
6827	P53-R273H mutation enhances colorectal cancer stemness through regulating specific lncRNAs. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 379.	3.5	59
6828	Breast cancer survival prediction using seven prognostic biomarker genes. <i>Oncology Letters</i> , 2019, 18, 2907-2916.	0.8	12
6829	Metabolomic and transcriptomic profiling of three types of litchi pericarps reveals that changes in the hormone balance constitute the molecular basis of the fruit cracking susceptibility of Litchi chinensis cv. Baitangying. <i>Molecular Biology Reports</i> , 2019, 46, 5295-5308.	1.0	16
6830	The RNA-seq approach to discriminate gene expression profiles in response to <i>Beauveria bassiana</i> and <i>Micrococcus luteus</i> microbial pathogens on <i>Actias selene</i> (Lepidoptera: Saturniidae). <i>Zootaxa</i> , 2019, 4591, 1.	0.2	0
6831	Comparative transcriptome and metabolite profiling of four tissues from <i>Alisma orientale</i> (Sam.) Juzep reveals its inflorescence developmental and medicinal characteristics. <i>Scientific Reports</i> , 2019, 9, 12310.	1.6	7
6832	The Analysis of Interface Normal Stress of Short Column of Square Concrete-Filled Steel Tube with Axial Compression. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019, 283, 012043.	0.2	0
6833	Clustering methods for single-cell RNA-sequencing expression data: performance evaluation with varying sample sizes and cell compositions. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.2	4
6834	Validation and delineation of a locus conferring <i>Fusarium</i> crown rot resistance on 1HL in barley by analysing transcriptomes from multiple pairs of near isogenic lines. <i>BMC Genomics</i> , 2019, 20, 650.	1.2	16
6835	Transcriptome profile of skeletal muscle at different developmental stages in Large White and Mashen pigs. <i>Canadian Journal of Animal Science</i> , 2019, 99, 867-880.	0.7	3
6836	Hydrogen Oxidation Influences Glycogen Accumulation in a Verrucomicrobial Methanotroph. <i>Frontiers in Microbiology</i> , 2019, 10, 1873.	1.5	15
6837	A Transcriptomic Analysis Reveals Diverse Regulatory Networks That Respond to Cold Stress in Strawberry ( <i>Fragaria</i> — <i>ananassa</i> ). <i>International Journal of Genomics</i> , 2019, 2019, 1-13.	0.8	16
6838	Roles of MYC-targeting long non-coding RNA MINCR in cell cycle regulation and apoptosis in non-small cell lung Cancer. <i>Respiratory Research</i> , 2019, 20, 202.	1.4	34
6839	Molecular Subtyping and Prognostic Assessment Based on Tumor Mutation Burden in Patients with Lung Adenocarcinomas. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4251.	1.8	29
6840	Transcriptome analysis to characterize the genes related to gonad growth and fatty acid metabolism in the sea urchin <i>Strongylocentrotus intermedius</i> . <i>Genes and Genomics</i> , 2019, 41, 1397-1415.	0.5	9
6841	Stable Redox-Cycling Nitroxide Tempol Has Antifungal and Immune-Modulatory Properties. <i>Frontiers in Microbiology</i> , 2019, 10, 1843.	1.5	5
6843	Artificially induced phased siRNAs promote virus resistance in transgenic plants. <i>Virology</i> , 2019, 537, 208-215.	1.1	11
6844	Transcriptome Reveals the Rice Response to Elevated Free Air CO <sub>2</sub> Concentration and TiO <sub>2</sub> Nanoparticles. <i>Environmental Science &amp; Technology</i> , 2019, 53, 11714-11724.	4.6	38
6845	Bogotá River anthropogenic contamination alters microbial communities and promotes spread of antibiotic resistance genes. <i>Scientific Reports</i> , 2019, 9, 11764.	1.6	29



#	ARTICLE	IF	CITATIONS
6846	Regional heterogeneity impacts gene expression in the subarctic zooplankter <i>Neocalanus flemingeri</i> in the northern Gulf of Alaska. <i>Communications Biology</i> , 2019, 2, 324.	2.0	12
6847	A Transcriptomic Study of the Tail Fat Deposition in Two Types of Hulun Buir Sheep According to Tail Size and Sex. <i>Animals</i> , 2019, 9, 655.	1.0	12
6848	Behavioural and chronic toxicity of fullerene to <i>Daphnia magna</i> : Mechanisms revealed by transcriptomic analysis. <i>Environmental Pollution</i> , 2019, 255, 113181.	3.7	16
6849	Transcriptome and Metabolite Profiling Reveal Novel Insights into Volatile Heterosis in the Tea Plant ( <i>Camellia Sinensis</i> ). <i>Molecules</i> , 2019, 24, 3380.	1.7	27
6850	Omics Technologies: A Hope for Translational Research in Bovine Tuberculosis. <i>Journal of Infectious Disease and Therapy</i> , 2019, 07, .	0.1	1
6851	Time-Course Transcriptome Analysis for Drug Repositioning in <i>Fusobacterium nucleatum</i> -Infected Human Gingival Fibroblasts. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 204.	1.8	10
6852	Progress and prospects of noncoding RNAs in insects. <i>Journal of Integrative Agriculture</i> , 2019, 18, 729-747.	1.7	21
6853	Metagenomics and metatranscriptomics analyses reveal oxygen detoxification and mixotrophic potentials of an enriched anammox culture in a continuous stirred-tank reactor. <i>Water Research</i> , 2019, 166, 115039.	5.3	57
6854	Malate-Dependent Carbon Utilization Enhances Central Metabolism and Contributes to Biological Fitness of <i>Laribacter hongkongensis</i> via CRP Regulation. <i>Frontiers in Microbiology</i> , 2019, 10, 1991.	1.5	2
6855	Gall Wasp Transcriptomes Unravel Potential Effectors Involved in Molecular Dialogues With Oak and Rose. <i>Frontiers in Physiology</i> , 2019, 10, 926.	1.3	33
6856	Early-life adversity and neurological disease: age-old questions and novel answers. <i>Nature Reviews Neurology</i> , 2019, 15, 657-669.	4.9	108
6857	Transcriptome analysis of hemocytes from the white shrimp <i>Litopenaeus vannamei</i> with the injection of dopamine. <i>Fish and Shellfish Immunology</i> , 2019, 94, 497-509.	1.6	21
6858	Neutrophils homing into the retina trigger pathology in early age-related macular degeneration. <i>Communications Biology</i> , 2019, 2, 348.	2.0	37
6859	Transcriptome analysis of <i>Plasmodium berghei</i> during exo-erythrocytic development. <i>Malaria Journal</i> , 2019, 18, 330.	0.8	46
6860	Telescope: Characterization of the retrotranscriptome by accurate estimation of transposable element expression. <i>PLoS Computational Biology</i> , 2019, 15, e1006453.	1.5	99
6861	lncRNA OSTN-AS1 May Represent a Novel Immune-Related Prognostic Marker for Triple-Negative Breast Cancer Based on Integrated Analysis of a ceRNA Network. <i>Frontiers in Genetics</i> , 2019, 10, 850.	1.1	42
6862	Chemical Ecology of <i>Capnodis tenebrionis</i> (L.) (Coleoptera: Buprestidae): Behavioral and Biochemical Strategies for Intraspecific and Host Interactions. <i>Frontiers in Physiology</i> , 2019, 10, 604.	1.3	16
6863	Gene Expression of <i>Haloferax volcanii</i> on Intermediate and Abundant Sources of Fixed Nitrogen. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4784.	1.8	4

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6864	A Discovery of Relevant Hepatoprotective Effects and Underlying Mechanisms of Dietary <i>Clostridium butyricum</i> Against Corticosterone-Induced Liver Injury in Pekin Ducks. <i>Microorganisms</i> , 2019, 7, 358.	1.6	8
6865	Pro-angiogenesis effect and transcriptome profile of Shuxinyin formula in zebrafish. <i>Phytomedicine</i> , 2019, 65, 153083.	2.3	8
6866	Transcriptome-based identification and characterization of genes responding to imidacloprid in <i>Myzus persicae</i> . <i>Scientific Reports</i> , 2019, 9, 13285.	1.6	17
6867	RNA-seq as a tool for evaluating human embryo competence. <i>Genome Research</i> , 2019, 29, 1705-1718.	2.4	31
6868	Combination of Transcriptomic, Proteomic, and Metabolomic Analysis Reveals the Ripening Mechanism of Banana Pulp. <i>Biomolecules</i> , 2019, 9, 523.	1.8	26
6869	Gene expression during the early stages of host perception and attachment in adult female <i>Rhipicephalus microplus</i> ticks. <i>Experimental and Applied Acarology</i> , 2019, 79, 107-124.	0.7	0
6870	Transcriptome analysis of the effect of GA3 in sugarcane culm. <i>3 Biotech</i> , 2019, 9, 376.	1.1	6
6871	eQTL mapping of rare variant associations using RNA-seq data: An evaluation of approaches. <i>PLoS ONE</i> , 2019, 14, e0223273.	1.1	2
6872	Integration of lipidomic and transcriptomic profiles reveals novel genes and regulatory mechanisms of <i>Schizochytrium</i> sp. in response to salt stress. <i>Bioresource Technology</i> , 2019, 294, 122231.	4.8	30
6873	Transcriptome sequencing reveals phagocytosis as the main immune response in the pathogen-challenged sea urchin <i>Strongylocentrotus intermedius</i> . <i>Fish and Shellfish Immunology</i> , 2019, 94, 780-791.	1.6	14
6874	Transcriptomic analysis of postharvest toon buds and key enzymes involved in terpenoid biosynthesis during cold storage. <i>Scientia Horticulturae</i> , 2019, 257, 108747.	1.7	10
6875	Metabolic engineering with ATP-citrate lyase and nitrogen source supplementation improves itaconic acid production in <i>Aspergillus niger</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 233.	6.2	23
6876	Identification of differential abundances of mRNA transcript in cumulus cells and <i>CCND1</i> associated with yak oocyte developmental competence. <i>Animal Reproduction Science</i> , 2019, 208, 106135.	0.5	10
6877	Realizing the potential of full-length transcriptome sequencing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190097.	1.8	92
6878	Integrating GWAS and Gene Expression Analysis Identifies Candidate Genes for Root Morphology Traits in Maize at the Seedling Stage. <i>Genes</i> , 2019, 10, 773.	1.0	31
6879	Transcriptome Analysis of <i>Sogatella furcifera</i> (Homoptera: Delphacidae) in Response to Sulfoxaflor and Functional Verification of Resistance-Related P450 Genes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4573.	1.8	16
6880	The Axial Organ and the Pharynx Are Sites of Hematopoiesis in the Sea Urchin. <i>Frontiers in Immunology</i> , 2019, 10, 870.	2.2	25
6881	Analysis of Small RNAs from <i>Solanum torvum</i> Swartz by Deep Sequencing. <i>Tropical Plant Biology</i> , 2019, 12, 44-54.	1.0	1

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6882	Discovery of potential transcriptional biomarkers in broiler chicken for detection of amantadine abuse based on RNA sequencing technology. <i>Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment</i> , 2019, 36, 254-269.	1.1	3
6883	HIV-1 infection increases microRNAs that inhibit Dicer1, HRB and HIV-EP2, thereby reducing viral replication. <i>PLoS ONE</i> , 2019, 14, e0211111.	1.1	22
6884	Big data challenges in genome informatics. <i>Biophysical Reviews</i> , 2019, 11, 51-54.	1.5	12
6885	Primary and Secondary Metabolic Effects of a Key Gene Deletion ( <i>YPL062W</i> ) in Metabolically Engineered Terpenoid-Producing <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	19
6886	Arabidopsis SME1 Regulates Plant Development and Response to Abiotic Stress by Determining Spliceosome Activity Specificity. <i>Plant Cell</i> , 2019, 31, 537-554.	3.1	42
6887	High Throughput mRNA Sequencing Reveals Potential Therapeutic Targets of Tao-Hong-Si-Wu Decoction in Experimental Middle Cerebral Artery Occlusion. <i>Frontiers in Pharmacology</i> , 2018, 9, 1570.	1.6	17
6888	Airway Smooth Muscle-Specific Transcriptomic Signatures of Glucocorticoid Exposure. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 110-120.	1.4	27
6889	Global Transcriptional Insights of Pollen-Pistil Interactions Commencing Self-Incompatibility and Fertilization in Tea [ <i>Camellia sinensis</i> (L.) O. Kuntze]. <i>International Journal of Molecular Sciences</i> , 2019, 20, 539.	1.8	34
6890	Disruption of TCF4 regulatory networks leads to abnormal cortical development and mental disabilities. <i>Molecular Psychiatry</i> , 2019, 24, 1235-1246.	4.1	63
6891	Comparative transcriptomics in <i>Leishmania braziliensis</i> : disclosing differential gene expression of coding and putative noncoding RNAs across developmental stages. <i>RNA Biology</i> , 2019, 16, 639-660.	1.5	20
6892	BMP signaling is required for amphioxus tail regeneration. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	8
6893	Comprehensive Expression Profiling Analysis of Pituitary Indicates that circRNA Participates in the Regulation of Sheep Estrus. <i>Genes</i> , 2019, 10, 90.	1.0	21
6894	Transcriptome analyses provide insights into the expression pattern and sequence similarity of several taxol biosynthesis-related genes in three <i>Taxus</i> species. <i>BMC Plant Biology</i> , 2019, 19, 33.	1.6	39
6895	LncRNA expression profile and ceRNA analysis in tomato during flowering. <i>PLoS ONE</i> , 2019, 14, e0210650.	1.1	30
6896	Transcriptome, enzyme activity and histopathology analysis reveal the effects of dietary carbohydrate on glycometabolism in juvenile largemouth bass, <i>Micropterus salmoides</i> . <i>Aquaculture</i> , 2019, 504, 39-51.	1.7	39
6897	Whole blood RNA sequencing reveals a unique transcriptomic profile in patients with ARDS following hematopoietic stem cell transplantation. <i>Respiratory Research</i> , 2019, 20, 15.	1.4	16
6898	Fibroblast growth factor-5 promotes spermatogonial stem cell proliferation via ERK and AKT activation. <i>Stem Cell Research and Therapy</i> , 2019, 10, 40.	2.4	28
6899	RNA-Seq and transcriptome analysis of nitrogen-deprivation responsive genes in <i>Dunaliella salina</i> TG strain. <i>Theoretical and Experimental Plant Physiology</i> , 2019, 31, 139-155.	1.1	5

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6900	Liver transcriptome data of <i>Esr1</i> knockout male rats reveals altered expression of genes involved in carbohydrate and lipid metabolism. <i>Data in Brief</i> , 2019, 22, 771-780.	0.5	7
6901	A bipartite boundary element restricts <i>UBE3A</i> imprinting to mature neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2181-2186.	3.3	50
6902	Effects of adult temperature on gene expression in a butterfly: identifying pathways associated with thermal acclimation. <i>BMC Evolutionary Biology</i> , 2019, 19, 32.	3.2	8
6903	A Host Factor GPNMB Restricts Porcine Circovirus Type 2 (PCV2) Replication and Interacts With PCV2 ORF5 Protein. <i>Frontiers in Microbiology</i> , 2019, 9, 3295.	1.5	12
6904	Secretome analysis of <i>Strongyloides venezuelensis</i> parasitic stages reveals that soluble and insoluble proteins are involved in its parasitism. <i>Parasites and Vectors</i> , 2019, 12, 21.	1.0	23
6905	Drug Repurposing: The Anthelmintics Niclosamide and Nitazoxanide Are Potent TMEM16A Antagonists That Fully Bronchodilate Airways. <i>Frontiers in Pharmacology</i> , 2019, 10, 51.	1.6	101
6906	Genome-wide analysis of DNA methylation in subcultured <i>Cordyceps militaris</i> . <i>Archives of Microbiology</i> , 2019, 201, 369-375.	1.0	19
6907	Comparative transcriptome analysis reveals key genes in the regulation of squalene and $\beta$ -sitosterol biosynthesis in <i>Torreyia grandis</i> . <i>Industrial Crops and Products</i> , 2019, 131, 182-193.	2.5	22
6908	Development of a novel cell-based assay to diagnose recurrent focal segmental glomerulosclerosis patients. <i>Kidney International</i> , 2019, 95, 708-716.	2.6	10
6909	Transcriptomic analysis of <i>Citrus clementina</i> mandarin fruits maturation reveals a MADS-box transcription factor that might be involved in the regulation of earliness. <i>BMC Plant Biology</i> , 2019, 19, 47.	1.6	27
6910	Analysis of the molecular basis of fruit cracking susceptibility in <i>Litchi chinensis</i> cv. Baitangying by transcriptome and quantitative proteome profiling. <i>Journal of Plant Physiology</i> , 2019, 234-235, 106-116.	1.6	28
6911	Genetic control of compound leaf development in the mungbean ( <i>Vigna radiata</i> L.). <i>Horticulture Research</i> , 2019, 6, 23.	2.9	22
6912	First step toward gene expression data integration: transcriptomic data acquisition with COMMAND>_. <i>BMC Bioinformatics</i> , 2019, 20, 54.	1.2	8
6913	Integration of Transcriptome, Proteome, and Metabolome Provides Insights into How Calcium Enhances the Mechanical Strength of Herbaceous Peony Inflorescence Stems. <i>Cells</i> , 2019, 8, 102.	1.8	34
6914	Divergent rRNAs as regulators of gene expression at the ribosome level. <i>Nature Microbiology</i> , 2019, 4, 515-526.	5.9	52
6915	Oxygen-mediated growth enhancement of an obligate anaerobic archaeon <i>Thermococcus onnurineus</i> NA1. <i>Journal of Microbiology</i> , 2019, 57, 138-142.	1.3	3
6916	Integrated analysis of high-throughput sequencing data shows abscisic acid-responsive genes and miRNAs in strawberry receptacle fruit ripening. <i>Horticulture Research</i> , 2019, 6, 26.	2.9	51
6917	The flagellin of candidate live biotherapeutic <i>Enterococcus gallinarum</i> MRx0518 is a potent immunostimulant. <i>Scientific Reports</i> , 2019, 9, 801.	1.6	34

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6918	Transcriptome sequencing in a 6-hydroxydopamine rat model of Parkinson's disease. <i>Genes and Genetic Systems</i> , 2019, 94, 61-69.	0.2	24
6919	Molecular Organization of Integrin-Based Adhesion Complexes in Mouse Embryonic Stem Cells. <i>ACS Biomaterials Science and Engineering</i> , 2019, 5, 3828-3842.	2.6	21
6920	Differential damage and repair of DNA-adducts induced by anti-cancer drug cisplatin across mouse organs. <i>Nature Communications</i> , 2019, 10, 309.	5.8	131
6921	Thinning alters the expression of the PpeSUT1 and PpeSUT4 sugar transporter genes and the accumulation of translocated sugars in the fruits of an early season peach variety. <i>Plant Growth Regulation</i> , 2019, 88, 283-296.	1.8	15
6922	Identification and molecular characterization of exosome-like vesicles derived from the <i>Taenia asiatica</i> adult worm. <i>Acta Tropica</i> , 2019, 198, 105036.	0.9	33
6923	How fall dormancy benefits alfalfa winter-survival? Physiologic and transcriptomic analyses of dormancy process. <i>BMC Plant Biology</i> , 2019, 19, 205.	1.6	15
6924	ChiCMaxima: a robust and simple pipeline for detection and visualization of chromatin looping in Capture Hi-C. <i>Genome Biology</i> , 2019, 20, 102.	3.8	25
6925	Retinal Gene Distribution and Functionality Implicated in Inherited Retinal Degenerations Can Reveal Disease-Relevant Pathways for Pharmacologic Intervention. <i>Pharmaceuticals</i> , 2019, 12, 74.	1.7	5
6926	Transcriptomic analysis provides insight into the mechanism of salinity adjustment in swimming crab <i>Portunus trituberculatus</i> . <i>Genes and Genomics</i> , 2019, 41, 961-971.	0.5	11
6927	Photosynthesis and yield response to elevated CO <sub>2</sub> , C4 plant foxtail millet behaves similarly to C3 species. <i>Plant Science</i> , 2019, 285, 239-247.	1.7	26
6928	Transcriptomic analysis of interstock-induced dwarfism in Sweet Persimmon ( <i>Diospyros kaki</i> Thunb.). <i>Horticulture Research</i> , 2019, 6, 51.	2.9	26
6929	Isolation and Expression Analysis of Growth-Related Genes at Different Growth Stages of Dinoflagellate <i>Alexandrium pacificum</i> . <i>Journal of Ocean University of China</i> , 2019, 18, 710-718.	0.6	2
6930	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple ( <i>Malus domestica</i> Borkh.) Buds with Diverse Flowering Capabilities Reveal Novel Insights into the Regulatory Mechanisms of Flower Bud Formation. <i>Plant and Cell Physiology</i> , 2019, 60, 1702-1721.	1.5	27
6931	Transcriptome changes in the phenylpropanoid pathway in senescing leaves of <i>Toona sinensis</i> . <i>Acta Physiologiae Plantarum</i> , 2019, 41, 126.	1.0	7
6932	Single-cell technologies in reproductive immunology. <i>American Journal of Reproductive Immunology</i> , 2019, 82, e13157.	1.2	9
6933	Single-Cell Sequencing in Precision Medicine. <i>Cancer Treatment and Research</i> , 2019, 178, 237-252.	0.2	19
6934	Physiological and transcriptomic analysis highlight key metabolic pathways in relation to drought tolerance in <i>Rhododendron delavayi</i> . <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 991-1008.	1.4	18
6935	Transcriptomic investigation of immune responses of the <i>Apis cerana cerana</i> larval gut infected by <i>Ascospaera apis</i> . <i>Journal of Invertebrate Pathology</i> , 2019, 166, 107210.	1.5	24

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6936	Optimal clustering with missing values. <i>BMC Bioinformatics</i> , 2019, 20, 321.	1.2	16
6937	Comprehensive transcriptomic view of the role of the LGALS12 gene in porcine subcutaneous and intramuscular adipocytes. <i>BMC Genomics</i> , 2019, 20, 509.	1.2	12
6938	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	1.1	8
6939	Selection and validation of reference genes of <i>Paeonia lactiflora</i> in growth development and light stress. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 1097-1105.	1.4	13
6940	Fibroblast growth factor homologous factor 1 stimulates Leydig cell regeneration from stem cells in male rats. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5618-5631.	1.6	15
6941	De novo transcriptome analysis of <i>Fraxinus velutina</i> Torr in response to NaCl stress. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	3
6942	Defining housekeeping genes suitable for RNA-seq analysis of the human allograft kidney biopsy tissue. <i>BMC Medical Genomics</i> , 2019, 12, 86.	0.7	29
6943	Immediate Dosage Compensation Is Triggered by the Deletion of Y-Linked Genes in <i>Silene latifolia</i> . <i>Current Biology</i> , 2019, 29, 2214-2221.e4.	1.8	21
6944	<i>Anaplasma phagocytophilum</i> modifies tick cell microRNA expression and upregulates isc-mir-79 to facilitate infection by targeting the Roundabout protein 2 pathway. <i>Scientific Reports</i> , 2019, 9, 9073.	1.6	12
6945	A transcriptome analysis reveals a role for the indole GLS-linked auxin biosynthesis in secondary dormancy in rapeseed ( <i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 264.	1.6	13
6946	Distribution and Characteristics of Transposable Elements in the Mulberry Genome. <i>Plant Genome</i> , 2019, 12, 180094.	1.6	5
6947	Genomic analysis reveals variant association with high altitude adaptation in native chickens. <i>Scientific Reports</i> , 2019, 9, 9224.	1.6	11
6948	Effect of de novo transcriptome assembly on transcript quantification. <i>Scientific Reports</i> , 2019, 9, 8304.	1.6	36
6949	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host coevolution. <i>Environmental Microbiology</i> , 2019, 21, 3683-3695.	1.8	47
6950	Comparative transcriptomic analysis of high- and low-oil <i>Camellia oleifera</i> reveals a coordinated mechanism for the regulation of upstream and downstream multigenes for high oleic acid accumulation. <i>3 Biotech</i> , 2019, 9, 257.	1.1	23
6951	Misassembly of long reads undermines de novo-assembled ethnicity-specific genomes: validation in a Chinese Han population. <i>Human Genetics</i> , 2019, 138, 757-769.	1.8	6
6952	De novo Assembly and Annotation of the Blood Transcriptome of the Southern Elephant Seal <i>Mirounga leonina</i> from the South Shetland Islands, Antarctica. <i>Ocean Science Journal</i> , 2019, 54, 307-315.	0.6	3
6953	Improved TGIRT-seq methods for comprehensive transcriptome profiling with decreased adapter dimer formation and bias correction. <i>Scientific Reports</i> , 2019, 9, 7953.	1.6	56

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6954	Physiological and transcriptomic analysis of yellow leaf coloration in <i>Populus deltoides</i> Marsh. PLoS ONE, 2019, 14, e0216879.	1.1	16
6955	Dissecting sex pheromone communication of <i>Mythimna separata</i> (Walker) in North China from receptor molecules and antennal lobes to behavior. Insect Biochemistry and Molecular Biology, 2019, 111, 103176.	1.2	26
6956	De novo transcriptome analysis of <i>Pleurotus djamor</i> to identify genes encoding CAZymes related to the decomposition of corn stalk lignocellulose. Journal of Bioscience and Bioengineering, 2019, 128, 529-536.	1.1	13
6957	Uncovering the cellular and humoral immune responses of <i>Antheraea pernyi</i> hemolymph to <i>Antheraea pernyi</i> nucleopolyhedrovirus infection by transcriptome analysis. Journal of Invertebrate Pathology, 2019, 166, 107205.	1.5	9
6958	Transcriptome analysis of atemoya pericarp elucidates the role of polysaccharide metabolism in fruit ripening and cracking after harvest. BMC Plant Biology, 2019, 19, 219.	1.6	38
6959	<i>Vitis vinifera</i> gene expression differential analysis assessing microarrays data pre-processing dynamism by RNA-Seq approach. Journal of Bioinformatics and Sequence Analysis, 2019, 10, 1-14.	0.5	0
6960	Defining the Independence of the Liver Circadian Clock. Cell, 2019, 177, 1448-1462.e14.	13.5	213
6961	SNP discovery in radiata pine using a de novo transcriptome assembly. Trees - Structure and Function, 2019, 33, 1505-1511.	0.9	5
6962	Computational Simulation of Adapter Length-Dependent LASSO Probe Capture Efficiency. Biomolecules, 2019, 9, 199.	1.8	3
6963	IL12 Abrogates Calcineurin-Dependent Immune Evasion during Leukemia Progression. Cancer Research, 2019, 79, 3702-3713.	0.4	7
6964	Conventionally used reference genes are not outstanding for normalization of gene expression in human cancer research. BMC Bioinformatics, 2019, 20, 245.	1.2	44
6965	ABioTrans: A Biostatistical Tool for Transcriptomics Analysis. Frontiers in Genetics, 2019, 10, 499.	1.1	7
6966	UDP-glucosyltransferases potentially contribute to imidacloprid resistance in <i>Aphis gossypii</i> glover based on transcriptomic and proteomic analyses. Pesticide Biochemistry and Physiology, 2019, 159, 98-106.	1.6	39
6967	Earlier demethylation of myogenic genes contributes to embryonic precocious terminal differentiation of myoblasts in miniature pigs. FASEB Journal, 2019, 33, 9638-9655.	0.2	11
6968	Global transcriptome profiling and functional analysis reveal that tissue-specific constitutive overexpression of cytochrome P450s confers tolerance to imidacloprid in palm weevils in date palm fields. BMC Genomics, 2019, 20, 440.	1.2	25
6969	Role of Cytokinin, Strigolactone, and Auxin Export on Outgrowth of Axillary Buds in Apple. Frontiers in Plant Science, 2019, 10, 616.	1.7	38
6970	Two-factor ANOVA of SSH and RNA-seq analysis reveal development-associated Pi-starvation genes in oilseed rape. Planta, 2019, 250, 1073-1088.	1.6	6
6971	Characterization of <i>Cucurbita maxima</i> Fruit Metabolomic Profiling and Transcriptome to Reveal Fruit Quality and Ripening Gene Expression Patterns. Journal of Plant Biology, 2019, 62, 203-216.	0.9	17

#	ARTICLE	IF	CITATIONS
6972	Giant group I intron in a mitochondrial genome is removed by RNA back-splicing. <i>BMC Molecular Biology</i> , 2019, 20, 16.	3.0	6
6973	RNA Sequencing Analysis of Chicken Cecum Tissues Following <i>Eimeria tenella</i> Infection in Vivo. <i>Genes</i> , 2019, 10, 420.	1.0	20
6974	Annotation and Expression of IDN2-like and FDM-like Genes in Sexual and Aposporous <i>Hypericum perforatum</i> L. accessions. <i>Plants</i> , 2019, 8, 158.	1.6	1
6975	Phenotypical profile and global transcriptomic profile of Hypervirulent <i>Klebsiella pneumoniae</i> due to carbapenemase-encoding plasmid acquisition. <i>BMC Genomics</i> , 2019, 20, 480.	1.2	17
6976	Zika virus antagonizes interferon response in patients and disrupts RIG-I-MAVS interaction through its CARD-TM domains. <i>Cell and Bioscience</i> , 2019, 9, 46.	2.1	42
6977	Inactivation of <i>farR</i> Causes High Rhodomyrtone Resistance and Increased Pathogenicity in <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1157.	1.5	14
6978	Characterization of mRNA profiles of the exosome-like vesicles in porcine follicular fluid. <i>PLoS ONE</i> , 2019, 14, e0217760.	1.1	51
6979	Integrated transcriptomic and secretomic approaches reveal critical pathogenicity factors in <i>Pseudofabrea citricarpa</i> inciting citrus target spot. <i>Microbial Biotechnology</i> , 2019, 12, 1260-1273.	2.0	8
6980	Overexpression of paralogues of the wheat expansin gene <i>TaEXPA8</i> improves low-temperature tolerance in <i>Arabidopsis</i> . <i>Plant Biology</i> , 2019, 21, 1119-1131.	1.8	26
6981	Transcriptome Profile Analysis of Winter Rapeseed ( <i>Brassica napus</i> L.) in Response to Freezing Stress, Reveal Potentially Connected Events to Freezing Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2771.	1.8	51
6982	Metagenomic analysis reveals that activated carbon aids anaerobic digestion of raw incineration leachate by promoting direct interspecies electron transfer. <i>Water Research</i> , 2019, 161, 570-580.	5.3	106
6983	Transcriptomic Sequencing of Airway Epithelial Cell NCI-H292 Induced by Synthetic Cationic Polypeptides. <i>BioMed Research International</i> , 2019, 2019, 1-13.	0.9	1
6984	Co-overexpression of AVP1 and OsSIZ1 in <i>Arabidopsis</i> substantially enhances plant tolerance to drought, salt, and heat stresses. <i>Scientific Reports</i> , 2019, 9, 7642.	1.6	30
6985	Transcriptomic analysis reveals insights into deep-sea adaptations of the dominant species, <i>Shinkaia crosnieri</i> (Crustacea: Decapoda: Anomura), inhabiting both hydrothermal vents and cold seeps. <i>BMC Genomics</i> , 2019, 20, 388.	1.2	23
6986	Transcriptomic responses of the clam <i>Meretrix meretrix</i> to the organophosphorus pesticide (dimethoate). <i>Ecotoxicology</i> , 2019, 28, 539-549.	1.1	10
6987	The Reference Genome Sequence of <i>Scutellaria baicalensis</i> Provides Insights into the Evolution of Wogonin Biosynthesis. <i>Molecular Plant</i> , 2019, 12, 935-950.	3.9	121
6988	The dynamics of mito-nuclear coevolution: A perspective from bivalve species with two different mechanisms of mitochondrial inheritance. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2019, 57, 534-547.	0.6	4
6989	Transcriptomic View of <i>Jatropha curcas</i> L. Inflorescence. , 2019, , 111-130.		0



#	ARTICLE	IF	CITATIONS
6990	Effects of NaCl stress on growth of <i>Portulaca oleracea</i> and underlying mechanisms. <i>Revista Brasileira De Botanica</i> , 2019, 42, 217-226.	0.5	14
6991	Transcript analyses reveal a comprehensive role of abscisic acid in modulating fruit ripening in Chinese jujube. <i>BMC Plant Biology</i> , 2019, 19, 189.	1.6	10
6992	Absolute quantification of translational regulation and burden using combined sequencing approaches. <i>Molecular Systems Biology</i> , 2019, 15, e8719.	3.2	61
6993	Comparative Transcriptomic Analysis Identifies a Range of Immunologically Related Functional Elaborations of Lymph Node Associated Lymphatic and Blood Endothelial Cells. <i>Frontiers in Immunology</i> , 2019, 10, 816.	2.2	35
6994	Molecular genetic testing methodologies in hematopoietic diseases: current and future methods. <i>International Journal of Laboratory Hematology</i> , 2019, 41, 102-116.	0.7	10
6995	Integrated Transcriptomic, Proteomic, and Metabolomics Analysis Reveals Peel Ripening of Harvested Banana under Natural Condition. <i>Biomolecules</i> , 2019, 9, 167.	1.8	38
6996	An integrated process of chemical precipitation and sulfate reduction for treatment of flue gas desulphurization wastewater from coal-fired power plant. <i>Journal of Cleaner Production</i> , 2019, 228, 63-72.	4.6	56
6997	Multiple SCN5A variant enhancers modulate its cardiac gene expression and the QT interval. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10636-10645.	3.3	22
6998	Upregulation of peroxide scavenging enzymes and multidrug efflux proteins highlight an active sodium hypochlorite response in <i>Pseudomonas fluorescens</i> biofilms. <i>Biofouling</i> , 2019, 35, 329-339.	0.8	7
6999	Identification of the defense-related gene VdWRKY53 from the wild grapevine <i>Vitis davidii</i> using RNA sequencing and ectopic expression analysis in <i>Arabidopsis</i> . <i>Hereditas</i> , 2019, 156, 14.	0.5	15
7000	Transcriptome analysis reveals pathways facilitating the growth of tobacco powdery mildew in <i>Arabidopsis</i> . <i>Phytopathology Research</i> , 2019, 1, .	0.9	9
7002	Superantigen SpeA attenuates the biofilm forming capacity of <i>Streptococcus pyogenes</i> . <i>Journal of Microbiology</i> , 2019, 57, 626-636.	1.3	10
7003	Transcriptomic comparison between developing seeds of yellow- and black-seeded <i>Brassica napus</i> reveals that genes influence seed quality. <i>BMC Plant Biology</i> , 2019, 19, 203.	1.6	40
7004	Fine-mapping and transcriptome analysis of BoGL-3, a wax-less gene in cabbage ( <i>Brassica oleracea</i> L. var. Tj ETQq1.1.0.784314 rgBT / Ov). <i>Frontiers in Plant Science</i> , 2019, 10, 12.	1.0	12
7005	Dynamics of repeat-associated plasticity in the aap gene family in <i>Anaplasma marginale</i> . <i>Gene: X</i> , 2019, 721, 100010.	2.3	1
7006	Gene expression profiles that shape high and low oil content sesames. <i>BMC Genetics</i> , 2019, 20, 45.	2.7	18
7007	Global Shifts in Gene Expression Profiles Accompanied with Environmental Changes in Cnidarian-Dinoflagellate Endosymbiosis. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2337-2347.	0.8	12
7008	The transcriptome analysis of the bamboo grasshopper provides insights into hypothermic stress acclimation. <i>International Journal of Biological Macromolecules</i> , 2019, 134, 237-246.	3.6	6

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7009	RNA-Seq analysis and transcriptome assembly of raspberry fruit ( <i>Rubus idaeus</i> 'Heritage') revealed several candidate genes involved in fruit development and ripening. <i>Scientia Horticulturae</i> , 2019, 254, 26-34.	1.7	15
7010	Computational Methods for Mapping, Assembly and Quantification for Coding and Non-coding Transcripts. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 628-637.	1.9	25
7011	Global transcriptome analysis provides new insights in <i>Thellungiella salsuginea</i> stress response. <i>Plant Biology</i> , 2019, 21, 796-804.	1.8	14
7012	Greater potency of adipocytes compared with preadipocytes under lipopolysaccharide exposure in grass carp <i>Ctenopharyngodon idella</i> . <i>Fish and Shellfish Immunology</i> , 2019, 91, 343-349.	1.6	3
7013	Improved annotation of the domestic pig genome through integration of Iso-Seq and RNA-seq data. <i>BMC Genomics</i> , 2019, 20, 344.	1.2	80
7014	Transcriptome Dataset of Leaf Tissue in Agave H11648. <i>Data</i> , 2019, 4, 62.	1.2	2
7015	Identification of a DNA N6-Adenine Methyltransferase Complex and Its Impact on Chromatin Organization. <i>Cell</i> , 2019, 177, 1781-1796.e25.	13.5	81
7016	Integrated Analysis of Transcriptomic, miRNA and Proteomic Changes of a Novel Hybrid Yellow Catfish Uncovers Key Roles for miRNAs in Heterosis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1437-1453.	2.5	30
7017	Hypothalamic transcriptome analysis reveals the neuroendocrine mechanisms in controlling broodiness of Muscovy duck ( <i>Cairina moschata</i> ). <i>PLoS ONE</i> , 2019, 14, e0207050.	1.1	12
7018	Performance Assessment and Selection of Normalization Procedures for Single-Cell RNA-Seq. <i>Cell Systems</i> , 2019, 8, 315-328.e8.	2.9	117
7019	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 139-173.	2.8	101
7020	Cytosporone B as a Biological Preservative: Purification, Fungicidal Activity and Mechanism of Action against <i>Geotrichum citri-aurantii</i> . <i>Biomolecules</i> , 2019, 9, 125.	1.8	11
7021	Post-transcriptional regulation through alternative splicing after infection with <i>Flavobacterium columnare</i> in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Fish and Shellfish Immunology</i> , 2019, 91, 188-193.	1.6	25
7022	Identification of global mRNA expression profiles and comprehensive bioinformatic analyses of abnormally expressed genes in cholestatic liver disease. <i>Gene</i> , 2019, 707, 9-21.	1.0	11
7023	Transcriptome profiling of anthocyanin biosynthesis in the peel of 'Granny Smith' apples ( <i>Malus domestica</i> ). <i>PLoS ONE</i> , 2019, 14, e0207050.	1.2	28
7024	Overlapped differentially expressed genes between acute lymphoblastic leukemia and chronic lymphocytic leukemia revealed potential key genes and pathways involved in leukemia. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 15980-15988.	1.2	2
7025	Carrot Genetics, Omics and Breeding Toolboxes. <i>Compendium of Plant Genomes</i> , 2019, , 225-245.	0.3	3
7026	Comparative Transcriptome Analysis in Eggplant Reveals Selection Trends during Eggplant Domestication. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	5

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7027	Comparative analysis of differentially expressed genes between the ovaries from pregnant and nonpregnant goats using RNA-Seq. <i>Journal of Biological Research</i> , 2019, 26, 3.	2.2	13
7028	Transcriptional profiling of cytochrome P450 genes in the liver of adult zebrafish, <i>&amp;lt;i&gt;Danio rerio</i> &lt;/i>. <i>Journal of Toxicological Sciences</i> , 2019, 44, 347-356.	0.7	16
7029	Human Macrophages Clear the Biovar Microtus Strain of <i>Yersinia pestis</i> More Efficiently Than Murine Macrophages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 111.	1.8	2
7030	Prediction of survival risks with adjusted gene expression through risk-gene networks. <i>Bioinformatics</i> , 2019, 35, 4898-4906.	1.8	1
7031	Transcriptional regulation of <i>Lonicera japonica</i> Thunb. during flower development as revealed by comprehensive analysis of transcription factors. <i>BMC Plant Biology</i> , 2019, 19, 198.	1.6	26
7032	A prognostic 11 long noncoding RNA expression signature for breast invasive carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16692-16702.	1.2	17
7033	PASS: A Proteomics Alternative Splicing Screening Pipeline. <i>Proteomics</i> , 2019, 19, e1900041.	1.3	6
7034	Next-Generation Sequencing and Emerging Technologies. <i>Seminars in Thrombosis and Hemostasis</i> , 2019, 45, 661-673.	1.5	168
7035	Follicle-stimulating hormone and luteinizing hormone increase Ca <sup>2+</sup> in the granulosa cells of mouse ovarian follicles. <i>Biology of Reproduction</i> , 2019, 101, 433-444.	1.2	14
7036	Iron Corrosion via Direct Metal-Microbe Electron Transfer. <i>MBio</i> , 2019, 10, .	1.8	107
7037	Comparative transcriptome analysis reveals potential evolutionary differences in adaptation of temperature and body shape among four Percidae species. <i>PLoS ONE</i> , 2019, 14, e0215933.	1.1	6
7038	De novo Characterization of the <i>Platycladus orientalis</i> Transcriptome and Analysis of Photosynthesis-Related Genes during Aging. <i>Forests</i> , 2019, 10, 393.	0.9	4
7039	De Novo Assembly and Comparative Transcriptome Profiling of <i>Anser anser</i> and <i>Anser cygnoides</i> Geese Species. <i>Embryonic Skin Feather Follicles</i> . <i>Genes</i> , 2019, 10, 351.	1.0	8
7040	Integration of mRNA and miRNA Analysis Reveals the Molecular Mechanism Underlying Salt and Alkali Stress Tolerance in Tobacco. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2391.	1.8	23
7041	RNA-seq in Skeletal Biology. <i>Current Osteoporosis Reports</i> , 2019, 17, 178-185.	1.5	32
7042	Identification of Transcription Factors Involved in the Regulation of Flowering in <i>Adonis Amurensis</i> Through Combined RNA-seq Transcriptomics and iTRAQ Proteomics. <i>Genes</i> , 2019, 10, 305.	1.0	17
7043	Effect of terahertz pulse on gene expression in human eye cells. <i>Chinese Physics B</i> , 2019, 28, 048703.	0.7	8
7044	Retinal Transcriptome Analysis in the Treatment of Endotoxin-Induced Uveitis with Tetramethylpyrazine Eye Drops. <i>Journal of Ocular Pharmacology and Therapeutics</i> , 2019, 35, 235-244.	0.6	3

#	ARTICLE	IF	CITATIONS
7045	Cereal Root Interactions with Soilborne Pathogensâ€”From Trait to Gene and Back. <i>Agronomy</i> , 2019, 9, 188.	1.3	11
7046	Identification of microRNA transcriptome reveals that miR-100 is involved in the renewal of porcine intestinal epithelial cells. <i>Science China Life Sciences</i> , 2019, 62, 816-828.	2.3	13
7047	Transcriptome data analyses of prostatic hyperplasia in <i>Esr2</i> knockout rats. <i>Data in Brief</i> , 2019, 24, 103826.	0.5	5
7048	Gender specific differences of immune competence in the sea cucumber <i>Apostichopus japonicus</i> before and after spawning. <i>Fish and Shellfish Immunology</i> , 2019, 90, 73-79.	1.6	12
7049	Complete assembly of the <i>Leishmania donovani</i> (HU3 strain) genome and transcriptome annotation. <i>Scientific Reports</i> , 2019, 9, 6127.	1.6	18
7050	RyÅ«tÅ« network-flow based transcriptome reconstruction. <i>BMC Bioinformatics</i> , 2019, 20, 190.	1.2	20
7051	The Stat3-Fam3a axis promotes muscle stem cell myogenic lineage progression by inducing mitochondrial respiration. <i>Nature Communications</i> , 2019, 10, 1796.	5.8	38
7052	Adipokines Regulate the Expression of Tumor-Relevant MicroRNAs. <i>Obesity Facts</i> , 2019, 12, 211-225.	1.6	27
7053	Identification and Characterization of Salt-Responsive MicroRNAs in <i>Vicia faba</i> by High-Throughput Sequencing. <i>Genes</i> , 2019, 10, 303.	1.0	23
7054	Comparative transcriptome analyses reveal changes of gene expression in fresh and cryopreserved yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) sperm and the effects of Cryoprotectant Me2SO. <i>International Journal of Biological Macromolecules</i> , 2019, 133, 457-465.	3.6	6
7055	Phosphoâ€RNAâ€seq: a modified small RNAâ€seq method that reveals circulating mRNA and lncRNA fragments as potential biomarkers in human plasma. <i>EMBO Journal</i> , 2019, 38, .	3.5	72
7056	Biogenesis and Function of Circular RNAs in Health and in Disease. <i>Frontiers in Pharmacology</i> , 2019, 10, 428.	1.6	92
7057	Transcriptome analysis of differentially expressed genes in the fore- and hind-intestine of ovate pompano <i>Trachinotus ovatus</i> . <i>Aquaculture</i> , 2019, 508, 76-82.	1.7	8
7058	Transcriptional Responses of the <i>Trichoplusia ni</i> Midgut to Oral Infection by the Baculovirus <i>Autographa californica</i> Multiple Nucleopolyhedrovirus. <i>Journal of Virology</i> , 2019, 93, .	1.5	20
7059	Lysosomal Dysfunction in Down Syndrome Is APP-Dependent and Mediated by APP-Î²CTF (C99). <i>Journal of Neuroscience</i> , 2019, 39, 5255-5268.	1.7	109
7060	Evaluation of osteoclast-derived exosomal miRNA under simulated microgravity conditions using next-generation sequencing. <i>Acta Astronautica</i> , 2019, 161, 75-86.	1.7	7
7061	Comparative transcriptomic analysis revealed the key pathways responsible for organic sulfur removal by thermophilic bacterium <i>Geobacillus thermoglucosidasius</i> W-2. <i>Science of the Total Environment</i> , 2019, 676, 639-650.	3.9	16
7062	Transcriptome analysis reveals molecular mechanisms of sclerotial development in the rice sheath blight pathogen <i>Rhizoctonia solani</i> AG1-IA. <i>Functional and Integrative Genomics</i> , 2019, 19, 743-758.	1.4	28

#	ARTICLE	IF	CITATIONS
7063	The Transcriptomic Toolbox: Resources for Interpreting Large Gene Expression Data within a Precision Medicine Context for Metabolic Disease Atherosclerosis. <i>Journal of Personalized Medicine</i> , 2019, 9, 21.	1.1	6
7064	Inheritance patterns of the transcriptome in hybrid chickens and their parents revealed by expression analysis. <i>Scientific Reports</i> , 2019, 9, 5750.	1.6	31
7065	Systematic analysis of the effects of different nitrogen source and ICDH knockout on glycolate synthesis in <i>Escherichia coli</i> . <i>Journal of Biological Engineering</i> , 2019, 13, 30.	2.0	9
7066	Contribution of H3K4 demethylase KDM5B to nucleosome organization in embryonic stem cells revealed by micrococcal nuclease sequencing. <i>Epigenetics and Chromatin</i> , 2019, 12, 20.	1.8	8
7067	Unravelling the mechanisms of PFOS toxicity by combining morphological and transcriptomic analyses in zebrafish embryos. <i>Science of the Total Environment</i> , 2019, 674, 462-471.	3.9	51
7068	Transcription factor TEAD1 is essential for vascular development by promoting vascular smooth muscle differentiation. <i>Cell Death and Differentiation</i> , 2019, 26, 2790-2806.	5.0	30
7069	C9â€“13 chlorinated paraffins cause immunomodulatory effects in adult C57BL/6 mice. <i>Science of the Total Environment</i> , 2019, 675, 110-121.	3.9	30
7070	Maize pentatricopeptide repeat protein DEK41 affects cis-splicing of mitochondrial nad4 intron 3 and is required for normal seed development. <i>Journal of Experimental Botany</i> , 2019, 70, 3795-3808.	2.4	35
7071	Genome-wide analyses and expression patterns under abiotic stress of NAC transcription factors in white pear ( <i>Pyrus bretschneideri</i> ). <i>BMC Plant Biology</i> , 2019, 19, 161.	1.6	41
7072	The protein elicitor Hrip1 enhances resistance to insects and early bolting and flowering in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2019, 14, e0216082.	1.1	7
7073	Longitudinal characterization of diet-induced genetic murine models of nonalcoholic steatohepatitis with metabolic, histological, and transcriptomic hallmarks of human patients. <i>Biology Open</i> , 2019, 8, .	0.6	22
7074	RNA-seq analysis of LPS-induced transcriptional changes and its possible implications for the adrenal gland dysregulation during sepsis. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 191, 105360.	1.2	14
7075	Postmortem brain tissue as an underutilized resource to study the molecular pathology of neuropsychiatric disorders across different ethnic populations. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 102, 195-207.	2.9	9
7076	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. <i>Genetics in Medicine</i> , 2019, 21, 2135-2144.	1.1	19
7077	ATP-Binding Cassette (ABC) Transporter Genes Involved in Pyrethroid Resistance in the Malaria Vector <i>Anopheles sinensis</i> : Genome-Wide Identification, Characteristics, Phylogenetics, and Expression Profile. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1409.	1.8	33
7078	Snakin-1 affects reactive oxygen species and ascorbic acid levels and hormone balance in potato. <i>PLoS ONE</i> , 2019, 14, e0214165.	1.1	29
7079	Transcriptome Studies in <i>Trypanosoma cruzi</i> Using RNA-seq. <i>Methods in Molecular Biology</i> , 2019, 1955, 35-45.	0.4	2
7080	An Integrated Approach to Plant Biology via Multi-Analogous Methods. , 2019, , 57-126.		0

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7081	Targeted delivery of hesperetin to cartilage attenuates osteoarthritis by bimodal imaging with Gd <sub>2</sub> (CO <sub>3</sub> ) <sub>3</sub> @PDA nanoparticles via TLR-2/NF- $\kappa$ B/Akt signaling. <i>Biomaterials</i> , 2019, 205, 50-63.	5.7	62
7082	Transcriptome profiling reveals genetic basis of disease resistance against <i>Corynespora cassiicola</i> in rubber tree ( <i>Hevea brasiliensis</i> ). <i>Current Plant Biology</i> , 2019, 17, 2-16.	2.3	22
7083	Digital gene expression profiling in larvae of <i>Tribolium castaneum</i> at different periods post UV-B exposure. <i>Ecotoxicology and Environmental Safety</i> , 2019, 174, 514-523.	2.9	10
7084	Effects of anti-inflammatory and adaptogenic herbal extracts on gene expression of eicosanoids signaling pathways in isolated brain cells. <i>Phytomedicine</i> , 2019, 60, 152881.	2.3	34
7085	Identification of leucoanthocyanidin reductase and anthocyanidin reductase genes involved in proanthocyanidin biosynthesis in <i>Malus crabapple</i> plants. <i>Plant Physiology and Biochemistry</i> , 2019, 139, 141-151.	2.8	39
7086	Integrated transcriptome and in vitro analysis revealed anti-proliferative effect of citral in human stomach cancer through apoptosis. <i>Scientific Reports</i> , 2019, 9, 4883.	1.6	12
7088	Fine mapping of <i>lcm1</i> , a gene conferring chlorophyll-deficient golden leaf in Chinese cabbage ( <i>Brassica</i> ) Tj ETQq0 0.0rgBT /Oyerlock 10	1.0	15
7089	Transcriptome analysis of peach ( <i>Prunus persica</i> ) fruit skin and differential expression of related pigment genes. <i>Scientia Horticulturae</i> , 2019, 250, 271-277.	1.7	10
7090	Caffeine Content and Related Gene Expression: Novel Insight into Caffeine Metabolism in <i>Camellia</i> Plants Containing Low, Normal, and High Caffeine Concentrations. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 3400-3411.	2.4	61
7091	Identification and expression of candidate chemosensory receptors in the white-spotted flower chafer, <i>Protaetia brevitarsis</i> . <i>Scientific Reports</i> , 2019, 9, 3339.	1.6	8
7092	<i>Znhit1</i> controls intestinal stem cell maintenance by regulating H2A.Z incorporation. <i>Nature Communications</i> , 2019, 10, 1071.	5.8	25
7093	BES/BZR Transcription Factor TaBZR2 Positively Regulates Drought Responses by Activation of <i>TaGST1</i> . <i>Plant Physiology</i> , 2019, 180, 605-620.	2.3	151
7094	Dysregulated Expression of microRNA-21 and Disease-Related Genes in Human Patients and in a Mouse Model of Alport Syndrome. <i>Human Gene Therapy</i> , 2019, 30, 865-881.	1.4	34
7095	Manganese Detoxification by MntE Is Critical for Resistance to Oxidative Stress and Virulence of <i>Staphylococcus aureus</i> . <i>MBio</i> , 2019, 10, .	1.8	38
7096	Distal chromosome 16p11.2 duplications containing <i>SH2B1</i> in patients with scoliosis. <i>Journal of Medical Genetics</i> , 2019, 56, 427-433.	1.5	11
7097	Effects of Early Intervention With Maternal Fecal Bacteria and Antibiotics on Liver Metabolome and Transcription in Neonatal Pigs. <i>Frontiers in Physiology</i> , 2019, 10, 171.	1.3	17
7098	Preparation of Frozen Liver Tissues for Integrated Omics Analysis. <i>Methods in Molecular Biology</i> , 2019, 1951, 167-178.	0.4	2
7099	Comparative transcriptome profiling of <i>Kappaphycus alvarezii</i> (Rhodophyta, Gigartinales) in response to two extreme temperature treatments: an RNA-seq-based resource for photosynthesis research. <i>European Journal of Phycology</i> , 2019, 54, 162-174.	0.9	6

#	ARTICLE	IF	CITATIONS
7100	Gene expression patterns indicate that a high-fatâ€“high-carbohydrate diet causes mitochondrial dysfunction in fish. <i>Genome</i> , 2019, 62, 53-67.	0.9	5
7101	Integrating Transcriptomic and GC-MS Metabolomic Analysis to Characterize Color and Aroma Formation during Tepal Development in <i>Lycoris longituba</i> . <i>Plants</i> , 2019, 8, 53.	1.6	42
7102	Assessment of a Highly Multiplexed RNA Sequencing Platform and Comparison to Existing High-Throughput Gene Expression Profiling Techniques. <i>Frontiers in Genetics</i> , 2019, 10, 150.	1.1	4
7103	Gene expression profiling of ovary identified eggshell proteins regulated by 20-hydroxyecdysone in <i>Bactrocera dorsalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 206-216.	0.4	7
7104	Complex regulatory network allows <i>Myriophyllum aquaticum</i> to thrive under high-concentration ammonia toxicity. <i>Scientific Reports</i> , 2019, 9, 4801.	1.6	11
7105	RNA-sequencing in ophthalmology research: considerations for experimental design and analysis. <i>Therapeutic Advances in Ophthalmology</i> , 2019, 11, 251584141983546.	0.8	6
7106	Differential Alternative Splicing Genes in Response to Boron Deficiency in <i>Brassica napus</i> . <i>Genes</i> , 2019, 10, 224.	1.0	12
7107	Identification and classification of differentially expressed genes in pyrethroid-resistant <i>Culex pipiens pallens</i> . <i>Molecular Genetics and Genomics</i> , 2019, 294, 861-873.	1.0	10
7108	Pretumor microenvironment of hepatocellular carcinoma: Cancerization or anticancerization?. <i>Gene</i> , 2019, 701, 46-54.	1.0	4
7109	Machine learning-powered antibiotics phenotypic drug discovery. <i>Scientific Reports</i> , 2019, 9, 5013.	1.6	63
7110	Investigating the Biological Relevance of <i>In Vitro</i> -Identified Putative Packaging Signals at the 5â€² Terminus of Satellite Tobacco Necrosis Virus 1 Genomic RNA. <i>Journal of Virology</i> , 2019, 93, .	1.5	9
7111	Comparative genomics reveals the unique evolutionary status of <i>Plasmodiophora brassicae</i> and the essential role of GPCR signaling pathways. <i>Phytopathology Research</i> , 2019, 1, .	0.9	17
7112	Quercetin Inhibits the Proliferation and Aflatoxins Biosynthesis of <i>Aspergillus flavus</i> . <i>Toxins</i> , 2019, 11, 154.	1.5	31
7114	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. <i>Human Genetics</i> , 2019, 138, 375-388.	1.8	6
7115	The motor protein Myo1c regulates transforming growth factor-Î²â€“signaling and fibrosis in podocytes. <i>Kidney International</i> , 2019, 96, 139-158.	2.6	20
7116	Integrated Analysis of LncRNA-mRNA Coexpression in the Extracellular Matrix of Developing Deciduous Teeth in Miniature Pigs. <i>BioMed Research International</i> , 2019, 2019, 1-9.	0.9	2
7117	A complete statistical model for calibration of RNA-seq counts using external spike-ins and maximum likelihood theory. <i>PLoS Computational Biology</i> , 2019, 15, e1006794.	1.5	9
7118	Analysis of Transcriptome and Epitranscriptome in Plants Using PacBio Iso-Seq and Nanopore-Based Direct RNA Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 253.	1.1	127

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7119	Unraveling the Contribution of High Temperature Stage to Jiang-Flavor Daqu, a Liquor Starter for Production of Chinese Jiang-Flavor Baijiu, With Special Reference to Metatranscriptomics. <i>Frontiers in Microbiology</i> , 2019, 10, 472.	1.5	46
7120	Transcriptome and chemical analysis reveal putative genes involved in flower color change in <i>Paeonia</i> 'Coral Sunset'. <i>Plant Physiology and Biochemistry</i> , 2019, 138, 130-139.	2.8	31
7121	Distinct isoforms of Nrf1 diversely regulate different subsets of its cognate target genes. <i>Scientific Reports</i> , 2019, 9, 2960.	1.6	26
7122	UDP-glycosyltransferase genes and their association and mutations associated with pyrethroid resistance in <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Malaria Journal</i> , 2019, 18, 62.	0.8	46
7123	Comparative Transcriptomic Analysis Provides Insight into the Domestication and Improvement of Pear ( <i>P. pyrifolia</i> ) Fruit. <i>Plant Physiology</i> , 2019, 180, 435-452.	2.3	33
7124	TCC-GUI: a Shiny-based application for differential expression analysis of RNA-Seq count data. <i>BMC Research Notes</i> , 2019, 12, 133.	0.6	87
7125	<i>Elymus nutans</i> genes for seed shattering and candidate gene-derived EST-SSR markers for germplasm evaluation. <i>BMC Plant Biology</i> , 2019, 19, 102.	1.6	14
7126	Functional genomics analysis of Phelan-McDermid syndrome 22q13 region during human neurodevelopment. <i>PLoS ONE</i> , 2019, 14, e0213921.	1.1	16
7127	Key Maize Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome and Physiological Analyses of Contrasting Inbred Lines. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1268.	1.8	78
7128	Purification and Functional Analysis of Plant Long Noncoding RNAs (lncRNA). <i>Methods in Molecular Biology</i> , 2019, 1933, 131-147.	0.4	6
7129	Surfaceome interrogation using an RNA-seq approach highlights leukemia initiating cell biomarkers in an LMO2 T cell transgenic model. <i>Scientific Reports</i> , 2019, 9, 5760.	1.6	8
7130	Omics: Potential Role in Early Phase Drug Development. , 2019, , 309-347.		0
7131	A Therapeutic Strategy for Chemotherapy-Resistant Gastric Cancer via Destabilization of Both $\beta$ -Catenin and RAS. <i>Cancers</i> , 2019, 11, 496.	1.7	9
7132	The regulatory actions of retinoic acid on M2 polarization of porcine macrophages. <i>Developmental and Comparative Immunology</i> , 2019, 98, 20-33.	1.0	26
7133	Disruption of ESR1 alters the expression of genes regulating hepatic lipid and carbohydrate metabolism in male rats. <i>Molecular and Cellular Endocrinology</i> , 2019, 490, 47-56.	1.6	26
7134	Integrated Transcriptomic and Proteomic Analysis of Human Eccrine Sweat Glands Identifies Missing and Novel Proteins. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1382-1395.	2.5	25
7135	Re-sequencing and transcriptome analysis reveal rich DNA variations and differential expressions of fertility-related genes in neo-tetraploid rice. <i>PLoS ONE</i> , 2019, 14, e0214953.	1.1	21
7136	Identification and functional analysis of microRNAs in rats following focal cerebral ischemia injury. <i>Molecular Medicine Reports</i> , 2019, 19, 4175-4184.	1.1	12



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7137	OsCDC48/48E complex is required for plant survival in rice ( <i>Oryza sativa</i> L.). <i>Plant Molecular Biology</i> , 2019, 100, 163-179.	2.0	8
7138	Whole RNA-sequencing and gene expression analysis of <i>Trichoderma harzianum</i> Tr-92 under chlamyospore-producing condition. <i>Genes and Genomics</i> , 2019, 41, 689-699.	0.5	11
7139	Comparative Transcriptome Analysis of Celery Leaf Blades Identified an R2R3-MYB Transcription Factor that Regulates Apigenin Metabolism. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 5265-5277.	2.4	17
7140	Transcriptomic analysis of <i>de novo</i> folate biosynthetic genes in <i>Lactobacillus plantarum</i> strain 4_3 in fermented soybean. <i>Food and Function</i> , 2019, 10, 2426-2438.	2.1	6
7141	Integrated miRNA-mRNA transcriptomic analysis reveals epigenetic-mediated embryonic muscle growth differences between Wuzhishan and Landrace pigs. <i>Journal of Animal Science</i> , 2019, 97, 1967-1978.	0.2	15
7142	Repeated pregnant mare serum gonadotropin-mediated oestrous synchronization alters gene expression in the ovaries and reduces reproductive performance in dairy goats. <i>Reproduction in Domestic Animals</i> , 2019, 54, 873-881.	0.6	11
7143	HSP superfamily of genes in the malaria vector <i>Anopheles sinensis</i> : diversity, phylogenetics and association with pyrethroid resistance. <i>Malaria Journal</i> , 2019, 18, 132.	0.8	17
7144	Comparative RNA sequencing reveals that HPV16 E6 abrogates the effect of E6*1 on ROS metabolism. <i>Scientific Reports</i> , 2019, 9, 5938.	1.6	17
7145	Enhanced production of antifungal lipopeptide iturin A by <i>Bacillus amyloliquefaciens</i> LL3 through metabolic engineering and culture conditions optimization. <i>Microbial Cell Factories</i> , 2019, 18, 68.	1.9	68
7146	GPR139 and Dopamine D2 Receptor Co-express in the Same Cells of the Brain and May Functionally Interact. <i>Frontiers in Neuroscience</i> , 2019, 13, 281.	1.4	20
7147	Prediction of Long Non-Coding RNAs Based on Deep Learning. <i>Genes</i> , 2019, 10, 273.	1.0	23
7148	Aligning the Aligners: Comparison of RNA Sequencing Data Alignment and Gene Expression Quantification Tools for Clinical Breast Cancer Research. <i>Journal of Personalized Medicine</i> , 2019, 9, 18.	1.1	17
7149	Comparative transcriptome analysis reveals the different roles between hepatopancreas and intestine of <i>Litopenaeus vannamei</i> in immune response to aflatoxin B1 (AFB1) challenge. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2019, 222, 1-10.	1.3	23
7150	Phenotyping a Dynamic Trait: Leaf Growth of Perennial Ryegrass Under Water Limiting Conditions. <i>Frontiers in Plant Science</i> , 2019, 10, 344.	1.7	23
7151	Transcriptional Profile Corroborates that bml Mutant Plays likely Role in Premature Leaf Senescence of Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 1708.	1.8	4
7152	A 17 gene panel for non-small cell lung cancer prognosis identified through integrative epigenomic-transcriptomic analyses of hypoxia-induced epithelial-mesenchymal transition. <i>Molecular Oncology</i> , 2019, 13, 1490-1502.	2.1	25
7153	MIR205HG Is a Long Noncoding RNA that Regulates Growth Hormone and Prolactin Production in the Anterior Pituitary. <i>Developmental Cell</i> , 2019, 49, 618-631.e5.	3.1	30
7154	Transcriptome analyses reveal key genes involved in skin color changes of 'Xinlimei'™ radish taproot. <i>Plant Physiology and Biochemistry</i> , 2019, 139, 528-539.	2.8	24

#	ARTICLE	IF	CITATIONS
7155	Novel Data Transformations for RNA-seq Differential Expression Analysis. <i>Scientific Reports</i> , 2019, 9, 4820.	1.6	28
7156	High olive oil diets enhance cervical tumour growth in mice: transcriptome analysis for potential candidate genes and pathways. <i>Lipids in Health and Disease</i> , 2019, 18, 76.	1.2	17
7157	High-Throughput Identification and Analysis of Novel Conotoxins from Three Vermivorous Cone Snails by Transcriptome Sequencing. <i>Marine Drugs</i> , 2019, 17, 193.	2.2	18
7158	Transcriptome sequencing to unravel the molecular mechanisms underlying the cuticle liquefaction of <i>Antheraea pernyi</i> following <i>Antheraea pernyi</i> nucleopolyhedrovirus challenge. <i>Molecular Immunology</i> , 2019, 109, 108-115.	1.0	6
7159	Pulsed light as an emerging technology to cause disruption for food and adjacent industries – Quo vadis?. <i>Trends in Food Science and Technology</i> , 2019, 88, 316-332.	7.8	78
7160	A statistical normalization method and differential expression analysis for RNA-seq data between different species. <i>BMC Bioinformatics</i> , 2019, 20, 163.	1.2	24
7161	Transcriptome Sequencing Analysis Provides Insights Into the Response to <i>Fusarium oxysporum</i> in <i>Lilium pumilum</i> . <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431983881.	0.6	9
7162	Physiological and Growth Response of Pepper ( <i>Capsicum annum</i> L.) Seedlings to Supplementary Red/Blue Light Revealed through Transcriptomic Analysis. <i>Agronomy</i> , 2019, 9, 139.	1.3	15
7163	Towards the definition of a detailed transcriptomic map of berry development. <i>BIO Web of Conferences</i> , 2019, 13, 01001.	0.1	1
7164	Gene expression profiles at different stages for formation of pearl sac and pearl in the pearl oyster <i>Pinctada fucata</i> . <i>BMC Genomics</i> , 2019, 20, 240.	1.2	26
7165	Alternative splicing, RNA-seq and drug discovery. <i>Drug Discovery Today</i> , 2019, 24, 1258-1267.	3.2	55
7166	RNA Isolation and Analysis of LncRNAs from Gametophytes of Maize. <i>Methods in Molecular Biology</i> , 2019, 1933, 67-86.	0.4	3
7167	Transcriptomic insight into antimicrobial peptide factors involved in the prophylactic immunity of crowded <i>Mythimna separata</i> larvae. <i>Developmental and Comparative Immunology</i> , 2019, 98, 34-41.	1.0	11
7168	Arbuscular mycorrhizal fungi induce the expression of specific retrotransposons in roots of sunflower ( <i>Helianthus annuus</i> L.). <i>PLoS ONE</i> , 2019, 14, e0212371.	1.1	17
7169	Molecular Mechanisms of Polybrominated Diphenyl Ethers (BDE-47, BDE-100, and BDE-153) in Human Breast Cancer Cells and Patient-Derived Xenografts. <i>Toxicological Sciences</i> , 2019, 169, 380-398.	1.4	30
7170	Transcriptional Dynamics of Grain Development in Barley ( <i>Hordeum vulgare</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 962.	1.8	29
7171	Adaptive laboratory evolution of a genome-reduced <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 935.	5.8	114
7172	De novo transcriptome analysis of <i>Taxus chinensis</i> var. <i>mairei</i> to identify significant pathways associated with the fruit color of this species. <i>Biochemical Systematics and Ecology</i> , 2019, 84, 1-7.	0.6	3

#	ARTICLE	IF	CITATIONS
7173	Serum exosomal microRNA letâ€“7iâ€“3p as candidate diagnostic biomarker for Kawasaki disease patients with coronary artery aneurysm. IUBMB Life, 2019, 71, 891-900.	1.5	19
7174	How well do RNA-Seq differential gene expression tools perform in a complex eukaryote? A case study in <i>Arabidopsis thaliana</i>. Bioinformatics, 2019, 35, 3372-3377.	1.8	9
7175	Role of RpoN from <i>Labrenzia aggregata</i> LZB033 ( <i>Rhodobacteraceae</i> ) in Formation of Flagella and Biofilms, Motility, and Environmental Adaptation. Applied and Environmental Microbiology, 2019, 85, .	1.4	19
7176	First RNA-seq approach to study fruit set and parthenocarpy in zucchini (Cucurbita pepo L.). BMC Plant Biology, 2019, 19, 61.	1.6	19
7177	Fine mapping of the major QTL for seed coat color in Brassica rapa var. Yellow Sarson by use of NIL populations and transcriptome sequencing for identification of the candidate genes. PLoS ONE, 2019, 14, e0209982.	1.1	12
7178	Identification and expression analysis of ceftriaxone resistance-related genes in Neisseria gonorrhoeae integrating RNA-Seq data and qRT-PCR validation. Journal of Global Antimicrobial Resistance, 2019, 16, 202-209.	0.9	19
7179	Blood-based analysis of type-2 diabetes mellitus susceptibility genes identifies specific transcript variants with deregulated expression and association with disease risk. Scientific Reports, 2019, 9, 1512.	1.6	21
7180	Deciphering global gene expression and regulation strategy in <i>Escherichia coli</i> during carbon limitation. Microbial Biotechnology, 2019, 12, 360-376.	2.0	11
7181	Itaconic acid degradation in Aspergillus niger: the role of unexpected bioconversion pathways. Fungal Biology and Biotechnology, 2019, 6, 1.	2.5	28
7182	&lt;p&gt;Establishment and characterization of the GC-030-35 cell line derived from gastric hepatoid adenocarcinoma&lt;/p&gt;. Cancer Management and Research, 2019, Volume 11, 1275-1287.	0.9	0
7183	De Novo Transcriptome Assembly of Agave H11648 by Illumina Sequencing and Identification of Cellulose Synthase Genes in Agave Species. Genes, 2019, 10, 103.	1.0	22
7184	Identification of Gene Expression Changes Associated With Uterine Receptivity in Mice. Frontiers in Physiology, 2019, 10, 125.	1.3	17
7185	Transcriptome Analysis of Male and Female Mature Gonads of Silver Sillago (Sillago sihama). Genes, 2019, 10, 129.	1.0	35
7186	Exploring the Diversity and Novelty of Toxin Genes in Naja sumatrana, the Equatorial Spitting Cobra from Malaysia through De Novo Venom-Gland Transcriptomics. Toxins, 2019, 11, 104.	1.5	31
7187	Using mouse genetics to understand human skeletal disease. Bone, 2019, 126, 27-36.	1.4	5
7188	Integrated analysis of mRNAs and long noncoding RNAs in the semen from Holstein bulls with high and low sperm motility. Scientific Reports, 2019, 9, 2092.	1.6	35
7189	Genome-Wide mRNA-Seq Profiling Reveals that<i>LEF1</i>and<i>SMAD3</i>Regulate Epithelialâ€“Mesenchymal Transition Through the Hippo Signaling Pathway During Palatal Fusion. Genetic Testing and Molecular Biomarkers, 2019, 23, 197-203.	0.3	4
7190	Genome-wide analysis and identification of the low potassium stress responsive gene SiMYB3 in foxtail millet (Setariaitalica L.). BMC Genomics, 2019, 20, 136.	1.2	15

#	ARTICLE	IF	CITATIONS
7191	Physiological and Transcriptomic Analysis of Tree Peony ( <i>Paeonia</i> section <i>Moutan</i> DC.) in Response to Drought Stress. <i>Forests</i> , 2019, 10, 135.	0.9	35
7193	Brain transcriptome of honey bees ( <i>Apis mellifera</i> ) exhibiting impaired olfactory learning induced by a sublethal dose of imidacloprid. <i>Pesticide Biochemistry and Physiology</i> , 2019, 156, 36-43.	1.6	61
7194	Kidney Organogenesis. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
7195	An integrated meta-omics approach reveals substrates involved in synergistic interactions in a bisphenol A (BPA)-degrading microbial community. <i>Microbiome</i> , 2019, 7, 16.	4.9	89
7196	Putative small RNAs controlling detoxification of industrial cyanide-containing wastewaters by <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>PLoS ONE</i> , 2019, 14, e0212032.	1.1	20
7197	How an ancient, salt-tolerant fruit crop, <i>Ficus carica</i> L., copes with salinity: a transcriptome analysis. <i>Scientific Reports</i> , 2019, 9, 2561.	1.6	26
7198	Integrated Omic Analyses Provide Evidence that a <i>Candidatus</i> <i>Accumulibacter phosphatis</i> Strain Performs Denitrification under Microaerobic Conditions. <i>MSystems</i> , 2019, 4, .	1.7	44
7199	CirGO: an alternative circular way of visualising gene ontology terms. <i>BMC Bioinformatics</i> , 2019, 20, 84.	1.2	84
7200	Enhancing co-translational folding of heterologous protein by deleting non-essential ribosomal proteins in <i>Pichia pastoris</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 38.	6.2	7
7201	RNA-Seq Revealed Expression of Many Novel Genes Associated With <i>Leishmania donovani</i> Persistence and Clearance in the Host Macrophage. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 17.	1.8	28
7202	Tricin levels and expression of flavonoid biosynthetic genes in developing grains of purple and brown pericarp rice. <i>PeerJ</i> , 2019, 7, e6477.	0.9	11
7203	Free-access copy-number variant detection tools for targeted next-generation sequencing data. <i>Mutation Research - Reviews in Mutation Research</i> , 2019, 779, 114-125.	2.4	46
7204	Lipid-Activated Nuclear Receptors. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
7205	Transcriptome analysis provides insights into the molecular mechanisms responsible for evisceration behavior in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 30, 143-157.	0.4	13
7206	Comparative sialotranscriptome analysis of the rare Chinese cicada <i>Subsalsaltria yangi</i> , with identification of candidate genes related to host-plant adaptation. <i>International Journal of Biological Macromolecules</i> , 2019, 130, 323-332.	3.6	7
7207	Representation and relative abundance of cell-type selective markers in whole-kidney RNA-Seq data. <i>Kidney International</i> , 2019, 95, 787-796.	2.6	89
7208	Comparative transcriptome analysis of genes involved in anthocyanin biosynthesis in the pink-white and red fruits of Chinese bayberry ( <i>Morella rubra</i> ). <i>Scientia Horticulturae</i> , 2019, 250, 278-286.	1.7	15
7209	LncRNA PCAT1 activates AKT and NF- $\kappa$ B signaling in castration-resistant prostate cancer by regulating the PHLPP/FKBP51/IKK $\beta$ complex. <i>Nucleic Acids Research</i> , 2019, 47, 4211-4225.	6.5	129

#	ARTICLE	IF	CITATIONS
7210	Whole gene transcriptomic analysis of PCB/biphenyl degrading <i>Rhodococcus jostii</i> ; RHA1. <i>Journal of General and Applied Microbiology</i> , 2019, 65, 173-179.	0.4	6
7211	Divergent gene expression levels between diploid and autotetraploid <i>Tolmiea</i> relative to the total transcriptome, the cell, and biomass. <i>American Journal of Botany</i> , 2019, 106, 280-291.	0.8	30
7212	RNA-sequencing analysis reveals transcriptional changes in the roots of low-cadmium-accumulating winter wheat under cadmium stress. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	16
7213	Identification and Expression Profiling of Odorant Receptor Protein Genes in <i>Sitophilus zeamais</i> (Coleoptera: Curculionioidea) Using RT-qPCR. <i>Neotropical Entomology</i> , 2019, 48, 538-551.	0.5	8
7214	RNA Sequencing in B-Cell Lymphomas. <i>Methods in Molecular Biology</i> , 2019, 1956, 283-303.	0.4	2
7215	A microRNA profile of saliva and the role of miR-375 in <i>Haemaphysalis longicornis</i> (Ixodida: Ixodidae). <i>Parasites and Vectors</i> , 2019, 12, 68.	1.0	12
7216	The Impact of the Wheat Rht-B1b Semi-Dwarfing Allele on Photosynthesis and Seed Development Under Field Conditions. <i>Frontiers in Plant Science</i> , 2019, 10, 51.	1.7	47
7217	Identification of Differentially Expressed Genes and Pathways for Abdominal Fat Deposition in Ovariectomized and Sham-Operated Chickens. <i>Genes</i> , 2019, 10, 155.	1.0	6
7218	Network-pharmacology-based identification of caveolin-1 as a key target of <i>Oldenlandia diffusa</i> to suppress breast cancer metastasis. <i>Biomedicine and Pharmacotherapy</i> , 2019, 112, 108607.	2.5	38
7219	Analysis of the Teashirt Target Genes in Ureteric Bud Development. <i>Methods in Molecular Biology</i> , 2019, 1926, 223-232.	0.4	1
7221	Transcriptome analysis of early downy mildew ( <i>Plasmopara viticola</i> ) defense in grapevines carrying the Asian resistance locus Rpv10. <i>Euphytica</i> , 2019, 215, 1.	0.6	20
7222	Molt-dependent transcriptome analysis of claw muscles in Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Genes and Genomics</i> , 2019, 41, 515-528.	0.5	14
7223	An Arabidopsis TIR-Lectin Two-Domain Protein Confers Defense Properties against <i>Tetranychus urticae</i> . <i>Plant Physiology</i> , 2019, 179, 1298-1314.	2.3	38
7224	Screening of endogenous strong promoters for enhanced production of medium-chain-length polyhydroxyalkanoates in <i>Pseudomonas mendocina</i> NK-01. <i>Scientific Reports</i> , 2019, 9, 1798.	1.6	44
7225	Transcriptomic analysis of genes involved in reproduction at different ages in <i>Daphnia pulex</i> (Branchiopoda, Cladocera). <i>Crustaceana</i> , 2019, 92, 1311-1335.	0.1	1
7226	Unraveling the key molecular events of grape berry ripening. <i>Acta Horticulturae</i> , 2019, , 241-248.	0.1	1
7227	Novel algorithm to extract multiple solutions for RNA sequence classification problem. , 2019, . .		0
7228	Transcriptome Aprofile of <i>Brassica rapa</i> L. Reveals the Involvement of Jasmonic Acid, Ethylene, and Brassinosteroid Signaling Pathways in Clubroot Resistance. <i>Agronomy</i> , 2019, 9, 589.	1.3	19

#	ARTICLE	IF	CITATIONS
7229	Targeting Long Non-Coding RNA splicing by novel candidate drug. , 2019, , .		0
7230	Mip6 binds directly to the Mex67 UBA domain to maintain low levels of Msn2/4 stressâ€dependent mRNAs. EMBO Reports, 2019, 20, e47964.	2.0	6
7231	Roles for Non-coding RNAs in Spatial Genome Organization. Frontiers in Cell and Developmental Biology, 2019, 7, 336.	1.8	14
7232	Reversion of tumor hepatocytes to normal hepatocytes during liver tumor regression in an oncogene transgenic zebrafish model. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	13
7233	Genome Sequencing and Transcriptome Analysis Reveal Recent Species-Specific Gene Duplications in the Plastic Gilthead Sea Bream ( <i>Sparus aurata</i> ). Frontiers in Marine Science, 2019, 6, .	1.2	26
7234	The Many Faces of Gene Regulation in Cancer: A Computational Oncogenomics Outlook. Genes, 2019, 10, 865.	1.0	34
7235	Technological advances in studying epigenetics biomarkers of prognostic potential for clinical research. , 2019, , 45-83.		1
7236	Comprehensive Analysis of the Expression Profiles of Long Non-Coding RNAs with Associated ceRNA Network Involved in the Colon Cancer Staging and Progression. Scientific Reports, 2019, 9, 16910.	1.6	19
7237	Characterization of cancer omics and drug perturbations in panels of lung cancer cells. Scientific Reports, 2019, 9, 19529.	1.6	13
7238	Differential immune response modulation in early <i>Leishmania amazonensis</i> infection of BALB/c and C57BL/6 macrophages based on transcriptome profiles. Scientific Reports, 2019, 9, 19841.	1.6	24
7239	Anatomy and RNA-Seq reveal important gene pathways regulating sex differentiation in a functionally Androdioecious tree, <i>Tapiscia sinensis</i> . BMC Plant Biology, 2019, 19, 554.	1.6	11
7240	Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of <i>Croton draco</i> (Euphorbiaceae). BMC Plant Biology, 2019, 19, 560.	1.6	7
7241	HY5 Contributes to Light-Regulated Root System Architecture Under a Root-Covered Culture System. Frontiers in Plant Science, 2019, 10, 1490.	1.7	32
7242	Transcriptome-wide association study identifies putative elicitors/suppressor of <i>Puccinia graminis</i> f. sp. <i>tritici</i> that modulate barley rpg4-mediated stem rust resistance. BMC Genomics, 2019, 20, 985.	1.2	6
7243	deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. Genome Biology, 2019, 20, 274.	3.8	41
7244	Transcriptomic Profiling Identifies Candidate Genes Involved in the Salt Tolerance of the Xerophyte <i>Pugionium cornutum</i> . Genes, 2019, 10, 1039.	1.0	9
7245	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. Science, 2019, 366, .	6.0	329
7246	Identification of tRNA-derived ncRNAs in TCGA and NCI-60 panel cell lines and development of the public database tRFexplorer. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	36

#	ARTICLE	IF	CITATIONS
7247	New gene expression regulators: Long non-coding RNAs. AIP Conference Proceedings, 2019, , .	0.3	0
7248	De novo Comparative Transcriptome Analysis of Genes Differentially Expressed in the Scion of Homografted and Heterografted Tomato Seedlings. Scientific Reports, 2019, 9, 20240.	1.6	24
7249	Comparison of liver gene expression by RNAseq and PCR analysis after 8 weeks of feeding soy protein isolate- or casein-based diets in an obese liver steatosis rat model. Food and Function, 2019, 10, 8218-8229.	2.1	9
7250	The review of transcriptome sequencing: principles, history and advances. IOP Conference Series: Earth and Environmental Science, 2019, 332, 042003.	0.2	6
7251	Development and Characterization of a Genetic Mouse Model of KRAS Mutated Colorectal Cancer. International Journal of Molecular Sciences, 2019, 20, 5677.	1.8	3
7252	Transcriptomic and Co-Expression Network Profiling of Shoot Apical Meristem Reveal Contrasting Response to Nitrogen Rate between Indica and Japonica Rice Subspecies. International Journal of Molecular Sciences, 2019, 20, 5922.	1.8	12
7253	Prioritizing candidate diseases-related metabolites based on literature and functional similarity. BMC Bioinformatics, 2019, 20, 574.	1.2	9
7254	Transcriptional profiling reveals differentially expressed genes involved in lipid biosynthesis during cacao seed development. Scientific Reports, 2019, 9, 17263.	1.6	2
7255	Multiplatform biomarker identification using a data-driven approach enables single-sample classification. BMC Bioinformatics, 2019, 20, 601.	1.2	4
7256	Characterization of antibiotic resistance genes in the species of the rumen microbiota. Nature Communications, 2019, 10, 5252.	5.8	68
7257	Dissection of gene expression datasets into clinically relevant interaction signatures via high-dimensional correlation maximization. Nature Communications, 2019, 10, 5417.	5.8	5
7258	STK-12 acts as a transcriptional brake to control the expression of cellulase-encoding genes in Neurospora crassa. PLoS Genetics, 2019, 15, e1008510.	1.5	19
7259	deltaRpkM: an R package for a rapid detection of differential gene presence between related bacterial genomes. BMC Bioinformatics, 2019, 20, 621.	1.2	3
7260	Transcriptome profiling using RNA-seq to provide insights into foxtail millet seedling tolerance to short-term water deficit stress induced by PEG-6000. Journal of Integrative Agriculture, 2019, 18, 2457-2471.	1.7	26
7261	The Making of a Flight Feather: Bio-architectural Principles and Adaptation. Cell, 2019, 179, 1409-1423.e17.	13.5	28
7262	Identification of key genes and regulators associated with carotenoid metabolism in apricot (Prunus) Tj ETQq1 1 0.784314 rgBT /Overlo 1.2 28	1.2	28
7263	Identification of novel citramalate biosynthesis pathways in Aspergillus niger. Fungal Biology and Biotechnology, 2019, 6, 19.	2.5	9
7264	RNASeqR: An R Package for Automated Two-Group RNA-Seq Analysis Workflow. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2023-2031.	1.9	6

#	ARTICLE	IF	CITATIONS
7265	CDSeq: A novel complete deconvolution method for dissecting heterogeneous samples using gene expression data. <i>PLoS Computational Biology</i> , 2019, 15, e1007510.	1.5	42
7266	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo ( <i>Phyllostachys violascens</i> ). <i>BMC Bioinformatics</i> , 2019, 20, 687.	1.2	14
7267	Transcriptome analysis of the almond moth, <i>Cadra cautella</i> , female abdominal tissues and identification of reproduction control genes. <i>BMC Genomics</i> , 2019, 20, 883.	1.2	4
7268	Mepiquat chloride promotes cotton lateral root formation by modulating plant hormone homeostasis. <i>BMC Plant Biology</i> , 2019, 19, 573.	1.6	21
7269	Differential alternative splicing regulation among hepatocellular carcinoma with different risk factors. <i>BMC Medical Genomics</i> , 2019, 12, 175.	0.7	11
7270	Reduced H3K27me3 leads to abnormal Hox gene expression in neural tube defects. <i>Epigenetics and Chromatin</i> , 2019, 12, 76.	1.8	28
7271	Hippocampal clock regulates memory retrieval via Dopamine and PKA-induced GluA1 phosphorylation. <i>Nature Communications</i> , 2019, 10, 5766.	5.8	43
7272	RNA-Seq Analysis Identifies Differentially Expressed Genes in Subcutaneous Adipose Tissue in Qaidaford Cattle, Cattle-Yak, and Angus Cattle. <i>Animals</i> , 2019, 9, 1077.	1.0	18
7273	A Hierarchical Machine Learning Model to Discover Gleason Grade-Specific Biomarkers in Prostate Cancer. <i>Diagnostics</i> , 2019, 9, 219.	1.3	21
7274	Wheat straw increases the defense response and resistance of watermelon monoculture to <i>Fusarium wilt</i> . <i>BMC Plant Biology</i> , 2019, 19, 551.	1.6	15
7275	Overexpressing GH3.1 and GH3.1L reduces susceptibility to <i>Xanthomonas citri</i> subsp. <i>citri</i> by repressing auxin signaling in citrus ( <i>Citrus sinensis</i> Osbeck). <i>PLoS ONE</i> , 2019, 14, e0220017.	1.1	37
7276	Comparative transcriptome analysis of hESC- and iPSC-derived lentoid bodies. <i>Scientific Reports</i> , 2019, 9, 18552.	1.6	15
7277	Joint between-sample normalization and differential expression detection through a, "0-regularized regression. <i>BMC Bioinformatics</i> , 2019, 20, 593.	1.2	1
7278	Transcriptional and post-transcriptional responses of diploid and autotetraploid <i>Paulownia tomentosa</i> — <i>Paulownia fortunei</i> under water-deficit condition. <i>Revista Brasileira De Botanica</i> , 2019, 42, 0.5 623-641.		6
7279	Imbalanced Regulation of Fungal Nutrient Transports According to Phosphate Availability in a Symbiosome Formed by Poplar, Sorghum, and <i>Rhizophagus irregularis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1617.	1.7	23
7280	Full-Length Transcriptome Sequencing and Different Chemotype Expression Profile Analysis of Genes Related to Monoterpenoid Biosynthesis in <i>Cinnamomum porrectum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 6230.	1.8	22
7281	Transcriptome Analysis Reveals the Molecular Mechanisms Underlying Adenosine Biosynthesis in Anamorph Strain of Caterpillar Fungus. <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	8
7282	Normalization Methods for the Analysis of Unbalanced Transcriptome Data: A Review. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 358.	2.0	72



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7283	Comparative transcriptome and histological analyses of wheat in response to phytotoxic aphid <i>Schizaphis graminum</i> and non-phytotoxic aphid <i>Sitobion avenae</i> feeding. <i>BMC Plant Biology</i> , 2019, 19, 547.	1.6	31
7284	The role and robustness of the Gini coefficient as an unbiased tool for the selection of Gini genes for normalising expression profiling data. <i>Scientific Reports</i> , 2019, 9, 17960.	1.6	25
7285	1. Genomic Technology/ Next-Generation Sequencing. , 2019, , 1-35.		0
7286	Single-Cell RNA Sequencing of the Cardiovascular System: New Looks for Old Diseases. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 6, 173.	1.1	47
7287	De novo sequencing of the transcriptome reveals regulators of the floral transition in <i>Fargesia macclureana</i> (Poaceae). <i>BMC Genomics</i> , 2019, 20, 1035.	1.2	8
7288	Immunity-related genes and signaling pathways under hypoxic stresses in <i>Haliotis diversicolor</i> : a transcriptome analysis. <i>Scientific Reports</i> , 2019, 9, 19741.	1.6	13
7289	Effect of growth rate on transcriptomic responses to immune stimulation in wild-type, domesticated, and GH-transgenic coho salmon. <i>BMC Genomics</i> , 2019, 20, 1024.	1.2	11
7290	Hair follicles transcriptome profiles in Bashang long-tailed chickens with different plumage colors. <i>Genes and Genomics</i> , 2019, 41, 1357-1367.	0.5	10
7291	Transcriptomic analysis of interactions between <i>Hyphantria cunea</i> larvae and nucleopolyhedrovirus. <i>Pest Management Science</i> , 2019, 75, 1024-1033.	1.7	21
7292	Comparative analysis of testis transcriptomes associated with male infertility in triploid cyprinid fish. <i>Reproduction, Fertility and Development</i> , 2019, 31, 248.	0.1	16
7293	<i>Xanthomonas campestris</i> Promotes Diffusible Signal Factor Biosynthesis and Pathogenicity by Utilizing Glucose and Sucrose from Host Plants. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 157-166.	1.4	12
7294	Transcriptome analysis of <i>Panax zingiberensis</i> identifies genes encoding oleanolic acid glucuronosyltransferase involved in the biosynthesis of oleanane-type ginsenosides. <i>Planta</i> , 2019, 249, 393-406.	1.6	37
7295	Obstructed defecation“an enteric neuropathy? An exploratory study of patient samples. <i>International Journal of Colorectal Disease</i> , 2019, 34, 193-196.	1.0	7
7296	Long noncoding RNA H19 participates in metformin-mediated inhibition of gastric cancer cell invasion. <i>Journal of Cellular Physiology</i> , 2019, 234, 4515-4527.	2.0	37
7297	Maternal control of seed weight in rapeseed ( <i>Brassica napus</i> L.): the causal link between the size of pod (mother, source) and seed (offspring, sink). <i>Plant Biotechnology Journal</i> , 2019, 17, 736-749.	4.1	37
7298	Genetic control of fatty acid composition in coconut ( <i>Cocos nucifera</i> ), African oil palm ( <i>Elaeis</i> ) Tj ETQq1 1 0.784314 1.65 BT /Overlock 107		17
7299	Insights into the intestine immune of <i>Marsupenaeus japonicus</i> under the white spot syndrome virus challenge using RNA sequencing. <i>Veterinary Immunology and Immunopathology</i> , 2019, 208, 25-33.	0.5	22
7300	QuanTP: A Software Resource for Quantitative Proteo-Transcriptomic Comparative Data Analysis and Informatics. <i>Journal of Proteome Research</i> , 2019, 18, 782-790.	1.8	6

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7301	Comparative transcriptome analysis provides comprehensive insights into the heat stress response of <i>Marsupenaeus japonicus</i> . <i>Aquaculture</i> , 2019, 502, 338-346.	1.7	22
7302	Bacterial Small RNAs in the Genus <i>Herbaspirillum</i> spp.. <i>International Journal of Molecular Sciences</i> , 2019, 20, 46.	1.8	2
7303	Constitutive Dicer1 phosphorylation accelerates metabolism and aging in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 960-969.	3.3	13
7304	Challenges and solutions for analysing dual <i>scRNA-seq</i> data for non-model host-pathogen systems. <i>Methods in Ecology and Evolution</i> , 2019, 10, 401-414.	2.2	5
7305	The Harderian gland transcriptomes of <i>Caraiba andreae</i> , <i>Cubophis cantherigerus</i> and <i>Tretanorhinus variabilis</i> , three colubroid snakes from Cuba. <i>Genomics</i> , 2019, 111, 1720-1727.	1.3	10
7306	Actively personalized vaccination trial for newly diagnosed glioblastoma. <i>Nature</i> , 2019, 565, 240-245.	13.7	637
7307	Analysis of differential gene expression by RNA-seq data in ABCG1 knockout mice. <i>Gene</i> , 2019, 689, 24-33.	1.0	12
7308	Ecdysis triggering hormone receptors regulate male courtship behavior via antennal lobe interneurons in <i>Drosophila</i> . <i>General and Comparative Endocrinology</i> , 2019, 278, 79-88.	0.8	11
7309	A comparative transcriptomic analysis provides insights into the cold-adaptation mechanisms of a psychrophilic yeast, <i>Glaciozyma antarctica</i> PI12. <i>Polar Biology</i> , 2019, 42, 541-553.	0.5	17
7310	RNA splicing analysis in genomic medicine. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 108, 61-71.	1.2	21
7311	Hyper-Editing of Cell-Cycle Regulatory and Tumor Suppressor RNA Promotes Malignant Progenitor Propagation. <i>Cancer Cell</i> , 2019, 35, 81-94.e7.	7.7	64
7312	Transcriptomic analysis of key genes involved in chlorogenic acid biosynthetic pathway and characterization of MaHCT from <i>Morus alba</i> L.. <i>Protein Expression and Purification</i> , 2019, 156, 25-35.	0.6	25
7313	Comparative transcriptomic characterization of the eyestalk in Pacific white shrimp ( <i>Litopenaeus</i> ) Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50	0.8	26
7314	Transcriptome analysis showed differences of two purebred cattle and their crossbreds. <i>Italian Journal of Animal Science</i> , 2019, 18, 70-79.	0.8	2
7315	Invasive cervical tumors with high and low HPV titer represent molecular subgroups with different disease etiology. <i>Carcinogenesis</i> , 2019, 40, 269-278.	1.3	4
7316	<i>Brittle Culm 1</i> Encodes a COBRA-Like Protein Involved in Secondary Cell Wall Cellulose Biosynthesis in <i>Sorghum</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 788-801.	1.5	28
7317	An Extracytoplasmic Function Sigma Factor Controls Cellulose Utilization by Regulating the Expression of an Outer Membrane Protein in <i>Cytophaga hutchinsonii</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	6
7318	A novel lncRNA-mediated trans-regulatory mechanism in the development of cleft palate in mouse. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e00522.	0.6	10

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7319	CINSARC signature as a prognostic marker for clinical outcome in sarcomas and beyond. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 124-129.	1.5	23
7320	<i>Saccharomyces cerevisiae</i> isolates with extreme hydrogen sulfide production showed different oxidative stress resistances responses during wine fermentation by RNA sequencing analysis. <i>Food Microbiology</i> , 2019, 79, 147-155.	2.1	8
7321	Transcriptomics and proteomics analyses of anti-cancer mechanisms of TR35 "An active fraction from Xinjiang Bactrian camel milk in esophageal carcinoma cell. <i>Clinical Nutrition</i> , 2019, 38, 2349-2359.	2.3	21
7322	SP1, MYC, CTNNB1, CREB1, JUN genes as potential therapy targets for neuropathic pain of brain. <i>Journal of Cellular Physiology</i> , 2019, 234, 6688-6695.	2.0	13
7323	Transcriptome-wide analysis of wild Asari (=Manila) clams affected by the Brown Muscle Disease: Etiology and impacts of the disease. <i>Fish and Shellfish Immunology</i> , 2019, 86, 179-185.	1.6	4
7324	Genome-wide identification and characterization of the Dof gene family in cassava ( <i>Manihot</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 3	1.6	29
7325	CLR4, a novel conserved transcription factor for cellulase gene expression in ascomycete fungi. <i>Molecular Microbiology</i> , 2019, 111, 373-394.	1.2	38
7326	Dimorphism of sex and gonad-development-related genes in male and female lined seahorse, <i>Hippocampus erectus</i> , based on transcriptome analyses. <i>Genomics</i> , 2019, 111, 260-266.	1.3	12
7327	The effect of dietary ginseng polysaccharide supplementation on porcine milk-derived esRNAs involved in the host immune responses. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2019, 103, 276-282.	1.0	6
7328	Exposure to nitrate alters the histopathology and gene expression in the liver of <i>Bufo gargarizans</i> tadpoles. <i>Chemosphere</i> , 2019, 217, 308-319.	4.2	15
7329	Insights into genes encoding respiratory burst oxidase homologs (RBOHs) in rubber tree ( <i>Hevea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	2.5	31
7330	Three vital RNA functions and interactions in the process of silk gland apoptosis in silkworm <i>Bombyx mori</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2019, 100, e21511.	0.6	5
7331	Assessment of agronomic parameters and gene expression profiling of flax ( <i>Linum usitatissimum</i> L.) upon treatment with brassinosteroid and its biosynthetic inhibitor. <i>Industrial Crops and Products</i> , 2019, 128, 270-281.	2.5	4
7332	Inherent DNA-binding specificities of the HIF1 and HIF2 transcription factors in chromatin. <i>EMBO Reports</i> , 2019, 20, .	2.0	143
7333	In vivo transcriptomic analysis of <i>Beauveria bassiana</i> reveals differences in infection strategies in <i>Galleria mellonella</i> and <i>Plutella xylostella</i> . <i>Pest Management Science</i> , 2019, 75, 1443-1452.	1.7	13
7334	Prospects of pan-genomics in barley. <i>Theoretical and Applied Genetics</i> , 2019, 132, 785-796.	1.8	38
7335	hnRNPDLL extensively regulates transcription and alternative splicing. <i>Gene</i> , 2019, 687, 125-134.	1.0	45
7336	Evolutionary and ecological functional genomics, from lab to the wild. <i>Plant Journal</i> , 2019, 97, 40-55.	2.8	39

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7337	Hydrophilic bile acids prevent liver damage caused by lack of biliary phospholipid in Mdr2 mice. <i>Journal of Lipid Research</i> , 2019, 60, 85-97.	2.0	28
7338	Identification and characterization of circular RNAs involved in mechanical force-induced periodontal ligament stem cells. <i>Journal of Cellular Physiology</i> , 2019, 234, 10166-10177.	2.0	34
7339	MicroRNAs profiles of Chinese Perch Brain (CPB) cells infected with <i>Siniperca chuatsi</i> rhabdovirus (SCRV). <i>Fish and Shellfish Immunology</i> , 2019, 84, 1075-1082.	1.6	16
7340	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 65-88.	3.6	172
7341	Transcriptome analysis of <i>Sclerotinia ginseng</i> and comparative analysis with the genome of <i>Sclerotinia sclerotiorum</i> . <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 30-41.	1.3	8
7342	Evaluation of the genetic stability of Sabin strains and the consistency of inactivated poliomyelitis vaccine made from Sabin strains using direct deep-sequencing. <i>Vaccine</i> , 2019, 37, 130-136.	1.7	5
7343	Comparative transcriptome analysis of diploid and triploid hybrid groupers ( <i>Epinephelus coioides</i> ) 2019, 111, 251-259.	1.3	10
7344	Genome-wide isoform-level analysis reveals tumor-specific isoforms for lung adenocarcinoma diagnosis and prognosis. <i>Cancer Genetics</i> , 2019, 230, 58-65.	0.2	3
7345	A secreted-Cu/Zn superoxide dismutase from <i>Microplitis bicoloratus</i> reduces reactive oxygen species triggered by symbiotic bracovirus. <i>Developmental and Comparative Immunology</i> , 2019, 92, 129-139.	1.0	6
7346	RNA-Seq analysis of gynocious and weak female cucumber revealing the cell cycle pathway may regulate sex determination in cucumber. <i>Gene</i> , 2019, 687, 289-297.	1.0	11
7347	Adaptive Particle Filtering for Fault Detection in Partially-Observed Boolean Dynamical Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	6
7348	Enriched networks of nucleoside/nucleotide and ribonucleoside/ribonucleotide metabolic processes and response to stimulus potentially conferred to drought adaptation of the epiphytic orchid <i>Dendrobium wangliangii</i> . <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 31-45.	1.4	13
7349	Novel prognostic markers within the CD44-stromal ligand network in pancreatic cancer. <i>Journal of Pathology: Clinical Research</i> , 2019, 5, 130-141.	1.3	13
7350	The rise of the distributions: why non-normality is important for understanding the transcriptome and beyond. <i>Biophysical Reviews</i> , 2019, 11, 89-94.	1.5	39
7351	Species-specific genes account for the differences in floral transition between continuous-flowering and once-flowering roses. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 312-319.	0.9	1
7352	Ochratoxin A Exposure Impairs Porcine Granulosa Cell Growth via the PI3K/AKT Signaling Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2679-2690.	2.4	36
7353	Integrative Transcriptome and Proteome Analysis Identifies Major Metabolic Pathways Involved in Pepper Fruit Development. <i>Journal of Proteome Research</i> , 2019, 18, 982-994.	1.8	40
7354	(Differential) Co-Expression Analysis of Gene Expression: A Survey of Best Practices. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	34

#	ARTICLE	IF	CITATIONS
7355	Integrative Analysis of MicroRNAome, Transcriptome, and Proteome during the Limb Regeneration of <i>Cynops orientalis</i> . <i>Journal of Proteome Research</i> , 2019, 18, 1088-1098.	1.8	7
7356	Rare mutations of <i>ADAM17</i> from TOFs induce hypertrophy in human embryonic stem cell-derived cardiomyocytes via HB-EGF signaling. <i>Clinical Science</i> , 2019, 133, 225-238.	1.8	12
7357	Transcriptomic and Metabolic Profiling Reveals "Green Ring" and "Red Ring" on Jujube Fruit upon Postharvest <i>Alternaria alternata</i> Infection. <i>Plant and Cell Physiology</i> , 2019, 60, 844-861.	1.5	21
7358	Comparative transcriptome analysis at seven time points during <i>Haematococcus pluvialis</i> motile cell growth and astaxanthin accumulation. <i>Aquaculture</i> , 2019, 503, 304-311.	1.7	15
7359	De novo leaf and root transcriptome analysis to explore biosynthetic pathway of Celangulin V in <i>Celastrus angulatus maxim.</i> <i>BMC Genomics</i> , 2019, 20, 7.	1.2	26
7360	Understanding the Resistance Mechanism in <i>Brassica napus</i> to Clubroot Caused by <i>Plasmodiophora brassicae</i> . <i>Phytopathology</i> , 2019, 109, 810-818.	1.1	16
7361	Responses of Fuji ( <i>Malus domestica</i> ) and Shandingzi ( <i>Malus baccata</i> ) apples to <i>Marssonina coronaria</i> infection revealed by comparative transcriptome analysis. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 87-95.	1.3	9
7362	Exploring the differential mechanisms of carotenoid biosynthesis in the yellow peel and red flesh of papaya. <i>BMC Genomics</i> , 2019, 20, 49.	1.2	32
7363	Bariatric Surgery Alters microRNA Content of Circulating Exosomes in Patients with Obesity. <i>Obesity</i> , 2019, 27, 264-271.	1.5	37
7364	Evolutionary aspects of direct or indirect selection for seed size and seed metabolites in <i>Brassica juncea</i> and diploid progenitor species. <i>Molecular Biology Reports</i> , 2019, 46, 1227-1238.	1.0	11
7365	Transcriptomic analysis of the red and green light responses in <i>Columba livia domestica</i> . <i>3 Biotech</i> , 2019, 9, 20.	1.1	5
7366	Gene expression profiling of <i>Bothriochloa ischaemum</i> leaves and roots under drought stress. <i>Gene</i> , 2019, 691, 77-86.	1.0	3
7367	De novo transcriptomic sequencing unraveled the molecular mechanisms of WMybA1 underlying the alteration of <i>Ficus lyrata</i> leaf color. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	4
7368	Transcriptomic and metabolomics analyses reveal metabolic characteristics of L-leucine- and L-valine-producing <i>Corynebacterium glutamicum</i> mutants. <i>Annals of Microbiology</i> , 2019, 69, 457-468.	1.1	9
7369	Abnormal energy identification of variable refrigerant flow air-conditioning systems based on data mining techniques. <i>Applied Thermal Engineering</i> , 2019, 150, 398-411.	3.0	17
7370	Liver transcriptome analysis and de novo annotation of the orange-spotted groupers ( <i>Epinephelus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 4f 50 97 To Proteomics, 2019, 29, 264-273.	0.4	29
7371	Characterization of the <i>Fundulus heteroclitus</i> embryo transcriptional response and development of a gene expression-based fingerprint of exposure for the alternative flame retardant, TBPH (bis) Tj ETQq0 0 0 rgBT /Overlock 10 4f 50 97 To	1.0	4
7372	Revisiting avian "missing" genes from de novo assembled transcripts. <i>BMC Genomics</i> , 2019, 20, 4.	1.2	36

#	ARTICLE	IF	CITATIONS
7373	Activation of the Bile Acid Pathway and No Observed Antimicrobial Peptide Sequences in the Skin of a Poison Frog. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 581-589.	0.8	1
7374	Enhanced Production of Hypocrellin A in Submerged Cultures of <i>Shiraia bambusicola</i> by Red Light. <i>Photochemistry and Photobiology</i> , 2019, 95, 812-822.	1.3	17
7375	Low-Bias RNA Sequencing of the HIV-2 Genome from Blood Plasma. <i>Journal of Virology</i> , 2019, 93, .	1.5	11
7376	ER $\alpha$ activation in obesity improves whole body metabolism via adipose tissue function and enhanced mitochondria biogenesis. <i>Molecular and Cellular Endocrinology</i> , 2019, 479, 147-158.	1.6	31
7377	Transcriptome profiling reveals key roles of phagosome and NOD-like receptor pathway in spotting diseased <i>Strongylocentrotus intermedius</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 521-531.	1.6	27
7378	Enrichment of rare genetic variants in astrocyte gene enriched co-expression modules altered in postmortem brain samples of schizophrenia. <i>Neurobiology of Disease</i> , 2019, 121, 305-314.	2.1	12
7379	Acute immune stress improves cell resistance to chemical poison damage in SP600125-induced polyploidy of fish cells in vitro. <i>Fish and Shellfish Immunology</i> , 2019, 84, 656-663.	1.6	9
7380	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. <i>ISME Journal</i> , 2019, 13, 738-751.	4.4	166
7381	Predominant Shift of Different P44-Expressing <i>Anaplasma phagocytophilum</i> in Infected HL-60, THP-1, NB4, and RF/6A Cell Lines. <i>Japanese Journal of Infectious Diseases</i> , 2019, 72, 73-80.	0.5	14
7382	Expression profiling of ABA and GA signaling cascades regulating bud dormancy in grape. <i>Scientia Horticulturae</i> , 2019, 246, 44-50.	1.7	7
7383	Plant Primary Metabolism Regulated by Nitrogen Contributes to Plant-Pathogen Interactions. <i>Plant and Cell Physiology</i> , 2019, 60, 329-342.	1.5	45
7384	Regulation of compound leaf development in mungbean ( <i>Vigna radiata</i> L.) by CUP-SHAPED COTYLEDON/NO APICAL MERISTEM (CUC/NAM) gene. <i>Planta</i> , 2019, 249, 765-774.	1.6	39
7385	RNA-Seq analysis of <i>Polyrhachis vicina</i> Roger and insights into the heat shock protein 90 and 70 families. <i>Cell Stress and Chaperones</i> , 2019, 24, 45-58.	1.2	3
7386	The light-induced transcription factor FtMYB116 promotes accumulation of rutin in <i>Fagopyrum tataricum</i> . <i>Plant, Cell and Environment</i> , 2019, 42, 1340-1351.	2.8	45
7387	TPMCalculator: one-step software to quantify mRNA abundance of genomic features. <i>Bioinformatics</i> , 2019, 35, 1960-1962.	1.8	149
7388	Transcriptome analysis provides insights into differentially expressed genes and long noncoding RNAs involved in sex-related differences in Amur sturgeon ( <i>Acipenser schrenckii</i> ). <i>Molecular Reproduction and Development</i> , 2019, 86, 132-144.	1.0	7
7389	Transcriptome profiling suggests roles of innate immunity and digestion metabolism in purplish Washington clam. <i>Genes and Genomics</i> , 2019, 41, 183-191.	0.5	8
7390	Comparative transcriptome analysis explores maternal to zygotic transition during <i>Eriocheir sinensis</i> early embryogenesis. <i>Gene</i> , 2019, 685, 12-20.	1.0	3

#	ARTICLE	IF	CITATIONS
7391	Development of tightly linked markers and identification of candidate genes for Fusarium crown rot resistance in barley by exploiting a near-isogenic line-derived population. <i>Theoretical and Applied Genetics</i> , 2019, 132, 217-225.	1.8	13
7392	Oncostatin M inhibits differentiation of rat stem Leydig cells in vivo and in vitro. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 426-438.	1.6	34
7393	Sexually dimorphic gene expression and transcriptome evolution provide mixed evidence for a fast effect in <i>Heliconius</i> . <i>Journal of Evolutionary Biology</i> , 2019, 32, 194-204.	0.8	31
7394	Differential expression of genes in greenbug ( <i>Schizaphis graminum</i> Rondani) treated by imidacloprid and RNA interference. <i>Pest Management Science</i> , 2019, 75, 1726-1733.	1.7	18
7395	Multifactorial Inheritance and Complex Diseases. , 2019, , 323-358.		3
7396	Microgravity-induced hepatogenic differentiation of rBMSCs on board the SJ-10 satellite. <i>FASEB Journal</i> , 2019, 33, 4273-4286.	0.2	19
7397	Control Interventions Can Impact Alveolarization and the Transcriptome in Developing Mouse Lungs. <i>Anatomical Record</i> , 2019, 302, 346-363.	0.8	6
7398	Reprogramming of gene expression in the CS 8 rice line overexpressing ADP glucose pyrophosphorylase induces a suppressor of starch biosynthesis. <i>Plant Journal</i> , 2019, 97, 1073-1088.	2.8	14
7399	Transcriptome Sequencing (RNA-Seq). , 2019, , 33-49.		1
7400	Identification, characterization and field testing of Brassica napus mutants producing high oleic oils. <i>Plant Journal</i> , 2019, 98, 33-41.	2.8	30
7401	The comparative analysis of phenotypic and whole transcriptome gene expression data of ascites susceptible versus ascites resistant chickens. <i>Molecular Biology Reports</i> , 2019, 46, 793-804.	1.0	2
7402	Repaired Shells of the Pearl Oyster Largely Recapitulate Normal Prismatic Layer Growth: A Proteomics Study of Shell Matrix Proteins. <i>ACS Biomaterials Science and Engineering</i> , 2019, 5, 519-529.	2.6	21
7403	Cotton fiber elongation requires the transcription factor GhMYB212 to regulate sucrose transportation into expanding fibers. <i>New Phytologist</i> , 2019, 222, 864-881.	3.5	66
7404	Genome and Transcriptome Sequencing of the Astaxanthin-Producing Green Microalga, <i>Haematococcus pluvialis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 166-173.	1.1	52
7405	CYP76B74 Catalyzes the 3-Hydroxylation of Geranylhydroquinone in Shikonin Biosynthesis. <i>Plant Physiology</i> , 2019, 179, 402-414.	2.3	33
7406	A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without a reference. <i>Functional and Integrative Genomics</i> , 2019, 19, 363-371.	1.4	2
7407	Molecular characterization of anthocyanin and betulinic acid biosynthesis in red and white mulberry fruits using high-throughput sequencing. <i>Food Chemistry</i> , 2019, 279, 364-372.	4.2	28
7408	A Novel R2R3-MYB Transcription Factor Contributes to Petal Blotch Formation by Regulating Organ-Specific Expression of <i>PsCHS</i> in Tree Peony ( <i>Paeonia suffruticosa</i> ). <i>Plant and Cell Physiology</i> , 2019, 60, 599-611.	1.5	77

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7409	Comparative transcriptome analysis reveals PERP upregulated during <i>Salmonella</i> Enteritidis challenge in laying ducks. <i>Journal of Cellular Physiology</i> , 2019, 234, 11330-11347.	2.0	5
7410	Diphthamide affects selenoprotein expression: Diphthamide deficiency reduces selenocysteine incorporation, decreases selenite sensitivity and pre-disposes to oxidative stress. <i>Redox Biology</i> , 2019, 20, 146-156.	3.9	17
7411	Transcriptomic analysis of bagging-treated ‘Pingguo’ pear shows that MYB4-like1, MYB4-like2, MYB1R1 and WDR involved in anthocyanin biosynthesis are up-regulated in fruit peels in response to light. <i>Scientia Horticulturae</i> , 2019, 244, 428-434.	1.7	22
7412	META RNA profiling: Multiplexed quantitation of targeted RNAs across large numbers of samples. <i>Methods</i> , 2019, 152, 41-47.	1.9	1
7413	Elucidating the microRNA-203 specific biological processes in glioblastoma cells from comprehensive RNA-sequencing transcriptome profiling. <i>Cellular Signalling</i> , 2019, 53, 22-38.	1.7	5
7414	Introduction to Non-coding RNAs and High Throughput Sequencing. , 2019, , 3-31.		1
7416	In-depth characterization of the pituitary transcriptome in Simmental and Chinese native cattle. <i>Domestic Animal Endocrinology</i> , 2019, 66, 35-42.	0.8	6
7417	miARma-Seq, a comprehensive pipeline for the simultaneous study and integration of miRNA and mRNA expression data. <i>Methods</i> , 2019, 152, 31-40.	1.9	24
7418	Oncogenic zinc finger protein ZNF322A promotes stem cell-like properties in lung cancer through transcriptional suppression of c-Myc expression. <i>Cell Death and Differentiation</i> , 2019, 26, 1283-1298.	5.0	18
7419	The alternatively spliced porcine Fc $\beta$ RI regulated PRRSV-ADE infection and proinflammatory cytokine production. <i>Developmental and Comparative Immunology</i> , 2019, 90, 186-198.	1.0	14
7420	A benchmarking of workflows for detecting differential splicing and differential expression at isoform level in human RNA-seq studies. <i>Briefings in Bioinformatics</i> , 2019, 20, 471-481.	3.2	31
7421	Performance Measurement and Comparative Transcriptome Analysis Revealed the Efforts on Hybrid Improvement of Qinchuan Cattle. <i>Animal Biotechnology</i> , 2019, 30, 13-20.	0.7	4
7422	A Unified Model for Joint Normalization and Differential Gene Expression Detection in RNA-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 442-454.	1.9	13
7423	Effect of normalization methods on the performance of supervised learning algorithms applied to HTSeq-FPKM-UQ data sets: 7SK RNA expression as a predictor of survival in patients with colon adenocarcinoma. <i>Briefings in Bioinformatics</i> , 2019, 20, 985-994.	3.2	55
7424	It is time to apply biclustering: a comprehensive review of biclustering applications in biological and biomedical data. <i>Briefings in Bioinformatics</i> , 2019, 20, 1450-1465.	3.2	42
7425	Response of Chinese fir seedlings to low phosphorus stress and analysis of gene expression differences. <i>Journal of Forestry Research</i> , 2019, 30, 183-192.	1.7	10
7426	Point-Based Methodology to Monitor and Control Gene Regulatory Networks via Noisy Measurements. <i>IEEE Transactions on Control Systems Technology</i> , 2019, 27, 1023-1035.	3.2	23
7427	RNA sequencing analysis of salt tolerance in soybean ( <i>Glycine max</i> ). <i>Genomics</i> , 2019, 111, 629-635.	1.3	34



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7428	Dynamic gene amplification and function diversification of grass-specific O-methyltransferase gene family. <i>Genomics</i> , 2019, 111, 687-695.	1.3	7
7429	Control of Gene Regulatory Networks Using Bayesian Inverse Reinforcement Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1250-1261.	1.9	43
7430	Testing equality of means in partially paired data with incompleteness in single response. <i>Statistical Methods in Medical Research</i> , 2019, 28, 1508-1522.	0.7	7
7431	A rank-based algorithm of differential expression analysis for small cell line data with statistical control. <i>Briefings in Bioinformatics</i> , 2019, 20, 482-491.	3.2	23
7432	ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 796-803.	1.9	5
7433	Modelling gene interaction networks from time-series gene expression data using evolving spiking neural networks. <i>Evolving Systems</i> , 2020, 11, 599-613.	2.4	2
7434	Whole Genome Shotgun Phylogenomics Resolves the Pattern and Timing of Swallowtail Butterfly Evolution. <i>Systematic Biology</i> , 2020, 69, 38-60.	2.7	65
7435	Lipopolysaccharide induces the differentiation of hepatic progenitor cells into myofibroblasts constitutes the hepatocarcinogenesis-associated microenvironment. <i>Cell Death and Differentiation</i> , 2020, 27, 85-101.	5.0	34
7436	APOBEC-mediated DNA alterations: A possible new mechanism of carcinogenesis in EBV-positive gastric cancer. <i>International Journal of Cancer</i> , 2020, 146, 181-191.	2.3	21
7437	Transcriptome Characterization of Gene Profiling During Early Stage of Nitric Oxide-Induced Adventitious Rooting in Mung Bean Seedlings. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 430-455.	2.8	6
7438	Transcriptome wide characterization of water deficit responsive grape mTERF transcription. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 102-113.	0.9	3
7439	Effect of the key histone modifications on the expression of genes related to breast cancer. <i>Genomics</i> , 2020, 112, 853-858.	1.3	14
7440	Screening and evaluating of long non-coding RNAs in prenatal and postnatal pituitary gland of sheep. <i>Genomics</i> , 2020, 112, 934-942.	1.3	19
7441	An empirical Bayesian ranking method, with applications to high throughput biology. <i>Bioinformatics</i> , 2020, 36, 177-185.	1.8	1
7442	Deregulation of Long Intergenic Non-coding RNAs in CD4+ T Cells of Lamina Propria in Crohn's Disease Through Transcriptome Profiling. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 96-109.	0.6	18
7443	Genome-wide identification and analysis of the eQTL lncRNAs in multiple sclerosis based on RNA-seq data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1023-1037.	3.2	35
7444	Differential gene expression profiles of human periodontal ligament cells preserved in Hank's balanced salt solution and milk. <i>Dental Traumatology</i> , 2020, 36, 58-68.	0.8	6
7445	Elicitor hydrophobin Hyd1 interacts with Ubiquitin-like to induce maize systemic resistance. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 509-526.	4.1	27

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7446	Comparative study on seasonal hair follicle cycling by analysis of the transcriptomes from cashmere and milk goats. <i>Genomics</i> , 2020, 112, 332-345.	1.3	44
7447	DFseq: Distribution-Free Method to Detect Differential Gene Expression for RNA-Sequencing Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 558-565.	1.9	0
7448	Effects of ammonia stress on the hemocytes of the Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Chemosphere</i> , 2020, 239, 124759.	4.2	66
7449	Transcriptome sequencing of okra ( <i>Abelmoschus esculentus</i> L. Moench) uncovers differently expressed genes responding to drought stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 155-170.	0.9	16
7451	A novel catalyst with variable active sites for the direct hydrogenation of waste oils into jet fuel. <i>Applied Catalysis B: Environmental</i> , 2020, 260, 118114.	10.8	35
7452	Quantitative Real-Time PCR. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	3
7454	Combined transcriptome and metabolome analysis identifies defence responses in spider mite-infested pepper ( <i>Capsicum annuum</i> ). <i>Journal of Experimental Botany</i> , 2020, 71, 330-343.	2.4	61
7455	Transcriptomic insight into cadmium-induced neurotoxicity in embryonic neural stem/progenitor cells. <i>Toxicology in Vitro</i> , 2020, 62, 104686.	1.1	20
7456	Identification of miRNA signature associated with BMP2 and chemosensitivity of TMZ in glioblastoma stem-like cells. <i>Genes and Diseases</i> , 2020, 7, 424-439.	1.5	16
7457	Comparative morphological and transcriptomic responses of lowland and upland rice to root-zone hypoxia. <i>Environmental and Experimental Botany</i> , 2020, 169, 103916.	2.0	17
7458	icSHAPE-pipe: A comprehensive toolkit for icSHAPE data analysis and evaluation. <i>Methods</i> , 2020, 178, 96-103.	1.9	20
7459	Time delay in seeking treatment for first episode schizophrenia: a retrospective study. <i>Microbial Biotechnology</i> , 2020, 14, 553-558.	0.9	7
7460	Exosome-Derived MiRNAs as Biomarkers of the Development and Progression of Intracranial Aneurysms. <i>Journal of Atherosclerosis and Thrombosis</i> , 2020, 27, 545-610.	0.9	31
7461	Transcriptome sequencing reveals genetic mechanisms of reproduction performance stimulated by dietary daidzein in laying Abreeder hens. <i>Theriogenology</i> , 2020, 142, 120-130.	0.9	6
7462	Comparative Metabolomic and Transcriptome Analysis Reveal Distinct Flavonoid Biosynthesis Regulation Between Petals of White and Purple <i>Phalaenopsis amabilis</i> . <i>Journal of Plant Growth Regulation</i> , 2020, 39, 823-840.	2.8	42
7463	Interspecific hybridisation and LTR-retrotransposon mobilisation-related structural variation in plants: A case study. <i>Genomics</i> , 2020, 112, 1611-1621.	1.3	10
7464	Pkd1-targeted mutation reveals a role for the Wolffian duct in autosomal dominant polycystic kidney disease. <i>Journal of Developmental Origins of Health and Disease</i> , 2020, 11, 78-85.	0.7	2
7465	Outcomes of a low birth weight phenotype on piglet gut microbial composition and intestinal transcriptomic profile. <i>Canadian Journal of Animal Science</i> , 2020, 100, 47-58.	0.7	2

#	ARTICLE	IF	CITATIONS
7466	Mitochondrial genes associated with pyrethroid resistance revealed by mitochondrial genome and transcriptome analyses in the malaria vector <i>Anopheles sinensis</i> (Diptera: Culicidae). <i>Pest Management Science</i> , 2020, 76, 769-778.	1.7	7
7467	Comparative transcriptome analysis reveals a gene expression profile that contributes to rhizome swelling in <i>Panax japonicus</i> var. <i>major</i> . <i>Plant Biosystems</i> , 2020, 154, 515-523.	0.8	6
7469	Towards the Reconstruction of Integrated Genome-Scale Models of Metabolism and Gene Expression. <i>Advances in Intelligent Systems and Computing</i> , 2020, , 173-181.	0.5	0
7470	A functional genetic screen defines the AKT-induced senescence signaling network. <i>Cell Death and Differentiation</i> , 2020, 27, 725-741.	5.0	40
7471	Transcriptome and proteome profiles of the diazotroph <i>Nitrospirillum amazonense</i> strain CBAmC in response to the sugarcane apoplast fluid. <i>Plant and Soil</i> , 2020, 451, 145-168.	1.8	15
7472	Characterization of the promoter, downstream target genes and recognition DNA sequence of <i>Mhy1</i> , a key filamentation-promoting transcription factor in the dimorphic yeast <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 2020, 66, 245-261.	0.8	14
7473	Transcriptome profiling and dimorphic expression of sex-related genes in fifth-instar nymphs of <i>Sogatella furcifera</i> , an important rice pest. <i>Genomics</i> , 2020, 112, 1105-1111.	1.3	7
7474	Stage-dependent differential gene expression profiles of cranial neural crest-like cells derived from mouse-induced pluripotent stem cells. <i>Medical Molecular Morphology</i> , 2020, 53, 28-41.	0.4	4
7475	Transcriptome analysis of self- and cross-pollinated pistils revealing candidate unigenes of self-incompatibility in <i>Camellia oleifera</i> . <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 19-31.	0.9	12
7476	Comparative transcriptome analysis of rhizome nodes and internodes in <i>Panax japonicus</i> var. <i>major</i> reveals candidate genes involved in the biosynthesis of triterpenoid saponins. <i>Genomics</i> , 2020, 112, 1112-1119.	1.3	7
7477	Transcriptomic analysis reveals biocontrol mechanisms of <i>Trichoderma harzianum</i> ACCC30371 under eight culture conditions. <i>Journal of Forestry Research</i> , 2020, 31, 1863-1873.	1.7	6
7478	Intestinal responses of the oriental fruit fly <i>Bactrocera dorsalis</i> (Hendel) after ingestion of an entomopathogenic bacterium strain. <i>Pest Management Science</i> , 2020, 76, 653-664.	1.7	7
7479	Gene expression during genital morphogenesis in the ground beetle <i>Carabus maiyasanus</i> . <i>Insect Science</i> , 2020, 27, 975-986.	1.5	4
7480	<i>TaD27</i> gene controls the tiller number in hexaploid wheat. <i>Plant Biotechnology Journal</i> , 2020, 18, 513-525.	4.1	64
7481	Comparative Transcriptome Analysis Reveals Different Host Cell Responses to Acute and Persistent Foot-and-Mouth Disease Virus Infection. <i>Virologica Sinica</i> , 2020, 35, 52-63.	1.2	7
7482	Compressed and Penalized Linear Regression. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 309-322.	0.9	2
7483	Metformin ameliorates stress-induced depression-like behaviors via enhancing the expression of BDNF by activating AMPK/CREB-mediated histone acetylation. <i>Journal of Affective Disorders</i> , 2020, 260, 302-313.	2.0	83
7484	Imprinted X chromosome inactivation impacts primitive endoderm differentiation in mouse blastocysts. <i>FEBS Letters</i> , 2020, 594, 913-923.	1.3	0

#	ARTICLE	IF	CITATIONS
7485	Transcriptomic and metabolomic responses in the livers of pigs to diets containing different non-starchy polysaccharides. <i>Journal of Functional Foods</i> , 2020, 64, 103590.	1.6	3
7486	RNA-Seq analysis of peripheral blood mononuclear cells reveals unique transcriptional signatures associated with radiotherapy response of nasopharyngeal carcinoma and prognosis of head and neck cancer. <i>Cancer Biology and Therapy</i> , 2020, 21, 139-146.	1.5	35
7487	Alternative splicing of a barley gene results in an excess-tillering and semi-dwarf mutant. <i>Theoretical and Applied Genetics</i> , 2020, 133, 163-177.	1.8	6
7488	Transcriptome analysis of <i>Aconitum carmichaelii</i> and exploration of the salsolinol biosynthetic pathway. <i>FÄ-toterapÄ-Äç</i> , 2020, 140, 104412.	1.1	7
7489	A Learning-Based Power Management Method for Networked Microgrids Under Incomplete Information. <i>IEEE Transactions on Smart Grid</i> , 2020, 11, 1193-1204.	6.2	85
7490	Production of ammonia as a low-cost and long-distance antibiotic strategy by <i>Streptomyces</i> species. <i>ISME Journal</i> , 2020, 14, 569-583.	4.4	52
7491	RNA sequencing and transcriptome analysis. , 2020, , 41-53.		0
7492	Anisotropic ridge/groove microstructure for regulating morphology and biological function of Schwann cells. <i>Applied Materials Today</i> , 2020, 18, 100468.	2.3	19
7493	Integrated transcriptomic and proteomic analyses of the tissues from the digestive gland of <i>Chlamys farreri</i> following cadmium exposure. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 974-983.	1.2	4
7494	Investigation of the genes associated with a male sterility mutant (msm) in Chinese cabbage ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.0	15
7495	Mutations in the miR396 binding site of the growth-regulating factor gene <i>VvGRF4</i> modulate inflorescence architecture in grapevine. <i>Plant Journal</i> , 2020, 101, 1234-1248.	2.8	19
7496	Transcriptional responses to starvation of pathogenic <i>Vibrio harveyi</i> strain DY1. <i>Journal of Oceanology and Limnology</i> , 2020, 38, 579-587.	0.6	3
7497	De novo transcriptomic analysis of light-induced flavonoid pathway, transcription factors in the flower buds of <i>Lonicera japonica</i> . <i>Trees - Structure and Function</i> , 2020, 34, 267-283.	0.9	14
7498	Transcriptome analysis and histopathology of the mud crab ( <i>Scylla paramamosain</i> ) after air exposure. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 228, 108652.	1.3	14
7499	Integrated transcriptomic and proteomic analyses of grass carp intestines after vaccination with a double-targeted DNA vaccine of <i>Vibrio mimicus</i> . <i>Fish and Shellfish Immunology</i> , 2020, 98, 641-652.	1.6	31
7500	Identification of two novel highly inducible promoters from <i>Bacillus licheniformis</i> by screening transcriptomic data. <i>Genomics</i> , 2020, 112, 1866-1871.	1.3	7
7501	A NAC-type transcription factor confers aluminium resistance by regulating cell wall-associated receptor kinase 1 and cell wall pectin. <i>Plant, Cell and Environment</i> , 2020, 43, 463-478.	2.8	63
7502	The control of red colour by a family of MYB transcription factors in octoploid strawberry ( <i>Fragaria</i> — <i>Ananassa</i> ) fruits. <i>Plant Biotechnology Journal</i> , 2020, 18, 1169-1184.	4.1	78

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7503	Homeotic transformation from stamen to petal in <i>Eriobotrya japonica</i> is associated with hormone signal transduction and reduction of the transcriptional activity of <i>EJA1</i> . <i>Physiologia Plantarum</i> , 2020, 168, 893-908.	2.6	16
7504	Transcriptomic analysis reveals that hepatopancreatic necrosis disease in <i>Eriocheir sinensis</i> (Chinese) Tj ETQq1 1 0.784314 rgBT /Ove	1.7	7
7505	Stopping transformed cancer cell growth by rigidity sensing. <i>Nature Materials</i> , 2020, 19, 239-250.	13.3	81
7506	A Model of Hormonal Regulation of Stamen Abortion during Pre-Meiosis of <i>Litsea cubeba</i> . <i>Genes</i> , 2020, 11, 48.	1.0	12
7507	The Use of High-Throughput Transcriptomics to Identify Pathways with Therapeutic Significance in Podocytes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 274.	1.8	7
7508	Transcriptomic profile analysis of non-coding RNAs involved in <i>Capsicum chinense</i> Jacq. fruit ripening. <i>Scientia Horticulturae</i> , 2020, 264, 109158.	1.7	13
7509	A Conceptual Framework for Abundance Estimation of Genomic Targets in the Presence of Ambiguous Short Sequencing Reads. <i>Journal of Computational Biology</i> , 2020, 27, 1232-1247.	0.8	1
7510	contamDE-Im: linear model-based differential gene expression analysis using next-generation RNA-seq data from contaminated tumor samples. <i>Bioinformatics</i> , 2020, 36, 2492-2499.	1.8	2
7511	Nonthermal Plasma Induces the Viable-but-Nonculturable State in <i>Staphylococcus aureus</i> via Metabolic Suppression and the Oxidative Stress Response. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	43
7512	Identification and Validation of Differentially Expressing Transcripts from Top and Bottom Internodes of High-Sucrose Sugarcane Variety CoJ64. <i>Sugar Tech</i> , 2020, 22, 89-97.	0.9	1
7513	Domestication and breeding changed tomato fruit transcriptome. <i>Journal of Integrative Agriculture</i> , 2020, 19, 120-132.	1.7	18
7514	Comparative transcriptome analysis of the genes involved in lipid biosynthesis pathway and regulation of oil body formation in <i>Torreya grandis</i> kernels. <i>Industrial Crops and Products</i> , 2020, 145, 112051.	2.5	24
7515	Molecular Insights into the Insensitivity of Lepidopteran Pests to Cycloxyaprid. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 982-988.	2.4	5
7516	Antennal transcriptome analysis and expression profiles of putative chemosensory soluble proteins in <i>Histia rhodope</i> Cramer (Lepidoptera: Zygaenidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100654.	0.4	12
7517	U1 snRNP regulates cancer cell migration and invasion in vitro. <i>Nature Communications</i> , 2020, 11, 1.	5.8	12,921
7518	The MNT transcription factor autoregulates its expression and supports proliferation in MYC-associated factor X (MAX)-deficient cells. <i>Journal of Biological Chemistry</i> , 2020, 295, 2001-2017.	1.6	10
7519	Endogenous Interleukin 18 Suppresses Liver Regeneration After Hepatectomy in Mice. <i>Liver Transplantation</i> , 2020, 26, 408-418.	1.3	5
7520	Differential Expression of the Transcription Factor GATA3 Specifies Lineage and Functions of Innate Lymphoid Cells. <i>Immunity</i> , 2020, 52, 83-95.e4.	6.6	52

#	ARTICLE	IF	CITATIONS
7521	Identifying Vitamin E Biosynthesis Genes in <i>Elaeis guineensis</i> by Genome-Wide Association Study. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 678-685.	2.4	7
7522	Disentangling sRNA-Seq data to study RNA communication between species. <i>Nucleic Acids Research</i> , 2020, 48, e21-e21.	6.5	8
7523	Inorganic nitrite increases the susceptibility of tilapia ( <i>Oreochromis niloticus</i> ) leucocytes to <i>Streptococcus agalactiae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 97, 1-11.	1.6	5
7524	Transcriptomic Changes in Liver of Juvenile <i>Cynoglossus semilaevis</i> following Perfluorooctane Sulfonate Exposure. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 556-564.	2.2	10
7525	A comparative transcriptomic analysis in late embryogenesis of the red claw crayfish <i>Cherax quadricarinatus</i> . <i>Molecular Genetics and Genomics</i> , 2020, 295, 299-311.	1.0	9
7526	Evaluating maize phenotypic variance, heritability, and yield relationships at multiple biological scales across agronomically relevant environments. <i>Plant, Cell and Environment</i> , 2020, 43, 880-902.	2.8	24
7527	Targeted misexpression of NAC052, acting in H3K4 demethylation, alters leaf morphological and anatomical traits in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 1434-1448.	2.4	4
7528	Statistical genetic concepts in psychiatric genomics. , 2020, , 103-116.		0
7529	Scalable and cost-effective ribonuclease-based rRNA depletion for transcriptomics. <i>Nucleic Acids Research</i> , 2020, 48, e20-e20.	6.5	42
7530	Transcriptomic analyses of <i>Pinus koraiensis</i> under different cold stresses. <i>BMC Genomics</i> , 2020, 21, 10.	1.2	29
7531	RNA sequencing reveals an additional Crz1-binding motif in promoters of its target genes in the human fungal pathogen <i>Candida albicans</i> . <i>Cell Communication and Signaling</i> , 2020, 18, 1.	2.7	103
7532	Bayesian mixture regression analysis for regulation of Pluripotency in ES cells. <i>BMC Bioinformatics</i> , 2020, 21, 3.	1.2	3
7533	Phage-specific metabolic reprogramming of virocells. <i>ISME Journal</i> , 2020, 14, 881-895.	4.4	133
7534	Unravelling the role of long non-coding RNA - LINC01087 in breast cancer. <i>Non-coding RNA Research</i> , 2020, 5, 1-10.	2.4	13
7535	The role of the bacterial protease Prc in the uropathogenesis of extraintestinal pathogenic <i>Escherichia coli</i> . <i>Journal of Biomedical Science</i> , 2020, 27, 14.	2.6	24
7536	Lipopolysaccharide-dependent transcriptional regulation of PU.1 in microglial cells. <i>Molecular and Cellular Toxicology</i> , 2020, 16, 51-61.	0.8	0
7537	Identification of differential gene expression related to epirubicin-induced cardiomyopathy in breast cancer patients. <i>Human and Experimental Toxicology</i> , 2020, 39, 393-401.	1.1	5
7538	In vitro antifungal activity of dimethyl trisulfide against <i>Colletotrichum gloeosporioides</i> from mango. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 4.	1.7	17

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7539	Analyses of mRNA-seq and miRNA-seq of the brain reveal the sex differences of gene expression and regulation before and during gonadal differentiation in 17 $\beta$ -estradiol or 17 $\alpha$ -methyltestosterone-induced olive flounder ( <i>Paralichthys olivaceus</i> ). <i>Molecular Reproduction and Development</i> , 2020, 87, 78-90.	1.0	10
7540	t-Distributed Stochastic Neighbor Embedding (t-SNE): A tool for eco-physiological transcriptomic analysis. <i>Marine Genomics</i> , 2020, 51, 100723.	0.4	113
7541	Comparison of sulfide-oxidizing <i>Sulfurimonas</i> strains reveals a new mode of thiosulfate formation in subsurface environments. <i>Environmental Microbiology</i> , 2020, 22, 1784-1800.	1.8	27
7542	Overcoming challenges and dogmas to understand the functions of pseudogenes. <i>Nature Reviews Genetics</i> , 2020, 21, 191-201.	7.7	151
7543	Levels of the endosymbiont <i>Rickettsia</i> in the whitefly <i>Bemisia tabaci</i> are influenced by the expression of vitellogenin. <i>Insect Molecular Biology</i> , 2020, 29, 241-255.	1.0	19
7544	Gain and loss of a transcription factor that regulates late trichothecene biosynthetic pathway genes in <i>Fusarium</i> . <i>Fungal Genetics and Biology</i> , 2020, 136, 103317.	0.9	13
7545	High-throughput omics in the precision medicine ecosystem. , 2020, , 19-31.		1
7546	Development of the transcriptome for a sediment ecotoxicological model species, <i>Chironomus dilutus</i> . <i>Chemosphere</i> , 2020, 244, 125541.	4.2	13
7547	Genomic and gene expression evidence of nonribosomal peptide and polyketide production among ruminal bacteria: a potential role in niche colonization?. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	9
7548	Transcriptome and weighted correlation network analyses provide insights into inflorescence stem straightness in <i>Paeonia lactiflora</i> . <i>Plant Molecular Biology</i> , 2020, 102, 239-252.	2.0	8
7549	Explaining Gene Expression Using Twenty-One MicroRNAs. <i>Journal of Computational Biology</i> , 2020, 27, 1157-1170.	0.8	5
7550	Application of fermentation process control to increase l-tryptophan production in <i>Escherichia coli</i> . <i>Biotechnology Progress</i> , 2020, 36, e2944.	1.3	9
7551	A novel single-base mutation in <i>CaBRI1</i> confers dwarf phenotype and brassinosteroid accumulation in pepper. <i>Molecular Genetics and Genomics</i> , 2020, 295, 343-356.	1.0	7
7552	Transcriptomic analysis of <i>Nibeia albiflora</i> skin in response to infection by <i>Cryptocaryon irritans</i> . <i>Fish and Shellfish Immunology</i> , 2020, 98, 819-831.	1.6	13
7553	Changes in the gene expression of chalkbrood resistance in <i>Apis mellifera</i> larvae infected by <i>Ascosphaera apis</i> . <i>Apidologie</i> , 2020, 51, 35-47.	0.9	2
7554	Prediction of miRNA interaction with mRNA of stroke candidate genes. <i>Neurological Sciences</i> , 2020, 41, 799-808.	0.9	16
7555	Root transcriptome analysis of <i>Saccharum spontaneum</i> uncovers key genes and pathways in response to low-temperature stress. <i>Environmental and Experimental Botany</i> , 2020, 171, 103935.	2.0	23
7556	Robust identification of differentially expressed genes from RNA-seq data. <i>Genomics</i> , 2020, 112, 2000-2010.	1.3	20

#	ARTICLE	IF	CITATIONS
7557	Multinucleated polyploid cardiomyocytes undergo an enhanced adaptability to hypoxia via mitophagy. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 138, 115-135.	0.9	12
7558	Transcriptomic Profiling of 3D Glioblastoma Tumoroids for the Identification of Mechanisms Involved in Anticancer Drug Resistance. <i>In Vivo</i> , 2020, 34, 199-211.	0.6	15
7559	In vitro resynthesis of lichenization reveals the genetic background of symbiosis-specific fungal-algal interaction in <i>Usnea hakonensis</i> . <i>BMC Genomics</i> , 2020, 21, 671.	1.2	27
7560	Insulin-like growth factor binding protein-2: a new circulating indicator of pulmonary arterial hypertension severity and survival. <i>BMC Medicine</i> , 2020, 18, 268.	2.3	15
7561	Increased comparability between RNA-Seq and microarray data by utilization of gene sets. <i>PLoS Computational Biology</i> , 2020, 16, e1008295.	1.5	18
7562	Gene Expression Analysis in Response to Vernalization in Chinese Cabbage (&i>Brassica Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.8	9
7563	Commentary: A Systematic Evaluation of Single Cell RNA-Seq Analysis Pipelines. <i>Frontiers in Genetics</i> , 2020, 11, 941.	1.1	5
7564	Comprehensive Transcriptomic Analysis for Developing Seeds of a Synthetic Brassica Hexaploid. <i>Plants</i> , 2020, 9, 1141.	1.6	3
7565	Genetic circuit characterization by inferring RNA polymerase movement and ribosome usage. <i>Nature Communications</i> , 2020, 11, 5001.	5.8	40
7566	Polyunsaturated Fatty Acids Influence LPS-Induced Inflammation of Fish Macrophages Through Differential Modulation of Pathogen Recognition and p38 MAPK/NF- $\kappa$ B Signaling. <i>Frontiers in Immunology</i> , 2020, 11, 559332.	2.2	15
7567	In silico Screening Unveil the Great Potential of Ruminant Bacteria Synthesizing Lasso Peptides. <i>Frontiers in Microbiology</i> , 2020, 11, 576738.	1.5	10
7568	Comparative transcriptome analysis of three invasive leafminer flies provides insights into interspecific competition. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 1664-1674.	3.6	8
7569	<i>OsWUS</i> promotes tiller bud growth by establishing weak apical dominance in rice. <i>Plant Journal</i> , 2020, 104, 1635-1647.	2.8	20
7570	Development and comparison of RNA-sequencing pipelines for more accurate SNP identification: practical example of functional SNP detection associated with feed efficiency in Nellore beef cattle. <i>BMC Genomics</i> , 2020, 21, 703.	1.2	14
7571	Overexpression of an ethylene-forming ACC oxidase (ACO) gene precedes the Minute Hilum seed coat phenotype in <i>Glycine max</i> . <i>BMC Genomics</i> , 2020, 21, 716.	1.2	3
7572	Impact of Ocean Warming and Acidification on Symbiosis Establishment and Gene Expression Profiles in Recruits of Reef Coral <i>Acropora intermedia</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 532447.	1.5	10
7573	Exogenous Melatonin Attenuates Post-Harvest Decay by Increasing Antioxidant Activity in Wax Apple ( <i>Syzygium samarangense</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 569779.	1.7	25
7574	Correlation Analysis of Expression Profile and Quantitative iTRAQ-LC-MS/MS Proteomics Reveals Resistance Mechanism Against TuMV in Chinese Cabbage ( <i>Brassica rapa ssp. pekinensis</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 963.	1.1	10



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7576	Altered redox regulation and S-glutathionylation of BiP contribute to bortezomib resistance in multiple myeloma. <i>Free Radical Biology and Medicine</i> , 2020, 160, 755-767.	1.3	30
7577	Comparative transcriptome analysis of eyestalk from the white shrimp <i>Litopenaeus vannamei</i> after the injection of dopamine. <i>Gene</i> , 2020, 763, 145115.	1.0	7
7578	Genome-wide dynamics of RNA synthesis, processing, and degradation without RNA metabolic labeling. <i>Genome Research</i> , 2020, 30, 1492-1507.	2.4	26
7579	Genome-Wide Network of lncRNA-mRNA During Ovine Oocyte Development From Germinal Vesicle to Metaphase II in vitro. <i>Frontiers in Physiology</i> , 2020, 11, 1019.	1.3	18
7580	OpenGDC: Unifying, Modeling, Integrating Cancer Genomic Data and Clinical Metadata. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 6367.	1.3	12
7581	A Unique Population of Regulatory T Cells in Heart Potentiates Cardiac Protection From Myocardial Infarction. <i>Circulation</i> , 2020, 142, 1956-1973.	1.6	104
7582	Multidrug resistance of <i>Penicillium expansum</i> to fungicides: whole transcriptome analysis of MDR strains reveals overexpression of efflux transporter genes. <i>International Journal of Food Microbiology</i> , 2020, 335, 108896.	2.1	29
7583	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. <i>Scientific Reports</i> , 2020, 10, 17925.	1.6	18
7584	Transcriptome analysis identifies key genes involved in carotenoid biosynthesis in the flesh of red pummelo ( <i>Citrus maxima</i> ). <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 614-622.	0.5	2
7585	Messenger RNA enrichment using synthetic oligo(T) click nucleic acids. <i>Chemical Communications</i> , 2020, 56, 13987-13990.	2.2	10
7586	Identification of key genes and important histone modifications in hepatocellular carcinoma. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2657-2669.	1.9	18
7587	OneStopRNAseq: A Web Application for Comprehensive and Efficient Analyses of RNA-Seq Data. <i>Genes</i> , 2020, 11, 1165.	1.0	25
7588	The Chromosome Level Genome and Genome-wide Association Study for the Agronomic Traits of <i>Panax Notoginseng</i> . <i>IScience</i> , 2020, 23, 101538.	1.9	34
7589	The E3 ubiquitin ligase HectD3 attenuates cardiac hypertrophy and inflammation in mice. <i>Communications Biology</i> , 2020, 3, 562.	2.0	17
7590	Transcriptional and physiological analyses of reduced density in apple provide insight into the regulation involved in photosynthesis. <i>PLoS ONE</i> , 2020, 15, e0239737.	1.1	4
7591	Comparative transcriptome analysis of <i>Phascolosoma esculenta</i> under different salinities. <i>Aquaculture and Fisheries</i> , 2020, 5, 323-330.	1.2	0
7592	Analysis of the <i>Prunellae Spica</i> transcriptome under salt stress. <i>Plant Physiology and Biochemistry</i> , 2020, 156, 314-322.	2.8	8
7593	Low stringency tests revealed differential gene expression in red maple ( <i>Acer rubrum</i> ) treated with low doses of nickel. <i>Plant Gene</i> , 2020, 24, 100251.	1.4	2

#	ARTICLE	IF	CITATIONS
7594	Understanding salt tolerance mechanism using transcriptome profiling and de novo assembly of wild tomato <i>Solanum chilense</i> . <i>Scientific Reports</i> , 2020, 10, 15835.	1.6	35
7595	Combined transcriptome sequencing and prokaryotic expression to investigate the key enzyme in the 2-C-methylerythritol-4-phosphate pathway of <i>Osmanthus fragrans</i> . <i>Functional Plant Biology</i> , 2020, 47, 945.	1.1	6
7596	IsoXpressor: A Tool to Assess Transcriptional Activity within Isochores. <i>Genome Biology and Evolution</i> , 2020, 12, 1573-1578.	1.1	3
7597	Global transcriptomic and proteomics analysis of <i>Lactobacillus plantarum</i> Y44 response to 2,2-azobis(2-methylpropionamide) dihydrochloride (AAPH) stress. <i>Journal of Proteomics</i> , 2020, 226, 103903.	1.2	8
7598	Translocation of PpNPR1 is required for Î²-aminobutyric acid-triggered resistance against <i>Rhizopus stolonifer</i> in peach fruit. <i>Scientia Horticulturae</i> , 2020, 272, 109556.	1.7	5
7599	Comparative Transcriptome Analysis Reveals the Potential Cardiovascular Protective Targets of the Thyroid Hormone Metabolite 3-Iodothyronamine (3-TIAM). <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	3
7600	A New Method to Obtain the Complete Genome Sequence of Multiple-Component Circular ssDNA Viruses by Transcriptome Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 832.	2.0	1
7601	A CTGF-YAP Regulatory Pathway Is Essential for Angiogenesis and Barrierogenesis in the Retina. <i>IScience</i> , 2020, 23, 101184.	1.9	33
7602	Transcriptome wide identification and characterization of regulatory genes involved in EAA metabolism and validation through expression analysis in different developmental stages of finger millet spikes. <i>3 Biotech</i> , 2020, 10, 347.	1.1	6
7603	HRT Atlas v1.0 database: redefining human and mouse housekeeping genes and candidate reference transcripts by mining massive RNA-seq datasets. <i>Nucleic Acids Research</i> , 2021, 49, D947-D955.	6.5	145
7604	HCN Channel Activity Balances Quiescence and Proliferation in Neural Stem Cells and Is a Selective Target for Neuroprotection During Cancer Treatment. <i>Molecular Cancer Research</i> , 2020, 18, 1522-1533.	1.5	6
7605	A Guide to Understanding "State-of-the-Art" Basic Research Techniques in Anesthesiology. <i>Anesthesia and Analgesia</i> , 2020, 131, 450-463.	1.1	2
7606	Transcriptional Profiling of Normal, Stenotic, and Regurgitant Human Aortic Valves. <i>Genes</i> , 2020, 11, 789.	1.0	14
7607	Transcriptome Characterization of Repressed Embryonic Myogenesis Due to Maternal Calorie Restriction. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 527.	1.8	2
7608	High temperature damage to fatty acids and carbohydrate metabolism in tall fescue by coupling deep transcriptome and metabolome analysis. <i>Ecotoxicology and Environmental Safety</i> , 2020, 203, 110943.	2.9	11
7609	Alternative splicing of flowering time gene FT is associated with halving of time to flowering in coconut. <i>Scientific Reports</i> , 2020, 10, 11640.	1.6	11
7610	Transcriptome and Hormone Analyses Revealed Insights into Hormonal and Vesicle Trafficking Regulation among <i>Olea europaea</i> Fruit Tissues in Late Development. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4819.	1.8	10
7611	Transcriptome Profiling of Abscisic Acid-Related Pathways in SNAC4/9-Silenced Tomato Fruits. <i>Transactions of Tianjin University</i> , 2020, 27, 473.	3.3	3

#	ARTICLE	IF	CITATIONS
7612	Transcriptomic analysis of flower opening response to relatively low temperatures in <i>Osmanthus fragrans</i> . <i>BMC Plant Biology</i> , 2020, 20, 337.	1.6	8
7613	Region and Cell Type Distribution of TCF4 in the Postnatal Mouse Brain. <i>Frontiers in Neuroanatomy</i> , 2020, 14, 42.	0.9	28
7614	Comparative transcriptomics analysis revealing flower trichome development during flower development in two <i>Lonicera japonica</i> Thunb. cultivars using RNA-seq. <i>BMC Plant Biology</i> , 2020, 20, 341.	1.6	8
7615	Foliage Intensity is an Important Cue of Habitat Location for <i>Empoasca onukii</i> . <i>Insects</i> , 2020, 11, 426.	1.0	9
7616	Large-Scale Production of Human iPSC-Derived Macrophages for Drug Screening. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4808.	1.8	62
7617	Transcriptomic Profiling of the Immune Response to Crowding Stress in Juvenile Turbot ( <i>Scophthalmus maximus</i> ). <i>Journal of Ocean University of China</i> , 2020, 19, 911-922.	0.6	4
7618	Networks of transcription factors. , 2020, , 137-155.		3
7619	Mucosal IgA Prevents Commensal <i>Candida albicans</i> Dysbiosis in the Oral Cavity. <i>Frontiers in Immunology</i> , 2020, 11, 555363.	2.2	35
7620	De novo assembly and analysis of the transcriptome of the <i>Dermacentor marginatus</i> genes differentially expressed after blood-feeding and long-term starvation. <i>Parasites and Vectors</i> , 2020, 13, 563.	1.0	9
7621	Genome-Wide Gene Expression Profiles Analysis Reveal Novel Insights into Drought Stress in Foxtail Millet ( <i>Setaria italica</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 8520.	1.8	17
7622	Long-Term Soy Protein Isolate Consumption Reduces Liver Steatosis Through Changes in Global Transcriptomics in Obese Zucker Rats. <i>Frontiers in Nutrition</i> , 2020, 7, 607970.	1.6	8
7623	Whole Transcriptome Analysis of Myeloid Dendritic Cells Reveals Distinct Genetic Regulation in Patients with Allergies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8640.	1.8	7
7624	Deep sequencing reveals a DAP1 regulatory haplotype that potentiates autoimmunity in systemic lupus erythematosus. <i>Genome Biology</i> , 2020, 21, 281.	3.8	8
7625	N6-Adenosine Methylation of <i>Socs1</i> mRNA Is Required to Sustain the Negative Feedback Control of Macrophage Activation. <i>Developmental Cell</i> , 2020, 55, 737-753.e7.	3.1	51
7626	Mutational landscape influences immunotherapy outcomes among patients with non-small-cell lung cancer with human leukocyte antigen supertype B44. <i>Nature Cancer</i> , 2020, 1, 1167-1175.	5.7	22
7627	Transcriptome Analysis Illuminates a Hub Role of <i>SREBP2</i> in Cholesterol Metabolism by $\pm$ -Mangostin. <i>ACS Omega</i> , 2020, 5, 31126-31136.	1.6	10
7628	Long Non-coding RNA H19 Regulates Porcine Satellite Cell Differentiation Through miR-140-5p/SOX4 and DBN1. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 518724.	1.8	16
7629	Genes Induced by <i>Panax Notoginseng</i> in a Rodent Model of Ischemia-Reperfusion Injury. <i>Journal of Immunology Research</i> , 2020, 2020, 1-13.	0.9	2

#	ARTICLE	IF	CITATIONS
7630	The Potential Effects of Curcumin on Pulmonary Fibroblasts of Idiopathic Pulmonary Fibrosis (IPF) – Approaching with Next-Generation Sequencing and Bioinformatics. <i>Molecules</i> , 2020, 25, 5458.	1.7	5
7631	ROP18-Mediated Transcriptional Reprogramming of HEK293T Cell Reveals New Roles of ROP18 in the Interplay Between <i>Toxoplasma gondii</i> and the Host Cell. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 586946.	1.8	6
7632	Validation of Housekeeping Genes for Gene Expression Analysis in Iwagaki Oyster ( <i>Crassostrea</i> ). <i>Journal of Shellfish Research</i> , 2020, 39, 1441-1446.	0.6	2
7633	Effects on the Liver Transcriptome in Baltic Salmon: Contributions of Contamination with Organohalogen Compounds and Origin of Salmon. <i>Environmental Science &amp; Technology</i> , 2020, 54, 15246-15256.	4.6	3
7634	A joint analysis strategy reveals genetic changes associated with artificial selection between egg-type and meat-type ducks. <i>Animal Genetics</i> , 2020, 51, 890-898.	0.6	5
7635	Transcriptome analysis of low phosphate stress response in the roots of masson pine ( <i>Pinus massoniana</i> ). <i>Plant Physiology and Biochemistry</i> , 2020, 150, 107431.	1.0	3
7636	Alternative Splicing: Expanding the Landscape of Cancer Biomarkers and Therapeutics. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9032.	1.8	28
7637	Identification of key gene networks controlling organic acid and sugar metabolism during watermelon fruit development by integrating metabolic phenotypes and gene expression profiles. <i>Horticulture Research</i> , 2020, 7, 193.	2.9	74
7638	Transcriptome and proteome profiling reveal complementary scavenger and immune features of rat liver sinusoidal endothelial cells and liver macrophages. <i>BMC Molecular and Cell Biology</i> , 2020, 21, 85.	1.0	21
7639	Satellite Cell Depletion Disrupts Transcriptional Coordination and Muscle Adaptation to Exercise. <i>Frontiers in Physiology</i> , 2020, 11, 579033.	1.1	43
7640	Transcriptome analyses reveals the dynamic nature of oil accumulation during seed development of <i>Plukenetia volubilis</i> L.. <i>Scientific Reports</i> , 2020, 10, 20467.	1.6	7
7641	Comparative Transcriptomics Analysis and Functional Study Reveal Important Role of High-Temperature Stress Response Gene <i>GmHSFA2</i> During Flower Bud Development of CMS-Based F1 in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 600217.	1.7	20
7642	SITC cancer immunotherapy resource document: a compass in the land of biomarker discovery. <i>Journal of Cancer</i> , 2020, 11, e000705.		20
7643	Identification of a quantitative trait loci (QTL) associated with ammonia tolerance in the Pacific white shrimp ( <i>Litopenaeus vannamei</i> ). <i>BMC Genomics</i> , 2020, 21, 857.	1.2	14
7644	Transcriptome analysis of xa5-mediated resistance to bacterial leaf streak in rice ( <i>Oryza sativa</i> L.). <i>Scientific Reports</i> , 2020, 10, 19439.	1.6	8
7645	The human transcriptome: implications for understanding, diagnosing, and treating human disease. <i>Journal of Molecular Biology</i> , 2020, 638, 113-138.		0
7646	Effects of <i>Vibrio parahaemolyticus</i> infection on physiological response, histopathology and transcriptome changes in the mud crab ( <i>Scylla paramamosain</i> ). <i>Fish and Shellfish Immunology</i> , 2020, 106, 197-204.	1.6	20
7647	Cognitive Phenotype and Differential Gene Expression in a Hippocampal Homologue in Two Species of Frog. <i>Integrative and Comparative Biology</i> , 2020, 60, 1007-1023.	0.9	11

#	ARTICLE	IF	CITATIONS
7648	Transcriptome analysis of the eggs of the silkworm pale red egg (rep-1) mutant at 36 hours after oviposition. <i>PLoS ONE</i> , 2020, 15, e0237242.	1.1	1
7649	Murine Long Noncoding RNA Morrbid Contributes in the Regulation of NRAS Splicing in Hepatocytes In Vitro. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5605.	1.8	6
7650	Molecular Characterization, Expression Pattern and Function Analysis of Glycine-Rich Protein Genes Under Stresses in Chinese Cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 774.	1.1	5
7651	An Integrative Analysis of Transcriptome, Proteome and Hormones Reveals Key Differentially Expressed Genes and Metabolic Pathways Involved in Flower Development in Loquat. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5107.	1.8	22
7652	mRNAs, proteins and the emerging principles of gene expression control. <i>Nature Reviews Genetics</i> , 2020, 21, 630-644.	7.7	576
7653	A hierarchical Bayesian mixture model for inferring the expression state of genes in transcriptomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19339-19346.	3.3	16
7654	Immune response of mollusk <i>Onchidium struma</i> to extremely low-frequency electromagnetic fields (ELF-EMF, 50ÂHz) exposure based on immune-related enzyme activity and De novo transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2020, 98, 574-584.	1.6	5
7655	The identification of differentially expressed genes in male and female gametophytes of simple thalloid liverwort <i>Pellia endiviifolia</i> sp. B using an RNA-seq approach. <i>Planta</i> , 2020, 252, 21.	1.6	3
7656	Utility of the "omics" in kidney disease: Methods of analysis, sampling considerations, and technical approaches in renal biomarkers. , 2020, , 19-153.		0
7657	Comparison of cadmium uptake and transcriptional responses in roots reveal key transcripts from high and low-cadmium tolerance ryegrass cultivars. <i>Ecotoxicology and Environmental Safety</i> , 2020, 203, 110961.	2.9	17
7658	Fine-tuning the metabolic rewiring and adaptation of translational machinery during an epithelial-mesenchymal transition in breast cancer cells. <i>Cancer &amp; Metabolism</i> , 2020, 8, 8.	2.4	5
7659	Human Cytomegalovirus Long Non-coding RNA1.2 Suppresses Extracellular Release of the Pro-inflammatory Cytokine IL-6 by Blocking NF-ÎB Activation. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 361.	1.8	12
7660	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
7661	Integrated transcriptomic and metabolomic analyses of yellow horn ( <i>Xanthoceras sorbifolia</i> ) in response to cold stress. <i>PLoS ONE</i> , 2020, 15, e0236588.	1.1	14
7662	Transcriptomic and proteomic analyses reveal new insights into the regulation of immune pathways during cyprinid herpesvirus 2 infection in vitro. <i>Fish and Shellfish Immunology</i> , 2020, 106, 167-180.	1.6	11
7663	Identification of the Key Regulatory Genes Involved in Elaborate Petal Development and Specialized Character Formation in <i>Nigella damascena</i> (Ranunculaceae). <i>Plant Cell</i> , 2020, 32, 3095-3112.	3.1	27
7664	Î-6 Polyunsaturated fatty acids (linoleic acid) activate both autophagy and antioxidation in a synergistic feedback loop via TOR-dependent and TOR-independent signaling pathways. <i>Cell Death and Disease</i> , 2020, 11, 607.	2.7	49
7665	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , 2020, 30, 1047-1059.	2.4	32

#	ARTICLE	IF	CITATIONS
7666	Transcription factor CncC potentially regulates the expression of multiple detoxification genes that mediate indoxacarb resistance in <i>Spodoptera litura</i> . <i>Insect Science</i> , 2021, 28, 1426-1438.	1.5	28
7667	Coordinated regulation of anthranilate metabolism and bacterial virulence by the GntR family regulator MpaR in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2020, 114, 857-869.	1.2	10
7669	Deployment of Genetic and Genomic Tools Toward Gaining a Better Understanding of Rice-Xanthomonas oryzae Interactions for Development of Durable Bacterial Blight Resistant Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 1152.	1.7	41
7670	New insights into the Manila clam and PAMPs interaction based on RNA-seq analysis of clam through in vitro challenges with LPS, PGN, and poly(I:C). <i>BMC Genomics</i> , 2020, 21, 531.	1.2	22
7671	Histological, Physiological and Transcriptomic Analysis Reveal Gibberellin-Induced Axillary Meristem Formation in Garlic ( <i>Allium sativum</i> ). <i>Plants</i> , 2020, 9, 970.	1.6	11
7672	Global transcriptome analysis of subterranean pod and seed in peanut ( <i>Arachis hypogaea</i> L.) unravels the complexity of fruit development under dark condition. <i>Scientific Reports</i> , 2020, 10, 13050.	1.6	8
7673	Development and validation of a four-microRNA signature for placenta accreta spectrum: an integrated competing endogenous RNA network analysis. <i>Annals of Translational Medicine</i> , 2020, 8, 919-919.	0.7	15
7674	Long-read assays shed new light on the transcriptome complexity of a viral pathogen. <i>Scientific Reports</i> , 2020, 10, 13822.	1.6	17
7675	Comprehensive Gene Analysis of IgG4-Related Ophthalmic Disease Using RNA Sequencing. <i>Journal of Clinical Medicine</i> , 2020, 9, 3458.	1.0	6
7676	scAPAttrap: identification and quantification of alternative polyadenylation sites from single-cell RNA-seq data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	24
7677	Suppression of the TGF- $\beta$ pathway by a macrolide antibiotic decreases fibrotic responses by ocular fibroblasts <i>in vitro</i> . <i>Royal Society Open Science</i> , 2020, 7, 200441.	1.1	5
7678	Patterns, Profiles, and Parsimony: Dissecting Transcriptional Signatures From Minimal Single-Cell RNA-Seq Output With SALSA. <i>Frontiers in Genetics</i> , 2020, 11, 511286.	1.1	1
7679	Low RIN Value for RNA-Seq Library Construction from Long-Term Stored Seeds: A Case Study of Barley Seeds. <i>Genes</i> , 2020, 11, 1190.	1.0	15
7680	Characterization of sediment toxicity in Shanghai Harbor using toxicity tests and digital gene expression analysis based on clams <i>Ruditapes phillipinarum</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 204, 111065.	2.9	2
7681	Characterization of Drought-Responsive Transcriptome During Seed Germination in Adzuki Bean ( <i>Vigna angularis</i> L.) by PacBio SMRT and Illumina Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 996.	1.1	16
7682	Comparative genomic and transcriptomic analyses of chemosensory genes in the citrus fruit fly <i>Bactrocera (Tetracus) minax</i> . <i>Scientific Reports</i> , 2020, 10, 18068.	1.6	10
7683	$\beta$ -aminobutyric acid induces priming defence against <i>Botrytis cinerea</i> in grapefruit by reducing intercellular redox status that modifies posttranslation of VvNPR1 and its interaction with VvTGA1. <i>Plant Physiology and Biochemistry</i> , 2020, 156, 552-565.	2.8	15
7684	Pulmonary toxicity and RNA sequencing analyses of mouse in response to exposure to cellulose nanofibrils. <i>Inhalation Toxicology</i> , 2020, 32, 388-401.	0.8	3

#	ARTICLE	IF	CITATIONS
7685	A clinically validated human capillary blood transcriptome test for global systems biology studies. <i>BioTechniques</i> , 2020, 69, 289-301.	0.8	15
7686	Post-Transcriptional Expression Control in Platelet Biogenesis and Function. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7614.	1.8	14
7687	Comparative transcriptome of reproductive axis in Chinese indigenous sheep with different FecB genotypes and prolificacies. <i>Animal Reproduction Science</i> , 2020, 223, 106624.	0.5	9
7688	Identification and preliminary characterization of chemosensory-related proteins in the gall fly, <i>Procecidochares utilis</i> by transcriptomic analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100724.	0.4	5
7689	Expression analysis of immune-associated genes in hemocytes of mud crab <i>Scylla paramamosain</i> under low salinity challenge. <i>Fish and Shellfish Immunology</i> , 2020, 107, 16-25.	1.6	9
7690	Coordinated analysis of exon and intron data reveals novel differential gene expression changes. <i>Scientific Reports</i> , 2020, 10, 15669.	1.6	6
7691	RNA-sequencing of the <i>Nyssomyia neivai</i> sialome: a sand fly-vector from a Brazilian endemic area for tegumentary leishmaniasis and pemphigus foliaceus. <i>Scientific Reports</i> , 2020, 10, 17664.	1.6	2
7692	Alternative splicing profiling provides insights into the molecular mechanisms of peanut peg development. <i>BMC Plant Biology</i> , 2020, 20, 488.	1.6	3
7693	Incremental prognostic value and underlying biological pathways of radiomics patterns in medulloblastoma. <i>EBioMedicine</i> , 2020, 61, 103093.	2.7	23
7694	The Globin Gene Family in Arthropods: Evolution and Functional Diversity. <i>Frontiers in Genetics</i> , 2020, 11, 858.	1.1	8
7695	Identification and Biotechnical Potential of a Gcn5-Related N-Acetyltransferase Gene in Enhancing Microalgal Biomass and Starch Production. <i>Frontiers in Plant Science</i> , 2020, 11, 544827.	1.7	1
7696	DoRWA3 from <i>Dendrobium officinale</i> Plays an Essential Role in Acetylation of Polysaccharides. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6250.	1.8	10
7697	Comparative Transcriptome Analysis of Pine Trees Treated with Resistance-Inducing Substances against the Nematode <i>Bursaphelenchus xylophilus</i> . <i>Genes</i> , 2020, 11, 1000.	1.0	9
7698	Evaluating genomic biomarkers associated with resistance or sensitivity to chemotherapy in patients with advanced breast and colorectal cancer. <i>Journal of Oncology Pharmacy Practice</i> , 2020, 27, 107815522095184.	0.5	2
7699	Transcriptome analysis of <i>Aedes aegypti</i> Aag2 cells in response to dengue virus-2 infection. <i>Parasites and Vectors</i> , 2020, 13, 421.	1.0	13
7700	The Effector Repertoire of the Hop Downy Mildew Pathogen <i>Pseudoperonospora humuli</i> . <i>Frontiers in Genetics</i> , 2020, 11, 910.	1.1	9
7701	Global Transcriptome and Correlation Analysis Reveal Cultivar-Specific Molecular Signatures Associated with Fruit Development and Fatty Acid Determination in <i>Camellia oleifera</i> Abel. <i>International Journal of Genomics</i> , 2020, 2020, 1-16.	0.8	10
7702	Sources of variation in cell-type RNA-Seq profiles. <i>PLoS ONE</i> , 2020, 15, e0239495.	1.1	20

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7703	Intermittent leucine pulses during continuous feeding alters novel components involved in skeletal muscle growth of neonatal pigs. <i>Amino Acids</i> , 2020, 52, 1319-1335.	1.2	11
7704	Combined proteomics and transcriptomics reveal the genetic basis underlying the differentiation of skin appendages and immunity in pangolin. <i>Scientific Reports</i> , 2020, 10, 14566.	1.6	4
7705	Optimal reference genes for gene expression analysis in polyploid of <i>Cyprinus carpio</i> and <i>Carassius auratus</i> . <i>BMC Genetics</i> , 2020, 21, 107.	2.7	5
7706	RNA-Seq profiling of microdissected glomeruli identifies potential biomarkers for human IgA nephropathy. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 319, F809-F821.	1.3	15
7707	Comparative Analysis of Mouse Decidualization Models at the Molecular Level. <i>Genes</i> , 2020, 11, 935.	1.0	11
7708	Molecular and metabolomic changes in the proximal colon of pigs infected with <i>Trichuris suis</i> . <i>Scientific Reports</i> , 2020, 10, 12853.	1.6	10
7709	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	13.7	549
7710	Necrotrophic lifestyle of <i>Rhizoctonia solani</i> AG3-PT during interaction with its host plant potato as revealed by transcriptome analysis. <i>Scientific Reports</i> , 2020, 10, 12574.	1.6	21
7711	Poisson-Tweedie mixed-effects model: A flexible approach for the analysis of longitudinal RNA-seq data. <i>Statistical Modelling</i> , 2020, , 1471082X2093601.	0.5	4
7712	<i>Periplaneta americana</i> Extracts Accelerate Liver Regeneration via a Complex Network of Pathways. <i>Frontiers in Pharmacology</i> , 2020, 11, 1174.	1.6	15
7713	RNA-Seq analysis of differentially expressed genes of <i>Staphylococcus epidermidis</i> isolated from postoperative endophthalmitis and the healthy conjunctiva. <i>Scientific Reports</i> , 2020, 10, 14234.	1.6	4
7714	Characterization of the DREBA4-Type Transcription Factor (SIDREBA4), Which Contributes to Heat Tolerance in Tomatoes. <i>Frontiers in Plant Science</i> , 2020, 11, 554520.	1.7	17
7715	Glucocorticoid receptor expression in multiple myeloma patients is a predictor of survival. <i>Leukemia and Lymphoma</i> , 2020, 61, 3493-3497.	0.6	4
7716	Auxin and Its Interaction With Ethylene Control Adventitious Root Formation and Development in Apple Rootstock. <i>Frontiers in Plant Science</i> , 2020, 11, 574881.	1.7	19
7717	Insecticidal and synergistic activity of dsRNAs targeting buprofezin-specific genes against the small brown planthopper, <i>Laodelphax striatellus</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21739.	0.6	5
7718	Integrated analysis of lncRNA, miRNA and mRNA reveals novel insights into the fertility regulation of large white sows. <i>BMC Genomics</i> , 2020, 21, 636.	1.2	11
7719	It's the Little Things (in Viral RNA). <i>MBio</i> , 2020, 11, .	1.8	11
7720	Transcriptomic, Morphological, and Developmental Comparison of Adult Honey Bee Queens ( <i>Apis</i> ) Tj ETQq1 1 0.784314 rgBT /Over 2020, 113, 2581-2587.	0.8	6



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7721	Integration of absolute multi-omics reveals dynamic protein-to-RNA ratios and metabolic interplay within mixed-domain microbiomes. <i>Nature Communications</i> , 2020, 11, 4708.	5.8	28
7722	Transcriptome Analysis of Different Tissues Reveals Key Genes Associated With Galanthamine Biosynthesis in <i>Lycoris longituba</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 519752.	1.7	13
7723	<i>Escherichia coli</i> Increases its ATP Concentration in Weakly Acidic Environments Principally through the Glycolytic Pathway. <i>Genes</i> , 2020, 11, 991.	1.0	22
7724	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020, 21, 239.	3.8	96
7725	Inhibitory effect of <i>Enterobacter cloacae</i> 3J1EC on <i>Aspergillus flavus</i> 3.4408 growth and aflatoxin production. <i>World Mycotoxin Journal</i> , 2020, 13, 259-266.	0.8	3
7726	Peripheral Blood RNA Sequencing Unravels a Differential Signature of Coding and Noncoding Genes by Types of Kidney Allograft Rejection. <i>Kidney International Reports</i> , 2020, 5, 1706-1721.	0.4	15
7727	Transcriptomic analysis reveals somatic embryogenesis-associated signaling pathways and gene expression regulation in maize ( <i>Zea mays</i> L.). <i>Plant Molecular Biology</i> , 2020, 104, 647-663.	2.0	9
7728	Transcriptome profiling revealed potentially important roles of defensive gene expression in the divergence of insect biotypes: a case study with the cereal aphid <i>Sitobion avenae</i> . <i>BMC Genomics</i> , 2020, 21, 546.	1.2	6
7730	Gene expression profiling of <i>Rhododendron pulchrum</i> leaves under drought stress. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	2
7731	2-Methoxy-1,4-naphthoquinone Induces Metabolic Shifts in <i>Penicillium Digitatum</i> Revealed by High-Dimensional Biological Data. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 9697-9706.	2.4	20
7732	A cosmopolitan fungal pathogen of dicots adopts an endophytic lifestyle on cereal crops and protects them from major fungal diseases. <i>ISME Journal</i> , 2020, 14, 3120-3135.	4.4	57
7733	Suppressed ABA signal transduction in the spike promotes sucrose use in the stem and reduces grain number in wheat under water stress. <i>Journal of Experimental Botany</i> , 2020, 71, 7241-7256.	2.4	22
7734	Transcriptome Dynamics during Black and White Sesame ( <i>Sesamum indicum</i> L.) Seed Development and Identification of Candidate Genes Associated with Black Pigmentation. <i>Genes</i> , 2020, 11, 1399.	1.0	25
7735	A Sec-Dependent Secretory Protein of the Huanglongbing-Associated Pathogen Suppresses Hypersensitive Cell Death in <i>Nicotiana benthamiana</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 594669.	1.5	16
7736	Characterization of Metabolites and Transcripts Involved in Flower Pigmentation in <i>Primula vulgaris</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 572517.	1.7	18
7737	More Than a Methanotroph: A Broader Substrate Spectrum for <i>Methylacidiphilum fumariolicum</i> SolV. <i>Frontiers in Microbiology</i> , 2020, 11, 604485.	1.5	20
7738	Next-Generation Sequencing Reveals Downregulation of the Wnt Signaling Pathway in Human Dysmature Cumulus Cells as a Hallmark for Evaluating Oocyte Quality. <i>Reproductive Medicine</i> , 2020, 1, 205-215.	0.3	5
7739	Strandedness during cDNA synthesis, the stranded parameter in htseq-count and analysis of RNA-Seq data. <i>Briefings in Functional Genomics</i> , 2020, 19, 339-342.	1.3	11

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7740	Engineering prokaryotic regulator IrrE to enhance stress tolerance in budding yeast. <i>Biotechnology for Biofuels</i> , 2020, 13, 193.	6.2	13
7741	Comparative transcriptome analysis of Sweetpotato ( <i>Ipomoea batatas</i> L.) and discovery of genes involved in starch biosynthesis. <i>Plant Biotechnology Reports</i> , 2020, 14, 713-723.	0.9	2
7742	Transcriptomic analysis of the ark shell <i>Scapharca kagoshimensis</i> : De novo assembly and identification of genes and pathways involved growth. <i>Aquaculture Reports</i> , 2020, 18, 100522.	0.7	5
7743	Data-Driven Statistical Approaches for Omics Data Analysis. , 2020, , 429-459.		0
7744	EGFR-rich extracellular vesicles derived from highly metastatic nasopharyngeal carcinoma cells accelerate tumour metastasis through PI3K/AKT pathway-suppressed ROS. <i>Journal of Extracellular Vesicles</i> , 2020, 10, e12003.	5.5	25
7745	Algorithms for ribosome traffic engineering and their potential in improving host cells' titer and growth rate. <i>Scientific Reports</i> , 2020, 10, 21202.	1.6	15
7746	Comparative transcriptome analysis of three gonadal development stages reveals potential genes involved in gametogenesis of the fluted giant clam ( <i>Tridacna squamosa</i> ). <i>BMC Genomics</i> , 2020, 21, 872.	1.2	12
7747	Transcriptome changes and polymyxin resistance of acid-adapted <i>Escherichia coli</i> O157:H7 ATCC 43889. <i>Gut Pathogens</i> , 2020, 12, 52.	1.6	2
7748	Delayed Comparison and Apriori Algorithm (DCAA): A Tool for Discovering Protein-Protein Interactions From Time-Series Phosphoproteomic Data. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 606570.	1.6	2
7749	RNA-Seq Whole Transcriptome Analysis of Bovine Mammary Epithelial Cells in Response to Intracellular <i>Staphylococcus aureus</i> . <i>Frontiers in Veterinary Science</i> , 2020, 7, 642.	0.9	9
7750	Engineering of a genome-reduced strain <i>Bacillus amyloliquefaciens</i> for enhancing surfactin production. <i>Microbial Cell Factories</i> , 2020, 19, 223.	1.9	34
7751	Efficient and cost-effective bacterial mRNA sequencing from low input samples through ribosomal RNA depletion. <i>BMC Genomics</i> , 2020, 21, 717.	1.2	22
7752	Gene Expression and miRNA Regulation Changes in Leaves of Rice Backcross Introgression Lines. <i>Agronomy</i> , 2020, 10, 1381.	1.3	0
7753	Sexual Differences in Physiological and Transcriptional Responses to Salinity Stress of <i>Salix linearistipularis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 517962.	1.7	13
7754	Genome-wide identification of candidate genes related to disease resistance and high biomass in tetraploid <i>Paulownia</i> . <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	3
7755	Comparative physiological and transcriptomic analysis of pear leaves under distinct training systems. <i>Scientific Reports</i> , 2020, 10, 18892.	1.6	5
7756	Genomic analysis of circular RNAs in heart. <i>BMC Medical Genomics</i> , 2020, 13, 167.	0.7	16
7757	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	11

#	ARTICLE	IF	CITATIONS
7758	Genome-Wide Characterization of the HSP20 Gene Family Identifies Potential Members Involved in Temperature Stress Response in Apple. <i>Frontiers in Genetics</i> , 2020, 11, 609184.	1.1	27
7759	PUR1± Promotes the Transcriptional Activation of PCK2 in Oesophageal Squamous Cell Carcinoma Cells. <i>Genes</i> , 2020, 11, 1301.	1.0	7
7760	Hydrogen peroxide is involved in strigolactone induced low temperature stress tolerance in rape seedlings ( <i>Brassica rapa</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 157, 402-415.	2.8	56
7761	Pectoral muscle transcriptome analyses reveal high-altitude adaptations in Tibetan chickens. <i>Animal Biology</i> , 2020, 70, 385-400.	0.6	3
7762	Lipidomic analyses reveal enhanced lipolysis in planthoppers feeding on resistant host plants. <i>Science China Life Sciences</i> , 2021, 64, 1502-1521.	2.3	12
7763	Dimethylformamide Inhibits Fungal Growth and Aflatoxin B1 Biosynthesis in <i>Aspergillus flavus</i> by Down-Regulating Glucose Metabolism and Amino Acid Biosynthesis. <i>Toxins</i> , 2020, 12, 683.	1.5	9
7764	Transcriptomics Uncovers the Response of Anammox Bacteria to Dissolved Oxygen Inhibition and the Subsequent Recovery Mechanism. <i>Environmental Science &amp; Technology</i> , 2020, 54, 14674-14685.	4.6	40
7765	Candidate resistance genes selection and transcriptome analysis for the early responses to <i>Plasmopara viticola</i> infection in grape cultivars. <i>Journal of Plant Pathology</i> , 2020, 102, 857-869.	0.6	6
7766	Knockdown of CTRP6 reduces the deposition of intramuscular and subcutaneous fat in pigs via different signaling pathways. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2020, 1865, 158729.	1.2	9
7767	Characterization and transcriptomic basis of biofilm formation by <i>Lactobacillus plantarum</i> J26 isolated from traditional fermented dairy products. <i>LWT - Food Science and Technology</i> , 2020, 125, 109333.	2.5	24
7768	Transcriptome profile analysis of two <i>Vicia faba</i> cultivars with contrasting salinity tolerance during seed germination. <i>Scientific Reports</i> , 2020, 10, 7250.	1.6	23
7769	Comparative Transcriptomic Analysis to Identify the Genes Related to Delayed Gland Morphogenesis in <i>Gossypium bickii</i> . <i>Genes</i> , 2020, 11, 472.	1.0	7
7770	Casparian strip membrane domain proteins in <i>Gossypium arboreum</i> : genome-wide identification and negative regulation of lateral root growth. <i>BMC Genomics</i> , 2020, 21, 340.	1.2	4
7771	Optimization of cultivation conditions for efficient production of carotenoid-rich DHA oil by <i>Schizochytrium</i> sp. S31. <i>Process Biochemistry</i> , 2020, 94, 190-197.	1.8	21
7772	DiCoExpress: a tool to process multifactorial RNAseq experiments from quality controls to co-expression analysis through differential analysis based on contrasts inside GLM models. <i>Plant Methods</i> , 2020, 16, 68.	1.9	29
7773	The G123 rice mutant, carrying a mutation in SE13, presents alterations in the expression patterns of photosynthetic and major flowering regulatory genes. <i>PLoS ONE</i> , 2020, 15, e0233120.	1.1	6
7774	Urinary Sediment Transcriptomic and Longitudinal Data to Investigate Renal Function Decline in Type 1 Diabetes. <i>Frontiers in Endocrinology</i> , 2020, 11, 238.	1.5	7
7775	Arginine Deiminase and Biotin Metabolism Signaling Pathways Play an Important Role in Human-Derived Serotype V, ST1 <i>Streptococcus agalactiae</i> Virulent Strain upon Infected Tilapia. <i>Animals</i> , 2020, 10, 849.	1.0	1

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7776	Transcriptome analysis reveals metabolic regulation mechanism of microalga <i>Chlorella pyrenoidosa</i> in response to the mixed culture with yeast <i>Yarrowia lipolytica</i> . <i>Journal of Applied Phycology</i> , 2020, 32, 2841-2849.	1.5	5
7777	Comparison of the Toxicity Effects of Tris(1,3-dichloro-2-propyl)phosphate (TDCIPP) with Tributyl Phosphate (TNBP) Reveals the Mechanism of the Apoptosis Pathway in Asian Freshwater Clams ( <i>Corbicula fluminea</i> ). <i>Environmental Science &amp; Technology</i> , 2020, 54, 6850-6858.	4.6	31
7778	Identification of biosynthetic pathways involved in flavonoid production in licorice by RNA-seq based transcriptome analysis. <i>Plant Growth Regulation</i> , 2020, 92, 15-28.	1.8	13
7779	Transcriptome analysis reveals rapid defence responses in wheat induced by phytotoxic aphid <i>Schizaphis graminum</i> feeding. <i>BMC Genomics</i> , 2020, 21, 339.	1.2	23
7780	Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving -Omics Era. <i>Plants</i> , 2020, 9, 591.	1.6	25
7781	Dark-rearing uncovers novel gene expression patterns in an obligate cave-dwelling fish. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 518-529.	0.6	6
7782	The Sophisticated Transcriptional Response Governed by Transposable Elements in Human Health and Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3201.	1.8	8
7783	The Interaction of lncRNA XLOC-2222497, AKR1C1, and Progesterone in Porcine Endometrium and Pregnancy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3232.	1.8	11
7784	Phagosomal removal of fungal melanin reprograms macrophage metabolism to promote antifungal immunity. <i>Nature Communications</i> , 2020, 11, 2282.	5.8	68
7785	piRNA and Transposon Dynamics in <i>Drosophila</i> : A Female Story. <i>Genome Biology and Evolution</i> , 2020, 12, 931-947.	1.1	20
7786	GATA-type transcription factor MrNsdD regulates dimorphic transition, conidiation, virulence and microsclerotium formation in the entomopathogenic fungus <i>Metarhizium rileyi</i> . <i>Microbial Biotechnology</i> , 2020, 13, 1489-1501.	2.0	6
7787	Transcriptomic analysis of poc1, a mitochondrial pentatricopeptide repeat protein mutant in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 209.	1.6	9
7788	Tree peony variegated flowers show a small insertion in the F3 <sup>TMH</sup> gene of the acyanic flower parts. <i>BMC Plant Biology</i> , 2020, 20, 211.	1.6	20
7789	Analyses of chemosensory genes provide insight into the evolution of behavioral differences to phytochemicals in <i>Bactrocera</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106858.	1.2	12
7790	Whole genome-wide chromosome fusion and new gene birth in the <i>Monopterus albus</i> genome. <i>Cell and Bioscience</i> , 2020, 10, 67.	2.1	16
7791	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4432-4439.	1.8	10
7792	Skipping of exon 10 in <i>Axl</i> pre-mRNA regulated by PTBP1 mediates invasion and metastasis process of liver cancer cells. <i>Theranostics</i> , 2020, 10, 5719-5735.	4.6	35
7793	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1330-1341.	1.9	16

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7794	Integrated omics in <i>Drosophila</i> uncover a circadian kinome. <i>Nature Communications</i> , 2020, 11, 2710.	5.8	23
7795	Isolation and Identification of Bovine Preadipocytes and Screening of MicroRNAs Associated with Adipogenesis. <i>Animals</i> , 2020, 10, 818.	1.0	19
7796	Transcriptomics in Toxicogenomics, Part II: Preprocessing and Differential Expression Analysis for High Quality Data. <i>Nanomaterials</i> , 2020, 10, 903.	1.9	31
7797	RNA-Seq transcriptomic analyses of <i>Antrodia camphorata</i> determine antroquinol and antrodin C biosynthetic mechanisms in their situ extractive fermentation. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 4252-4262.	1.7	7
7798	Characterization of fosfomycin heteroresistance among multidrug-resistant <i>Escherichia coli</i> isolates from hospitalized patients in Rio de Janeiro, Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 584-593.	0.9	8
7799	Transcriptome Analysis of Gene Expression in <i>Demococcus abyssii</i> HZAU 226 under Lysozyme Stress. <i>Microorganisms</i> , 2020, 8, 707.	1.6	10
7800	Weighted Gene Correlation Network Meta-Analysis Reveals Functional Candidate Genes Associated with High- and Sub-Fertile Reproductive Performance in Beef Cattle. <i>Genes</i> , 2020, 11, 543.	1.0	14
7801	Transcriptome analysis of grass carp ( <i>Ctenopharyngodon idella</i> ) between fast- and slow-growing fish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100688.	0.4	27
7802	Transcriptional Analysis Reveals Key Genes in the Pathogenesis of Nifedipine-Induced Gingival Overgrowth. <i>Analytical Cellular Pathology</i> , 2020, 2020, 1-11.	0.7	3
7803	Transcriptional analyses reveal the molecular mechanism governing shade tolerance in the invasive plant <i>Solidago canadensis</i> . <i>Ecology and Evolution</i> , 2020, 10, 4391-4406.	0.8	11
7804	EDeepSSP: Explainable deep neural networks for exact splice sites prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050024.	0.3	12
7805	Non-coding RNAs in Nervous System Development and Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 273.	1.8	43
7806	Comparative analyses of leaf cuticular lipids of two succulent xerophytes of the Ordos Plateau ( <i>Gobi</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf <i>Experimental Botany</i> , 2020, 177, 104129.	2.0	5
7807	Ribosome profiling in plants: what is not lost in translation?. <i>Journal of Experimental Botany</i> , 2020, 71, 5323-5332.	2.4	21
7808	Degradation of MicroRNA miR-466d-3p by Japanese Encephalitis Virus NS3 Facilitates Viral Replication and Interleukin-1 $\beta$ Expression. <i>Journal of Virology</i> , 2020, 94, .	1.5	11
7809	Comparing transcriptome expression profiles to reveal the mechanisms of salt tolerance and exogenous glycine betaine mitigation in maize seedlings. <i>PLoS ONE</i> , 2020, 15, e0233616.	1.1	25
7810	Genome-Wide Analysis of Basic Helix-Loop-Helix Transcription Factors to Elucidate Candidate Genes Related to Fruit Ripening and Stress in Banana ( <i>Musa acuminata</i> L. AAA Group, cv. Cavendish). <i>Frontiers in Plant Science</i> , 2020, 11, 650.	1.7	15
7811	Adipogenesis, Osteogenesis, and Chondrogenesis of Human Mesenchymal Stem/Stromal Cells: A Comparative Transcriptome Approach. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 561.	1.8	73

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7812	Distinct long non-coding RNA and mRNA expression profiles in the hippocampus of an attention deficit hyperactivity disorder model in spontaneously hypertensive rats and control wistar Kyoto rats. <i>Brain Research Bulletin</i> , 2020, 161, 177-196.	1.4	5
7813	Pheromone biosynthetic pathway and chemoreception proteins in sex pheromone gland of <i>Eogystia hippophaecolus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100702.	0.4	1
7814	Lysophosphatidic Acid Increases Maturation of Brush Borders and SGLT1 Activity in MYO5B-deficient Mice, a Model of Microvillus Inclusion Disease. <i>Gastroenterology</i> , 2020, 159, 1390-1405.e20.	0.6	23
7815	Comparative transcriptome analysis between a resistant and a susceptible Chinese cabbage in response to <i>Hyaloperonospora brassicae</i> . <i>Plant Signaling and Behavior</i> , 2020, 15, 1777373.	1.2	7
7816	Rare and <i>de novo</i> duplications containing <i>SHOX</i> in clubfoot. <i>Journal of Medical Genetics</i> , 2020, 57, 851-857.	1.5	8
7817	Identification of Functional SSR Markers in Freshwater Ornamental Shrimps <i>Neocaridina denticulata</i> Using Transcriptome Sequencing. <i>Marine Biotechnology</i> , 2020, 22, 772-785.	1.1	15
7818	Handling multi-mapped reads in RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1569-1576.	1.9	44
7819	The involvement of the phytohormone ethylene in the adaptation of <i>Arabidopsis</i> rosettes to enhanced atmospheric carbon dioxide concentrations. <i>Environmental and Experimental Botany</i> , 2020, 177, 104128.	2.0	5
7820	Transcriptomic analysis of <i>Listeria monocytogenes</i> under pulsed magnetic field treatment. <i>Food Research International</i> , 2020, 133, 109195.	2.9	19
7821	Introducing <a href="http://www.axolotl-omics.org">www.axolotl-omics.org</a> – an integrated -omics data portal for the axolotl research community. <i>Experimental Cell Research</i> , 2020, 394, 112143.	1.2	18
7822	Transcriptome profiling of the flowering transition in saffron ( <i>Crocus sativus</i> L.). <i>Scientific Reports</i> , 2020, 10, 9680.	1.6	28
7823	Metabolic mechanisms of <i>Coilia nasus</i> in the natural food intake state during migration. <i>Genomics</i> , 2020, 112, 3294-3305.	1.3	9
7824	A rare single nucleotide variant in <i>Pm5e</i> confers powdery mildew resistance in common wheat. <i>New Phytologist</i> , 2020, 228, 1011-1026.	3.5	92
7825	RNA Sequencing for Gene Expression Profiles in Peripheral Blood Mononuclear Cells with Ankylosing Spondylitis RNA. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3
7826	Colanic acid biosynthesis in <i>Escherichia coli</i> is dependent on lipopolysaccharide structure and glucose availability. <i>Microbiological Research</i> , 2020, 239, 126527.	2.5	26
7827	Unveiling the complexity of the litchi transcriptome and pericarp browning by single-molecule long-read sequencing. <i>Postharvest Biology and Technology</i> , 2020, 168, 111252.	2.9	11
7828	Genome-wide DNA methylation analysis of paulownia with phytoplasma infection. <i>Gene</i> , 2020, 755, 144905.	1.0	3
7829	Comparative analysis of the ovarian transcriptome reveals novel insights into fertility differences in Large White sows. <i>Genes and Genomics</i> , 2020, 42, 715-725.	0.5	6

#	ARTICLE	IF	CITATIONS
7830	Characterization of antiviral immune response induced by poly(I:C) in macrophages of farmed large yellow croaker ( <i>Larimichthys crocea</i> ). <i>Fish and Shellfish Immunology</i> , 2020, 104, 663-672.	1.6	11
7831	Transcriptome Analysis by RNA-Seq Reveals Genes Related to Plant Height in Two Sets of Parent-hybrid Combinations in Easter lily ( <i>Lilium longiflorum</i> ). <i>Scientific Reports</i> , 2020, 10, 9082.	1.6	19
7832	Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
7833	Triphenyltin chloride reduces the development of rat adrenal cortex during puberty. <i>Food and Chemical Toxicology</i> , 2020, 143, 111479.	1.8	7
7834	Metagenomics as a Tool To Monitor Reclaimed-Water Quality. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
7835	Gene coexpression network analysis and tissue-specific profiling of gene expression in jute ( <i>Corchorus capsularis</i> L.). <i>BMC Genomics</i> , 2020, 21, 406.	1.2	7
7836	The Brittle Rachis Trait in Species Belonging to the Triticeae and Its Controlling Genes <i>Btr1</i> and <i>Btr2</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1000.	1.7	12
7837	Identification and Distribution of NBS-Encoding Resistance Genes of <i>Dactylis glomerata</i> L. and Its Expression Under Abiotic and Biotic Stress. <i>Biochemical Genetics</i> , 2020, 58, 824-847.	0.8	7
7838	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	13.5	508
7839	Risk assessment of cardiotoxicity to zebrafish ( <i>Danio rerio</i> ) by environmental exposure to triclosan and its derivatives. <i>Environmental Pollution</i> , 2020, 265, 114995.	3.7	25
7840	Heterotrophic Thaumarchaea with Small Genomes Are Widespread in the Dark Ocean. <i>MSystems</i> , 2020, 5, .	1.7	50
7841	Metabolic regulation of ethanol-type fermentation of anaerobic acidogenesis at different pH based on transcriptome analysis of <i>Ethanoligenens harbinense</i> . <i>Biotechnology for Biofuels</i> , 2020, 13, 101.	6.2	10
7842	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	5.8	43
7843	Caloric restriction attenuates C57BL/6 mouse lung injury and extra-pulmonary toxicity induced by real ambient particulate matter exposure. <i>Particle and Fibre Toxicology</i> , 2020, 17, 22.	2.8	22
7844	Oxidative stress induces monocyte-myofibroblast transdifferentiation through p38 in pancreatic ductal adenocarcinoma. <i>Clinical and Translational Medicine</i> , 2020, 10, e41.	1.7	34
7845	Cucumber <i>Fusarium</i> wilt resistance induced by intercropping with celery differs from that induced by the cucumber genotype and is related to sulfur-containing allelochemicals. <i>Scientia Horticulturae</i> , 2020, 271, 109475.	1.7	12
7846	Identification of population-level differentially expressed genes in one-phenotype data. <i>Bioinformatics</i> , 2020, 36, 4283-4290.	1.8	7
7847	Comparison of the Transcriptome of the Ovine Mammary Gland in Lactating and Non-lactating Small-Tailed Han Sheep. <i>Frontiers in Genetics</i> , 2020, 11, 472.	1.1	13

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7848	Transcriptomic Evidence Reveals the Molecular Basis for Functional Differentiation of Hemocytes in a Marine Invertebrate, <i>Crassostrea gigas</i> . <i>Frontiers in Immunology</i> , 2020, 11, 911.	2.2	24
7849	Exploring DNA Variant Segregation Types Enables Mapping Loci for Recessive Phenotypic Suppression of Columnar Growth in Apple. <i>Frontiers in Plant Science</i> , 2020, 11, 692.	1.7	5
7850	Transcription Factor GmWRKY142 Confers Cadmium Resistance by Up-Regulating the Cadmium Tolerance 1-Like Genes. <i>Frontiers in Plant Science</i> , 2020, 11, 724.	1.7	44
7851	Genome-wide analysis of long noncoding RNA profiles in Vero cells infected with porcine epidemic diarrhea virus. <i>Archives of Virology</i> , 2020, 165, 1969-1977.	0.9	2
7852	Transcriptomic analysis of resistant and susceptible cabbage lines reveals differential expressions and candidate genes involved in cabbage early responses to black rot. <i>3 Biotech</i> , 2020, 10, 308.	1.1	7
7853	The atypical chemokine receptor ACKR3/CXCR7 is a broad-spectrum scavenger for opioid peptides. <i>Nature Communications</i> , 2020, 11, 3033.	5.8	74
7854	A Simple, Cost-Effective, and Robust Method for rRNA Depletion in RNA-Sequencing Studies. <i>MBio</i> , 2020, 11, .	1.8	72
7855	Transcriptomic and metabolomic analyses of <i>Lycium ruthenicum</i> and <i>Lycium barbarum</i> fruits during ripening. <i>Scientific Reports</i> , 2020, 10, 4354.	1.6	17
7856	RNA Sequencing-Associated Study Identifies <i>GmDRR1</i> as Positively Regulating the Establishment of Symbiosis in Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 798-807.	1.4	10
7858	Genomic, transcriptomic, and metabolic characterizations of <i>Escherichia coli</i> adapted to branched-chain higher alcohol tolerance. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4171-4184.	1.7	7
7859	Comparative RNA sequencing based transcriptome profiling of regular bearing and alternate bearing mango ( <i>Mangifera indica</i> L.) varieties reveals novel insights into the regulatory mechanisms underlying alternate bearing. <i>Biotechnology Letters</i> , 2020, 42, 1035-1050.	1.1	16
7860	Global Transcriptome Profiling of <i>Enterobacter</i> Strain NRS-1 in Response to Hydrogen Peroxide Stress Treatment. <i>Applied Biochemistry and Biotechnology</i> , 2020, 191, 1638-1652.	1.4	3
7861	<i>Bacillus velezensis</i> LG37: transcriptome profiling and functional verification of GlnK and MnrA in ammonia assimilation. <i>BMC Genomics</i> , 2020, 21, 215.	1.2	6
7862	Effects of fenclorim on rice physiology, gene transcription and pretilachlor detoxification ability. <i>BMC Plant Biology</i> , 2020, 20, 100.	1.6	27
7863	Identification of small RNAs involved in nitrogen fixation in <i>Anabaena</i> sp. PCC 7120 based on RNA-seq under steady state conditions. <i>Annals of Microbiology</i> , 2020, 70, .	1.1	5
7864	Tetrahydrobiopterin Plays a Functionally Significant Role in Lipogenesis in the Oleaginous Fungus <i>Mortierella alpina</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 250.	1.5	7
7865	Aberrant hydroxymethylation of <i>ANGPTL4</i> is associated with selective intrauterine growth restriction in monozygotic twin pregnancies. <i>Epigenetics</i> , 2020, 15, 887-899.	1.3	10
7866	Enhancer occlusion transcripts regulate the activity of human enhancer domains via transcriptional interference: a computational perspective. <i>Nucleic Acids Research</i> , 2020, 48, 3435-3454.	6.5	5



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7867	Transcriptomic and Exometabolomic Profiling Reveals Antagonistic and Defensive Modes of <i>Clonostachys rosea</i> Action Against <i>Fusarium graminearum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 842-858.	1.4	23
7868	Evaluation of Seven Different RNA-Seq Alignment Tools Based on Experimental Data from the Model Plant <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 1720.	1.8	29
7869	Identification and phylogenetics of <i>Spodoptera frugiperda</i> chemosensory proteins based on antennal transcriptome data. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100680.	0.4	19
7870	Effects of prenatal bisphenol A exposure on the hepatic transcriptome and proteome in rat offspring. <i>Science of the Total Environment</i> , 2020, 720, 137568.	3.9	20
7871	Intravenous delivery of microRNA-133b along with Argonaute-2 enhances spinal cord recovery following cervical contusion in mice. <i>Spine Journal</i> , 2020, 20, 1138-1151.	0.6	10
7872	Classification models for Invasive Ductal Carcinoma Progression, based on gene expression data-trained supervised machine learning. <i>Scientific Reports</i> , 2020, 10, 4113.	1.6	23
7873	pyBedGraph: a python package for fast operations on 1D genomic signal tracks. <i>Bioinformatics</i> , 2020, 36, 3234-3235.	1.8	1
7874	Transcriptome analysis of metabolic pathways associated with oil accumulation in developing seed kernels of <i>Styrax tonkinensis</i> , a woody biodiesel species. <i>BMC Plant Biology</i> , 2020, 20, 121.	1.6	21
7875	Multiple Small RNAs Interact to Co-regulate Ethanol Tolerance in <i>Zymomonas mobilis</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 155.	2.0	9
7876	Skewed X-Chromosome Inactivation and Compensatory Upregulation of Escape Genes Precludes Major Clinical Symptoms in a Female With a Large Xq Deletion. <i>Frontiers in Genetics</i> , 2020, 11, 101.	1.1	19
7877	Whole-Genome Uterine Artery Transcriptome Profiling and Alternative Splicing Analysis in Rat Pregnancy. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2079.	1.8	3
7878	A quinone-dependent dehydrogenase and two NADPH-dependent aldo/keto reductases detoxify deoxynivalenol in wheat via epimerization in a <i>Devolia</i> strain. <i>Food Chemistry</i> , 2020, 321, 126703.	4.2	40
7879	Comparative high-throughput analysis of the <i>Trypanosoma cruzi</i> response to organometallic compounds. <i>Metallomics</i> , 2020, 12, 813-828.	1.0	10
7880	The <i>Litsea</i> genome and the evolution of the laurel family. <i>Nature Communications</i> , 2020, 11, 1675.	5.8	80
7881	Epigenomic Regulatory Mechanism in Vegetative Phase Transition of <i>Malus hupehensis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4812-4829.	2.4	10
7882	RNA-Seq based transcriptome analysis reveals the molecular mechanism of triterpenoid biosynthesis in <i>Glycyrrhiza glabra</i> . <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020, 30, 127102.	1.0	12
7883	Maternal exposure to zearalenone in masculinization window affects the fetal Leydig cell development in rat male fetus. <i>Environmental Pollution</i> , 2020, 263, 114357.	3.7	10
7884	High dose of dietary vitamin D3 modulated the yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) splenic innate immune response after <i>Edwardsiella ictaluri</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 100, 41-48.	1.6	17

#	ARTICLE	IF	CITATIONS
7885	Novel insights into cardiac regeneration based on differential fetal and adult ovine heart transcriptomic analysis. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2020, 318, H994-H1007.	1.5	11
7886	Physiological and transcriptomic analyses reveal the mechanisms underlying the salt tolerance of <i>Zoysia japonica</i> Steud. <i>BMC Plant Biology</i> , 2020, 20, 114.	1.6	21
7887	Loci associated with variation in gene expression and growth in juvenile salmon are influenced by the presence of a growth hormone transgene. <i>BMC Genomics</i> , 2020, 21, 185.	1.2	5
7888	Probe Signal Values in mRNA Arrays Imply an Excessive Involvement of Neutrophil FCGR1 in Tuberculosis. <i>Frontiers in Medicine</i> , 2020, 7, 19.	1.2	1
7889	Identification of the Differentially Expressed Genes of Muscle Growth and Intramuscular Fat Metabolism in the Development Stage of Yellow Broilers. <i>Genes</i> , 2020, 11, 244.	1.0	17
7890	Investigation of a Novel Salt Stress-Responsive Pathway Mediated by Arabidopsis DEAD-Box RNA Helicase Gene AtRH17 Using RNA-Seq Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1595.	1.8	15
7891	Identification of a combination of transcription factors that synergistically increases endothelial cell barrier resistance. <i>Scientific Reports</i> , 2020, 10, 3886.	1.6	40
7892	MIXnorm: normalizing RNA-seq data from formalin-fixed paraffin-embedded samples. <i>Bioinformatics</i> , 2020, 36, 3401-3408.	1.8	6
7893	Genome Architecture Facilitates Phenotypic Plasticity in the Honeybee ( <i>Apis mellifera</i> ). <i>Molecular Biology and Evolution</i> , 2020, 37, 1964-1978.	3.5	30
7894	A transcriptomic view of the ability of nascent hexaploid wheat to tolerate aneuploidy. <i>BMC Plant Biology</i> , 2020, 20, 97.	1.6	10
7895	Whole Transcriptome Analysis of Mesenchyme Tissue in Sika Deer Antler Revealed the CeRNAs Regulatory Network Associated With Antler Development. <i>Frontiers in Genetics</i> , 2019, 10, 1403.	1.1	16
7896	Physiological and Transcriptome Profiling Analyses Reveal Important Roles of Coronatine in Improving Drought Tolerance of Tobacco. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1346-1358.	2.8	14
7897	Integrative transcriptomics and proteomics analysis constructs a new molecular model for ovule abortion in the female-sterile line of <i>Pinus tabulaeformis</i> Carr.. <i>Plant Science</i> , 2020, 294, 110462.	1.7	8
7898	Diagnosis of Mendelian Inherited Disorders in Dogs: Brief Literature Review. <i>Bulletin of University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca: Veterinary Medicine</i> , 2020, 77, 9-14.	0.1	0
7899	Transcriptome analysis of the <i>Sepia pharaonis</i> : Identification of low salinity stress-related information and microsatellite markers. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100705.	0.4	3
7900	Glutathione peroxidase 5 deficiency induces lipid metabolism regulated by reactive oxygen species in <i>Chlamydomonas reinhardtii</i> . <i>Microbial Pathogenesis</i> , 2020, 147, 104358.	1.3	5
7901	Transcriptome and cell wall degrading enzyme-related gene analysis of <i>Pestalotiopsis neglecta</i> in response to sodium phophorbide a. <i>Pesticide Biochemistry and Physiology</i> , 2020, 169, 104639.	1.6	5
7902	Expression regulation of MALATE SYNTHASE involved in glyoxylate cycle during protocorm development in <i>Phalaenopsis aphrodite</i> (Orchidaceae). <i>Scientific Reports</i> , 2020, 10, 10123.	1.6	8

#	ARTICLE	IF	CITATIONS
7903	Functional Genomics of Healthy and Pathological Fetal Membranes. <i>Frontiers in Physiology</i> , 2020, 11, 687.	1.3	1
7904	Tobacco RNA-dependent RNA polymerase 1 affects the expression of defence-related genes in <i>Nicotiana benthamiana</i> upon Tomato leaf curl Gujarat virus infection. <i>Planta</i> , 2020, 252, 11.	1.6	16
7905	Robust principal component analysis for accurate outlier sample detection in RNA-Seq data. <i>BMC Bioinformatics</i> , 2020, 21, 269.	1.2	47
7906	An embryo lethal transgenic line manifests global expression changes and elevated protein/oil ratios in heterozygous soybean plants. <i>PLoS ONE</i> , 2020, 15, e0233721.	1.1	2
7907	Comparison of Normalization Methods for Analysis of TempO-Seq Targeted RNA Sequencing Data. <i>Frontiers in Genetics</i> , 2020, 11, 594.	1.1	13
7908	Light-harvesting chlorophyll a/b-binding protein-coding genes in jatropha and the comparison with castor, cassava and arabidopsis. <i>PeerJ</i> , 2020, 8, e8465.	0.9	18
7909	Fulvic acid increases forage legume growth inducing preferential up-regulation of nodulation and signalling-related genes. <i>Journal of Experimental Botany</i> , 2020, 71, 5689-5704.	2.4	19
7910	Effect of germination potential on storage lipids and transcriptome changes in premature developing seeds of oilseed rape ( <i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 2839-2852.	1.8	5
7911	Knocking Out Non-muscle Myosin II in Retinal Ganglion Cells Promotes Long-Distance Optic Nerve Regeneration. <i>Cell Reports</i> , 2020, 31, 107537.	2.9	33
7912	Global Reprogramming of Gene Transcription in <i>Trichoderma reesei</i> by Overexpressing an Artificial Transcription Factor for Improved Cellulase Production and Identification of Ypr1 as an Associated Regulator. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 649.	2.0	6
7913	A censored Poisson model based approach to the analysis of RNA-seq data. <i>Quantitative Biology</i> , 2020, 8, 155-171.	0.3	1
7914	Maternal ageing causes changes in DNA methylation and gene expression profiles in mouse oocytes. <i>Zygote</i> , 2020, 28, 360-366.	0.5	4
7915	A Unique Energy-Saving Strategy during Hibernation Revealed by Multi-Omics Analysis in the Chinese Alligator. <i>IScience</i> , 2020, 23, 101202.	1.9	12
7916	Microplastics negatively impact embryogenesis and modulate the immune response of the marine medaka <i>Oryzias melastigma</i> . <i>Marine Pollution Bulletin</i> , 2020, 158, 111349.	2.3	44
7917	Future of Probiotics and Prebiotics and the Implications for Early Career Researchers. <i>Frontiers in Microbiology</i> , 2020, 11, 1400.	1.5	30
7918	Different nitrogen forms differentially affect Cd uptake and accumulation in dwarf Polish wheat ( <i>Triticum polonicum</i> L.) seedlings. <i>Journal of Hazardous Materials</i> , 2020, 400, 123209.	6.5	35
7919	Expansions of chemosensory gene orthologs among selected tsetse fly species and their expressions in <i>Glossina morsitans morsitans</i> tsetse fly. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008341.	1.3	9
7920	Transcriptional analysis for the difference in carotenoids accumulation in flesh and peel of white-fleshed loquat fruit. <i>PLoS ONE</i> , 2020, 15, e0233631.	1.1	5

#	ARTICLE	IF	CITATIONS
7921	Nitrate deficiency decreased photosynthesis and oxidation-reduction processes, but increased cellular transport, lignin biosynthesis and flavonoid metabolism revealed by RNA-Seq in <i>Oryza sativa</i> leaves. <i>PLoS ONE</i> , 2020, 15, e0235975.	1.1	25
7922	Transcriptome Analysis Reveals Potential Roles of Abscisic Acid and Polyphenols in Adaptation of <i>Onobrychis viciifolia</i> to Extreme Environmental Conditions in the Qinghai-Tibetan Plateau. <i>Biomolecules</i> , 2020, 10, 967.	1.8	7
7924	Whole-genome landscape of H3K4me3, H3K36me3 and H3K9ac and their association with gene expression during <i>Paulownia witchesâ€™ broom</i> disease infection and recovery processes. <i>3 Biotech</i> , 2020, 10, 336.	1.1	7
7925	Comparative transcriptome analysis on four types of gonadal tissues of blotched snakehead ( <i>Channa</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 100708.	0.4	4
7926	Breathing fresh air into respiratory research with single-cell RNA sequencing. <i>European Respiratory Review</i> , 2020, 29, 200060.	3.0	11
7927	Growth performance and transcriptomic response of <i>Calliptamus abbreviatus</i> Ikonn (Orthoptera:) Tj ETQq1 1 0.784314 rgBT /Overl 605-612.	0.5	2
7928	Comparative transcriptomic and physiological analyses of contrasting hybrid cultivars ND476 and ZX978 identify important differentially expressed genes and pathways regulating drought stress tolerance in maize. <i>Genes and Genomics</i> , 2020, 42, 937-955.	0.5	5
7929	Integrated analysis on biochemical profiling and transcriptome revealed nitrogen-driven difference in accumulation of saponins in a medicinal plant <i>Panax notoginseng</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 154, 564-580.	2.8	15
7930	Association between Serum Essential Metal Elements and the Risk of Schizophrenia in China. <i>Scientific Reports</i> , 2020, 10, 10875.	1.6	22
7931	Responses of Soybean Genes in the Substituted Segments of Segment Substitution Lines Following a <i>Xanthomonas</i> Infection. <i>Frontiers in Plant Science</i> , 2020, 11, 972.	1.7	5
7932	mTORC1 coordinates an immediate unfolded protein response-related transcriptome in activated B cells preceding antibody secretion. <i>Nature Communications</i> , 2020, 11, 723.	5.8	72
7933	The developmental dynamics of the sweet sorghum root transcriptome elucidate the differentiation of apoplastic barriers. <i>Plant Signaling and Behavior</i> , 2020, 15, 1724465.	1.2	10
7934	RNA-seq reveals novel mechanistic targets of withaferin A in prostate cancer cells. <i>Carcinogenesis</i> , 2020, 41, 778-789.	1.3	20
7935	Differential expression of lncRNAs during silicosis and the role of LOC103691771 in myofibroblast differentiation induced by TGF- $\beta$ 1. <i>Biomedicine and Pharmacotherapy</i> , 2020, 125, 109980.	2.5	17
7936	Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp <i>Cotesia vestalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100657.	0.4	18
7937	MicroRNA expression profiling of caudal fin cell of <i>C. auratus gibelio</i> upon cyprinid herpesvirus 2 infection. <i>Developmental and Comparative Immunology</i> , 2020, 107, 103637.	1.0	5
7938	Cysteine Protease Inhibitors Reduce Enzymatic Browning of Potato by Lowering the Accumulation of Free Amino Acids. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 2467-2476.	2.4	32
7939	A universal pipeline for mobile mRNA detection and insights into heterografting advantages under chilling stress. <i>Horticulture Research</i> , 2020, 7, 13.	2.9	20

#	ARTICLE	IF	CITATIONS
7940	Read Mapping and Transcript Assembly: A Scalable and High-Throughput Workflow for the Processing and Analysis of Ribonucleic Acid Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 1361.	1.1	20
7941	FastMM: an efficient toolbox for personalized constraint-based metabolic modeling. <i>BMC Bioinformatics</i> , 2020, 21, 67.	1.2	6
7942	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020, 15, 2-16.	0.7	9
7943	Ribonucleic Acid Sequence Characterization by Negative Electron Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 4436-4444.	3.2	19
7944	Testis transcriptome profiling identified genes involved in spermatogenic arrest of cattleyak. <i>PLoS ONE</i> , 2020, 15, e0229503.	1.1	23
7945	Comparative Transcriptomics Analysis of Testicular miRNA from Cryptorchid and Normal Horses. <i>Animals</i> , 2020, 10, 338.	1.0	5
7946	Comparative Transcriptome Analysis of the Gills from the Chinese Mitten Crab ( <i>Eriocheir japonica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5020, .	0.4	3
7947	Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020, 35, 377-393.	0.4	43
7948	The novel bZIP transcription factor Fpo1 negatively regulates perithecial development by modulating carbon metabolism in the ascomycete fungus <i>Fusarium graminearum</i> . <i>Environmental Microbiology</i> , 2020, 22, 2596-2612.	1.8	15
7949	Transcriptome analysis of life stages of the house cricket, <i>Acheta domesticus</i> , to improve insect crop production. <i>Scientific Reports</i> , 2020, 10, 3471.	1.6	20
7950	Transition From Acute to Chronic Pain in Lower Extremity Fracture Patients. <i>Nursing Research</i> , 2020, 69, 149-156.	0.8	2
7951	Deep RNA-seq analysis reveals key responding aspects of wild banana relative resistance to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4. <i>Functional and Integrative Genomics</i> , 2020, 20, 551-562.	1.4	10
7952	Metabolic dependencies govern microbial syntrophies during methanogenesis in an anaerobic digestion ecosystem. <i>Microbiome</i> , 2020, 8, 22.	4.9	91
7953	High-Throughput Transcriptome Profiling in Drug and Biomarker Discovery. <i>Frontiers in Genetics</i> , 2020, 11, 19.	1.1	111
7954	Phytochemical and comparative transcriptome analyses reveal different regulatory mechanisms in the terpenoid biosynthesis pathways between <i>Matricaria recutita</i> L. and <i>Chamaemelum nobile</i> L.. <i>BMC Genomics</i> , 2020, 21, 169.	1.2	11
7955	Transcriptional reprogramming strategies and miRNA-mediated regulation networks of <i>Taxus media</i> induced into callus cells from tissues. <i>BMC Genomics</i> , 2020, 21, 168.	1.2	8
7956	Proteome interrogation using gold nanoprobe to identify targets of arctigenin in fish parasites. <i>Journal of Nanobiotechnology</i> , 2020, 18, 32.	4.2	10
7957	Identification and expression of main genes involved in non-target site resistance mechanisms to fenoxaprop-ethyl in <i>Beckmannia syzigachne</i> . <i>Pest Management Science</i> , 2020, 76, 2619-2626.	1.7	34

#	ARTICLE	IF	CITATIONS
7958	Comprehensive transcriptome analysis and tissue-specific profiling of gene expression in jute ( <i>Corchorus olitorius</i> L.). <i>Industrial Crops and Products</i> , 2020, 146, 112101.	2.5	13
7959	Comparative transcriptome analysis in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ) for DEGs of Ogura-, Polima-CMS and their shared maintainer. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 719-731.	1.4	10
7960	Higher sensitivity towards light stress and ocean acidification in an Arctic sea-ice-associated diatom compared to a pelagic diatom. <i>New Phytologist</i> , 2020, 226, 1708-1724.	3.5	26
7961	Transcriptomic and Metabolic Analyses Provide New Insights into the Apple Fruit Quality Decline during Long-Term Cold Storage. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4699-4716.	2.4	32
7962	Androgen receptor with short polyglutamine tract preferably enhances Wnt/ $\beta$ -catenin-mediated prostatic tumorigenesis. <i>Oncogene</i> , 2020, 39, 3276-3291.	2.6	9
7963	Nanoengineered Osteoinductive Bioink for 3D Bioprinting Bone Tissue. <i>ACS Applied Materials &amp; Interfaces</i> , 2020, 12, 15976-15988.	4.0	109
7964	Bioinformatics for Cancer Immunotherapy. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	1
7965	Genomic Designing of Climate-Smart Vegetable Crops. , 2020, , .		3
7966	Different diets can affect the digestion and immunity of common carp ( <i>Cyprinus carpio</i> ) according to enzyme activity assay and transcriptome sequencing. <i>Aquaculture</i> , 2020, 523, 735176.	1.7	4
7967	Targeted metabolic engineering of committed steps improves anti-cancer drug camptothecin production in <i>Ophiorrhiza pumila</i> hairy roots. <i>Industrial Crops and Products</i> , 2020, 148, 112277.	2.5	49
7968	AhHDA1-mediated AhGLK1 promoted chlorophyll synthesis and photosynthesis regulates recovery growth of peanut leaves after water stress. <i>Plant Science</i> , 2020, 294, 110461.	1.7	13
7969	Transcriptome analysis of terpenoid biosynthetic genes and simple sequence repeat marker screening in <i>Eucommia ulmoides</i> . <i>Molecular Biology Reports</i> , 2020, 47, 1979-1990.	1.0	13
7970	Identification of two recessive etiolation genes ( <i>py1</i> , <i>py2</i> ) in pakchoi ( <i>Brassica rapa</i> L. ssp. <i>chinensis</i> ). <i>BMC Plant Biology</i> , 2020, 20, 68.	1.6	5
7971	The Genome-Wide Analysis of RALF-Like Genes in Strawberry (Wild and Cultivated) and Five Other Plant Species (Rosaceae). <i>Genes</i> , 2020, 11, 174.	1.0	6
7972	Genome-Wide Identification of Aluminum-Activated Malate Transporter (ALMT) Gene Family in Rubber Trees ( <i>Hevea brasiliensis</i> ) Highlights Their Involvement in Aluminum Detoxification. <i>Forests</i> , 2020, 11, 142.	0.9	14
7973	20(S)-Protopanaxatriol promotes the binding of P53 and DNA to regulate the antitumor network via multiomic analysis. <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 1020-1035.	5.7	18
7974	A systems approach to infectious disease. <i>Nature Reviews Genetics</i> , 2020, 21, 339-354.	7.7	72
7975	Electroacupuncture Alleviates Experimental Chronic Inflammatory Pain by Inhibiting Calcium Voltage-Gated Channel-Mediated Inflammation. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-10.	0.5	5

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7976	Metabolic Profiling and Transcriptome Analysis of Mulberry Leaves Provide Insights into Flavonoid Biosynthesis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 1494-1504.	2.4	45
7977	Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic DPYD structural variant. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004713.	0.5	5
7978	Comparative transcriptome analysis of <i>Locusta migratoria tibetensis</i> Chen (Orthoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66	0.8	10
7979	Custom selected reference genes outperform pre-defined reference genes in transcriptomic analysis. <i>BMC Genomics</i> , 2020, 21, 35.	1.2	19
7980	Sorafenib Inhibits Ribonucleotide Reductase Regulatory Subunit M2 (RRM2) in Hepatocellular Carcinoma Cells. <i>Biomolecules</i> , 2020, 10, 117.	1.8	39
7981	Metabolic Adaptation to Sulfur of Hyperthermophilic <i>Palaeococcus pacificus</i> DY20341T from Deep-Sea Hydrothermal Sediments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 368.	1.8	8
7982	Life and death: A systematic comparison of antemortem and postmortem gene expression. <i>Gene</i> , 2020, 731, 144349.	1.0	16
7983	Transcriptomic Analysis of Testicular Gene Expression in Normal and Cryptorchid Horses. <i>Animals</i> , 2020, 10, 102.	1.0	5
7984	A computational genome-wide analysis of long terminal repeats retrotransposon expression in sunflower roots ( <i>Helianthus annuus</i> L.). <i>Genetica</i> , 2020, 148, 13-23.	0.5	12
7985	Genome wide characterization of the SERK/SERL gene family in <i>Phalaenopsis equestris</i> , <i>Dendrobium catenatum</i> and <i>Apostasia shenzhenica</i> (Orchidaceae). <i>Computational Biology and Chemistry</i> , 2020, 85, 107210.	1.1	3
7986	Classification of Kidney Cancer Data Using Cost-Sensitive Hybrid Deep Learning Approach. <i>Symmetry</i> , 2020, 12, 154.	1.1	26
7987	Transcriptome sequencing analysis reveals silver nanoparticles antifungal molecular mechanism of the soil fungi <i>Fusarium solani</i> species complex. <i>Journal of Hazardous Materials</i> , 2020, 388, 122063.	6.5	50
7988	Transcriptomic analysis of an <i>l</i> -threonine- $\epsilon$ -producing <i>Escherichia coli</i> TWFO01. <i>Biotechnology and Applied Biochemistry</i> , 2020, 67, 414-429.	1.4	8
7989	Tissue-Resident PDGFR <sup>hi</sup> Progenitor Cells Contribute to Fibrosis versus Healing in a Context- and Spatiotemporally Dependent Manner. <i>Cell Reports</i> , 2020, 30, 555-570.e7.	2.9	43
7990	MerP/MerT-mediated mechanism: A different approach to mercury resistance and bioaccumulation by marine bacteria. <i>Journal of Hazardous Materials</i> , 2020, 388, 122062.	6.5	21
7991	Transcriptome Analysis Unravels Metabolic and Molecular Pathways Related to Fruit Sac Granulation in a Late-Ripening Navel Orange ( <i>Citrus sinensis</i> Osbeck). <i>Plants</i> , 2020, 9, 95.	1.6	26
7992	A recessive high-density pod mutant resource of <i>Brassica napus</i> . <i>Plant Science</i> , 2020, 293, 110411.	1.7	8
7993	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. <i>Journal of Computational Biology</i> , 2020, 27, 442-457.	0.8	6

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7994	Genome-wide transcriptional response of papain-like cysteine protease-mediated resistance against <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice. <i>Plant Cell Reports</i> , 2020, 39, 457-472.	2.8	19
7995	Integrated analysis of mRNA-miRNA expression in <i>Tilapia</i> infected with <i>Tilapia lake virus</i> (TiLV) and identifies primarily immuneresponse genes. <i>Fish and Shellfish Immunology</i> , 2020, 99, 208-226.	1.6	21
7996	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cancer and their Molecular Characteristics. <i>Scientific Reports</i> , 2020, 10, 1212.	1.6	62
7997	Selection and Validation of Appropriate Reference Genes for Quantitative RT-PCR Analysis in <i>Rubia yunnanensis</i> Diels Based on Transcriptome Data. <i>BioMed Research International</i> , 2020, 2020, 1-19.	0.9	12
7998	An operon consisting of a P-type ATPase gene and a transcriptional regulator gene responsible for cadmium resistances in <i>Bacillus vietnamensis</i> 151â€™6 and <i>Bacillus marisflavi</i> 151â€™25. <i>BMC Microbiology</i> , 2020, 20, 18.	1.3	22
7999	Transcriptome analysis reveals key genes involved in the regulation of nicotine biosynthesis at early time points after topping in tobacco ( <i>Nicotiana tabacum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 30.	1.6	22
8000	Host Transcriptional Response of <i>Sclerotinia sclerotiorum</i> Induced by the Mycoparasite <i>Coniothyrium minitans</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 183.	1.5	4
8001	Growth and Spatial Control of Murine Neural Stem Cells on Reflectin Films. <i>ACS Biomaterials Science and Engineering</i> , 2020, 6, 1311-1320.	2.6	4
8002	RNA sequencing by direct tagmentation of RNA/DNA hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2886-2893.	3.3	86
8003	The biochemistry of headgroup exchange during triacylglycerol synthesis in canola. <i>Plant Journal</i> , 2020, 103, 83-94.	2.8	18
8004	Choice of library size normalization and statistical methods for differential gene expression analysis in balanced two-group comparisons for RNA-seq studies. <i>BMC Genomics</i> , 2020, 21, 75.	1.2	29
8005	Concomitant phytonutrient and transcriptome analysis of mature fruit and leaf tissues of tomato ( <i>Solanum lycopersicum</i> L. cv. Oregon Spring) grown using organic and conventional fertilizer. <i>PLoS ONE</i> , 2020, 15, e0227429.	1.1	14
8006	RNA sequencing analyses of gene expressions in a canine macrophages cell line DH82 infected with canine distemper virus. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104206.	1.0	4
8007	Transcriptomic profiles reveal that inactivated iridovirus and rhabdovirus bivalent vaccine elicits robust adaptive immune responses against lethal challenge in marbled sleepy goby. <i>Fish and Shellfish Immunology</i> , 2020, 98, 429-437.	1.6	6
8008	Comparative transcriptome analysis of olfactory epithelium in large yellow croaker: Evidence for olfactory adaptation to feed phagostimulant in fish. <i>Aquaculture</i> , 2020, 519, 734920.	1.7	4
8009	3â€™Pool-seq: an optimized cost-efficient and scalable method of whole-transcriptome gene expression profiling. <i>BMC Genomics</i> , 2020, 21, 64.	1.2	12
8010	CRISPR-cas3 of <i>Salmonella</i> Upregulates Bacterial Biofilm Formation and Virulence to Host Cells by Targeting Quorum-Sensing Systems. <i>Pathogens</i> , 2020, 9, 53.	1.2	56
8011	The (p)ppGpp-mediated stringent response regulatory system globally inhibits primary metabolism and activates secondary metabolism in <i>Pseudomonas protegens</i> H78. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3061-3079.	1.7	13



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8012	A constitutive and drought-responsive mRNA undergoes long-distance transport in pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 74	1.7	25
8013	MdMYB8 is associated with flavonol biosynthesis via the activation of the MdFLS promoter in the fruits of <i>Malus crabapple</i> . <i>Horticulture Research</i> , 2020, 7, 19.	2.9	39
8014	Methoprene-Induced Genes in Workers of Formosan Subterranean Termites ( <i>Coptotermes formosanus</i> ) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 74	1.0	7
8015	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
8016	Transcriptome analysis reveals insight into molecular hydrogen-induced cadmium tolerance in alfalfa: the prominent role of sulfur and (homo)glutathione metabolism. <i>BMC Plant Biology</i> , 2020, 20, 58.	1.6	43
8017	Genome Survey and Transcriptome Analysis on Mycelia and Primordia of <i>Agaricus blazei</i> . <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	6
8018	Global Transcriptomic Analysis of Zebrafish Glucagon Receptor Mutant Reveals Its Regulated Metabolic Network. <i>International Journal of Molecular Sciences</i> , 2020, 21, 724.	1.8	7
8019	Differential Gene Profiling of the Heartwood Formation Process in <i>Taiwania cryptomerioides</i> Hayata Xylem Tissues. <i>International Journal of Molecular Sciences</i> , 2020, 21, 960.	1.8	11
8020	Physiological and Anatomical Differences and Differentially Expressed Genes Reveal Yellow Leaf Coloration in Shumard Oak. <i>Plants</i> , 2020, 9, 169.	1.6	13
8021	The RNA degradome: a precious resource for deciphering RNA processing and regulation codes in plants. <i>RNA Biology</i> , 2020, 17, 1223-1227.	1.5	5
8022	Three-dimensional genetic networks among seed oil-related traits, metabolites and genes reveal the genetic foundations of oil synthesis in soybean. <i>Plant Journal</i> , 2020, 103, 1103-1124.	2.8	26
8023	<i>Puccinia triticina</i> pathotypes THTT and THTS display complex transcript profiles on wheat cultivar Thatcher. <i>BMC Genetics</i> , 2020, 21, 48.	2.7	7
8024	Transcriptome analysis and immune-related genes expression reveals the immune responses of <i>Macrobrachium rosenbergii</i> infected by <i>Enterobacter cloacae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 101, 66-77.	1.6	28
8025	Transcriptome profiling of developing testes and spermatogenesis in the Mongolian horse. <i>BMC Genetics</i> , 2020, 21, 46.	2.7	14
8026	Comparative Transcriptome Analyses of <i>Schistosoma japonicum</i> Derived From SCID Mice and BALB/c Mice: Clues to the Abnormality in Parasite Growth and Development. <i>Frontiers in Microbiology</i> , 2020, 11, 274.	1.5	5
8027	Transcriptomic and Physiological Responses to Oxidative Stress in a <i>Chlamydomonas reinhardtii</i> Glutathione Peroxidase Mutant. <i>Genes</i> , 2020, 11, 463.	1.0	16
8028	Homoeolog expression bias and expression level dominance (ELD) in four tissues of natural allotetraploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2020, 21, 330.	1.2	34
8029	Benchmarking RNA-seq differential expression analysis methods using spike-in and simulation data. <i>PLoS ONE</i> , 2020, 15, e0232271.	1.1	27

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8030	Tissue memory CD4+ T cells expressing IL-7 receptor-alpha (CD127) preferentially support latent HIV-1 infection. <i>PLoS Pathogens</i> , 2020, 16, e1008450.	2.1	34
8031	Physiological and transcriptomic analysis of "Whangkeumbae"™ pear core browning during low-temperature storage. <i>Gene Expression Patterns</i> , 2020, 36, 119113.	0.3	9
8032	Glyoxylic acid overcomes 1-MCP-induced blockage of fruit ripening in <i>Pyrus communis</i> L. var. "Dâ"™Anjou"™. <i>Scientific Reports</i> , 2020, 10, 7084.	1.6	14
8033	Expression Profile Analysis of the Cell Cycle in Diploid and Tetraploid <i>Carassius auratus</i> red var.. <i>Frontiers in Genetics</i> , 2020, 11, 203.	1.1	3
8034	Analysis of lncRNA UCA1-related downstream pathways and molecules of cisplatin resistance in lung adenocarcinoma. <i>Journal of Clinical Laboratory Analysis</i> , 2020, 34, e23312.	0.9	9
8036	Gene expression in <i>Rhizoglyphus irregularis</i> at two different time points of mycorrhiza establishment in <i>Helianthus annuus</i> roots, as revealed by RNA-seq analysis. <i>Mycorrhiza</i> , 2020, 30, 373-387.	1.3	11
8037	Plasmodesmata play a critical role in promoting the germination of floral buds in <i>Ilex verticillata</i> . <i>Plant Growth Regulation</i> , 2020, 91, 349-357.	1.8	3
8038	Expression profile of genes involved in ramie flavonoids biosynthesis pathway and regulation of flavanone 3-hydroxylase (BnF3H) in response to aquatic environment. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	1
8039	Transcriptome profiling of mild-salt responses in <i>Lycium ruthenicum</i> early seedlings to reveal salinity-adaptive strategies. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	2
8040	Transcriptomic response to ammonia-N stress in the hepatopancreas of swimming crab <i>Portunus trituberculatus</i> . <i>Marine Life Science and Technology</i> , 2020, 2, 135-145.	1.8	8
8041	Overexpression of LiTPS2 from a cultivar of lily ( <i>Lilium "Siberia"™</i> ) enhances the monoterpenoids content in tobacco flowers. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 391-399.	2.8	24
8042	Transcriptomics in RCC. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 742-754.	0.8	6
8043	Effects of drought stress on physiological responses and gene expression changes in herbaceous peony ( <i>Paeonia lactiflora</i> Pall.). <i>Plant Signaling and Behavior</i> , 2020, 15, 1746034.	1.2	23
8044	Transcriptome of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> PccS1 infected in calla plants in vivo highlights a spatiotemporal expression pattern of genes related to virulence, adaptation, and host response. <i>Molecular Plant Pathology</i> , 2020, 21, 871-891.	2.0	22
8045	Magnaporthe oryzae Auxiliary Activity Protein MoAa91 Functions as Chitin-Binding Protein To Induce Appressorium Formation on Artificial Inductive Surfaces and Suppress Plant Immunity. <i>MBio</i> , 2020, 11, .	1.8	38
8046	Capital Breeding in a Diapausing Copepod: A Transcriptomics Analysis. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	10
8047	The Encystment-Related MicroRNAs and Its Regulation Molecular Mechanism in <i>Pseudourostyla cristata</i> Revealed by High Throughput Small RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2309.	1.8	5
8048	Genome-Wide Identification and Characterization of Drought Stress Responsive microRNAs in Tibetan Wild Barley. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2795.	1.8	29

#	ARTICLE	IF	CITATIONS
8049	Insights into the Synthesis, Secretion and Curing of Barnacle Cyprid Adhesive via Transcriptomic and Proteomic Analyses of the Cement Gland. <i>Marine Drugs</i> , 2020, 18, 186.	2.2	10
8051	Specific genes and sequence variation in pathotype 7 of the clubroot pathogen <i>Plasmodiophora brassicae</i> . <i>European Journal of Plant Pathology</i> , 2020, 157, 17-28.	0.8	4
8052	Phytochrome Coordinates with a hnRNP to Regulate Alternative Splicing via an Exonic Splicing Silencer. <i>Plant Physiology</i> , 2020, 182, 243-254.	2.3	24
8053	Transcriptome alterations in HepG2 cells induced by shRNA knockdown and overexpression of TMEM2 gene. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 1576-1584.	0.6	3
8054	Statistics in the Genomic Era. <i>Genes</i> , 2020, 11, 443.	1.0	1
8055	Sequencing Strategies for Fusion Gene Detection. <i>BioEssays</i> , 2020, 42, 2000016.	1.2	18
8056	Metabolic engineering of <i>Cupriavidus necator</i> H16 for improved chemoautotrophic growth and PHB production under oxygen-limiting conditions. <i>Metabolic Engineering</i> , 2020, 61, 11-23.	3.6	40
8057	Generation of an enteric smooth muscle cell line from the pig ileum. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	3
8058	Contributions of Gene Modules Regulated by Essential Noncoding RNA in Colon Adenocarcinoma Progression. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	1
8059	Transcriptome analysis to unravel the gene expression profile of ovarian follicular development in Magang goose. <i>Journal of Reproduction and Development</i> , 2020, 66, 331-340.	0.5	7
8060	Characterization and expression analysis of four members genes of flavanone 3-hydroxylase families from <i>Chamaemelum nobile</i> . <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2020, 48, 102-115.	0.5	4
8061	Computational Oncology in the Multi-Omics Era: State of the Art. <i>Frontiers in Oncology</i> , 2020, 10, 423.	1.3	59
8062	Physiological Change and Transcriptome Analysis of Chinese Wild <i>Vitis amurensis</i> and <i>Vitis vinifera</i> in Response to Cold Stress. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 478-490.	1.0	19
8063	Transcriptome signatures in the brain of a migratory songbird. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100681.	0.4	16
8064	Gene expression on the fly: A transcriptome-level view of <i>Drosophila</i> 's immune response to the opportunistic fungal pathogen <i>Aspergillus flavus</i> . <i>Infection, Genetics and Evolution</i> , 2020, 82, 104308.	1.0	2
8065	Understory and canopy additions of nitrogen differentially affect carbon and nitrogen metabolism of <i>Psychotria rubra</i> in an evergreen broad-leaved forest. <i>Science of the Total Environment</i> , 2020, 724, 138183.	3.9	15
8066	Circular RNA expression alteration in whole blood of premature infants with periventricular white matter damage. <i>Genomics</i> , 2020, 112, 2875-2885.	1.3	10
8067	CCL5 derived from tumor-associated macrophages promotes prostate cancer stem cells and metastasis via activating $\beta$ -catenin/STAT3 signaling. <i>Cell Death and Disease</i> , 2020, 11, 234.	2.7	143

#	ARTICLE	IF	CITATIONS
8068	Mobile genomics: tools and techniques for tackling transposons. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190345.	1.8	39
8069	Gene Balance Predicts Transcriptional Responses Immediately Following Ploidy Change in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2020, 32, 1434-1448.	3.1	60
8070	Insights into response to food intake in anadromous <i>Coilia nasus</i> through stomach transcriptome analysis. <i>Aquaculture Research</i> , 2020, 51, 2799-2812.	0.9	7
8071	Nuclear actin regulates inducible transcription by enhancing RNA polymerase II clustering. <i>Science Advances</i> , 2020, 6, eaay6515.	4.7	81
8072	New Diagnostic Approaches for Undiagnosed Rare Genetic Diseases. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 351-372.	2.5	58
8073	The functions of ocu-miR-205 in regulating hair follicle development in Rex rabbits. <i>BMC Developmental Biology</i> , 2020, 20, 8.	2.1	15
8074	Automation of Spatial Transcriptomics library preparation to enable rapid and robust insights into spatial organization of tissues. <i>BMC Genomics</i> , 2020, 21, 298.	1.2	19
8075	BAMscale: quantification of next-generation sequencing peaks and generation of scaled coverage tracks. <i>Epigenetics and Chromatin</i> , 2020, 13, 21.	1.8	40
8076	Misuse of RPKM or TPM normalization when comparing across samples and sequencing protocols. <i>Rna</i> , 2020, 26, 903-909.	1.6	215
8077	Interferon-complement loop in transplant-associated thrombotic microangiopathy. <i>Blood Advances</i> , 2020, 4, 1166-1177.	2.5	41
8078	Identification and expression analysis of WRKY gene family under drought stress in peanut ( <i>Arachis</i> ). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	1.1	38
8079	Transcriptome Analysis Reveals the Neuro-Immune Interactions in Duck Tembusu Virus-Infected Brain. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2402.	1.8	23
8080	Comparative Genomics and Transcriptomics Analyses Reveal a Unique Environmental Adaptability of <i>Vibrio fujianensis</i> . <i>Microorganisms</i> , 2020, 8, 555.	1.6	12
8081	Analyses of microRNAs and transcriptomes in the midgut of <i>Spodoptera litura</i> feeding on <i>Brassica juncea</i> . <i>Insect Science</i> , 2021, 28, 533-547.	1.5	6
8082	RNA-seq Transcriptome Profiling of the Halophyte <i>Salicornia persica</i> in Response to Salinity. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 707-721.	2.8	11
8083	Reference genome and annotation updates lead to contradictory prognostic predictions in gene expression signatures: a case study of resected stage I lung adenocarcinoma. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
8084	RSVdb: a comprehensive database of transcriptome RNA structure. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	5
8085	Development of an RNA sequencing-based prognostic gene signature in multiple myeloma. <i>British Journal of Haematology</i> , 2021, 192, 310-321.	1.2	12

#	ARTICLE	IF	CITATIONS
8086	Bioinformatics analysis of WRKY transcription factors in grape and their potential roles prediction in sugar and abscisic acid signaling pathway. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 67-80.	0.9	9
8087	Comparative transcriptome and microbiota analyses provide new insights into the adverse effects of industrial trans fatty acids on the small intestine of C57BL/6 mice. <i>European Journal of Nutrition</i> , 2021, 60, 975-987.	1.8	9
8088	Unveiling the shade nature of cyanic leaves: A view from the "blue absorbing side" of anthocyanins. <i>Plant, Cell and Environment</i> , 2021, 44, 1119-1129.	2.8	31
8089	Cytochrome P450s <i>CYP380C6</i> and <i>CYP380C9</i> in green peach aphid facilitate its adaptation to indole glucosinolate-mediated plant defense. <i>Pest Management Science</i> , 2021, 77, 148-158.	1.7	13
8090	Metatranscriptomics reveals the gene functions and metabolic properties of the major microbial community during Chinese Sichuan Paocai fermentation. <i>Food Microbiology</i> , 2021, 98, 103573.	2.1	28
8091	Transcriptional identification of differentially expressed genes associated with division of labor in <i>Apis cerana cerana</i> . <i>Insect Science</i> , 2021, 28, 457-471.	1.5	0
8092	Deciphering cell-cell interactions and communication from gene expression. <i>Nature Reviews Genetics</i> , 2021, 22, 71-88.	7.7	575
8093	Integrative, normalization-insusceptible statistical analysis of RNA-Seq data, with improved differential expression and unbiased downstream functional analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
8094	Transcriptome analysis of two lines of <i>Brassica oleracea</i> in response to early infection with <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Canadian Journal of Plant Pathology</i> , 2021, 43, 127-139.	0.8	14
8095	First de novo transcriptome assembly of Iwagaki oyster, <i>Crassostrea nippona</i> , and comparative evolutionary analysis of salinity-stress response genes in <i>Crassostrea</i> oysters. <i>Marine Genomics</i> , 2021, 56, 100805.	0.4	7
8096	The Pre-Implantation Embryo Induces Uterine Inflammatory Reaction in Mice. <i>Reproductive Sciences</i> , 2021, 28, 60-68.	1.1	2
8097	Transcriptome Analysis of Dimorphic Fungus <i>Sporothrix schenckii</i> Exposed to Temperature Stress. <i>International Microbiology</i> , 2021, 24, 25-35.	1.1	4
8098	Integrated metabolite-transcriptomics and functional characterization reveals that the wheat auxin receptor TIR1 negatively regulates defense against <i>Fusarium graminearum</i> . <i>Journal of Integrative Plant Biology</i> , 2021, 63, 340-352.	4.1	53
8099	Genome-wide identification of the maize 2OGD superfamily genes and their response to <i>Fusarium verticillioides</i> and <i>Fusarium graminearum</i> . <i>Gene</i> , 2021, 764, 145078.	1.0	14
8100	A virtual sequencer reveals the dephasing patterns in error-correction code DNA sequencing. <i>National Science Review</i> , 2021, 8, nwaa227.	4.6	3
8101	Immunotranscriptome analysis of <i>Plutella xylostella</i> reveals differences in innate immune responses to low and high virulence <i>Beauveria bassiana</i> strain challenges. <i>Pest Management Science</i> , 2021, 77, 1070-1080.	1.7	10
8102	Pectin lyase enhances cotton resistance to <i>Verticillium</i> wilt by inducing cell apoptosis of <i>Verticillium dahliae</i> . <i>Journal of Hazardous Materials</i> , 2021, 404, 124029.	6.5	18
8103	In-depth transcriptome unveils the cadmium toxicology and a novel metallothionein in silkworm. <i>Chemosphere</i> , 2021, 273, 128522.	4.2	6

#	ARTICLE	IF	CITATIONS
8104	Addition of genistein to the fermentation process reduces citrinin production by <i>Monascus</i> via changes at the transcription level. <i>Food Chemistry</i> , 2021, 343, 128410.	4.2	21
8105	Nitric oxide affects seed oil accumulation and fatty acid composition through protein S-nitrosation. <i>Journal of Experimental Botany</i> , 2021, 72, 385-397.	2.4	7
8106	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. <i>Meat Science</i> , 2021, 173, 108378.	2.7	17
8107	Comprehensive analyses of degradative enzymes associated with mesotrione-degraded process in rice for declining environmental risks. <i>Science of the Total Environment</i> , 2021, 758, 143618.	3.9	18
8108	Experimental evidence for long-term coexistence of copiotrophic and oligotrophic bacteria in pelagic surface seawater. <i>Environmental Microbiology</i> , 2021, 23, 1162-1173.	1.8	7
8109	Combining quantitative trait locus and co-expression analysis allowed identification of new candidates for oil accumulation in rapeseed. <i>Journal of Experimental Botany</i> , 2021, 72, 1649-1660.	2.4	12
8111	Exploring Core Response Mechanisms to Multiple Environmental Stressors Via A Genome-Wide Study in the Brown Alga <i>Saccharina japonica</i> (Laminariales, Phaeophyceae). <i>Journal of Phycology</i> , 2021, 57, 345-354.	1.0	7
8112	Ribosome-Targeting Antibiotics Impair T Cell Effector Function and Ameliorate Autoimmunity by Blocking Mitochondrial Protein Synthesis. <i>Immunity</i> , 2021, 54, 68-83.e6.	6.6	51
8113	Development of Transcriptome Analysis Methods. , 2021, , 462-471.		2
8114	Mechanism of early germination inhibition of fresh walnuts ( <i>Juglans regia</i> ) with gamma radiation uncovered by transcriptomic profiling of embryos during storage. <i>Postharvest Biology and Technology</i> , 2021, 172, 111380.	2.9	5
8115	Lower Airway Dysbiosis Affects Lung Cancer Progression. <i>Cancer Discovery</i> , 2021, 11, 293-307.	7.7	139
8116	Deep sequencing of the transcriptome from murine lung infected with H5N8 subtype avian influenza virus with combined substitutions I283M and K526R in PB2 gene. <i>Infection, Genetics and Evolution</i> , 2021, 87, 104672.	1.0	3
8117	Multiple-genotypes transcriptional analysis revealed candidate genes and nucleotide variants for improvement of quality characteristics in tea ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Genomics</i> , 2021, 113, 305-316.	1.3	10
8118	Mechanisms for the stimulatory effects of a five-component mixture of antibiotics in <i>Microcystis aeruginosa</i> at transcriptomic and proteomic levels. <i>Journal of Hazardous Materials</i> , 2021, 406, 124722.	6.5	41
8119	Ammonia oxidation at pH 2.5 by a new gammaproteobacterial ammonia-oxidizing bacterium. <i>ISME Journal</i> , 2021, 15, 1150-1164.	4.4	39
8120	Transcriptome analysis in <i>Takifugu rubripes</i> and <i>Dicentrarchus labrax</i> gills during <i>Cryptocaryon irritans</i> infection. <i>Journal of Fish Diseases</i> , 2021, 44, 249-262.	0.9	10
8121	Rht semi-dwarfing alleles increase the abundance of high molecular weight glutenin subunits. <i>Cereal Chemistry</i> , 2021, 98, 337-345.	1.1	1
8122	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio harveyi</i> infection. <i>Aquaculture Research</i> , 2021, 52, 1855-1875.	0.9	3

#	ARTICLE	IF	CITATIONS
8123	Deciphering the molecular regulatory mechanism orchestrating ovary development of the Pacific whiteleg shrimp <i>Litopenaeus vannamei</i> through integrated transcriptomic analysis of reproduction-related organs. <i>Aquaculture</i> , 2021, 533, 736160.	1.7	10
8124	Innate Immunity Promotes Sleep through Epidermal Antimicrobial Peptides. <i>Current Biology</i> , 2021, 31, 564-577.e12.	1.8	35
8125	Ectopic expression of antifreeze protein gene from <i>Ammopiptanthus nanus</i> confers chilling tolerance in maize. <i>Crop Journal</i> , 2021, 9, 924-933.	2.3	10
8126	Contextualized Protein-Protein Interactions. <i>Patterns</i> , 2021, 2, 100153.	3.1	8
8127	Study of dynamics of genes involved in biosynthesis and accumulation of scopoletin at different growth stages of <i>Forssk.</i> <i>Phytochemistry</i> , 2021, 182, 112594.	1.4	5
8128	HeRA: an atlas of enhancer RNAs across human tissues. <i>Nucleic Acids Research</i> , 2021, 49, D932-D938.	6.5	27
8129	Physiological and transcription analyses reveal the regulatory mechanism of melatonin in inducing drought resistance in loquat ( <i>Eriobotrya japonica</i> Lindl.) seedlings. <i>Environmental and Experimental Botany</i> , 2021, 181, 104291.	2.0	54
8130	Systematic prediction of autophagy-related proteins using <i>Arabidopsis thaliana</i> interactome data. <i>Plant Journal</i> , 2021, 105, 708-720.	2.8	9
8131	RNA-Sequencing Analysis Pipeline for Prognostic Marker Identification in Cancer. <i>Methods in Molecular Biology</i> , 2021, 2174, 119-131.	0.4	1
8132	Bipartite tight spectral clustering (BiTSC) algorithm for identifying conserved gene co-clusters in two species. <i>Bioinformatics</i> , 2021, 37, 1225-1233.	1.8	3
8133	Gene co-expression and alternative splicing analysis of key metabolic tissues to unravel the regulatory signatures of fatty acid composition in cattle. <i>RNA Biology</i> , 2021, 18, 854-862.	1.5	13
8134	A tail-based test to detect differential expression in RNA-sequencing data. <i>Statistical Methods in Medical Research</i> , 2021, 30, 261-276.	0.7	2
8135	Comprehensive analysis of the translátome reveals the relationship between the translational and transcriptional control in high fat diet-induced liver steatosis. <i>RNA Biology</i> , 2021, 18, 863-874.	1.5	12
8136	<i>ANCA</i> : Alignment-Based Network Construction Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 512-524.	1.9	14
8137	Transcriptomes of the interaction between <i>Fusarium verticillioides</i> and a <i>Streptomyces</i> strain reveal the fungal defense strategy under the pressure of a potential biocontrol agent. <i>Fungal Biology</i> , 2021, 125, 78-88.	1.1	9
8138	Recursive Convolutional Neural Networks for Epigenomics. , 2021, , .		0
8139	Next Generation Sequencing: Transcriptomics. , 2021, , 1-11.		0
8140	Transcriptome profiling analysis of two contrasting barley genotypes in general combining ability for yield traits. <i>Revista Brasileira De Botanica</i> , 2021, 44, 117-123.	0.5	0

#	ARTICLE	IF	CITATIONS
8141	Comparative Transcriptome Profile Analysis of Longissimus dorsi Muscle Tissues From Two Goat Breeds With Different Meat Production Performance Using RNA-Seq. <i>Frontiers in Genetics</i> , 2020, 11, 619399.	1.1	18
8142	Molecular mechanism underlying <i>Pyropia haitanensis</i> PhHsp22-mediated increase in the high-temperature tolerance of <i>Chlamydomonas reinhardtii</i> . <i>Journal of Applied Phycology</i> , 2021, 33, 1137-1148.	1.5	9
8143	Transcriptome profiling analysis reveals involvement of SAM cycle and methionine pathway in low potassium tolerance in barley. <i>Current Plant Biology</i> , 2021, 25, 100190.	2.3	6
8144	Differential Expression With RNA-Seq Data. , 2021, , 313-323.		0
8145	RNA-Sequencing and Transcriptome Analysis after Stimulation in. <i>Methods in Molecular Biology</i> , 2021, 2319, 25-30.	0.4	0
8146	Screening and functional analysis of potential &lt;i>S&lt;/i> genes in &lt;i>Chrysanthemum morifolium&lt;/i>. <i>Ornamental Plant Research</i> , 2021, 1, 1-11.	0.2	1
8147	The new chimeric chiron genes evolved essential roles in zebrafish embryonic development by regulating NAD+ levels. <i>Science China Life Sciences</i> , 2021, 64, 1929-1948.	2.3	6
8148	A broad introduction to RNA-Seq. <i>WikiJournal of Science</i> , 2021, 4, 4.	0.1	0
8149	Recent Advances in Multi-Omics and Breeding Approaches Towards Drought Tolerance in Crops. , 2021, , 333-359.		1
8150	Transcriptome of Lingzhi. <i>Compendium of Plant Genomes</i> , 2021, , 89-116.	0.3	0
8151	Next-Generation Sequencing (NGS). , 2021, , 305-327.		3
8152	Transcriptomic response of <i>Anopheles gambiae</i> sensu stricto mosquito larvae to Curry tree ( <i>Murraya</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	88
8153	Guanosine-5â€²-triphosphate cyclohydrolase 1 regulated long noncoding RNAs are potential targets for microglial activation in neuropathic pain. <i>Neural Regeneration Research</i> , 2021, 16, 596.	1.6	6
8154	Nuclear Factor-Y (NF-Y), the Key Player in Plant Growth and Development: Prediction and Characterization of <i>Vanilla planifolia</i> . <i>Current Biotechnology</i> , 2021, 9, 269-280.	0.2	1
8155	Whole-transcriptome analysis of differentially expressed genes in the mutant and normal capitula of <i>Chrysanthemum morifolium</i> . <i>BMC Genomic Data</i> , 2021, 22, 2.	0.7	15
8156	Transcriptome and degradome sequencing reveals changes in <i>Populusâ€™uramericana</i> â€™Nevaâ€™™ caused by its allelopathic response to p-hydroxybenzoic acid. <i>Journal of Forestry Research</i> , 2021, 32, 2155-2168.	1.7	3
8157	De novo venom gland transcriptomics of <i>Calliophis bivirgata flaviceps</i> : uncovering the complexity of toxins from the Malayan blue coral snake. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2021, 27, e20210024.	0.8	3
8158	Transcriptome Profiles in the Spleen of the Chinese Giant Salamander ( <i>Andrias davidianus</i> ) Challenged with <i>Citrobacter freundii</i> . <i>Russian Journal of Bioorganic Chemistry</i> , 2021, 47, 252-260.	0.3	1



#	ARTICLE	IF	CITATIONS
8159	Processing and Analysis of RNA-seq Data from Public Resources. <i>Methods in Molecular Biology</i> , 2021, 2243, 81-94.	0.4	14
8160	Metabolic and Transcriptional Analysis of Recombinant <i>Saccharomyces Cerevisiae</i> for Xylose Fermentation: A Feasible and Efficient Approach. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 2425-2434.	3.9	1
8162	Integrative genomics of aging. , 2021, , 151-171.		1
8163	Library Preparation Based on Transposase Assisted RNA/DNA Hybrid Co-Tagmentation for Next-Generation Sequencing of Human Noroviruses. <i>Viruses</i> , 2021, 13, 65.	1.5	3
8165	Genomic and proteomic mechanisms and models in toxicity and safety evaluation of nutraceuticals. , 2021, , 289-297.		0
8166	Computational intelligence for genomic data. , 2021, , 247-260.		0
8167	Intestinal transcriptomes in Kazakh sheep with different haplotypes after experimental <i>Echinococcus granulosus</i> infection. <i>Parasite</i> , 2021, 28, 14.	0.8	3
8168	Transcriptomics in rare diseases. , 2021, , 215-228.		0
8170	Robustness of differential gene expression analysis of RNA-seq. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3470-3481.	1.9	39
8171	Transcriptomic analysis reveals essential microRNAs after peripheral nerve injury. <i>Neural Regeneration Research</i> , 2021, 16, 1865.	1.6	13
8172	Dmrt1 regulates the immune response by repressing the TLR4 signaling pathway in goat male germline stem cells. <i>Zoological Research</i> , 2021, 42, 14-27.	0.9	24
8173	OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	1
8174	GH directly inhibits steatosis and liver injury in a sex-dependent and IGF1-independent manner. <i>Journal of Endocrinology</i> , 2021, 248, 31-44.	1.2	19
8175	RAP: A Web Tool for RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2284, 393-415.	0.4	0
8176	PM4NGS, a project management framework for next-generation sequencing data analysis. <i>GigaScience</i> , 2021, 10, .	3.3	0
8177	High mobility group box 1 mediates inflammatory response of astrocytes via cyclooxygenase 2/prostaglandin E2 signaling following spinal cord injury. <i>Neural Regeneration Research</i> , 2021, 16, 1848.	1.6	13
8178	Dynamic Expression Analysis and Introgressive Gene Identification of Fiber Length Using Chromosome Segment Substitution Lines from <i>G. hirsutum</i> × <i>G. barbadense</i> . <i>Phyton</i> , 2021, 90, 129-144.	0.4	2
8179	Utilization of Phenol as Carbon Source by the Thermoacidophilic Archaeon <i>Saccharolobus solfataricus</i> P2 Is Limited by Oxygen Supply and the Cellular Stress Response. <i>Frontiers in Microbiology</i> , 2020, 11, 587032.	1.5	2

#	ARTICLE	IF	CITATIONS
8180	Simultaneous profiling of <i>Arabidopsis thaliana</i> and <i>Vibrio vulnificus</i> MO6-24/O transcriptomes by dual RNA-seq analysis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2084-2096.	1.9	5
8181	Relevance of Metatranscriptomics in Symbiotic Associations Between Plants and Rhizosphere Microorganisms. , 2021, , 59-90.		2
8182	Effect of fulvic acid on barnyardgrass ( <i>Echinochloa crus-galli</i> ) seedling growth under flooding conditions. <i>Weed Science</i> , 2021, 69, 192-202.	0.8	4
8184	Transcriptome analysis of immune response against <i>Siniperca chuatsi</i> rhabdovirus infection in mandarin fish <i>Siniperca chuatsi</i> . <i>Journal of Fish Diseases</i> , 2021, 44, 675-687.	0.9	12
8185	Transcriptome profiling reveals candidate genes associated with cold stress in mulberry. <i>Revista Brasileira De Botanica</i> , 2021, 44, 125-137.	0.5	9
8186	Rapid Identification of a Candidate Gene Related to Fiber Strength Using a Superior Chromosome Segment Substitution Line from <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> via Bulk Segregant RNA-Sequencing. <i>Phyton</i> , 2021, 90, 837-858.	0.4	0
8187	Host Transcriptomic Response Following Administration of Rotavirus Vaccine in Infants™ Mimics Wild Type Infection. <i>Frontiers in Immunology</i> , 2020, 11, 580219.	2.2	4
8188	RNA sequencing. , 2021, , 61-73.		0
8189	Alternative Polyadenylation in response to temperature stress contributes to gene regulation in <i>Populus trichocarpa</i> . <i>BMC Genomics</i> , 2021, 22, 53.	1.2	9
8190	Digital Gene Expression Analysis of Huanglongbing Affected Mandarins ( <i>Citrus reticulata</i> Blanco) In Response to Thermotherapy. <i>Horticultural Plant Journal</i> , 2021, 7, 1-12.	2.3	5
8191	Phospho-RNAseq Profiling of Extracellular mRNAs and lncRNAs. <i>Methods in Molecular Biology</i> , 2021, 2348, 257-271.	0.4	0
8192	YhJC is a novel transcriptional regulator required for <i>Shigella flexneri</i> virulence. <i>Virulence</i> , 2021, 12, 1661-1671.	1.8	7
8193	High heterogeneity undermines generalization of differential expression results in RNA-Seq analysis. <i>Human Genomics</i> , 2021, 15, 7.	1.4	20
8194	Induced defense response in red mango fruit against <i>Colletotrichum gloeosporioides</i> . <i>Horticulture Research</i> , 2021, 8, 17.	2.9	26
8195	Transcriptome sequencing, data-based screening, and functional investigation of <i>MdWRKY75d</i> and <i>MdWRKY75e</i> in disease-resistant apples. <i>Journal of Plant Interactions</i> , 2021, 16, 462-473.	1.0	3
8196	Orf165 is associated with cytoplasmic male sterility in pepper. <i>Genetics and Molecular Biology</i> , 2021, 44, e20210030.	0.6	2
8197	Machine Learning Perspective in Cancer Research. <i>Advances in Medical Diagnosis, Treatment, and Care</i> , 2021, , 142-163.	0.1	2
8198	FLINO: a new method for immunofluorescence bioimage normalization. <i>Bioinformatics</i> , 2022, 38, 520-526.	1.8	12

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8199	QuickIsoSeq for Isoform Quantification in Large-Scale RNA Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2284, 135-145.	0.4	1
8200	Identification of Key Histone Modifications and Their Regulatory Regions on Gene Expression Level Changes in Chronic Myelogenous Leukemia. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 621578.	1.8	6
8201	Enhanced Biosynthesis of Chlorogenic Acid and Its Derivatives in Methyl-Jasmonate-Treated <i>Gardenia jasminoides</i> Cells: A Study on Metabolic and Transcriptional Responses of Cells. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 604957.	2.0	8
8202	Identification of candidate genes influencing anthocyanin biosynthesis during the development and ripening of red and white strawberry fruits via comparative transcriptome analysis. <i>PeerJ</i> , 2021, 9, e10739.	0.9	15
8203	Genome-wide transcriptome reveals mechanisms underlying Rlm1-mediated blackleg resistance on canola. <i>Scientific Reports</i> , 2021, 11, 4407.	1.6	3
8205	Molecular mechanisms of fat deposition: <i>IL-6</i> is a hub gene in fat lipolysis, comparing thin-tailed with fat-tailed sheep breeds. <i>Archives Animal Breeding</i> , 2021, 64, 53-68.	0.5	7
8207	Proteomic and Transcriptomic Techniques to Decipher the Molecular Evolution of Venoms. <i>Toxins</i> , 2021, 13, 154.	1.5	11
8208	Multi-omics analysis reveals the glycolipid metabolism response mechanism in the liver of genetically improved farmed Tilapia ( <i>GIFT, Oreochromis niloticus</i> ) under hypoxia stress. <i>BMC Genomics</i> , 2021, 22, 105.	1.2	34
8210	Chemosensory genes in the head of <i>Spodoptera litura</i> larvae. <i>Bulletin of Entomological Research</i> , 2021, 111, 454-463.	0.5	16
8212	Comparative transcriptome analysis of differentially expressed genes related to the physiological changes of yellow-green leaf mutant of maize. <i>PeerJ</i> , 2021, 9, e10567.	0.9	7
8214	Predominantly inverse modulation of gene expression in genomically unbalanced disomic haploid maize. <i>Plant Cell</i> , 2021, 33, 901-916.	3.1	22
8215	<i>Pichia galeiformis</i> Induces Resistance in Postharvest Citrus by Activating the Phenylpropanoid Biosynthesis Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 2619-2631.	2.4	65
8216	<i>Methylobacterium thermophilum</i> AP8, a Novel Methane- and Hydrogen-Oxidizing Bacterium Isolated From Volcanic Soil on Pantelleria Island, Italy. <i>Frontiers in Microbiology</i> , 2021, 12, 637762.	1.5	14
8217	Phenotypic Resemblance to Neuropsychiatric Disorder and Altered mRNA Profiles in Cortex and Hippocampus Underlying <i>IL15R1</i> Knockout. <i>Frontiers in Neuroscience</i> , 2020, 14, 582279.	1.4	4
8218	Comparative transcriptome analysis of sesquiterpene biosynthesis and functional characterization of sesquiterpene synthases in <i>Leonurus sibiricus</i> L. <i>Planta</i> , 2021, 253, 71.	1.6	5
8219	Galaxy and MEAN Stack to Create a User-Friendly Workflow for the Rational Optimization of Cancer Chemotherapy. <i>Frontiers in Genetics</i> , 2021, 12, 624259.	1.1	6
8220	Alzheimer's Risk Gene <i>TREM2</i> Determines Functional Properties of New Type of Human iPSC-Derived Microglia. <i>Frontiers in Immunology</i> , 2020, 11, 617860.	2.2	32
8221	Gene duplication at the <i>Fascicled ear1</i> locus controls the fate of inflorescence meristem cells in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	16

#	ARTICLE	IF	CITATIONS
8222	CIRCexplorer pipelines for circRNA annotation and quantification from non-polyadenylated RNA-seq datasets. <i>Methods</i> , 2021, 196, 3-10.	1.9	18
8223	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. <i>Journal of Dairy Science</i> , 2021, 104, 1928-1950.	1.4	19
8224	An Alternative Splicing Variant of PtRD26 Delays Leaf Senescence by Regulating Multiple NAC Transcription Factors in <i>Populus</i> . <i>Plant Cell</i> , 2021, 33, 1594-1614.	3.1	74
8225	Two Tomato ( <i>Solanum lycopersicum</i> ) Thaumatin-Like Protein Genes Confer Enhanced Resistance to Late Blight ( <i>Phytophthora infestans</i> ). <i>Phytopathology</i> , 2021, 111, 1790-1799.	1.1	3
8226	WACS: improving ChIP-seq peak calling by optimally weighting controls. <i>BMC Bioinformatics</i> , 2021, 22, 69.	1.2	3
8227	Comparative Transcriptomics and RNA-Seq-Based Bulk Segregant Analysis Reveals Genomic Basis Underlying <i>Cronartium ribicola</i> vcr2 Virulence. <i>Frontiers in Microbiology</i> , 2021, 12, 602812.	1.5	6
8228	Transcriptome-Wide High-Throughput m6A Sequencing of Differential m6A Methylation Patterns in the Human Rheumatoid Arthritis Fibroblast-Like Synoviocytes Cell Line MH7A. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 575-586.	1.6	30
8229	De Novo Venom-Gland Transcriptomics of Spine-Bellied Sea Snake ( <i>Hydrophis curtus</i> ) from Penang, Malaysia—Next-Generation Sequencing, Functional Annotation and Toxinological Correlation. <i>Toxins</i> , 2021, 13, 127.	1.5	9
8230	A snapshot of translation in <i>Mycobacterium tuberculosis</i> during exponential growth and nutrient starvation revealed by ribosome profiling. <i>Cell Reports</i> , 2021, 34, 108695.	2.9	16
8231	Space: the final frontier – achieving single-cell, spatially resolved transcriptomics in plants. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 179-188.	1.1	13
8232	Extensive profiling of the expressions of tRNAs and tRNA-derived fragments (tRFs) reveals the complexities of tRNA and tRF populations in plants. <i>Science China Life Sciences</i> , 2021, 64, 495-511.	2.3	23
8233	Comparative analysis of embryo proper and suspensor transcriptomes in plant embryos with different morphologies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
8234	Optimized expression of Hfq protein increases <i>Escherichia coli</i> growth. <i>Journal of Biological Engineering</i> , 2021, 15, 7.	2.0	5
8235	Identification of a Glycolysis-Related LncRNA Signature to Predict Survival in Diffuse Glioma Patients. <i>Frontiers in Oncology</i> , 2020, 10, 597877.	1.3	12
8236	Freshwater sponge hosts and their green algae symbionts: a tractable model to understand intracellular symbiosis. <i>PeerJ</i> , 2021, 9, e10654.	0.9	11
8237	Integrated metabolic profiling and transcriptome analysis of pigment accumulation in <i>Lonicera japonica</i> flower petals during colour-transition. <i>BMC Plant Biology</i> , 2021, 21, 98.	1.6	36
8238	Uniform genomic data analysis in the NCI Genomic Data Commons. <i>Nature Communications</i> , 2021, 12, 1226.	5.8	61
8239	Electrokinetic identification of ribonucleotide monophosphates (rNMPs) using thermoplastic nanochannels. <i>Journal of Chromatography A</i> , 2021, 1638, 461892.	1.8	7

#	ARTICLE	IF	CITATIONS
8240	NF- $\kappa$ B pathway play a role in SCD1 deficiency-induced ceramide <i>de novo</i> synthesis. <i>Cancer Biology and Therapy</i> , 2021, 22, 164-174.	1.5	6
8241	De Novo Transcriptomic Analyses Revealed Some Detoxification Genes and Related Pathways Responsive to Noposion Yihaogong <sup>®</sup> 5% EC (Lambda-Cyhalothrin 5%) Exposure in <i>Spodoptera frugiperda</i> Third-Instar Larvae. <i>Insects</i> , 2021, 12, 132.	1.0	16
8242	Transcriptome Analysis of Responses to Dengue Virus 2 Infection in <i>Aedes albopictus</i> (Skuse) C6/36 Cells. <i>Viruses</i> , 2021, 13, 343.	1.5	6
8243	Improving isobutanol tolerance and titers through EMS mutagenesis in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	5
8244	RNA binding protein GNL3 up-regulates IL24 and PTN to promote the development of osteoarthritis. <i>Life Sciences</i> , 2021, 267, 118926.	2.0	11
8245	A chromosome-level genome of the mud crab ( <i>Scylla paramamosain</i> estampador) provides insights into the evolution of chemical and light perception in this crustacean. <i>Molecular Ecology Resources</i> , 2021, 21, 1299-1317.	2.2	17
8246	Metabolomic and transcriptional profiling reveals bioenergetic stress and activation of cell death and inflammatory pathways <i>in vivo</i> after neuronal deletion of NAMPT. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2021, 41, 0271678X2199262.	2.4	12
8247	Cross-species RNA-seq for deciphering host-microbe interactions. <i>Nature Reviews Genetics</i> , 2021, 22, 361-378.	7.7	52
8248	Splicing regulation in brain and testis: common themes for highly specialized organs. <i>Cell Cycle</i> , 2021, 20, 480-489.	1.3	22
8249	Sialotranscriptomics of the argasid tick <i>Ornithodoros moubata</i> along the trophogonic cycle. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009105.	1.3	16
8250	Non-canonical PD-1 signaling in cancer and its potential implications in clinic. , 2021, 9, e001230.		15
8251	DNA methylation analysis improves the prognostication of acute myeloid leukemia. <i>EJHaem</i> , 2021, 2, 211-218.	0.4	5
8252	<i>Escherichia coli</i> segments its controls on carbon-dependent gene expression into global and specific regulations. <i>Microbial Biotechnology</i> , 2021, 14, 1084-1106.	2.0	4
8253	Postharvest Dehydration Temperature Modulates the Transcriptomic Programme and Flavonoid Profile of Grape Berries. <i>Foods</i> , 2021, 10, 687.	1.9	11
8254	Application of a dissolved oxygen control strategy to increase the expression of <i>Streptococcus suis</i> glutamate dehydrogenase in <i>Escherichia coli</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 60.	1.7	3
8255	Identifying Novel Cell Glycolysis-Related Gene Signature Predictive of Overall Survival in Gastric Cancer. <i>BioMed Research International</i> , 2021, 2021, 1-12.	0.9	5
8256	Multiplexed Analysis of Retinal Gene Expression and Chromatin Accessibility Using scRNA-Seq and scATAC-Seq. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	2
8257	Comparative Transcriptome Analysis of Early- and Late-Bolting Traits in Chinese Cabbage ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT <sub>11</sub> /Overlock	1.1	11

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8258	Identification and validation of a five-lncRNA prognostic signature related to Glioma using bioinformatics analysis. <i>BMC Cancer</i> , 2021, 21, 251.	1.1	9
8259	Transcriptome Analysis Unravels Key Factors Involved in Response to Potassium Deficiency and Feedback Regulation of K <sup>+</sup> Uptake in Cotton Roots. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3133.	1.8	15
8260	An integrated transcriptomic and proteomic approach to identify the main <i>Torymus sinensis</i> venom components. <i>Scientific Reports</i> , 2021, 11, 5032.	1.6	18
8261	Integrated transcriptome and in vitro analysis revealed antiproliferative effects on human gastric cancer cells by a benzimidazole-quinoline copper(II) complex. <i>Process Biochemistry</i> , 2021, 102, 286-295.	1.8	8
8262	Mutation of the Cytochrome P450 <i>CYP360A8</i> Gene Increases Sensitivity to Paraquat in <i>Daphnia magna</i> . <i>Environmental Toxicology and Chemistry</i> , 2021, 40, 1279-1288.	2.2	17
8263	Construction and Application of an <i>Escherichia coli</i> Strain Lacking 62 Genes Responsible for the Biosynthesis of Enterobacterial Common Antigen and Flagella. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 4153-4163.	2.4	6
8264	Deep sequencing of the <i>Sanghuangporus vaninii</i> transcriptome reveals dynamic landscapes of candidate genes involved in the biosynthesis of active compounds. <i>Archives of Microbiology</i> , 2021, 203, 2315-2324.	1.0	9
8265	Transcriptome and metabolome analyses reveal the pivotal role of hydrogen sulfide in promoting submergence tolerance in <i>Arabidopsis</i> . <i>Environmental and Experimental Botany</i> , 2021, 183, 104365.	2.0	17
8266	Structure-based decoupling of the pro- and anti-inflammatory functions of interleukin-10. <i>Science</i> , 2021, 371, .	6.0	79
8267	Evolutionary Changes in the Interaction of miRNA With mRNA of Candidate Genes for Parkinson's Disease. <i>Frontiers in Genetics</i> , 2021, 12, 647288.	1.1	6
8268	Identification of a putative candidate gene encoding 7-dehydrocholesterol reductase involved in brassinosteroids biosynthesis for compact plant architecture in Cucumber ( <i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2023-2034.	1.8	9
8269	Combined Transcriptome Analysis Reveals the Ovule Abortion Regulatory Mechanisms in the Female Sterile Line of <i>Pinus tabulaeformis</i> Carr.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3138.	1.8	0
8270	SMIXnorm: Fast and Accurate RNA-Seq Data Normalization for Formalin-Fixed Paraffin-Embedded Samples. <i>Frontiers in Genetics</i> , 2021, 12, 650795.	1.1	2
8272	Transcriptomic, Biochemical, and Morphological Study Reveals the Mechanism of Inhibition of <i>Pseudopestalotiopsis camelliae-sinensis</i> by Phenazine-1-Carboxylic Acid. <i>Frontiers in Microbiology</i> , 2021, 12, 618476.	1.5	8
8273	Comparative transcriptome analysis of the gills of <i>Procambarus clarkii</i> provide novel insights into the response mechanism of ammonia stress tolerance. <i>Molecular Biology Reports</i> , 2021, 48, 2611-2618.	1.0	10
8274	Single-cell RNA sequencing: A new opportunity for retinal research. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1652.	3.2	2
8275	Unveiling the long non-coding RNA profile of porcine reproductive and respiratory syndrome virus-infected porcine alveolar macrophages. <i>BMC Genomics</i> , 2021, 22, 177.	1.2	11
8276	A MAPK/miR-29 Axis Suppresses Melanoma by Targeting MAFG and MYBL2. <i>Cancers</i> , 2021, 13, 1408.	1.7	16

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8277	Transcriptomic analysis identifies upregulation of secreted phosphoprotein $\hat{A}$ 1 in silicotic rats. <i>Experimental and Therapeutic Medicine</i> , 2021, 21, 579.	0.8	9
8278	Genome-wide transcriptome profiling uncovers differential miRNAs and lncRNAs in ovaries of Hu sheep at different developmental stages. <i>Scientific Reports</i> , 2021, 11, 5865.	1.6	16
8279	Transcriptomic and Metabolomic Basis of Short- and Long-Term Post-Harvest UV-C Application in Regulating Grape Berry Quality Development. <i>Foods</i> , 2021, 10, 625.	1.9	13
8280	The mechanism of sesame resistance against <i>Macrophomina phaseolina</i> was revealed via a comparison of transcriptomes of resistant and susceptible sesame genotypes. <i>BMC Plant Biology</i> , 2021, 21, 159.	1.6	16
8281	Initial Hepatitis C Virus Infection of Adult Hepatocytes Triggers a Temporally Structured Transcriptional Program Containing Diverse Pro- and Antiviral Elements. <i>Journal of Virology</i> , 2021, 95, .	1.5	13
8282	The phytotoxin COR induces transcriptional reprogramming of photosynthetic, hormonal and defence networks in tomato. <i>Plant Biology</i> , 2021, 23, 69-79.	1.8	10
8283	Diapause vs. reproductive programs: transcriptional phenotypes in a keystone copepod. <i>Communications Biology</i> , 2021, 4, 426.	2.0	16
8284	The case for using mapped exonic non-duplicate reads when reporting RNA-sequencing depth: examples from pediatric cancer datasets. <i>GigaScience</i> , 2021, 10, .	3.3	2
8285	Transcription factor WRKY22 regulates canker susceptibility in sweet orange ( <i>Citrus sinensis</i> Osbeck) by enhancing cell enlargement and CsLOB1 expression. <i>Horticulture Research</i> , 2021, 8, 50.	2.9	35
8286	RNA $\hat{E}$ seq analysis of knocking out the neuroprotective proton $\hat{E}$ sensitive GPR68 on basal and acute ischemia $\hat{E}$ induced transcriptome changes and signaling in mouse brain. <i>FASEB Journal</i> , 2021, 35, e21461.	0.2	9
8287	Long, Noncoding RNA Dysregulation in Glioblastoma. <i>Cancers</i> , 2021, 13, 1604.	1.7	18
8288	Exploring TERRA during <i>Leishmania major</i> developmental cycle and continuous in vitro passages. <i>International Journal of Biological Macromolecules</i> , 2021, 174, 573-586.	3.6	9
8289	Fresh Crab Plays an Important Role as a Nutrient Reservoir for the Rapid Propagation of <i>Vibrio vulnificus</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 645860.	1.5	1
8290	Comparative transcriptome and metabolome analysis of <i>Ostrinia furnacalis</i> female adults under UV-A exposure. <i>Scientific Reports</i> , 2021, 11, 6797.	1.6	8
8291	Purification and characterization of a novel and conserved TPR-domain protein that binds both Hsp90 and Hsp70 and is expressed in all developmental stages of <i>Leishmania major</i> . <i>Biochimie</i> , 2021, 182, 51-60.	1.3	2
8292	Transcriptome from opaque cornea of Fanconi anemia patient uncovers fibrosis and two connected players. <i>Molecular Genetics and Metabolism Reports</i> , 2021, 26, 100712.	0.4	0
8293	Characterization of Pre $\hat{E}$ mRNA Splicing and Spliceosomal Machinery in <i>Porphyridium purpureum</i> and Evolutionary Implications for Red Algae. <i>Journal of Eukaryotic Microbiology</i> , 2021, 68, e12844.	0.8	5
8294	Decoding the interspecies interaction in anammox process with inorganic feeding through metagenomic and metatranscriptomic analysis. <i>Journal of Cleaner Production</i> , 2021, 288, 125691.	4.6	33

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8295	The Role of lncRNA AF117829.1 in the Immunological Pathogenesis of Severe Aplastic Anaemia. <i>Oxidative Medicine and Cellular Longevity</i> , 2021, 2021, 1-19.	1.9	1
8296	High oil accumulation in tuber of yellow nutsedge compared to purple nutsedge is associated with more abundant expression of genes involved in fatty acid synthesis and triacylglycerol storage. <i>Biotechnology for Biofuels</i> , 2021, 14, 54.	6.2	6
8297	Discovering the Mechanisms of Wikstroelide E as a Potential HIV-Latency-Reversing Agent by Transcriptome Profiling. <i>Journal of Natural Products</i> , 2021, 84, 1022-1033.	1.5	10
8299	Immune-related genes of the larval <i>Holotrichia parallela</i> in response to entomopathogenic nematodes <i>Heterorhabditis beicheriana</i> LF. <i>BMC Genomics</i> , 2021, 22, 192.	1.2	7
8301	Growth on Formic Acid Is Dependent on Intracellular pH Homeostasis for the Thermoacidophilic Methanotroph <i>Methylacidiphilum</i> sp. RTK17.1. <i>Frontiers in Microbiology</i> , 2021, 12, 651744.	1.5	12
8302	smiFISH and embryo segmentation for single-cell multi-gene RNA quantification in arthropods. <i>Communications Biology</i> , 2021, 4, 352.	2.0	20
8304	Transcriptomic analysis provides insights into candidate genes and molecular pathways involved in growth of Manila clam <i>Ruditapes philippinarum</i> . <i>Functional and Integrative Genomics</i> , 2021, 21, 341-353.	1.4	13
8305	IRF1 governs the differential interferon-stimulated gene responses in human monocytes and macrophages by regulating chromatin accessibility. <i>Cell Reports</i> , 2021, 34, 108891.	2.9	46
8306	Transcriptome Analysis Identifies Candidate Genes and Signaling Pathways Associated With Feed Efficiency in Xiayan Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 607719.	1.1	12
8307	Transcriptional Analyses of Acute Exposure to Methylmercury on Erythrocytes of Loggerhead Sea Turtle. <i>Toxics</i> , 2021, 9, 70.	1.6	2
8308	A Comparative Transcriptome Analysis of Human and Porcine Choroid Plexus Cells in Response to <i>Streptococcus suis</i> Serotype 2 Infection Points to a Role of Hypoxia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 639620.	1.8	5
8309	Identification of putative ingestion-related olfactory receptor genes in the Chinese mitten crab ( <i>Eriocheir japonica sinensis</i> ). <i>Genes and Genomics</i> , 2021, 43, 479-490.	0.5	1
8310	RGB1 Regulates Grain Development and Starch Accumulation Through Its Effect on OsYUC11-Mediated Auxin Biosynthesis in Rice Endosperm Cells. <i>Frontiers in Plant Science</i> , 2021, 12, 585174.	1.7	16
8312	Network Analyses Predict Small RNAs That Might Modulate Gene Expression in the Testis and Epididymis of <i>Bos indicus</i> Bulls. <i>Frontiers in Genetics</i> , 2021, 12, 610116.	1.1	7
8314	Comprehensive RNA-Seq Analysis of Potential Therapeutic Targets of Ganâ€œDouâ€œFuâ€œMu Decoction for Treatment of Wilson Disease Using a Toxic Milk Mouse Model. <i>Frontiers in Pharmacology</i> , 2021, 12, 622268.	1.6	5
8315	Nitric oxide donor sodium nitroprusside-induced transcriptional changes and hypocrellin biosynthesis of <i>Shiraia</i> sp. S9. <i>Microbial Cell Factories</i> , 2021, 20, 92.	1.9	13
8317	Transcriptomics analysis reveals the effect of <i>Broussonetia papyrifera</i> L. fermented feed on meat quality traits in fattening lamb. <i>PeerJ</i> , 2021, 9, e11295.	0.9	8
8319	Integrated analysis of miRNAome and transcriptome reveals miRNA-mRNA network regulation in <i>Vibrio alginolyticus</i> infected thick shell mussel <i>Mytilus coruscus</i> . <i>Molecular Immunology</i> , 2021, 132, 217-226.	1.0	6



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8320	Transcriptome-Wide Analyses Provide Insights into Development of the <i>Hedychium coronarium</i> Flower, Revealing Potential Roles of PTL. <i>Journal of Plant Biology</i> , 2021, 64, 431-445.	0.9	2
8321	Construction of an <i>Escherichia coli</i> Strain Lacking Fimbriae by Deleting 64 Genes and Its Application for Efficient Production of Poly(3-Hydroxybutyrate) and $\alpha$ -Threonine. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0038121.	1.4	6
8322	Sharing biological data: why, when, and how. <i>FEBS Letters</i> , 2021, 595, 847-863.	1.3	26
8323	Coordinated interactions between endothelial cells and macrophages in the islet microenvironment promote $\beta$ cell regeneration. <i>Npj Regenerative Medicine</i> , 2021, 6, 22.	2.5	14
8324	Transcriptome profiling of runner formation induced by exogenous gibberellin in <i>Fragaria vesca</i> . <i>Scientia Horticulturae</i> , 2021, 281, 109966.	1.7	5
8325	Biomarkers of cholestasis. <i>Biomarkers in Medicine</i> , 2021, 15, 437-454.	0.6	11
8326	Toxicity of silver nanoparticles (AgNPs) in the model ciliate <i>Paramecium multimicronucleatum</i> : Molecular mechanisms of activation are dose- and particle size-dependent. <i>European Journal of Protistology</i> , 2021, 81, 125792.	0.5	2
8327	Transcriptomic investigation of embryonic pectoral muscle reveals increased myogenic processes in Shitou geese compared to Wuzong geese. <i>British Poultry Science</i> , 2021, 62, 650-657.	0.8	9
8328	Comparative Transcriptome Analysis of Key Genes and Pathways Activated in Response to Fat Deposition in Two Sheep Breeds With Distinct Tail Phenotype. <i>Frontiers in Genetics</i> , 2021, 12, 639030.	1.1	14
8329	Actin-Related Protein 4 Interacts with PIE1 and Regulates Gene Expression in <i>Arabidopsis</i> . <i>Genes</i> , 2021, 12, 520.	1.0	8
8330	Transcriptomic and Physiological Analysis Reveal That $\Delta$ -Linolenic Acid Biosynthesis Responds to Early Chilling Tolerance in Pumpkin Rootstock Varieties. <i>Frontiers in Plant Science</i> , 2021, 12, 669565.	1.7	15
8331	Identification of the molecular regulation of differences in lipid deposition in dedifferentiated preadipocytes from different chicken tissues. <i>BMC Genomics</i> , 2021, 22, 232.	1.2	13
8332	Non-linear Normalization for Non-UMI Single Cell RNA-Seq. <i>Frontiers in Genetics</i> , 2021, 12, 612670.	1.1	3
8333	Developing a Riboswitch-Mediated Regulatory System for Metabolic Flux Control in Thermophilic <i>Bacillus methanolicus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4686.	1.8	6
8334	High ELF4 expression in human cancers is associated with worse disease outcomes and increased resistance to anticancer drugs. <i>PLoS ONE</i> , 2021, 16, e0248984.	1.1	14
8335	Endosperm-based incompatibilities in hybrid monkeyflowers. <i>Plant Cell</i> , 2021, 33, 2235-2257.	3.1	14
8336	Single-Cell Transcriptomics: Current Methods and Challenges in Data Acquisition and Analysis. <i>Frontiers in Neuroscience</i> , 2021, 15, 591122.	1.4	53
8337	Transcriptome integrated metabolic modeling of carbon assimilation underlying storage root development in cassava. <i>Scientific Reports</i> , 2021, 11, 8758.	1.6	8

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8338	The protective effect and mechanism of epidermal growth factor on necrotizing enterocolitis in a neonatal rat model. <i>Translational Pediatrics</i> , 2021, 10, 900-913.	0.5	3
8339	SMART approaches for genome-wide analyses of skeletal muscle stem and niche cells. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2021, 56, 284-300.	2.3	0
8340	Sequence deeper without sequencing more: Bayesian resolution of ambiguously mapped reads. <i>PLoS Computational Biology</i> , 2021, 17, e1008926.	1.5	8
8341	Polee: RNA-Seq analysis using approximate likelihood. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab046.	1.5	1
8342	<tt>pyrpipe</tt>: a Python package for RNA-Seq workflows. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab049.	1.5	14
8343	Genomic and transcriptomic studies on chilling injury in peach and nectarine. <i>Postharvest Biology and Technology</i> , 2021, 174, 111444.	2.9	16
8344	Identification of two UDP-glycosyltransferases involved in the main oleanane-type ginsenosides in <i>Panax japonicus</i> var. major. <i>Planta</i> , 2021, 253, 91.	1.6	11
8345	Identification of key regulators responsible for dysregulated networks in osteoarthritis by large-scale expression analysis. <i>Journal of Orthopaedic Surgery and Research</i> , 2021, 16, 259.	0.9	8
8346	Transcriptome Analysis Provides Insights into the Mechanism of Astaxanthin Enrichment in a Mutant of the Ridgetail White Prawn <i>Exopalaemon carinicauda</i> . <i>Genes</i> , 2021, 12, 618.	1.0	8
8347	Important ecophysiological roles of non-dominant Actinobacteria in plant residue decomposition, especially in less fertile soils. <i>Microbiome</i> , 2021, 9, 84.	4.9	87
8348	Physiological and Transcriptomic Analysis Provide Insight into Low Temperature Enhancing Hypericin Biosynthesis in <i>Hypericum perforatum</i> . <i>Molecules</i> , 2021, 26, 2294.	1.7	5
8350	Integrated Analysis of the Transcriptome and Metabolome Revealed Candidate Genes Involved in GA3-Induced Dormancy Release in <i>Leymus chinensis</i> Seeds. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4161.	1.8	10
8351	Combined Transcriptomic and Proteomic Analysis of <i>Myzus persicae</i> , the Green Peach Aphid, Infected with Cucumber Mosaic Virus. <i>Insects</i> , 2021, 12, 372.	1.0	12
8352	Identification of transcriptional subtypes in lung adenocarcinoma and squamous cell carcinoma through integrative analysis of microarray and RNA sequencing data. <i>Scientific Reports</i> , 2021, 11, 8709.	1.6	8
8353	The KbvR Regulator Contributes to Capsule Production, Outer Membrane Protein Biosynthesis, Antiphagocytosis, and Virulence in <i>Klebsiella pneumoniae</i> . <i>Infection and Immunity</i> , 2021, 89, .	1.0	5
8354	Comprehensive RNA-Seq Profiling Reveals Temporal and Tissue-Specific Changes in Gene Expression in Spragueâ€Dawley Rats as Response to Heat Stress Challenges. <i>Frontiers in Genetics</i> , 2021, 12, 651979.	1.1	11
8355	Ovarian transcriptomic analysis of black Muscovy duck at the early, peak and late egg-laying stages. <i>Gene</i> , 2021, 777, 145449.	1.0	8
8356	RNA alternative splicing prediction with discrete compositional energy network. , 2021, , .		2

#	ARTICLE	IF	CITATIONS
8357	Proteomic and Transcriptomic Analyses Reveal Pathological Changes in the Entorhinal Cortex Region that Correlate Well with Dysregulation of Ion Transport in Patients with Alzheimer's Disease. <i>Molecular Neurobiology</i> , 2021, 58, 4007-4027.	1.9	10
8358	Integration of Transformative Platforms for the Discovery of Causative Genes in Cardiovascular Diseases. <i>Cardiovascular Drugs and Therapy</i> , 2021, 35, 637-654.	1.3	2
8359	The histone variant SL_H2A.Z regulates carotenoid biosynthesis and gene expression during tomato fruit ripening. <i>Horticulture Research</i> , 2021, 8, 85.	2.9	18
8360	Estimation of peptide elongation times from ribosome profiling spectra. <i>Nucleic Acids Research</i> , 2021, 49, 5124-5142.	6.5	5
8361	Study on the mechanism of production of Î³-PGA and nattokinase in <i>Bacillus subtilis</i> natto based on RNA-seq analysis. <i>Microbial Cell Factories</i> , 2021, 20, 83.	1.9	21
8362	Transcriptional and Metabolic Response of Wine-Related <i>Lactiplantibacillus plantarum</i> to Different Conditions of Aeration and Nitrogen Availability. <i>Fermentation</i> , 2021, 7, 68.	1.4	3
8363	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021, 22, 121.	3.8	51
8364	Antennal transcriptome sequencing and identification of candidate chemoreceptor proteins from an invasive pest, the American palm weevil, <i>Rhynchophorus palmarum</i> . <i>Scientific Reports</i> , 2021, 11, 8334.	1.6	17
8365	A new era for plant science: spatial single-cell transcriptomics. <i>Current Opinion in Plant Biology</i> , 2021, 60, 102041.	3.5	51
8366	The tissue protective functions of interleukin-22 can be decoupled from pro-inflammatory actions through structure-based design. <i>Immunity</i> , 2021, 54, 660-672.e9.	6.6	36
8367	Integrated metabolomics and transcriptomics reveal the differences in fruit quality of the red and white <i>Fragaria pentaphylla</i> morphs. <i>Food Bioscience</i> , 2021, 40, 100896.	2.0	9
8368	Integrated transcriptomics and metabolites at different growth stages reveals the regulation mechanism of bolting and flowering of <i>Angelica sinensis</i> . <i>Plant Biology</i> , 2021, 23, 574-582.	1.8	13
8369	Kaempferol induces ROS-dependent apoptosis in pancreatic cancer cells via TGM2-mediated Akt/mTOR signaling. <i>BMC Cancer</i> , 2021, 21, 396.	1.1	69
8370	Metabolic, Organoleptic and Transcriptomic Impact of <i>Saccharomyces cerevisiae</i> Genes Involved in the Biosynthesis of Linear and Substituted Esters. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4026.	1.8	4
8371	<i>Leishmania major</i> RUVBL1 has a hexameric conformation in solution and, in the presence of RUVBL2, forms a heterodimer with ATPase activity. <i>Archives of Biochemistry and Biophysics</i> , 2021, 703, 108841.	1.4	4
8372	3D Bioprinting Allows the Establishment of Long-Term 3D Culture Model for Chronic Lymphocytic Leukemia Cells. <i>Frontiers in Immunology</i> , 2021, 12, 639572.	2.2	26
8374	A novel diagnostic signature based on three circulating exosomal miRNAs for chronic obstructive pulmonary disease. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 717.	0.8	12
8375	Studies on the control effect of <i>Bacillus subtilis</i> on wheat powdery mildew. <i>Pest Management Science</i> , 2021, 77, 4375-4382.	1.7	20

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8376	Molecular insights into plant desiccation tolerance: transcriptomics, proteomics and targeted metabolite profiling in <i>Craterostigma plantagineum</i> . <i>Plant Journal</i> , 2021, 107, 377-398.	2.8	40
8377	Transcriptome analysis reveals hub genes in the hepatopancreas of <i>Exopalaemon carinicauda</i> in response to hypoxia and reoxygenation. <i>Aquaculture International</i> , 2021, 29, 1785-1811.	1.1	2
8378	Anti-bias training for (sc)RNA-seq: experimental and computational approaches to improve precision. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	8
8379	Transcriptome and metabolite profiling analyses provide insight into volatile compounds of the apple cultivar 'Ruixue'™ and its parents during fruit development. <i>BMC Plant Biology</i> , 2021, 21, 231.	1.6	33
8380	In vitro transcriptomes analysis identifies some special genes involved in pathogenicity difference of the <i>Beauveria bassiana</i> against different insect hosts. <i>Microbial Pathogenesis</i> , 2021, 154, 104824.	1.3	12
8381	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	1.2	4
8382	Supplemental Effects of Functional Oils on the Modulation of Mucosa-Associated Microbiota, Intestinal Health, and Growth Performance of Nursery Pigs. <i>Animals</i> , 2021, 11, 1591.	1.0	17
8384	Integrated omics analyses reveal differential gene expression and potential for cooperation between denitrifying polyphosphate and glycogen accumulating organisms. <i>Environmental Microbiology</i> , 2021, 23, 3274-3293.	1.8	17
8385	Liver Transcriptome Dynamics During Hibernation Are Shaped by a Shifting Balance Between Transcription and RNA Stability. <i>Frontiers in Physiology</i> , 2021, 12, 662132.	1.3	11
8386	Aging affects artemisinin synthesis in <i>Artemisia annua</i> . <i>Scientific Reports</i> , 2021, 11, 11297.	1.6	1
8387	Omics-Based Identification of Shared and Gender Disparity Routes in Hras12V-Induced Hepatocarcinogenesis: An Important Role for Dlk1-Dio3 Genomic Imprinting Region. <i>Frontiers in Genetics</i> , 2021, 12, 620594.	1.1	3
8388	Genome-wide DNA methylation analysis and biochemical responses provide insights into the initial domestication of halophyte <i>Puccinellia tenuiflora</i> . <i>Plant Cell Reports</i> , 2021, 40, 1181-1197.	2.8	2
8389	A systematic comparison of normalization methods for eQTL analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
8390	Facultative symbiosis with a saprotrophic soil fungus promotes potassium uptake in American sweetgum trees. <i>Plant, Cell and Environment</i> , 2021, 44, 2793-2809.	2.8	23
8391	Integrated study of circRNA, lncRNA, miRNA, and mRNA networks in mediating the effects of testicular heat exposure. <i>Cell and Tissue Research</i> , 2021, 386, 127-143.	1.5	6
8392	Advances in understanding the molecular pathology of gynecological malignancies: the role and potential of RNA sequencing. <i>International Journal of Gynecological Cancer</i> , 2021, 31, 1159-1164.	1.2	0
8393	Asymmetric expression of homoeologous genes contributes to dietary adaption of an allodiploid hybrid fish derived from <i>Megalobrama amblycephala</i> (♀) × <i>Culter alburnus</i> (♂). <i>BMC Genomics</i> , 2021, 22, 362.	1.2	2
8394	Characterization of the small RNA transcriptomes of cell protrusions and cell bodies of highly metastatic hepatocellular carcinoma cells via RNA sequencing. <i>Oncology Letters</i> , 2021, 22, 568.	0.8	4

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8395	Trimethylamine <i>N</i> -oxide is a new plant molecule that promotes abiotic stress tolerance. <i>Science Advances</i> , 2021, 7, .	4.7	12
8396	Autoactivation of Translation Causes the Bloom of <i>Prorocentrum donghaiense</i> in Harmful Algal Blooms. <i>Journal of Proteome Research</i> , 2021, 20, 3179-3187.	1.8	1
8398	Genome-Centric Metatranscriptomics Analysis Reveals the Role of Hydrochar in Anaerobic Digestion of Waste Activated Sludge. <i>Environmental Science &amp; Technology</i> , 2021, 55, 8351-8361.	4.6	77
8399	Transcriptomic and Metabolomic Studies Reveal Mechanisms of Effects of CPPU-Mediated Fruit-Setting on Attenuating Volatile Attributes of Melon Fruit. <i>Agronomy</i> , 2021, 11, 1007.	1.3	4
8400	Hormone Orchestrates a Hierarchical Transcriptional Cascade That Regulates AI-Induced De Novo Root Regeneration in Tea Nodal Cutting. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 5858-5870.	2.4	6
8401	LTR-retrotransposon dynamics in common fig ( <i>Ficus carica</i> L.) genome. <i>BMC Plant Biology</i> , 2021, 21, 221.	1.6	5
8402	Fitness Costs of Chlorantraniliprole Resistance Related to the SeNPF Overexpression in the <i>Spodoptera exigua</i> (Lepidoptera: Noctuidae). <i>International Journal of Molecular Sciences</i> , 2021, 22, 5027.	1.8	6
8403	Evaluation of morphological traits, hormonal metabolism, and transcriptional abundance in bitter melon ( <i>Momordica charantia</i> L.) plants in response to ethephon inducement. <i>Scientia Horticulturae</i> , 2021, 282, 110033.	1.7	3
8404	Comparative transcriptomic analysis reveals an association of gibel carp fatty liver with ferroptosis pathway. <i>BMC Genomics</i> , 2021, 22, 328.	1.2	7
8405	Metabolome and Transcriptome Integration Reveals Insights Into Flavor Formation of "Crimson" Watermelon Flesh During Fruit Development. <i>Frontiers in Plant Science</i> , 2021, 12, 629361.	1.7	24
8406	Systematic analysis of differentially expressed ZmMYB genes related to drought stress in maize. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1295-1309.	1.4	6
8407	Comparative analysis of latex transcriptomes reveals the potential mechanisms underlying rubber molecular weight variations between the <i>Hevea brasiliensis</i> clones RRIM600 and Reyan7-33-97. <i>BMC Plant Biology</i> , 2021, 21, 244.	1.6	6
8408	Antifungal mechanism of <i>Bacillus amyloliquefaciens</i> strain GKT04 against <i>Fusarium</i> wilt revealed using genomic and transcriptomic analyses. <i>MicrobiologyOpen</i> , 2021, 10, e1192.	1.2	13
8409	VvWRKY22 transcription factor interacts with VvSnRK1.1/VvSnRK1.2 and regulates sugar accumulation in grape. <i>Biochemical and Biophysical Research Communications</i> , 2021, 554, 193-198.	1.0	24
8410	<i>Oryzias latipes</i> in <i>Sanya</i> Does Not Contain the Male Sex-Determining Gene <i>dmy</i> . <i>Animals</i> , 2021, 11, 1327.	1.0	7
8411	Spontaneous Cell Detachment and Reattachment in Cancer Cell Lines: An In Vitro Model of Metastasis and Malignancy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4929.	1.8	3
8412	High resolution RNA-seq profiling of genes encoding ribosomal proteins across different organs and developmental stages in <i>Arabidopsis thaliana</i> . <i>Plant Direct</i> , 2021, 5, e00320.	0.8	5
8413	The dissection of R genes and locus Pc5.1 in <i>Phytophthora capsici</i> infection provides a novel view of disease resistance in peppers. <i>BMC Genomics</i> , 2021, 22, 372.	1.2	15

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8414	CSCS: a chromatin state interface for Chinese Spring bread wheat. <i>ABIOTECH</i> , 2021, 2, 357-364.	1.8	3
8415	Implication of a Key Region of Six <i>Bacillus cereus</i> Genes Involved in Siroheme Synthesis, Nitrite Reductase Production and Iron Cluster Repair in the Bacterial Response to Nitric Oxide Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5079.	1.8	4
8417	Fullerene C60 Protects Against Intestinal Injury from Deoxynivalenol Toxicity by Improving Antioxidant Capacity. <i>Life</i> , 2021, 11, 491.	1.1	6
8418	Applications of single-cell and bulk RNA sequencing in onco-immunology. <i>European Journal of Cancer</i> , 2021, 149, 193-210.	1.3	62
8419	Not just shades of grey: life is full of colour for the ocellate river stingray ( <i>Potamotrygon motoro</i> ). <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	8
8420	Effect of fixed-time artificial insemination on corpus luteum gene expression at the day 16 and 25 pregnancy of gilt. <i>Animal Biotechnology</i> , 2021, , 1-9.	0.7	1
8421	Transcriptome analysis of <i>Ehrlichia ruminantium</i> in the ruminant host at the tick bite site and in the tick vector salivary glands. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101646.	1.1	1
8422	Comparative transcriptome combined with biochemical and physiological analyses provide new insights toward cadmium accumulation with two contrasting <i>Nicotiana</i> species. <i>Physiologia Plantarum</i> , 2021, 173, 369-383.	2.6	8
8424	Comparative transcriptome analysis of the gills of <i>Cardisoma armatum</i> provides novel insights into the terrestrial adaptive related mechanism of air exposure stress. <i>Genomics</i> , 2021, 113, 1193-1202.	1.3	8
8425	Benchmarking association analyses of continuous exposures with RNA-seq in observational studies. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
8426	Comparative evaluation of full-length isoform quantification from RNA-Seq. <i>BMC Bioinformatics</i> , 2021, 22, 266.	1.2	15
8427	The Potential Genes Mediate the Pathogenicity of Allogeneic CD4+T Cell in aGVHD Mouse Model. <i>BioMed Research International</i> , 2021, 2021, 1-19.	0.9	2
8428	circRNA landscape of non-pregnant endometrium during the estrus cycle in dairy goats. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1346-1358.	1.7	1
8429	A native conjugative plasmid confers potential selective advantages to plant growth-promoting <i>Bacillus velezensis</i> strain GH1-13. <i>Communications Biology</i> , 2021, 4, 582.	2.0	3
8430	De novo transcriptome analysis and identification of reproduction control genes from the red palm weevil <i>Rhynchophorus ferrugineus</i> . <i>PLoS ONE</i> , 2021, 16, e0251278.	1.1	6
8431	Genome-wide identification and expression analysis of the WRKY transcription factor family in flax ( <i>Linum usitatissimum</i> L.). <i>BMC Genomics</i> , 2021, 22, 375.	1.2	15
8432	Albino seedling lethality 4; Chloroplast 30S Ribosomal Protein S1 is Required for Chloroplast Ribosome Biogenesis and Early Chloroplast Development in Rice. <i>Rice</i> , 2021, 14, 47.	1.7	10
8433	Interaction Between the Intestinal Microbial Community and Transcriptome Profile in Common Carp ( <i>Cyprinus carpio</i> L.). <i>Frontiers in Microbiology</i> , 2021, 12, 659602.	1.5	11

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8434	Tissue-specific transcriptome analyses reveal candidate genes for stilbene, flavonoid and anthraquinone biosynthesis in the medicinal plant <i>Polygonum cuspidatum</i> . <i>BMC Genomics</i> , 2021, 22, 353.	1.2	18
8435	Exposure to 1-Butanol Exemplifies the Response of the Thermoacidophilic Archaeon <i>Sulfolobus acidocaldarius</i> to Solvent Stress. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
8436	Transcriptome Analysis of Light-Regulated Monoterpenes Biosynthesis in Leaves of <i>Mentha canadensis</i> L. <i>Plants</i> , 2021, 10, 930.	1.6	10
8437	Transcriptome analysis of <i>Apis mellifera</i> under benomyl stress to discriminate the gene expression in response to development and immune systems. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2021, 56, 1-12.	0.7	5
8440	Post-diapause transcriptomic restarts: insight from a high-latitude copepod. <i>BMC Genomics</i> , 2021, 22, 409.	1.2	6
8441	Genome-wide DNA methylation and transcription analysis in tongue and biceps femoris muscles of cloned pigs with macroglossia. <i>Animal Genetics</i> , 2021, 52, 608-620.	0.6	1
8442	Post-mating gene expression of Mexican fruit fly females: disentangling the effects of the male accessory glands. <i>Insect Molecular Biology</i> , 2021, 30, 480-496.	1.0	10
8443	Identification of the Potential Gene Regulatory Networks and Therapeutics in Aged Mice With Postoperative Neurocognitive Disorder. <i>Frontiers in Neuroscience</i> , 2021, 15, 689188.	1.4	11
8444	Impact of scaffolding protein TNRC6 paralogs on gene expression and splicing. <i>Rna</i> , 2021, 27, 1004-1016.	1.6	10
8445	Co-expression of hydrolase genes improves seed germination of <i>Sinopodophyllum hexandrum</i> . <i>Industrial Crops and Products</i> , 2021, 164, 113414.	2.5	10
8446	Transcriptome sequencing analysis of primary fibroblasts: a new insight into postoperative abdominal adhesion. <i>Surgery Today</i> , 2021, , 1.	0.7	0
8447	Chaperone-mediated coupling of subunit availability to activation of flagellar Type III secretion. <i>Molecular Microbiology</i> , 2021, 116, 538-549.	1.2	8
8448	Transcriptome Profiling Reveals a Novel Mechanism of Antiviral Immunity Upon Sacbrood Virus Infection in Honey Bee Larvae ( <i>Apis cerana</i> ). <i>Frontiers in Microbiology</i> , 2021, 12, 615893.	1.5	10
8449	Integrative analysis of histomorphology, transcriptome and whole genome resequencing identified DIO2 gene as a crucial gene for the protuberant knob located on forehead in geese. <i>BMC Genomics</i> , 2021, 22, 487.	1.2	5
8451	Transcriptome sequencing and comparative analysis of differentially expressed genes in the roots of <i>Musa Paradisiaca</i> under salt stress. <i>Plant Biotechnology Reports</i> , 2021, 15, 389-401.	0.9	3
8452	De novo Transcriptome Assembly and Comparative Analysis Highlight the Primary Mechanism Regulating the Response to Selenium Stimuli in Oats ( <i>Avena sativa</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 625520.	1.7	2
8453	Linking Chromosomal Silencing With Xist Expression From Autosomal Integrated Transgenes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 693154.	1.8	5
8455	Analysis of lncRNA, miRNA, and mRNA Expression Profiling in Type I IFN and Type II IFN Overexpressed in Porcine Alveolar Macrophages. <i>International Journal of Genomics</i> , 2021, 2021, 1-28.	0.8	5

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8456	A scaling-free minimum enclosing ball method to detect differentially expressed genes for RNA-seq data. <i>BMC Genomics</i> , 2021, 22, 479.	1.2	4
8457	Quasi-essentiality of RNase Y in <i>Bacillus subtilis</i> is caused by its critical role in the control of mRNA homeostasis. <i>Nucleic Acids Research</i> , 2021, 49, 7088-7102.	6.5	12
8458	Downregulation of the photosynthetic machinery and carbon storage signaling pathways mediate La2O3 nanoparticle toxicity on radish taproot formation. <i>Journal of Hazardous Materials</i> , 2021, 411, 124971.	6.5	23
8459	RNA Engineering for Public Health: Innovations in RNA-Based Diagnostics and Therapeutics. <i>Annual Review of Chemical and Biomolecular Engineering</i> , 2021, 12, 263-286.	3.3	8
8460	Functional analysis of colonization factor antigen I positive enterotoxigenic <i>Escherichia coli</i> identifies genes implicated in survival in water and host colonization. <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
8461	Rapid and accurate alignment of nucleotide conversion sequencing reads with HISAT-3N. <i>Genome Research</i> , 2021, 31, 1290-1295.	2.4	104
8462	Selective delignification of poplar wood with a newly isolated white-rot basidiomycete <i>Peniophora incarnata</i> T-7 by submerged fermentation to enhance saccharification. <i>Biotechnology for Biofuels</i> , 2021, 14, 135.	6.2	17
8463	Gene expression profile of the taimen <i>Hucho taimen</i> in response to acute temperature changes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100824.	0.4	2
8464	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. <i>Frontiers in Genetics</i> , 2021, 12, 655707.	1.1	30
8465	Comparative transcriptome between male fertile and male sterile alfalfa ( <i>Medicago varia</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1487-1498.	1.4	2
8466	Comparative transcriptome analysis of <i>Salix cupularis</i> under drought stress. <i>Global Ecology and Conservation</i> , 2021, 27, e01532.	1.0	3
8467	A method to analyze time expression profiles demonstrated in a database of chili pepper fruit development. <i>Scientific Reports</i> , 2021, 11, 13181.	1.6	4
8468	Comparative transcriptome analysis reveals key genes associated with pigmentation in radish ( <i>Raphanus sativus</i> L.) skin and flesh. <i>Scientific Reports</i> , 2021, 11, 11434.	1.6	9
8469	De novo assembly and Transcriptome Analysis of the <i>Momordica charantia</i> Seedlings Responding to methyl jasmonate using 454 pyrosequencing. <i>Gene Expression Patterns</i> , 2021, 40, 119160.	0.3	3
8470	Homeotic transformation from stamen to petal in <i>Lilium</i> is associated with MADS-box genes and hormone signal transduction. <i>Plant Growth Regulation</i> , 2021, 95, 49-64.	1.8	8
8471	Transcriptional responses for biosynthesis of ginsenoside in arbuscular mycorrhizal fungi-treated <i>Panax quinquefolius</i> L. seedlings using RNA-seq. <i>Plant Growth Regulation</i> , 2021, 95, 83-96.	1.8	11
8472	Comparative Transcriptome Analysis Demonstrates the Positive Effect of the Cyclic AMP Receptor Protein Crp on Daptomycin Biosynthesis in <i>Streptomyces roseosporus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 618029.	2.0	6
8473	MicroRNA transcriptome analysis of oriental river prawn <i>Macrobrachium nipponense</i> in responding to starvation stress. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100820.	0.4	2



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8474	Analysis of miRNA and mRNA reveals core interaction networks and pathways of dexamethasone-induced immunosuppression in chicken bursa of Fabricius. <i>Molecular Immunology</i> , 2021, 134, 34-47.	1.0	12
8475	Identification of Key Gene Networks Associated With Cell Wall Components Leading to Flesh Firmness in Watermelon. <i>Frontiers in Plant Science</i> , 2021, 12, 630243.	1.7	14
8476	Target identification for small-molecule discovery in the FOXO3a tumor-suppressor pathway using a biodiverse peptide library. <i>Cell Chemical Biology</i> , 2021, 28, 1602-1615.e9.	2.5	6
8477	TCF11 Has a Potent Tumor-Repressing Effect Than Its Prototypic Nrf1 <sup>±</sup> by Definition of Both Similar Yet Different Regulatory Profiles, With a Striking Disparity From Nrf2. <i>Frontiers in Oncology</i> , 2021, 11, 707032.	1.3	10
8478	How Machine Learning and Statistical Models Advance Molecular Diagnostics of Rare Disorders Via Analysis of RNA Sequencing Data. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 647277.	1.6	12
8479	Large lipid transfer proteins in hepatopancreas of the mud crab <i>Scylla paramamosain</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100801.	0.4	4
8480	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. <i>Journal of Translational Medicine</i> , 2021, 19, 269.	1.8	151
8481	A Tissue-Specific Landscape of Alternative Polyadenylation, lncRNAs, TFs, and Gene Co-expression Networks in <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 705321.	1.7	12
8482	Hydrogen Sulfide Alleviates Alkaline Salt Stress by Regulating the Expression of MicroRNAs in <i>Malus hupehensis</i> Rehd. Roots. <i>Frontiers in Plant Science</i> , 2021, 12, 663519.	1.7	8
8483	MUREN: a robust and multi-reference approach of RNA-seq transcript normalization. <i>BMC Bioinformatics</i> , 2021, 22, 386.	1.2	4
8484	Diagnosis of Fungal Plant Pathogens Using Conventional and Molecular Approaches. , 0, , .		5
8485	<i>Tropilaelaps mercedesae</i> parasitism changes behavior and gene expression in honey bee workers. <i>PLoS Pathogens</i> , 2021, 17, e1009684.	2.1	5
8486	In silico-driven analysis of the <i>Glossina morsitans morsitans</i> antennae transcriptome in response to repellent or attractant compounds. <i>PeerJ</i> , 2021, 9, e11691.	0.9	2
8488	SlbBX20 interacts with the COP9 signalosome subunit SICSN5-2 to regulate anthocyanin biosynthesis by activating SlDFR expression in tomato. <i>Horticulture Research</i> , 2021, 8, 163.	2.9	27
8489	Transcriptomic diversity in longissimus thoracis muscles of Barbari and Changthangi goat breeds of India. <i>Genomics</i> , 2021, 113, 1639-1646.	1.3	10
8491	Comparative Transcriptome and Endophytic Bacterial Community Analysis of <i>Morchella conica</i> SH. <i>Frontiers in Microbiology</i> , 2021, 12, 682356.	1.5	3
8492	Transcriptome and Small RNA Combined Sequencing Analysis of Cold Tolerance in Non-heading Chinese Cabbage. <i>Frontiers in Genetics</i> , 2021, 12, 605292.	1.1	0
8493	Comprehensive Genomic and Transcriptomic Analysis of Three Synchronous Primary Tumours and a Recurrence from a Head and Neck Cancer Patient. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7583.	1.8	3

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8494	Germ cells: ENCODE™s forgotten cell type. <i>Biology of Reproduction</i> , 2021, 105, 761-766.	1.2	0
8495	The <i>Welwitschia</i> genome reveals a unique biology underpinning extreme longevity in deserts. <i>Nature Communications</i> , 2021, 12, 4247.	5.8	51
8496	Machine learning methods to model multicellular complexity and tissue specificity. <i>Nature Reviews Materials</i> , 2021, 6, 717-729.	23.3	13
8497	pMGF505-7R determines pathogenicity of African swine fever virus infection by inhibiting IL-1 $\beta$ and type I IFN production. <i>PLoS Pathogens</i> , 2021, 17, e1009733.	2.1	83
8498	Transcriptome analysis reveals the mechanism associated with dynamic changes in fatty acid and phytosterol content in foxtail millet ( <i>Setaria italica</i> ) during seed development. <i>Food Research International</i> , 2021, 145, 110429.	2.9	15
8499	A Detailed Spatial Expression Analysis of Wing Phenotypes Reveals Novel Patterns of Odorant Binding Proteins in the Soybean Aphid, <i>Aphis glycines</i> . <i>Frontiers in Physiology</i> , 2021, 12, 702973.	1.3	3
8500	Combined analysis of carotenoid metabolites and the transcriptome to reveal the molecular mechanism underlying fruit colouration in zucchini ( <i>Cucurbita pepo</i> L.). <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100021.	0.9	14
8501	MicroRNAs Involved in the Therapeutic Functions of Noni ( <i>Morinda citrifolia</i> L.) Fruit Juice in the Treatment of Acute Gouty Arthritis in Mice Induced with Monosodium Urate. <i>Foods</i> , 2021, 10, 1638.	1.9	7
8502	Analyzing the gonadal transcriptome of the frog <i>Hoplobatrachus rugulosus</i> to identify genes involved in sex development. <i>BMC Genomics</i> , 2021, 22, 552.	1.2	7
8503	Seasonal Variation in Transcriptomic Profiling of <i>Tetrastigma hemsleyanum</i> Fully Developed Tuberos Roots Enriches Candidate Genes in Essential Metabolic Pathways and Phytohormone Signaling. <i>Frontiers in Plant Science</i> , 2021, 12, 659645.	1.7	12
8504	Global transcriptomic changes in glomerular endothelial cells in mice with podocyte depletion and glomerulosclerosis. <i>Cell Death and Disease</i> , 2021, 12, 687.	2.7	5
8505	Common response of dominant plants in typical grassland of Inner Mongolia to long-term overgrazing revealed by transcriptome analysis. <i>Grassland Science</i> , 2021, 67, 352.	0.6	1
8507	Application of single cell genomics to focal epilepsies: A call to action. <i>Brain Pathology</i> , 2021, 31, e12958.	2.1	8
8508	Exploiting Single-Cell Tools in Gene and Cell Therapy. <i>Frontiers in Immunology</i> , 2021, 12, 702636.	2.2	21
8509	Single-cell analysis of mosquito hemocytes identifies signatures of immune cell subtypes and cell differentiation. <i>ELife</i> , 2021, 10, .	2.8	31
8510	Rhizospheric pathogen proliferation and ROS production is associated with premature senescence of the <i>osvha-a1</i> rice mutant. <i>Journal of Experimental Botany</i> , 2021, 72, 7247-7263.	2.4	2
8511	Biochemical and genetic changes revealing the enhanced lipid accumulation in <i>Desmodium</i> sp. mutated by atmospheric and room temperature plasma. <i>Renewable Energy</i> , 2021, 172, 368-381.	4.3	11
8512	Comparative transcriptome analyses of the liver between <i>Xenocypris microlepis</i> and <i>Xenocypris davidi</i> under low copper exposure. <i>Aquatic Toxicology</i> , 2021, 236, 105850.	1.9	5

#	ARTICLE	IF	CITATIONS
8513	Gene network analysis to determine the effect of hypoxia-associated genes on brain damages and tumorigenesis using an avian model. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 100.	1.5	2
8514	Identification and Expression Profile of Chemosensory Genes in the Small Hive Beetle <i>Aethina tumida</i> . <i>Insects</i> , 2021, 12, 661.	1.0	8
8515	Identification and comparative expression analysis of odorant-binding proteins in the reproductive system and antennae of <i>Athetis dissimilis</i> . <i>Scientific Reports</i> , 2021, 11, 13941.	1.6	9
8516	Transcriptome Profiling of <i>Micromelalopha troglodyta</i> (Lepidoptera: Notodontidae) Larvae under Tannin Stress Using Solexa Sequencing Technology. <i>Journal of Entomological Science</i> , 2021, 56, 321-342.	0.2	1
8517	Transcriptome analysis of resistant and susceptible mulberry responses to <i>Meloidogyne enterolobii</i> infection. <i>BMC Plant Biology</i> , 2021, 21, 338.	1.6	5
8518	Differentially expressed genes involved in immune pathways from yellowhead catfish ( <i>Tachysurus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook 340-345.	3.6	8
8519	Transcriptome analysis reveals new insight of duck Tembusu virus (DTMUV)-infected DF-1 cells. <i>Research in Veterinary Science</i> , 2021, 137, 150-158.	0.9	8
8520	Linking plasmid-based beta-lactamases to their bacterial hosts using single-cell fusion PCR. <i>ELife</i> , 2021, 10, .	2.8	18
8521	Comparative Transcriptome Analysis of Milk Somatic Cells During Lactation Between Two Intensively Reared Dairy Sheep Breeds. <i>Frontiers in Genetics</i> , 2021, 12, 700489.	1.1	4
8522	Genetic and Transcriptomic Analysis Reveal the Molecular Basis of Photoperiod-Regulated Flowering in <i>Xishuangbanna Cucumber</i> ( <i>Cucumis sativus</i> L. var. <i>xishuangbannensis</i> Qi et Yuan). <i>Genes</i> , 2021, 12, 1064.	1.0	10
8523	Transcriptome, degradome and physiological analysis provide new insights into the mechanism of inhibition of litchi fruit senescence by melatonin. <i>Plant Science</i> , 2021, 308, 110926.	1.7	23
8524	Comparative Transcriptome Analysis of Human Adipose-Derived Stem Cells Undergoing Osteogenesis in 2D and 3D Culture Conditions. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7939.	1.8	6
8525	Pre-conditioning modifies the TME to enhance solid tumor CAR T cell efficacy and endogenous protective immunity. <i>Molecular Therapy</i> , 2021, 29, 2335-2349.	3.7	51
8526	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021, 39, 1563-1573.	9.4	115
8527	Spatial Transcriptomics: Molecular Maps of the Mammalian Brain. <i>Annual Review of Neuroscience</i> , 2021, 44, 547-562.	5.0	28
8528	Comparative transcriptomic analysis of ovaries from high and low egg-laying <i>Lingyun black</i> bone chickens. <i>Veterinary Medicine and Science</i> , 2021, 7, 1867-1880.	0.6	8
8529	ROS/RNS Balancing, Aerobic Fermentation Regulation and Cell Cycle Control – a Complex Early Trait (CoV-MAC-TED™) for Combating SARS-CoV-2-Induced Cell Reprogramming. <i>Frontiers in Immunology</i> , 2021, 12, 673692.	2.2	12
8530	Olfactory Proteins and Their Expression Profiles in the <i>Eucalyptus</i> Pest <i>Endoclyta signifier</i> Larvae. <i>Frontiers in Physiology</i> , 2021, 12, 682537.	1.3	5

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8531	RNA sequencing identified novel target genes for <i>Adansonia digitata</i> in breast and colon cancer cells. <i>Science Progress</i> , 2021, 104, 003685042110320.	1.0	5
8532	Isolation of cycloeucaleanol cycloisomerase (CYC1) by expressed sequence tag mining in fenugreek ( <i>Trigonella foenum-graecum</i> ). <i>Acta Horticulturae</i> , 2021, , 301-306.	0.1	0
8533	Time-Course Transcriptome Profiling of a Poxvirus Using Long-Read Full-Length Assay. <i>Pathogens</i> , 2021, 10, 919.	1.2	4
8535	Insights into the multitrophic interactions between the biocontrol agent <i>Bacillus subtilis</i> MBI 600, the pathogen <i>Botrytis cinerea</i> and their plant host. <i>Microbiological Research</i> , 2021, 248, 126752.	2.5	24
8536	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. <i>Cell Reports Methods</i> , 2021, 1, 100041.	1.4	3
8537	Sex-Biased Gene Expression of <i>Mesobuthus martensii</i> Collected from Gansu Province, China, Reveals Their Different Therapeutic Potentials. <i>Evidence-based Complementary and Alternative Medicine</i> , 2021, 2021, 1-15.	0.5	3
8538	The epithelial potassium channel Kir7.1 is stimulated by progesterone. <i>Journal of General Physiology</i> , 2021, 153, .	0.9	6
8539	Transcriptional Landscape and Splicing Efficiency in <i>Arabidopsis</i> Mitochondria. <i>Cells</i> , 2021, 10, 2054.	1.8	3
8540	UBCH5 Family Members Differentially Impact Stabilization of Mutant p53 via RNF128 Iso1 During Barrett's Progression to Esophageal Adenocarcinoma. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 13, 129-149.	2.3	2
8541	ACTAR: A novel approach for transcriptome assembly and abundance estimation using an adapted genetic algorithm from RNA-seq data. <i>Computers in Biology and Medicine</i> , 2021, 135, 104646.	3.9	1
8542	Transcriptomics of different tissues of blueberry and diversity analysis of rhizosphere fungi under cadmium stress. <i>BMC Plant Biology</i> , 2021, 21, 389.	1.6	8
8543	Linking circular intronic RNA degradation and function in transcription by RNase H1. <i>Science China Life Sciences</i> , 2021, 64, 1795-1809.	2.3	43
8544	Comparative Transcriptome Analysis to Identify Candidate Genes for FaRCg1 Conferring Resistance Against <i>Colletotrichum gloeosporioides</i> in Cultivated Strawberry ( <i>Fragaria Ananassa</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 730444.	1.1	5
8545	Transcriptomic markers of fungal growth, respiration and carbon-use efficiency. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	6
8546	Utilization of Transcriptome, Small RNA, and Degradome Sequencing to Provide Insights Into Drought Stress and Rewatering Treatment in <i>Medicago ruthenica</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 675903.	1.7	9
8548	Pan-cancer analysis of pathway-based gene expression pattern at the individual level reveals biomarkers of clinical prognosis. <i>Cell Reports Methods</i> , 2021, 1, 100050.	1.4	10
8549	Joint Modeling of RNAseq and Radiomics Data for Glioma Molecular Characterization and Prediction. <i>Frontiers in Medicine</i> , 2021, 8, 705071.	1.2	3
8551	Localized and Systemic Inflammatory Mediators in a Murine Acute Mastitis Model. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4053-4067.	1.6	1

#	ARTICLE	IF	CITATIONS
8552	Microbial signatures in the lower airways of mechanically ventilated COVID-19 patients associated with poor clinical outcome. <i>Nature Microbiology</i> , 2021, 6, 1245-1258.	5.9	101
8553	Transcriptional Analysis of Infection With Early or Late Isolates From the 2013–2016 West Africa Ebola Virus Epidemic Does Not Suggest Attenuated Pathogenicity as a Result of Genetic Variation. <i>Frontiers in Microbiology</i> , 2021, 12, 714817.	1.5	3
8554	High Transcriptional Activity and Diverse Functional Repertoires of Hundreds of Giant Viruses in a Coastal Marine System. <i>MSystems</i> , 2021, 6, e0029321.	1.7	30
8555	Identification and Validation of Four Novel Promoters for Gene Engineering with Broad Suitability across Species. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1154-1162.	0.9	1
8556	Osteogenic ability using porous hydroxyapatite scaffold-based delivery of human placenta-derived mesenchymal stem cells. <i>Experimental and Therapeutic Medicine</i> , 2021, 22, 1091.	0.8	2
8557	Haloalkaliphilic denitrifiers-dependent sulfate-reducing bacteria thrive in nitrate-enriched environments. <i>Water Research</i> , 2021, 201, 117354.	5.3	11
8558	Emerging roles of a pivotal lncRNA SBF2-AS1 in cancers. <i>Cancer Cell International</i> , 2021, 21, 417.	1.8	10
8559	Isoform Age - Splice Isoform Profiling Using Long-Read Technologies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 711733.	1.6	31
8560	Null mutation in <i>sspA</i> of <i>Cronobacter sakazakii</i> influences its tolerance to environmental stress. <i>Canadian Journal of Microbiology</i> , 2021, 67, 902-918.	0.8	0
8561	Characterization and comparative analysis of transcriptional profiles of porcine colostrum and mature milk at different parities. <i>BMC Genomic Data</i> , 2021, 22, 25.	0.7	3
8562	Transcriptome and Metabolome Analyses of the Flowers and Leaves of <i>Chrysanthemum dichrum</i> . <i>Frontiers in Genetics</i> , 2021, 12, 716163.	1.1	6
8564	A systematic evaluation of the computational tools for lncRNA identification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
8565	Extended in vivo transcriptomes of two ascoviruses with different tissue tropisms reveal alternative mechanisms for enhancing virus reproduction in hemolymph. <i>Scientific Reports</i> , 2021, 11, 16402.	1.6	4
8566	Elucidating the Venom Diversity in Sri Lankan Spectacled Cobra ( <i>Naja naja</i> ) through De Novo Venom Gland Transcriptomics, Venom Proteomics and Toxicity Neutralization. <i>Toxins</i> , 2021, 13, 558.	1.5	8
8567	Increase in carbohydrate content and variation in microbiome are related to the drought tolerance of <i>Codonopsis pilosula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 165, 19-35.	2.8	12
8568	Optimal Brassinosteroid Levels Are Required for Soybean Growth and Mineral Nutrient Homeostasis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8400.	1.8	9
8569	Co-culture model of B-cell acute lymphoblastic leukemia recapitulates a transcription signature of chemotherapy-refractory minimal residual disease. <i>Scientific Reports</i> , 2021, 11, 15840.	1.6	16
8570	Comparison of gene expression in the red imported fire ant ( <i>Solenopsis invicta</i> ) under different temperature conditions. <i>Scientific Reports</i> , 2021, 11, 16476.	1.6	8

#	ARTICLE	IF	CITATIONS
8571	Resource Allocation During the Transition to Diazotrophy in <i>Klebsiella oxytoca</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 718487.	1.5	5
8572	Genome Fractionation and Loss of Heterozygosity in Hybrids and Polyploids: Mechanisms, Consequences for Selection, and Link to Gene Function. <i>Molecular Biology and Evolution</i> , 2021, 38, 5255-5274.	3.5	7
8573	A novel melatonin-regulated lncRNA suppresses TPA-induced oral cancer cell motility through replenishing PRUNE2 expression. <i>Journal of Pineal Research</i> , 2021, 71, e12760.	3.4	45
8574	Transcription factor BZR2 activates chitinase <i>Cht20.2</i> transcription to confer resistance to wheat stripe rust. <i>Plant Physiology</i> , 2021, 187, 2749-2762.	2.3	21
8575	Morphological, Physiological, and Molecular Responses of Sweetly Fragrant <i>Luculia gratissima</i> During the Floral Transition Stage Induced by Short-Day Photoperiod. <i>Frontiers in Plant Science</i> , 2021, 12, 715683.	1.7	0
8576	Improve isobutanol tolerance and production by engineering of TATA-binding protein Spt15 in <i>Saccharomyces cerevisiae</i> . <i>Letters in Applied Microbiology</i> , 2021, 73, 694-707.	1.0	0
8578	Comparative Transcriptomic Analysis Reveals the Effects of Drought on the Biosynthesis of Methyleugenol in <i>Asarum sieboldii</i> Miq.. <i>Biomolecules</i> , 2021, 11, 1233.	1.8	8
8579	HTS-Based Diagnostics of Sugarcane Viruses: Seasonal Variation and Its Implications for Accurate Detection. <i>Viruses</i> , 2021, 13, 1627.	1.5	12
8581	Transcriptome Adaptation of the Ovine Mammary Gland to Dietary Supplementation of Extruded Linseed. <i>Animals</i> , 2021, 11, 2707.	1.0	2
8582	Competition-based screening helps to secure the evolutionary stability of a defensive microbiome. <i>BMC Biology</i> , 2021, 19, 205.	1.7	10
8583	Transcriptome characterization and expression profile of <i>Coix lacryma-jobi</i> L. in response to drought. <i>PLoS ONE</i> , 2021, 16, e0256875.	1.1	10
8584	Over-expression of the bottlenose dolphin <i>Hoxd13</i> gene in zebrafish provides new insights into the cetacean flipper formation. <i>Genomics</i> , 2021, 113, 2925-2933.	1.3	2
8585	Relaxed selection on male mitochondrial genes in DUI bivalves eases the need for mitonuclear coevolution. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1722-1736.	0.8	10
8587	Transcriptional Controls for Early Bolting and Flowering in <i>Angelica sinensis</i> . <i>Plants</i> , 2021, 10, 1931.	1.6	13
8588	Positive selection of skeleton-related genes during duck domestication revealed by whole genome sequencing. <i>Bmc Ecology and Evolution</i> , 2021, 21, 165.	0.7	6
8589	Transcriptome analysis of pacific white shrimp ( <i>Penaeus vannamei</i> ) intestines and hepatopancreas in response to <i>Enterocytozoon hepatopenaei</i> (EHP) infection. <i>Journal of Invertebrate Pathology</i> , 2021, 186, 107665.	1.5	14
8590	<i>Hermetia illucens</i> (L.) (Diptera: Stratiomyidae) Odorant Binding Proteins and Their Interactions with Selected Volatile Organic Compounds: An In Silico Approach. <i>Insects</i> , 2021, 12, 814.	1.0	25
8591	An extremely promiscuous terpenoid synthase from the Lamiaceae plant <i>Colquhounia coccinea</i> var. <i>mollis</i> catalyzes the formation of sester-/di-/sesqui-/mono-terpenoids. <i>Plant Communications</i> , 2021, 2, 100233.	3.6	7

#	ARTICLE	IF	CITATIONS
8592	Differential transcript usage analysis of bulk and single-cell RNA-seq data with DTUrtle. <i>Bioinformatics</i> , 2021, 37, 3781-3787.	1.8	10
8593	Animal-eRNAdb: a comprehensive animal enhancer RNA database. <i>Nucleic Acids Research</i> , 2022, 50, D46-D53.	6.5	14
8594	Exogenous Antioxidants Improve the Accumulation of Saturated and Polyunsaturated Fatty Acids in <i>Schizochytrium</i> sp. PKU#Mn4. <i>Marine Drugs</i> , 2021, 19, 559.	2.2	11
8595	Molecular underpinnings of the early brain developmental response to differential feeding in the honey bee <i>Apis mellifera</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194732.	0.9	5
8596	Transcriptome Analysis Reveals an Inhibitory Effect of Dihydrotestosterone-Treated 2D- and 3D-Cultured Dermal Papilla Cells on Hair Follicle Growth. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 724310.	1.8	7
8597	Metabolomic and Transcriptomic Changes Induced by Potassium Deficiency During <i>Sarocladium oryzae</i> Infection Reveal Insights into Rice Sheath Rot Disease Resistance. <i>Rice</i> , 2021, 14, 81.	1.7	10
8598	SNORA42 promotes oesophageal squamous cell carcinoma development through triggering the DHX9/p65 axis. <i>Genomics</i> , 2021, 113, 3015-3029.	1.3	6
8599	Optogenetic modeling of human neuromuscular circuits in Duchenne muscular dystrophy with CRISPR and pharmacological corrections. <i>Science Advances</i> , 2021, 7, eabi8787.	4.7	14
8600	Newt regeneration genes regulate Wingless signaling to restore patterning in <i>Drosophila</i> eye. <i>IScience</i> , 2021, 24, 103166.	1.9	9
8601	Physiological, biochemical and transcription effects of roxithromycin before and after phototransformation in <i>Chlorella pyrenoidosa</i> . <i>Aquatic Toxicology</i> , 2021, 238, 105911.	1.9	14
8602	Integrated multiomics analysis identifies molecular landscape perturbations during hyperammonemia in skeletal muscle and myotubes. <i>Journal of Biological Chemistry</i> , 2021, 297, 101023.	1.6	10
8603	Molecular regulation of anthocyanin discoloration under water stress and high solar irradiance in pluckable shoots of purple tea cultivar. <i>Planta</i> , 2021, 254, 85.	1.6	8
8604	Advances in Understanding Leishmania Pathobiology: What Does RNA-Seq Tell Us?. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 702240.	1.8	11
8605	Analysis of weighted gene co-expression network of triterpenoid-related transcriptome characteristics from different strains of <i>Wolfiporia cocos</i> . <i>Scientific Reports</i> , 2021, 11, 18207.	1.6	2
8606	Comparative metabolomic and transcriptomic analyses revealed the differential accumulation of secondary metabolites during the ripening process of acerola cherry ( <i>Malpighia</i> ) Tj ETQq0 0 0 rgBT /Overlact 10 Tf 50 177 Td (		
8607	Identification of N6-Methyladenosine-Related lncRNAs for Subtype Identification and Risk Stratification in Gastric Adenocarcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 725181.	1.3	9
8608	Human Cytomegalovirus RNA2.7 Is Required for Upregulating Multiple Cellular Genes To Promote Cell Motility and Viral Spread Late in Lytic Infection. <i>Journal of Virology</i> , 2021, 95, e0069821.	1.5	2
8609	The potential for mitigation of methane emissions in ruminants through the application of metagenomics, metabolomics, and other -OMICS technologies. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	8

#	ARTICLE	IF	CITATIONS
8611	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	14
8612	Genomic insights into the origin, domestication and diversification of <i>Brassica juncea</i> . <i>Nature Genetics</i> , 2021, 53, 1392-1402.	9.4	66
8613	Metabolite profiling and transcriptome analyses reveal novel regulatory mechanisms of melatonin biosynthesis in hickory. <i>Horticulture Research</i> , 2021, 8, 196.	2.9	27
8614	Integrated Analysis of Liver Transcriptome, miRNA, and Proteome of Chinese Indigenous Breed Ningxiang Pig in Three Developmental Stages Uncovers Significant miRNA-mRNA-Protein Networks in Lipid Metabolism. <i>Frontiers in Genetics</i> , 2021, 12, 709521.	1.1	3
8615	Transcriptional Landscapes of Long Non-coding RNAs and Alternative Splicing in <i>Pyricularia oryzae</i> Revealed by RNA-Seq. <i>Frontiers in Plant Science</i> , 2021, 12, 723636.	1.7	3
8616	DNA hypomethylation leads to cGAS-induced autoinflammation in the epidermis. <i>EMBO Journal</i> , 2021, 40, e108234.	3.5	17
8617	Transcriptome profiling reveals new insights into the roles of neuronal nitric oxide synthase on macrophage polarization towards classically activated phenotype. <i>PLoS ONE</i> , 2021, 16, e0257908.	1.1	1
8618	A Brief Summary of Current Therapeutic Strategies for Spinal Cord Injury. <i>Engineering</i> , 2021, , .	3.2	0
8620	A Comparison of Short- and Long-Term Soy Protein Isolate Intake and Its Ability to Reduce Liver Steatosis in Obese Zucker Rats Through Modifications of Genes Involved in Inflammation and Lipid Transport. <i>Journal of Medicinal Food</i> , 2021, 24, 1010-1016.	0.8	1
8621	Non-homologous chromosome pairing during meiosis in haploid <i>Brassica rapa</i> . <i>Plant Cell Reports</i> , 2021, 40, 2421-2434.	2.8	1
8622	Transcriptomic analysis for differential expression of genes involved in secondary metabolite production in <i>Narcissus pseudonarcissus</i> field derived bulb and in vitro callus. <i>Industrial Crops and Products</i> , 2021, 168, 113615.	2.5	4
8623	Platelet transcriptome profiles provide potential therapeutic targets for elderly acute myelocytic leukemia patients. <i>Journal of Translational Medicine</i> , 2021, 19, 388.	1.8	2
8624	Characteristics of steroidogenesis-related factors in the musk gland of Chinese forest musk deer ( <i>Moschus berezovskii</i> ). <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021, 212, 105916.	1.2	8
8625	Stability analysis of reference genes for RT-qPCR assays involving compatible and incompatible <i>Ralstonia solanacearum</i> -tomato "Hawaii 7996"™ interactions. <i>Scientific Reports</i> , 2021, 11, 18719.	1.6	7
8626	Genome-wide identification of ascorbate-glutathione cycle gene families in soybean ( <i>Glycine max</i> ) reveals gene duplication events and specificity of gene members linked to development and stress conditions. <i>International Journal of Biological Macromolecules</i> , 2021, 187, 528-543.	3.6	12
8627	Silicon Alleviates the Disease Severity of <i>Sclerotinia</i> Stem Rot in Rapeseed. <i>Frontiers in Plant Science</i> , 2021, 12, 721436.	1.7	4
8628	Analysis of mRNA and Long Non-Coding RNA Expression Profiles in Developing Yorkshire Pig Spleens. <i>Animals</i> , 2021, 11, 2768.	1.0	5
8629	FrogCap: A modular sequence capture probe-set for phylogenomics and population genetics for all frogs, assessed across multiple phylogenetic scales. <i>Molecular Ecology Resources</i> , 2022, 22, 1100-1119.	2.2	17



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8631	The transcriptomic revolution and radiation biology. <i>International Journal of Radiation Biology</i> , 2022, 98, 428-438.	1.0	7
8632	Transcriptomic and Metabolomic Analyses Reveals That Exogenous Methyl Jasmonate Regulates Galanthamine Biosynthesis in <i>Lycoris longituba</i> Seedlings. <i>Frontiers in Plant Science</i> , 2021, 12, 713795.	1.7	9
8636	Prospects and challenges of cancer systems medicine: from genes to disease networks. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
8637	Integrated mRNA and miRNA Expression Analyses of <i>Pinus massoniana</i> Roots and Shoots in Long-Term Response to Phosphate Deficiency. <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	5
8638	RNA-Seq-Based Profiling of pl Mutant Reveals Transcriptional Regulation of Anthocyanin Biosynthesis in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 9787.	1.8	4
8639	Functional Analysis of Keto-Acid Reductoisomerase ILVC in the Entomopathogenic Fungus <i>Metarhizium robertsii</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 737.	1.5	2
8640	The Transporter-Mediated Cellular Uptake and Efflux of Pharmaceutical Drugs and Biotechnology Products: How and Why Phospholipid Bilayer Transport Is Negligible in Real Biomembranes. <i>Molecules</i> , 2021, 26, 5629.	1.7	14
8641	Relationship between HSPA1A-regulated gene expression and alternative splicing in mouse cardiomyocytes and cardiac hypertrophy. <i>Journal of Thoracic Disease</i> , 2021, 13, 5517-5533.	0.6	2
8642	Transcriptome sequencing reveals terpene biosynthesis pathway genes accounting for volatile terpene of tree peony. <i>Planta</i> , 2021, 254, 67.	1.6	11
8643	The role of glutathione-mediated triacylglycerol synthesis in the response to ultra-high cadmium stress in <i>Auxenochlorella protothecoides</i> . <i>Journal of Environmental Sciences</i> , 2021, 108, 58-69.	3.2	12
8644	RNA-seq and nuclear proteomics provide insights into the lactation regulation mechanism of goat transfected IGF-I and GH recombinant vectors. <i>Growth Hormone and IGF Research</i> , 2021, 60-61, 101428.	0.5	0
8645	Targeting epigenetics and lncRNAs in liver disease: From mechanisms to therapeutics. <i>Pharmacological Research</i> , 2021, 172, 105846.	3.1	7
8646	Nitrogen assimilation and gene regulation of two Kentucky bluegrass cultivars differing in response to nitrate supply. <i>Scientia Horticulturae</i> , 2021, 288, 110315.	1.7	7
8647	Effects of sodium salicylate and time postpartum on mammary tissue proliferation, gene transcript profile, and DNA methylation. <i>Journal of Dairy Science</i> , 2021, 104, 11259-11276.	1.4	1
8648	Adaptive Reprogramming During Early Seed Germination Requires Temporarily Enhanced Fermentation-A Critical Role for Alternative Oxidase Regulation That Concerns Also Microbiota Effectiveness. <i>Frontiers in Plant Science</i> , 2021, 12, 686274.	1.7	10
8649	Phenotypic and transcriptomic changes in the corneal epithelium following exposure to cigarette smoke. <i>Environmental Pollution</i> , 2021, 287, 117540.	3.7	6
8650	Ammonium-nitrogen addition at the seedling stage does not reduce grain cadmium concentration in two common wheat ( <i>Triticum aestivum</i> L.) cultivars. <i>Environmental Pollution</i> , 2021, 286, 117575.	3.7	9
8651	N-acyl-homoserine-lactones signaling as a critical control point for phosphorus entrapment by multi-species microbial aggregates. <i>Water Research</i> , 2021, 204, 117627.	5.3	19

#	ARTICLE	IF	CITATIONS
8652	A promoter engineering-based strategy enhances polyhydroxyalkanoate production in <i>Pseudomonas putida</i> KT2440. <i>International Journal of Biological Macromolecules</i> , 2021, 191, 608-617.	3.6	24
8653	Transcriptomic analysis reveals key genes associated with the biosynthesis regulation of phenolics in fresh-cut pitaya fruit ( <i>Hylocereus undatus</i> ). <i>Postharvest Biology and Technology</i> , 2021, 181, 111684.	2.9	15
8654	The impact of gene-body H3K36me3 patterns on gene expression level changes in chronic myelogenous leukemia. <i>Gene</i> , 2021, 802, 145862.	1.0	3
8655	Responses of sediment resistome, virulence factors and potential pathogens to decades of antibiotics pollution in a shrimp aquafarm. <i>Science of the Total Environment</i> , 2021, 794, 148760.	3.9	26
8656	Cultivar-, stress duration- and leaf age-specific hub genes and co-expression networks responding to waterlogging in barley. <i>Environmental and Experimental Botany</i> , 2021, 191, 104599.	2.0	9
8657	A RING type ubiquitin ligase PhCUL4 is involved in thermotolerance of <i>Pyropia haitanensis</i> . <i>Algal Research</i> , 2021, 59, 102448.	2.4	6
8658	Comparative transcriptome analysis reveals changes in gene expression in sea cucumber ( <i>Holothuria</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf D: Genomics and Proteomics, 2021, 40, 100883.	0.4	12
8659	Tetrahydroxy stilbene glycoside regulates TGF- $\beta$ 2/fractalkine/CX3CR1 based on network pharmacology in APP/PS1 mouse model. <i>Neuropeptides</i> , 2021, 90, 102197.	0.9	1
8660	Transcriptomic changes upon epoxiconazole exposure in a human stem cell-based model of developmental toxicity. <i>Chemosphere</i> , 2021, 284, 131225.	4.2	9
8661	Transcriptomic analyses of the acute aerial and ammonia stress response in the gill and liver of large-scale loach ( <i>Paramisgurnus dabryanus</i> ). <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2021, 250, 109185.	1.3	11
8662	Systems biology under heat stress in Indian cattle. <i>Gene</i> , 2021, 805, 145908.	1.0	4
8663	Transcriptome sequencing provides insights into the mechanism of hypoxia adaption in bighead carp ( <i>Hypophthalmichthys nobilis</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100891.	0.4	8
8664	Transcriptomic profiling of <i>Paulownia elongata</i> in response to heat stress. <i>Plant Gene</i> , 2021, 28, 100330.	1.4	0
8665	Advances in mRNA 5-methylcytosine modifications: Detection, effectors, biological functions, and clinical relevance. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 575-593.	2.3	37
8666	Wild relatives of plants as sources for the development of abiotic stress tolerance in plants. , 2022, , 471-518.		13
8667	Skin transcriptome and physiological analyses reveal the metabolic and immune responses of yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) to acute hypoxia. <i>Aquaculture</i> , 2022, 546, 737277.	1.7	12
8668	A multi-omic screening approach for the discovery of thermoactive glycoside hydrolases. <i>Extremophiles</i> , 2021, 25, 101-114.	0.9	6
8669	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing. <i>BMC Genomics</i> , 2021, 22, 69.	1.2	12

#	ARTICLE	IF	CITATIONS
8670	In Silico Prediction for ncRNAs in Prokaryotes. <i>Methods in Molecular Biology</i> , 2021, 2328, 277-285.	0.4	0
8671	Differences between common endothelial cell models (primary human aortic endothelial cells and) Tj ETQq1 1 0.784314 rgBT /Overlook <i>Research in Biotechnology</i> , 2021, 3, 135-145.	1.9	6
8672	Transcriptomic profile of VEGF-regulated genes in human cervical epithelia. <i>Cell and Tissue Research</i> , 2021, 384, 771-788.	1.5	3
8673	Transcriptome analysis reveals salinity responses in four Tartary buckwheat cultivars. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 564-578.	0.9	6
8674	Transcriptome landscapes of differentially expressed genes related to fat deposits in Nandan-Yao chicken. <i>Functional and Integrative Genomics</i> , 2021, 21, 113-124.	1.4	14
8675	Analysis of Transcriptional Profiling of Chamber-Specific Human Cardiac Myocytes Derived from. <i>Methods in Molecular Biology</i> , 2021, 2320, 219-232.	0.4	0
8676	Genome and transcriptome of <i>Papaver somniferum</i> Chinese landrace CHM indicates that massive genome expansion contributes to high benzyloisoquinoline alkaloid biosynthesis. <i>Horticulture Research</i> , 2021, 8, 5.	2.9	22
8677	A Systematic Review of Applications of Machine Learning in Cancer Prediction and Diagnosis. <i>Archives of Computational Methods in Engineering</i> , 2021, 28, 4875-4896.	6.0	24
8678	Genome-Wide Ribosome Profiling of the <i>Plasmodium falciparum</i> Intraerythrocytic Developmental Cycle. <i>Methods in Molecular Biology</i> , 2021, 2252, 57-87.	0.4	0
8680	Construction and Analysis of a ceRNA Network in Cardiac Fibroblast During Fibrosis Based on in vivo and in vitro Data. <i>Frontiers in Genetics</i> , 2020, 11, 503256.	1.1	7
8681	Human adipose-derived stromal/stem cells are distinct from dermal fibroblasts as evaluated by biological characterization and RNA sequencing. <i>Cell Biochemistry and Function</i> , 2021, 39, 442-454.	1.4	3
8682	Transcriptome Analysis Reveals Candidate Genes Involved in Anthocyanin Biosynthesis in Flowers of the Pagoda Tree ( <i>Sophora japonica</i> L.). <i>Journal of Plant Growth Regulation</i> , 2022, 41, 1-14.	2.8	11
8683	YjbH mediates the oxidative stress response and infection by regulating SpxA1 and the phosphoenolpyruvate-carbohydrate phosphotransferase system (PTS) in <i>Listeria monocytogenes</i> . <i>Gut Microbes</i> , 2021, 13, 1-19.	4.3	6
8684	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	14
8685	MiR-33a plays a crucial role in the proliferation of bovine preadipocytes. <i>Adipocyte</i> , 2021, 10, 189-200.	1.3	8
8687	Adversarial generation of gene expression data. <i>Bioinformatics</i> , 2022, 38, 730-737.	1.8	23
8688	Melatonin improves the maturation and developmental ability of bovine oocytes by up-regulating GJA4 to enhance gap junction intercellular communication. <i>Reproduction, Fertility and Development</i> , 2021, 33, 760-771.	0.1	6
8689	Functional roles of antisense enhancer RNA for promoting prostate cancer progression. <i>Theranostics</i> , 2021, 11, 1780-1794.	4.6	24

#	ARTICLE	IF	CITATIONS
8691	Retina Development in Vertebrates: Systems Biology Approaches to Understanding Genetic Programs. <i>BioEssays</i> , 2020, 42, e1900187.	1.2	17
8692	Transcriptomic analysis on responses of the liver and kidney of finishing pigs fed cadmium contaminated rice. <i>Journal of the Science of Food and Agriculture</i> , 2018, 98, 2964-2972.	1.7	9
8693	Gene Annotation Methods. , 2009, , 121-136.		2
8694	Galaxy: A Gateway to Tools in e-Science. <i>Computer Communications and Networks</i> , 2011, , 145-177.	0.8	20
8695	Analysis of RNA Sequencing Data Using CLC Genomics Workbench. <i>Methods in Molecular Biology</i> , 2020, 2102, 61-113.	0.4	50
8696	Cap Analysis of Gene Expression (CAGE): A Quantitative and Genome-Wide Assay of Transcription Start Sites. <i>Methods in Molecular Biology</i> , 2020, 2120, 277-301.	0.4	22
8697	Statistical and Bioinformatics Analysis of Data from Bulk and Single-Cell RNA Sequencing Experiments. <i>Methods in Molecular Biology</i> , 2021, 2194, 143-175.	0.4	12
8698	Guidelines for Setting Up a mRNA Sequencing Experiment and Best Practices for Bioinformatic Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2264, 137-162.	0.4	1
8699	Bioinformatics Techniques for Understanding and Analyzing Tree Gene Expression Data. , 2012, , 17-38.		2
8700	Transcriptome Profiling. , 2013, , 117-127.		1
8701	Biotechnology for Drought and Salinity Tolerance of Crops. , 2014, , 97-113.		3
8702	Regulation of Eukaryotic Cell Differentiation by Long Non-coding RNAs. , 2013, , 15-67.		4
8703	Next-Generation Sequencing Applied to Flower Development: RNA-Seq. <i>Methods in Molecular Biology</i> , 2014, 1110, 401-411.	0.4	12
8704	RNA Sequencing: From Sample Preparation to Analysis. <i>Methods in Molecular Biology</i> , 2014, 1164, 51-65.	0.4	16
8705	Methods to Detect Transcribed Pseudogenes: RNA-Seq Discovery Allows Learning Through Features. <i>Methods in Molecular Biology</i> , 2014, 1167, 157-183.	0.4	8
8706	RNA Sequencing of FACS-Sorted Immune Cell Populations from Zebrafish Infection Models to Identify Cell Specific Responses to Intracellular Pathogens. <i>Methods in Molecular Biology</i> , 2014, 1197, 261-274.	0.4	40
8707	Omics Approaches to Macrophage Biology. , 2014, , 587-615.		1
8708	Global Analysis of Transcription Factor-Binding Sites in Yeast Using ChIP-Seq. <i>Methods in Molecular Biology</i> , 2014, 1205, 231-255.	0.4	4

#	ARTICLE	IF	CITATIONS
8709	Quantifying Entire Transcriptomes by Aligned RNA-Seq Data. <i>Methods in Molecular Biology</i> , 2015, 1269, 163-172.	0.4	1
8710	Quality Control of RNA-Seq Experiments. <i>Methods in Molecular Biology</i> , 2015, 1269, 137-146.	0.4	51
8711	Transcriptome Analysis of Feline Infectious Peritonitis Virus Infection. <i>Methods in Molecular Biology</i> , 2015, 1282, 241-250.	0.4	21
8712	Transcriptomics Using Axolotls. <i>Methods in Molecular Biology</i> , 2015, 1290, 309-319.	0.4	2
8713	Deep Sequencing of Cardiac MicroRNA-mRNA Interactomes in Clinical and Experimental Cardiomyopathy. <i>Methods in Molecular Biology</i> , 2015, 1299, 27-49.	0.4	15
8714	In Silico HLA Typing Using Standard RNA-Seq Sequence Reads. <i>Methods in Molecular Biology</i> , 2015, 1310, 247-258.	0.4	13
8715	Transcriptional Profiling of <i>Candida albicans</i> in the Host. <i>Methods in Molecular Biology</i> , 2016, 1356, 17-29.	0.4	8
8716	Single-Cell Transcriptome Analysis of T Cells. <i>Methods in Molecular Biology</i> , 2019, 2048, 155-205.	0.4	3
8717	Generation and Interpretation of Context-Specific Human Protein-Protein Interaction Networks with HIPPIE. <i>Methods in Molecular Biology</i> , 2020, 2074, 135-144.	0.4	4
8718	High-Throughput SuperSAGE. <i>Methods in Molecular Biology</i> , 2011, 687, 135-146.	0.4	10
8719	Identifying mRNA Editing Deaminase Targets by RNA-Seq. <i>Methods in Molecular Biology</i> , 2011, 718, 103-119.	0.4	7
8720	Microarray mRNA Expression Profiling to Study Cystic Fibrosis. <i>Methods in Molecular Biology</i> , 2011, 742, 193-212.	0.4	11
8721	RNA Sequencing. <i>Methods in Molecular Biology</i> , 2011, 759, 125-132.	0.4	14
8722	Identification of Imprinted Loci by Transcriptome Sequencing. <i>Methods in Molecular Biology</i> , 2012, 925, 79-88.	0.4	5
8723	The Principles of RNA Structure Architecture. <i>Methods in Molecular Biology</i> , 2014, 1097, 33-43.	0.4	4
8724	High-Throughput Approaches for MicroRNA Expression Analysis. <i>Methods in Molecular Biology</i> , 2014, 1107, 91-103.	0.4	20
8725	High-Throughput RNA-Seq for Allelic or Locus-Specific Expression Analysis in Arabidopsis-Related Species, Hybrids, and Allotetraploids. <i>Methods in Molecular Biology</i> , 2014, 1112, 33-48.	0.4	3
8726	Inference of Allele-Specific Expression from RNA-seq Data. <i>Methods in Molecular Biology</i> , 2014, 1112, 49-69.	0.4	8

#	ARTICLE	IF	CITATIONS
8727	Next Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine in Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1168, 9-30.	0.8	114
8729	What Is the Transcriptome and How it is Evaluated?. , 2014, , 3-48.		5
8730	Characterization of DNA-Protein Interactions: Design and Analysis of ChIP-Seq Experiments. , 2016, , 223-260.		3
8731	Eukaryotic Single-Cell mRNA Sequencing. , 2016, , 343-365.		1
8732	Transcriptomics and Proteomics of Foodborne Bacterial Pathogens. , 2017, , 167-200.		1
8733	Gene Expression Profiling. , 2017, , 1-6.		1
8735	The Importance of Genetic and Epigenetic Research in the Brassica Vegetables in the Face of Climate Change. , 2020, , 161-255.		15
8736	Classifying Big DNA Methylation Data: A Gene-Oriented Approach. <i>Communications in Computer and Information Science</i> , 2018, , 138-149.	0.4	2
8737	Discriminant Analysis and Normalization Methods for Next-Generation Sequencing Data. <i>ICSA Book Series in Statistics</i> , 2018, , 365-384.	0.0	1
8738	Inference of Isoforms from Short Sequence Reads. <i>Lecture Notes in Computer Science</i> , 2010, , 138-157.	1.0	18
8739	Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments. <i>Lecture Notes in Computer Science</i> , 2010, , 397-409.	1.0	6
8740	Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data. <i>Lecture Notes in Computer Science</i> , 2010, , 202-214.	1.0	17
8741	Statistical and Computational Studies on Alternative Splicing. , 2011, , 31-53.		4
8743	Renaissance of the Regulatory RNAs. , 2012, , 3-22.		1
8744	Detection of Alternatively Spliced or Processed RNAs in Cancer Using Oligonucleotide Microarray. <i>Cancer Treatment and Research</i> , 2013, 158, 25-40.	0.2	1
8745	A Novel Combinatorial Method for Estimating Transcript Expression with RNA-Seq: Bounding the Number of Paths. <i>Lecture Notes in Computer Science</i> , 2013, , 85-98.	1.0	3
8746	A Polynomial Delay Algorithm for the Enumeration of Bubbles with Length Constraints in Directed Graphs and Its Application to the Detection of Alternative Splicing in RNA-seq Data. <i>Lecture Notes in Computer Science</i> , 2013, , 99-111.	1.0	6
8747	Brain changes in iron loading disorders. , 2012, , 17-29.		4

#	ARTICLE	IF	CITATIONS
8748	Surveying <i>Entamoeba histolytica</i> Transcriptome Using Massively Parallel cDNA Sequencing. , 2015, , 99-117.		1
8749	Global Approaches to Alternative Splicing and Its Regulation—Recent Advances and Open Questions. <i>Translational Bioinformatics</i> , 2016, , 37-71.	0.0	2
8750	Introduction to Isoform Sequencing Using Pacific Biosciences Technology (Iso-Seq). <i>Translational Bioinformatics</i> , 2016, , 141-160.	0.0	55
8751	An Update on Transcriptome Sequencing of Hairy Root Cultures of Medicinally Important Plants. , 2018, , 295-310.		2
8752	Plant Genetic Engineering and GM Crops: Merits and Demerits. , 2019, , 155-229.		4
8753	Genomics and Transcriptomics Advance in Plant Sciences. <i>Energy, Environment, and Sustainability</i> , 2019, , 419-448.	0.6	5
8754	Transcriptome profiling and digital gene expression analysis of the skin of Dybowski's frog ( <i>Rana</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5799-5808.	1.7	10
8755	Mapping and characterization of major QTL for spike traits in common wheat. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1295-1307.	1.4	15
8756	Integrin-Mediated Focal Anchorage Drives Epithelial Zippering during Mouse Neural Tube Closure. <i>Developmental Cell</i> , 2020, 52, 321-334.e6.	3.1	46
8757	De novo transcriptome analysis of the mussel <i>Perna viridis</i> after exposure to the toxic dinoflagellate <i>Prorocentrum lima</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 192, 110265.	2.9	25
8758	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. <i>Research in Veterinary Science</i> , 2018, 117, 85-91.	0.9	19
8759	Impact of Sequencing Depth and Library Preparation on Toxicological Interpretation of RNA-Seq Data in a "Three-Sample" Scenario. <i>Chemical Research in Toxicology</i> , 2021, 34, 529-540.	1.7	8
8760	Accurate quantification of dystrophin mRNA and exon skipping levels in Duchenne Muscular Dystrophy. <i>Laboratory Investigation</i> , 0, , .	1.7	2
8762	BCL9/STAT3 regulation of transcriptional enhancer networks promote DCIS progression. <i>Npj Breast Cancer</i> , 2020, 6, 12.	2.3	10
8763	Red versus green leaves: transcriptomic comparison of foliar senescence between two <i>Prunus cerasifera</i> genotypes. <i>Scientific Reports</i> , 2020, 10, 1959.	1.6	8
8764	Evidence for the Involvement of Vernalization-related Genes in the Regulation of Cold-induced Ripening in "D'Anjou" and "Bartlett" Pear Fruit. <i>Scientific Reports</i> , 2020, 10, 8478.	1.6	10
8765	Detrimental effects of flame retardant, PBB153, exposure on sperm and future generations. <i>Scientific Reports</i> , 2020, 10, 8567.	1.6	32
8766	Different expression of lipid metabolism-related genes in Shandong black cattle and Luxi cattle based on transcriptome analysis. <i>Scientific Reports</i> , 2020, 10, 21915.	1.6	31

#	ARTICLE	IF	CITATIONS
8767	Loss of CBX2 induces genome instability and senescence-associated chromosomal rearrangements. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	15
8768	TBro: visualization and management of de novo transcriptomes. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw146.	1.4	3
8769	Homeobox transcription factor OsZHD2 promotes root meristem activity in rice by inducing ethylene biosynthesis. <i>Journal of Experimental Botany</i> , 2020, 71, 5348-5364.	2.4	24
8770	Re-examination of MAGE-A3 as a T-cell Therapeutic Target. <i>Journal of Immunotherapy</i> , 2021, 44, 95-105.	1.2	15
8771	Clinical Impact of High-Throughput Gene Expression Studies in Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2009, 4, 109-118.	0.5	22
8772	Combined infection with Tomato yellow leaf curl virus and <i>Rickettsia</i> influences fecundity, attraction to infected plants and expression of immunity-related genes in the whitefly <i>Bemisia tabaci</i> . <i>Journal of General Virology</i> , 2019, 100, 721-731.	1.3	17
8773	A long and abundant non-coding RNA in <i>Lactobacillus salivarius</i> . <i>Microbial Genomics</i> , 2017, 3, e000126.	1.0	6
8774	A survey of <i>Fusobacterium nucleatum</i> genes modulated by host cell infection. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
8775	Mycoparasitism illuminated by genome and transcriptome sequencing of <i>Coniothyrium minitans</i> , an important biocontrol fungus of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>Microbial Genomics</i> , 2020, 6, .	1.0	15
8776	Complete genome of a unicellular parasite ( <i>Antonospora locustae</i> ) and transcriptional interactions with its host locust. <i>Microbial Genomics</i> , 2020, 6, .	1.0	4
8777	Dual transcriptome analysis reveals differential gene expression modulation influenced by <i>Leishmania</i> arginase and host genetic background. <i>Microbial Genomics</i> , 2020, 6, .	1.0	9
8778	Role of dihydrofolate reductase in tetrahydrobiopterin biosynthesis and lipid metabolism in the oleaginous fungus <i>Mortierella alpina</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 1544-1553.	0.7	9
8900	De novo transcriptome assembly and developmental mode specific gene expression of <i>Pygospio elegans</i> . <i>Evolution &amp; Development</i> , 2017, 19, 205-217.	1.1	13
8901	Altered gene expression signatures by calcitonin gene-related peptide promoted mast cell activity in the colon of stress-induced visceral hyperalgesia mice. <i>Neurogastroenterology and Motility</i> , 2021, 33, e14073.	1.6	11
8902	Systematic analysis of 1298 RNA-Seq samples and construction of a comprehensive soybean ( <i>Glycine</i> ) Tj ETQq0,0 0 rgBT/Overlock	2.8	54
8903	NSR-seq transcriptional profiling enables identification of a gene signature of <i>Plasmodium falciparum</i> parasites infecting children. <i>Journal of Clinical Investigation</i> , 2011, 121, 1119-1129.	3.9	72
8904	Inflammatory priming predisposes mice to age-related retinal degeneration. <i>Journal of Clinical Investigation</i> , 2012, 122, 2989-3001.	3.9	55
8905	5â€²RNA-Seq identifies Fhl1 as a genetic modifier in cardiomyopathy. <i>Journal of Clinical Investigation</i> , 2014, 124, 1364-1370.	3.9	58



#	ARTICLE	IF	CITATIONS
8906	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	78
8908	Exploring features and function of Ss-riok-3 , an enigmatic kinase gene from <i>Strongyloides stercoralis</i> . <i>Parasites and Vectors</i> , 2014, 7, 561.	1.0	1
8912	Transcriptomic response to three osmotic stresses in gills of hybrid tilapia ( <i>Oreochromis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,662 Td (	1.2	47
8913	Transcriptome of pleuropodia from locust embryos supports that these organs produce enzymes enabling the larva to hatch. <i>Frontiers in Zoology</i> , 2020, 17, 4.	0.9	7
8914	Physiological and transcriptome changes induced by exogenous putrescine in anthurium under chilling stress. , 2020, 61, 28.		7
8916	WHEAT GENOMICS: PRESENT STATUS AND FUTURE PROSPECTS. , 2014, , 129-196.		2
8917	Efficient Experimental Design and Analysis Strategies for the Detection of Differential Expression Using RNA-Sequencing. , 2014, , 279-310.		2
8918	RSEM. , 2014, , 41-74.		31
8919	A primer for generating and using transcriptome data and gene sets. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	6
8920	The Prognostic Value of m6A RNA Methylation Regulators in Colon Adenocarcinoma. <i>Medical Science Monitor</i> , 2019, 25, 9435-9445.	0.5	51
8921	Analysis of Circular RNA in <i>Caenorhabditis elegans</i> . <i>Hans Journal of Computational Biology</i> , 2015, 05, 17-28.	0.0	14
8922	RSEQREP: RNA-Seq Reports, an open-source cloud-enabled framework for reproducible RNA-Seq data processing, analysis, and result reporting. <i>F1000Research</i> , 2017, 6, 2162.	0.8	7
8923	RSEQREP: RNA-Seq Reports, an open-source cloud-enabled framework for reproducible RNA-Seq data processing, analysis, and result reporting. <i>F1000Research</i> , 2017, 6, 2162.	0.8	12
8924	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	372
8925	Thousands of exon skipping events differentiate among splicing patterns in sixteen human tissues. <i>F1000Research</i> , 2013, 2, 188.	0.8	293
8926	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	0.8	2,612
8927	Advances in analyzing RNA diversity in eukaryotic transcriptomes: peering through the Omics lens. <i>F1000Research</i> , 2016, 5, 2668.	0.8	3
8928	Rapid transcriptional responses to serum exposure are associated with sensitivity and resistance to antibody-mediated complement killing in invasive <i>Salmonella Typhimurium</i> ST313. <i>Wellcome Open Research</i> , 2019, 4, 74.	0.9	8

#	ARTICLE	IF	CITATIONS
8929	Genome Sequencing Analysis of Macrophomina Phaseolina Resistant and Susceptible Castor Genotype. <i>Biosciences, Biotechnology Research Asia</i> , 2018, 15, 195-215.	0.2	4
8930	RNA-seq Using Next Generation Sequencing. <i>Materials and Methods</i> , 0, 3, .	0.0	18
8931	Differential expression analysis methods for ribonucleic acid-sequencing data. <i>OA Bioinformatics</i> , 2013, 1, .	0.0	2
8932	Most "Dark Matter" Transcripts Are Associated With Known Genes. <i>PLoS Biology</i> , 2010, 8, e1000371.	2.6	377
8933	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015, 11, e1004491.	1.5	11
8934	Mixture models reveal multiple positional bias types in RNA-Seq data and lead to accurate transcript concentration estimates. <i>PLoS Computational Biology</i> , 2017, 13, e1005515.	1.5	18
8935	Synergistic and Dose-Controlled Regulation of Cellulase Gene Expression in <i>Penicillium oxalicum</i> . <i>PLoS Genetics</i> , 2015, 11, e1005509.	1.5	174
8936	Secondary Structure across the Bacterial Transcriptome Reveals Versatile Roles in mRNA Regulation and Function. <i>PLoS Genetics</i> , 2015, 11, e1005613.	1.5	168
8937	Genome-Wide and Experimental Resolution of Relative Translation Elongation Speed at Individual Gene Level in Human Cells. <i>PLoS Genetics</i> , 2016, 12, e1005901.	1.5	36
8938	Robust stratification of breast cancer subtypes using differential patterns of transcript isoform expression. <i>PLoS Genetics</i> , 2017, 13, e1006589.	1.5	53
8939	In the hunt for genomic markers of metabolic resistance to pyrethroids in the mosquito <i>Aedes aegypti</i> : An integrated next-generation sequencing approach. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005526.	1.3	73
8940	L-arginine availability and arginase activity: Characterization of amino acid permease 3 in <i>Leishmania amazonensis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006025.	1.3	35
8941	3'-End Sequencing for Expression Quantification (3SEQ) from Archival Tumor Samples. <i>PLoS ONE</i> , 2010, 5, e8768.	1.1	123
8942	Using Deep RNA Sequencing for the Structural Annotation of the <i>Laccaria Bicolor</i> Mycorrhizal Transcriptome. <i>PLoS ONE</i> , 2010, 5, e9780.	1.1	32
8943	Digital Genome-Wide ncRNA Expression, Including SnoRNAs, across 11 Human Tissues Using PolyA-Neutral Amplification. <i>PLoS ONE</i> , 2010, 5, e11779.	1.1	108
8944	SAW: A Method to Identify Splicing Events from RNA-Seq Data Based on Splicing Fingerprints. <i>PLoS ONE</i> , 2010, 5, e12047.	1.1	7
8945	Reduced Expression of IFIH1 Is Protective for Type 1 Diabetes. <i>PLoS ONE</i> , 2010, 5, e12646.	1.1	82
8946	Reference-Free Validation of Short Read Data. <i>PLoS ONE</i> , 2010, 5, e12681.	1.1	23

#	ARTICLE	IF	CITATIONS
8947	De Novo Analysis of Transcriptome Dynamics in the Migratory Locust during the Development of Phase Traits. PLoS ONE, 2010, 5, e15633.	1.1	215
8948	A Comparison of Single Molecule and Amplification Based Sequencing of Cancer Transcriptomes. PLoS ONE, 2011, 6, e17305.	1.1	48
8949	Effects of Nickel Treatment on H3K4 Trimethylation and Gene Expression. PLoS ONE, 2011, 6, e17728.	1.1	37
8950	Comparative Transcriptome Analyses Indicate Molecular Homology of Zebrafish Swimbladder and Mammalian Lung. PLoS ONE, 2011, 6, e24019.	1.1	139
8951	Unstable Transcripts in Arabidopsis Allotetraploids Are Associated with Nonadditive Gene Expression in Response to Abiotic and Biotic Stresses. PLoS ONE, 2011, 6, e24251.	1.1	32
8952	Epigenetic Regulation of MicroRNA Genes and the Role of miR-34b in Cell Invasion and Motility in Human Melanoma. PLoS ONE, 2011, 6, e24922.	1.1	63
8953	Expression Profiling without Genome Sequence Information in a Non-Model Species, Pandalid Shrimp ( <i>Pandalus latirostris</i> ), by Next-Generation Sequencing. PLoS ONE, 2011, 6, e26043.	1.1	38
8954	A Low-Cost Library Construction Protocol and Data Analysis Pipeline for Illumina-Based Strand-Specific Multiplex RNA-Seq. PLoS ONE, 2011, 6, e26426.	1.1	135
8955	RNA-Seq Reveals an Integrated Immune Response in Nucleated Erythrocytes. PLoS ONE, 2011, 6, e26998.	1.1	130
8956	Transcriptome Analysis of the Oriental Fruit Fly ( <i>Bactrocera dorsalis</i> ). PLoS ONE, 2011, 6, e29127.	1.1	135
8957	Fast Computation and Applications of Genome Mappability. PLoS ONE, 2012, 7, e30377.	1.1	458
8958	Isoform Diversity and Regulation in Peripheral and Central Neurons Revealed through RNA-Seq. PLoS ONE, 2012, 7, e30417.	1.1	51
8959	Transcriptome Analysis of the Model Protozoan, <i>Tetrahymena thermophila</i> , Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
8960	Development of Genomic Resources for Pacific Herring through Targeted Transcriptome Pyrosequencing. PLoS ONE, 2012, 7, e30908.	1.1	22
8961	Insights into SCP/TAPS Proteins of Liver Flukes Based on Large-Scale Bioinformatic Analyses of Sequence Datasets. PLoS ONE, 2012, 7, e31164.	1.1	24
8962	RNA-seq Reveals Novel Transcriptome of Genes and Their Isoforms in Human Pulmonary Microvascular Endothelial Cells Treated with Thrombin. PLoS ONE, 2012, 7, e31229.	1.1	42
8963	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
8964	Identification of Vascular and Hematopoietic Genes Downstream of <i>etsrp</i> by Deep Sequencing in Zebrafish. PLoS ONE, 2012, 7, e31658.	1.1	26

#	ARTICLE	IF	CITATIONS
8965	RNA-seq Analysis Reveals That an ECF $\sigma$ Factor, AcsS, Regulates Achromobactin Biosynthesis in <i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a. <i>PLoS ONE</i> , 2012, 7, e34804.	1.1	18
8966	Generation and Analysis of a Mouse Intestinal Metatranscriptome through Illumina Based RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e36009.	1.1	52
8967	Transcriptome Sequencing Revealed Significant Alteration of Cortical Promoter Usage and Splicing in Schizophrenia. <i>PLoS ONE</i> , 2012, 7, e36351.	1.1	89
8968	Gene Mapping via Bulked Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406.	1.1	297
8969	High-Throughput Sequencing to Reveal Genes Involved in Reproduction and Development in <i>Bactrocera dorsalis</i> (Diptera: Tephritidae). <i>PLoS ONE</i> , 2012, 7, e36463.	1.1	57
8970	A Complete Sequence and Transcriptomic Analyses of Date Palm ( <i>Phoenix dactylifera</i> L.) Mitochondrial Genome. <i>PLoS ONE</i> , 2012, 7, e37164.	1.1	106
8971	Conserved Expression Signatures between Medaka and Human Pigment Cell Tumors. <i>PLoS ONE</i> , 2012, 7, e37880.	1.1	35
8972	Molecular Effects of Doxycycline Treatment on Pterygium as Revealed by Massive Transcriptome Sequencing. <i>PLoS ONE</i> , 2012, 7, e39359.	1.1	20
8973	A Retinoblastoma Orthologue Is a Major Regulator of S-Phase, Mitotic, and Developmental Gene Expression in <i>Dictyostelium</i> . <i>PLoS ONE</i> , 2012, 7, e39914.	1.1	11
8974	Transcriptome Profiling of the Cancer, Adjacent Non-Tumor and Distant Normal Tissues from a Colorectal Cancer Patient by Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e41001.	1.1	68
8975	Comprehensive Identification and Annotation of Cell Type-Specific and Ubiquitous CTCF-Binding Sites in the Human Genome. <i>PLoS ONE</i> , 2012, 7, e41374.	1.1	119
8976	Novel Insights into the Transcriptome of <i>Dirofilaria immitis</i> . <i>PLoS ONE</i> , 2012, 7, e41639.	1.1	15
8977	Establishment of Mouse Teratocarcinomas Stem Cells Line and Screening Genes Responsible for Malignancy. <i>PLoS ONE</i> , 2012, 7, e43955.	1.1	5
8978	Allele-Biased Expression in Differentiating Human Neurons: Implications for Neuropsychiatric Disorders. <i>PLoS ONE</i> , 2012, 7, e44017.	1.1	84
8979	Deep Insight into the <i>Ganoderma lucidum</i> by Comprehensive Analysis of Its Transcriptome. <i>PLoS ONE</i> , 2012, 7, e44031.	1.1	60
8980	The Social Brain: Transcriptome Assembly and Characterization of the Hippocampus from a Social Subterranean Rodent, the Colonial Tuco-Tuco ( <i>Ctenomys sociabilis</i> ). <i>PLoS ONE</i> , 2012, 7, e45524.	1.1	21
8981	Transcriptomic Responses to Salinity Stress in the Pacific Oyster <i>Crassostrea gigas</i> . <i>PLoS ONE</i> , 2012, 7, e46244.	1.1	159
8982	Transcriptome Sequencing and De Novo Analysis for Ma Bamboo ( <i>Dendrocalamus latiflorus</i> Munro) Using the Illumina Platform. <i>PLoS ONE</i> , 2012, 7, e46766.	1.1	104

#	ARTICLE	IF	CITATIONS
8983	Reanalysis of RNA-Sequencing Data Reveals Several Additional Fusion Genes with Multiple Isoforms. PLoS ONE, 2012, 7, e48745.	1.1	72
8984	Nuclear RNA Sequencing of the Mouse Erythroid Cell Transcriptome. PLoS ONE, 2012, 7, e49274.	1.1	35
8985	Simultaneous RNA-Seq Analysis of a Mixed Transcriptome of Rice and Blast Fungus Interaction. PLoS ONE, 2012, 7, e49423.	1.1	242
8986	Transcriptome Analysis of Male and Female <i>Sebastiscus marmoratus</i> . PLoS ONE, 2012, 7, e50676.	1.1	16
8987	Evaluation of the Effects of Erythritol on Gene Expression in <i>Brucella abortus</i> . PLoS ONE, 2012, 7, e50876.	1.1	27
8988	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree <i>Pongamia pinnata</i> . PLoS ONE, 2012, 7, e51687.	1.1	73
8989	Genome-Wide Transcriptome and Proteome Analysis on Different Developmental Stages of <i>Cordyceps militaris</i> . PLoS ONE, 2012, 7, e51853.	1.1	78
8990	Comparative Transcriptome Analysis of the Accessory Sex Gland and Testis from the Chinese Mitten Crab ( <i>Eriocheir sinensis</i> ). PLoS ONE, 2013, 8, e53915.	1.1	54
8991	RNA-Seq for Enrichment and Analysis of IRF5 Transcript Expression in SLE. PLoS ONE, 2013, 8, e54487.	1.1	42
8992	Transcriptome Analysis of Cytokinin Response in Tomato Leaves. PLoS ONE, 2013, 8, e55090.	1.1	36
8993	Transcriptome Profiling of the Goose ( <i>Anser cygnoides</i> ) Ovaries Identify Laying and Broodiness Phenotypes. PLoS ONE, 2013, 8, e55496.	1.1	66
8994	Consequences of Normalizing Transcriptomic and Genomic Libraries of Plant Genomes Using a Duplex-Specific Nuclease and Tetramethylammonium Chloride. PLoS ONE, 2013, 8, e55913.	1.1	37
8995	Transcriptome and Proteome Exploration to Provide a Resource for the Study of <i>Agrocybe aegerita</i> . PLoS ONE, 2013, 8, e56686.	1.1	56
8996	De novo Transcriptome Sequencing Reveals a Considerable Bias in the Incidence of Simple Sequence Repeats towards the Downstream of "Pre-miRNAs"™ of Black Pepper. PLoS ONE, 2013, 8, e56694.	1.1	51
8997	Sequencing and Comparative Analysis of the Straw Mushroom ( <i>Volvariella volvacea</i> ) Genome. PLoS ONE, 2013, 8, e58294.	1.1	143
8998	Transcriptomic Events Involved in Melon Mature-Fruit Abscission Comprise the Sequential Induction of Cell-Wall Degrading Genes Coupled to a Stimulation of Endo and Exocytosis. PLoS ONE, 2013, 8, e58363.	1.1	82
8999	Transcriptome of the Alternative Ethanol Production Strain <i>Dekkera bruxellensis</i> CBS 11270 in Sugar Limited, Low Oxygen Cultivation. PLoS ONE, 2013, 8, e58455.	1.1	36
9000	RNA-Seq Reveals Activation of Both Common and Cytokine-Specific Pathways following Neutrophil Priming. PLoS ONE, 2013, 8, e58598.	1.1	92

#	ARTICLE	IF	CITATIONS
9001	Transcriptome Analysis on Chinese Shrimp <i>Fenneropenaeus chinensis</i> during WSSV Acute Infection. PLoS ONE, 2013, 8, e58627.	1.1	128
9002	Genes Related to Ion-Transport and Energy Production Are Upregulated in Response to CO <sub>2</sub> -Driven pH Decrease in Corals: New Insights from Transcriptome Analysis. PLoS ONE, 2013, 8, e58652.	1.1	152
9003	Transcriptome Profiling of <i>Chironomus kiinensis</i> under Phenol Stress Using Solexa Sequencing Technology. PLoS ONE, 2013, 8, e58914.	1.1	18
9004	The Patterns of Histone Modifications in the Vicinity of Transcription Factor Binding Sites in Human Lymphoblastoid Cell Lines. PLoS ONE, 2013, 8, e60002.	1.1	18
9005	Study of Global Transcriptional Changes of N-GlcNAc <sub>2</sub> Proteins-Producing T24 Bladder Carcinoma Cells under Glucose Deprivation. PLoS ONE, 2013, 8, e60397.	1.1	12
9006	Identification of Transcriptome SNPs for Assessing Allele-Specific Gene Expression in a Super-Hybrid Rice Xieyou9308. PLoS ONE, 2013, 8, e60668.	1.1	12
9007	In-Depth Transcriptomic Analysis on Giant Freshwater Prawns. PLoS ONE, 2013, 8, e60839.	1.1	32
9008	Transcriptomic and Proteomic Responses of Sweetpotato Whitefly, <i>Bemisia tabaci</i> , to Thiamethoxam. PLoS ONE, 2013, 8, e61820.	1.1	58
9009	A Global Transcriptional Switch between the Attack and Growth Forms of <i>Bdellovibrio bacteriovorus</i> . PLoS ONE, 2013, 8, e61850.	1.1	76
9010	Exploring Differentially Expressed Genes by RNA-Seq in Cashmere Goat ( <i>Capra hircus</i> ) Skin during Hair Follicle Development and Cycling. PLoS ONE, 2013, 8, e62704.	1.1	59
9011	Transcriptome Sequencing and De Novo Analysis of the Copepod <i>Calanus sinicus</i> Using 454 GS FLX. PLoS ONE, 2013, 8, e63741.	1.1	43
9012	Characterization of Transcriptional Complexity during Longissimus Muscle Development in Bovines Using High-Throughput Sequencing. PLoS ONE, 2013, 8, e64356.	1.1	57
9013	Transcriptome Sequencing and De Novo Analysis of a Cytoplasmic Male Sterile Line and Its Near-Isogenic Restorer Line in Chili Pepper ( <i>Capsicum annum</i> L.). PLoS ONE, 2013, 8, e65209.	1.1	60
9014	Global Transcriptional and Phenotypic Analyses of <i>Escherichia coli</i> O157:H7 Strain Xuzhou21 and Its pO157_Sal Cured Mutant. PLoS ONE, 2013, 8, e65466.	1.1	11
9015	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. PLoS ONE, 2013, 8, e66521.	1.1	4
9016	Strategies for Wheat Stripe Rust Pathogenicity Identified by Transcriptome Sequencing. PLoS ONE, 2013, 8, e67150.	1.1	110
9017	Tracing the Transcriptomic Changes in Synthetic Trigenomic allohexaploids of Brassica Using an RNA-Seq Approach. PLoS ONE, 2013, 8, e68883.	1.1	39
9018	Changes in the Transcriptome of the Human Endometrial Ishikawa Cancer Cell Line Induced by Estrogen, Progesterone, Tamoxifen, and Mifepristone (RU486) as Detected by RNA-Sequencing. PLoS ONE, 2013, 8, e68907.	1.1	42

#	ARTICLE	IF	CITATIONS
9019	A New Omics Data Resource of <i>Pleurocybella porrigens</i> for Gene Discovery. PLoS ONE, 2013, 8, e69681.	1.1	12
9020	Differential Programming of B Cells in AID Deficient Mice. PLoS ONE, 2013, 8, e69815.	1.1	26
9021	De Novo Transcriptome of <i>Brassica juncea</i> Seed Coat and Identification of Genes for the Biosynthesis of Flavonoids. PLoS ONE, 2013, 8, e71110.	1.1	49
9022	Identification of an Imprinted Gene Cluster in the X-Inactivation Center. PLoS ONE, 2013, 8, e71222.	1.1	18
9023	De Novo Sequencing and Transcriptome Analysis of <i>Wolfiporia cocos</i> to Reveal Genes Related to Biosynthesis of Triterpenoids. PLoS ONE, 2013, 8, e71350.	1.1	42
9024	Large Scale Comparison of Gene Expression Levels by Microarrays and RNAseq Using TCGA Data. PLoS ONE, 2013, 8, e71462.	1.1	189
9025	Transcriptome Characteristics and Six Alternative Expressed Genes Positively Correlated with the Phase Transition of Annual Cambial Activities in Chinese Fir ( <i>Cunninghamia lanceolata</i> (Lamb.) Hook). PLoS ONE, 2013, 8, e71562.	1.1	26
9026	Impact of Library Preparation on Downstream Analysis and Interpretation of RNA-Seq Data: Comparison between Illumina PolyA and NuGEN Ovation Protocol. PLoS ONE, 2013, 8, e71745.	1.1	19
9027	Identification of the Novel Candidate Genes and Variants in Boar Liver Tissues with Divergent Skatole Levels Using RNA Deep Sequencing. PLoS ONE, 2013, 8, e72298.	1.1	26
9028	Transcriptome Analysis of Chlorantraniliprole Resistance Development in the Diamondback Moth <i>Plutella xylostella</i> . PLoS ONE, 2013, 8, e72314.	1.1	68
9029	Erg Channel Is Critical in Controlling Cell Volume during Cell Cycle in Embryonic Stem Cells. PLoS ONE, 2013, 8, e72409.	1.1	5
9030	Transcript Assembly and Quantification by RNA-Seq Reveals Differentially Expressed Genes between Soft-Endocarp and Hard-Endocarp Hawthorns. PLoS ONE, 2013, 8, e72910.	1.1	30
9031	An Analysis of the <i>Athetis lepigone</i> Transcriptome from Four Developmental Stages. PLoS ONE, 2013, 8, e73911.	1.1	38
9032	Determination of sRNA Expressions by RNA-seq in <i>Yersinia pestis</i> Grown In Vitro and during Infection. PLoS ONE, 2013, 8, e74495.	1.1	58
9033	An Organic Acid Based Counter Selection System for Cyanobacteria. PLoS ONE, 2013, 8, e76594.	1.1	62
9034	The Fumagillin Gene Cluster, an Example of Hundreds of Genes under <i>veA</i> Control in <i>Aspergillus fumigatus</i> . PLoS ONE, 2013, 8, e77147.	1.1	45
9035	The Pituitary Gland of the European Eel Reveals Massive Expression of Genes Involved in the Melanocortin System. PLoS ONE, 2013, 8, e77396.	1.1	15
9036	Extension of Life Span by Impaired Glucose Metabolism in <i>Caenorhabditis elegans</i> Is Accompanied by Structural Rearrangements of the Transcriptomic Network. PLoS ONE, 2013, 8, e77776.	1.1	18

#	ARTICLE	IF	CITATIONS
9037	Comprehensive RNA-Seq Expression Analysis of Sensory Ganglia with a Focus on Ion Channels and GPCRs in Trigeminal Ganglia. PLoS ONE, 2013, 8, e79523.	1.1	121
9038	Comparative Transcriptome Analysis of Salivary Glands of Two Populations of Rice Brown Planthopper, <i>Nilaparvata lugens</i> , That Differ in Virulence. PLoS ONE, 2013, 8, e79612.	1.1	100
9039	The Venom Gland Transcriptome of <i>Latrodectus tredecimguttatus</i> Revealed by Deep Sequencing and cDNA Library Analysis. PLoS ONE, 2013, 8, e81357.	1.1	60
9040	Next Generation Sequencing Analysis of Human Platelet PolyA+ mRNAs and rRNA-Depleted Total RNA. PLoS ONE, 2013, 8, e81809.	1.1	56
9041	The Utility of Shallow RNA-Seq for Documenting Differential Gene Expression in Genes with High and Low Levels of Expression. PLoS ONE, 2013, 8, e84160.	1.1	11
9042	Transforming RNA-Seq Data to Improve the Performance of Prognostic Gene Signatures. PLoS ONE, 2014, 9, e85150.	1.1	127
9043	Dual Targeting of MEK and PI3K Pathways Attenuates Established and Progressive Pulmonary Fibrosis. PLoS ONE, 2014, 9, e86536.	1.1	24
9044	Transcriptomic Analysis of Endangered Chinese Salamander: Identification of Immune, Sex and Reproduction-Related Genes and Genetic Markers. PLoS ONE, 2014, 9, e87940.	1.1	50
9045	Deep RNA Sequencing Reveals Hidden Features and Dynamics of Early Gene Transcription in <i>Paramecium bursaria</i> Chlorella Virus 1. PLoS ONE, 2014, 9, e90989.	1.1	65
9046	Transcriptome Immune Analysis of the Invasive Beetle <i>Octodonta nipae</i> (Maulik) (Coleoptera: Tj ETQq1 1 0.784314 rgBT /Overlock 101 PLoS ONE, 2014, 9, e91482.	1.1	26
9047	Isl1 and Pou4f2 Form a Complex to Regulate Target Genes in Developing Retinal Ganglion Cells. PLoS ONE, 2014, 9, e92105.	1.1	37
9048	Identification of Genes Differentially Expressed in Myogenin Knock-Down Bovine Muscle Satellite Cells during Differentiation through RNA Sequencing Analysis. PLoS ONE, 2014, 9, e92447.	1.1	35
9049	SNP Discovery from Transcriptome of the Swimbladder of <i>Takifugu rubripes</i> . PLoS ONE, 2014, 9, e92502.	1.1	14
9050	Towards Decrypting Cryptobiosis—Analyzing Anhydrobiosis in the Tardigrade <i>Milnesium tardigradum</i> Using Transcriptome Sequencing. PLoS ONE, 2014, 9, e92663.	1.1	53
9051	RNA Sequence Reveals Mouse Retinal Transcriptome Changes Early after Axonal Injury. PLoS ONE, 2014, 9, e93258.	1.1	68
9052	Genome-Wide Transcriptional Profiling of Skin and Dorsal Root Ganglia after Ultraviolet-B-Induced Inflammation. PLoS ONE, 2014, 9, e93338.	1.1	46
9053	TraV: A Genome Context Sensitive Transcriptome Browser. PLoS ONE, 2014, 9, e93677.	1.1	22
9054	ZBED6 Modulates the Transcription of Myogenic Genes in Mouse Myoblast Cells. PLoS ONE, 2014, 9, e94187.	1.1	19



#	ARTICLE	IF	CITATIONS
9055	Rapid Development of Microsatellite Markers for <i>Callosobruchus chinensis</i> Using Illumina Paired-End Sequencing. PLoS ONE, 2014, 9, e95458.	1.1	22
9056	Time Course Transcriptome Changes in <i>Shewanella</i> algae in Response to Salt Stress. PLoS ONE, 2014, 9, e96001.	1.1	24
9057	De Novo Assembly of Expressed Transcripts and Global Transcriptomic Analysis from Seedlings of the Paper Mulberry ( <i>Broussonetia kazinoki</i> x <i>Broussonetia papyifera</i> ). PLoS ONE, 2014, 9, e97487.	1.1	21
9058	RNA Sequencing Analysis of the Gametophyte Transcriptome from the Liverwort, <i>Marchantia polymorpha</i> . PLoS ONE, 2014, 9, e97497.	1.1	40
9059	Characterization of Natural Antisense Transcript, Sclerotia Development and Secondary Metabolism by Strand-Specific RNA Sequencing of <i>Aspergillus flavus</i> . PLoS ONE, 2014, 9, e97814.	1.1	13
9060	Digital Gene-Expression Profiling Analysis of the Cholesterol-Lowering Effects of Alfalfa Saponin Extract on Laying Hens. PLoS ONE, 2014, 9, e98578.	1.1	20
9061	Identification of Maize Long Non-Coding RNAs Responsive to Drought Stress. PLoS ONE, 2014, 9, e98958.	1.1	148
9062	Energy Metabolism in <i>Mycobacterium gilvum</i> PYR-GCK: Insights from Transcript Expression Analyses Following Two States of Induction. PLoS ONE, 2014, 9, e99464.	1.1	4
9063	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. PLoS ONE, 2014, 9, e99720.	1.1	66
9064	RNA-Seq Analysis Implicates Detoxification Pathways in Ovine Mycotoxin Resistance. PLoS ONE, 2014, 9, e99975.	1.1	10
9065	Transcriptome Profiling Reveals Higher Vertebrate Orthologous of Intra-Cytoplasmic Pattern Recognition Receptors in Grey Bamboo Shark. PLoS ONE, 2014, 9, e100018.	1.1	19
9066	Molecular Characterization and Differential Expression of Olfactory Genes in the Antennae of the Black Cutworm Moth <i>Agrotis ipsilon</i> . PLoS ONE, 2014, 9, e103420.	1.1	66
9067	Small RNA Profile in Moso Bamboo Root and Leaf Obtained by High Definition Adapters. PLoS ONE, 2014, 9, e103590.	1.1	16
9068	Fatty Acid Profile and Unigene-Derived Simple Sequence Repeat Markers in Tung Tree ( <i>Vernicia fordii</i> ). PLoS ONE, 2014, 9, e105298.	1.1	23
9069	De Novo Assembly and Characterization of the Fruit Transcriptome of Chinese Jujube ( <i>Ziziphus jujuba</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 2014, 9, e106438.	1.1	27
9070	Identification and Expression of Fructose-1,6-Bisphosphate Aldolase Genes and Their Relations to Oil Content in Developing Seeds of Tea Oil Tree ( <i>Camellia oleifera</i> ). PLoS ONE, 2014, 9, e107422.	1.1	44
9071	Thermal Stress Triggers Broad <i>Pocillopora damicornis</i> Transcriptomic Remodeling, while <i>Vibrio coralliilyticus</i> Infection Induces a More Targeted Immuno-Suppression Response. PLoS ONE, 2014, 9, e107672.	1.1	80
9072	Transcriptome Sequencing and Identification of Cold Tolerance Genes in Hardy <i>Corylus</i> Species (C.) Tj ETQq1 1 0.784314 rgBT /Overlock 14	1.1	14

#	ARTICLE	IF	CITATIONS
9073	Study on the Regulatory Mechanism of the Lipid Metabolism Pathways during Chicken Male Germ Cell Differentiation Based on RNA-Seq. PLoS ONE, 2015, 10, e0109469.	1.1	6
9074	Comparative Transcriptomics between <i>Synechococcus</i> PCC 7942 and <i>Synechocystis</i> PCC 6803 Provide Insights into Mechanisms of Stress Acclimation. PLoS ONE, 2014, 9, e109738.	1.1	63
9075	Antennal-Expressed Ammonium Transporters in the Malaria Vector Mosquito <i>Anopheles gambiae</i> . PLoS ONE, 2014, 9, e111858.	1.1	39
9076	RNA-Seq Analysis of <i>Quercus pubescens</i> Leaves: De Novo Transcriptome Assembly, Annotation and Functional Markers Development. PLoS ONE, 2014, 9, e112487.	1.1	49
9077	Growth Hormone-Regulated mRNAs and miRNAs in Chicken Hepatocytes. PLoS ONE, 2014, 9, e112896.	1.1	25
9078	Comparison of the Transcriptome between Two Cotton Lines of Different Fiber Color and Quality. PLoS ONE, 2014, 9, e112966.	1.1	26
9079	Deep Sequencing of the Murine Olfactory Receptor Neuron Transcriptome. PLoS ONE, 2015, 10, e0113170.	1.1	74
9080	Transcriptome Analysis of Neonatal Larvae after Hyperthermia-Induced Seizures in the Contractile Silkworm, <i>Bombyx mori</i> . PLoS ONE, 2014, 9, e113214.	1.1	5
9081	Genetic Insights into <i>Graminella nigrifrons</i> Competence for Maize fine streak virus Infection and Transmission. PLoS ONE, 2014, 9, e113529.	1.1	10
9082	De Novo Assembly and Transcriptome Analysis of the Mediterranean Fruit Fly <i>Ceratitis capitata</i> Early Embryos. PLoS ONE, 2014, 9, e114191.	1.1	17
9083	RNA-Seq Analysis of Equine Conceptus Transcripts during Embryo Fixation and Capsule Disappearance. PLoS ONE, 2014, 9, e114414.	1.1	3
9084	Identification of Regulatory Genes Implicated in Continuous Flowering of Longan ( <i>Dimocarpus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.1	26
9085	Transcriptional Analyses of Natural Leaf Senescence in Maize. PLoS ONE, 2014, 9, e115617.	1.1	51
9086	Selective Calcium Sensitivity in Immature Glioma Cancer Stem Cells. PLoS ONE, 2014, 9, e115698.	1.1	23
9087	A Note on an Exon-Based Strategy to Identify Differentially Expressed Genes in RNA-Seq Experiments. PLoS ONE, 2014, 9, e115964.	1.1	12
9088	Transcriptome Sequencing and Characterization of Japanese Scallop <i>Patinopecten yessoensis</i> from Different Shell Color Lines. PLoS ONE, 2015, 10, e0116406.	1.1	51
9089	Transcriptional Regulation and Adaptation to a High-Fiber Environment in <i>Bacillus subtilis</i> HH2 Isolated from Feces of the Giant Panda. PLoS ONE, 2015, 10, e0116935.	1.1	20
9090	Transcriptomic Analysis of American Ginseng Seeds during the Dormancy Release Process by RNA-Seq. PLoS ONE, 2015, 10, e0118558.	1.1	19

#	ARTICLE	IF	CITATIONS
9091	Isoform Switch of Pyruvate Kinase M1 Indeed Occurs but Not to Pyruvate Kinase M2 in Human Tumorigenesis. PLoS ONE, 2015, 10, e0118663.	1.1	25
9092	Comparative Transcriptome Analysis of Anthurium "Albama" and Its Anthocyanin-Loss Mutant. PLoS ONE, 2015, 10, e0119027.	1.1	17
9093	Transcriptome Sequence Analysis of an Ornamental Plant, Ananas comosus var. bracteatus, Revealed the Potential Unigenes Involved in Terpenoid and Phenylpropanoid Biosynthesis. PLoS ONE, 2015, 10, e0119153.	1.1	21
9094	Modifying Effects of Vitamin E on Chlorpyrifos Toxicity in Atlantic Salmon. PLoS ONE, 2015, 10, e0119250.	1.1	43
9095	Involvement of CitCHX and CitDIC in Developmental-Related and Postharvest-Hot-Air Driven Citrate Degradation in Citrus Fruits. PLoS ONE, 2015, 10, e0119410.	1.1	15
9096	Comparative Transcriptome Analysis of Genes Involved in Anthocyanin Biosynthesis in the Red and Yellow Fruits of Sweet Cherry ( <i>Prunus avium</i> L.). PLoS ONE, 2015, 10, e0121164.	1.1	112
9097	Comparative Transcriptome Profiling of the Maize Primary, Crown and Seminal Root in Response to Salinity Stress. PLoS ONE, 2015, 10, e0121222.	1.1	31
9098	Identification of Candidate Odorant Receptors in Asian Corn Borer <i>Ostrinia furnacalis</i> . PLoS ONE, 2015, 10, e0121261.	1.1	50
9099	Transcriptome Analysis of <i>Bombyx mori</i> Larval Midgut during Persistent and Pathogenic Cytoplasmic Polyhedrosis Virus Infection. PLoS ONE, 2015, 10, e0121447.	1.1	63
9100	A Next Generation Semiconductor Based Sequencing Approach for the Identification of Meat Species in DNA Mixtures. PLoS ONE, 2015, 10, e0121701.	1.1	58
9101	Repositioning of Memantine as a Potential Novel Therapeutic Agent against Meningitic <i>E. coli</i> "Induced Pathogenicities through Disease-Associated Alpha7 Cholinergic Pathway and RNA Sequencing-Based Transcriptome Analysis of Host Inflammatory Responses. PLoS ONE, 2015, 10, e0121911.	1.1	22
9102	Transcriptome Analysis of Post-Hatch Breast Muscle in Legacy and Modern Broiler Chickens Reveals Enrichment of Several Regulators of Myogenic Growth. PLoS ONE, 2015, 10, e0122525.	1.1	44
9103	Glutathione S-Transferase (GST) Gene Diversity in the Crustacean <i>Calanus finmarchicus</i> "Contributors to Cellular Detoxification. PLoS ONE, 2015, 10, e0123322.	1.1	53
9104	De Novo Assembly and Transcriptome Analysis of Wheat with Male Sterility Induced by the Chemical Hybridizing Agent SQ-1. PLoS ONE, 2015, 10, e0123556.	1.1	28
9105	Exploring Triacylglycerol Biosynthetic Pathway in Developing Seeds of Chia ( <i>Salvia hispanica</i> L.): A Transcriptomic Approach. PLoS ONE, 2015, 10, e0123580.	1.1	29
9106	A Powerful Statistical Approach for Large-Scale Differential Transcription Analysis. PLoS ONE, 2015, 10, e0123658.	1.1	4
9107	Do Housekeeping Genes Exist?. PLoS ONE, 2015, 10, e0123691.	1.1	42
9108	RNA-Seq Analysis and Gene Discovery of <i>Andrias davidianus</i> Using Illumina Short Read Sequencing. PLoS ONE, 2015, 10, e0123730.	1.1	26

#	ARTICLE	IF	CITATIONS
9109	Transcriptomic Analysis of Drought Stress Responses in <i>Ammopiptanthus mongolicus</i> Leaves Using the RNA-Seq Technique. PLoS ONE, 2015, 10, e0124382.	1.1	51
9110	Regulation of HbPIP2;3, a Latex-Abundant Water Transporter, Is Associated with Latex Dilution and Yield in the Rubber Tree ( <i>Hevea brasiliensis</i> Muell. Arg.). PLoS ONE, 2015, 10, e0125595.	1.1	20
9111	RNA-Seq Based De Novo Transcriptome Assembly and Gene Discovery of <i>Cistanche deserticola</i> Fleshy Stem. PLoS ONE, 2015, 10, e0125722.	1.1	14
9112	Combining GWAS and RNA-Seq Approaches for Detection of the Causal Mutation for Hereditary Junctional Epidermolysis Bullosa in Sheep. PLoS ONE, 2015, 10, e0126416.	1.1	15
9113	Probe Region Expression Estimation for RNA-Seq Data for Improved Microarray Comparability. PLoS ONE, 2015, 10, e0126545.	1.1	15
9114	Whitefly Genome Expression Reveals Host-Symbiont Interaction in Amino Acid Biosynthesis. PLoS ONE, 2015, 10, e0126751.	1.1	28
9115	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. PLoS ONE, 2015, 10, e0126911.	1.1	42
9116	Different Astrocytic Activation between Adult <i>Gekko japonicus</i> and Rats during Wound Healing In Vitro. PLoS ONE, 2015, 10, e0127663.	1.1	10
9117	Whole-Transcriptome Analysis of Differentially Expressed Genes in the Vegetative Buds, Floral Buds and Buds of <i>Chrysanthemum morifolium</i> . PLoS ONE, 2015, 10, e0128009.	1.1	54
9118	Transcriptome Profiling of the Potato ( <i>Solanum tuberosum</i> L.) Plant under Drought Stress and Water-Stimulus Conditions. PLoS ONE, 2015, 10, e0128041.	1.1	100
9119	Male- and Female-Biased Gene Expression of Olfactory-Related Genes in the Antennae of Asian Corn Borer, <i>Ostrinia furnacalis</i> (Guené) (Lepidoptera: Crambidae). PLoS ONE, 2015, 10, e0128550.	1.1	33
9120	Generation of a Transcriptome in a Model Lepidopteran Pest, <i>Heliothis virescens</i> , Using Multiple Sequencing Strategies for Profiling Midgut Gene Expression. PLoS ONE, 2015, 10, e0128563.	1.1	18
9121	Comparative Transcriptome Analysis of White and Purple Potato to Identify Genes Involved in Anthocyanin Biosynthesis. PLoS ONE, 2015, 10, e0129148.	1.1	75
9122	Defining the Human Brain Proteome Using Transcriptomics and Antibody-Based Profiling with a Focus on the Cerebral Cortex. PLoS ONE, 2015, 10, e0130028.	1.1	44
9123	Comparative Transcriptome Analysis Reveals the Influence of Abscisic Acid on the Metabolism of Pigments, Ascorbic Acid and Folic Acid during Strawberry Fruit Ripening. PLoS ONE, 2015, 10, e0130037.	1.1	54
9124	DELTA: A Distal Enhancer Locating Tool Based on AdaBoost Algorithm and Shape Features of Chromatin Modifications. PLoS ONE, 2015, 10, e0130622.	1.1	57
9125	Transcriptome Response Signatures Associated with the Overexpression of a Mitochondrial Uncoupling Protein (AtUCP1) in Tobacco. PLoS ONE, 2015, 10, e0130744.	1.1	11
9126	Comparison of Gene Coexpression Profiles and Construction of Conserved Gene Networks to Find Functional Modules. PLoS ONE, 2015, 10, e0132039.	1.1	9

#	ARTICLE	IF	CITATIONS
9127	Widespread Polycistronic Transcripts in Fungi Revealed by Single-Molecule mRNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0132628.	1.1	340
9128	Comparative Transcriptome Analysis Reveals Sex-Biased Gene Expression in Juvenile Chinese Mitten Crab <i>Eriocheir sinensis</i> . <i>PLoS ONE</i> , 2015, 10, e0133068.	1.1	42
9129	Identification of Oxygen-Responsive Transcripts in the Silage Inoculant <i>Lactobacillus buchneri</i> CD034 by RNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0134149.	1.1	19
9130	Transcriptomic Analysis of <i>Paeonia delavayi</i> Wild Population Flowers to Identify Differentially Expressed Genes Involved in Purple-Red and Yellow Petal Pigmentation. <i>PLoS ONE</i> , 2015, 10, e0135038.	1.1	36
9131	Transcriptome Analysis of the Preterm Rabbit Lung after Seven Days of Hyperoxic Exposure. <i>PLoS ONE</i> , 2015, 10, e0136569.	1.1	21
9132	Cross Platform Standardisation of an Experimental Pipeline for Use in the Identification of Dysregulated Human Circulating MiRNAs. <i>PLoS ONE</i> , 2015, 10, e0137389.	1.1	7
9133	Transcriptomic Analyses of the Biological Effects of Airborne PM2.5 Exposure on Human Bronchial Epithelial Cells. <i>PLoS ONE</i> , 2015, 10, e0138267.	1.1	72
9134	Ovarian Transcriptome Analysis of <i>Portunus trituberculatus</i> Provides Insights into Genes Expressed during Phase III and IV Development. <i>PLoS ONE</i> , 2015, 10, e0138862.	1.1	20
9135	Transcriptomic Analysis of the Anterior Silk Gland in the Domestic Silkworm ( <i>Bombyx mori</i> ) – Insight into the Mechanism of Silk Formation and Spinning. <i>PLoS ONE</i> , 2015, 10, e0139424.	1.1	25
9136	Differential Regulation of Gene and Protein Expression by Zinc Oxide Nanoparticles in Hen's Ovarian Granulosa Cells: Specific Roles of Nanoparticles. <i>PLoS ONE</i> , 2015, 10, e0140499.	1.1	30
9137	Molecular Characterization and Expression Profiling of Odorant-Binding Proteins in <i>Apolygus lucorum</i> . <i>PLoS ONE</i> , 2015, 10, e0140562.	1.1	64
9138	Molecular Characterization and Differential Expression of an Olfactory Receptor Gene Family in the White-Backed Planthopper <i>Sogatella furcifera</i> Based on Transcriptome Analysis. <i>PLoS ONE</i> , 2015, 10, e0140605.	1.1	21
9139	Transcriptome Analysis in <i>Haematococcus pluvialis</i> : Astaxanthin Induction by Salicylic Acid (SA) and Jasmonic Acid (JA). <i>PLoS ONE</i> , 2015, 10, e0140609.	1.1	47
9140	Gene Structures, Evolution, Classification and Expression Profiles of the Aquaporin Gene Family in Castor Bean ( <i>Ricinus communis</i> L.). <i>PLoS ONE</i> , 2015, 10, e0141022.	1.1	35
9141	Gene Expression Analysis of Pak Choi in Response to Vernalization. <i>PLoS ONE</i> , 2015, 10, e0141446.	1.1	20
9142	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0141586.	1.1	95
9143	Union Exon Based Approach for RNA-Seq Gene Quantification: To Be or Not to Be?. <i>PLoS ONE</i> , 2015, 10, e0141910.	1.1	25
9144	Transcriptomic Analysis of Myocardial Ischemia Using the Blood of Rat. <i>PLoS ONE</i> , 2015, 10, e0141915.	1.1	2

#	ARTICLE	IF	CITATIONS
9145	Genome-Wide Identification of New Reference Genes for qRT-PCR Normalization under High Temperature Stress in Rice Endosperm. <i>PLoS ONE</i> , 2015, 10, e0142015.	1.1	30
9146	Large-Scale Transcriptome Analysis of Cucumber and <i>Botrytis cinerea</i> during Infection. <i>PLoS ONE</i> , 2015, 10, e0142221.	1.1	55
9147	Transcriptome Analysis of Blunt Snout Bream ( <i>Megalobrama amblycephala</i> ) Reveals Putative Differential Expression Genes Related to Growth and Hypoxia. <i>PLoS ONE</i> , 2015, 10, e0142801.	1.1	20
9148	454 Pyrosequencing of Olive ( <i>Olea europaea</i> L.) Transcriptome in Response to Salinity. <i>PLoS ONE</i> , 2015, 10, e0143000.	1.1	37
9149	Tissue Restricted Splice Junctions Originate Not Only from Tissue-Specific Gene Loci, but Gene Loci with a Broad Pattern of Expression. <i>PLoS ONE</i> , 2015, 10, e0144302.	1.1	20
9150	Whole Transcriptome Analysis Provides Insights into Molecular Mechanisms for Molting in <i>Litopenaeus vannamei</i> . <i>PLoS ONE</i> , 2015, 10, e0144350.	1.1	86
9151	The Activation-Induced Assembly of an RNA/Protein Interactome Centered on the Splicing Factor U2AF2 Regulates Gene Expression in Human CD4 T Cells. <i>PLoS ONE</i> , 2015, 10, e0144409.	1.1	15
9152	From Insect to Man: <i>Photorhabdus</i> Sheds Light on the Emergence of Human Pathogenicity. <i>PLoS ONE</i> , 2015, 10, e0144937.	1.1	33
9153	Using RNA-seq to Profile Gene Expression of Spikelet Development in Response to Temperature and Nitrogen during Meiosis in Rice ( <i>Oryza sativa</i> L.). <i>PLoS ONE</i> , 2015, 10, e0145532.	1.1	12
9154	Differential Expression of Hepatic Genes of the Greater Horseshoe Bat ( <i>Rhinolophus ferrumequinum</i> ) between the Summer Active and Winter Torpid States. <i>PLoS ONE</i> , 2015, 10, e0145702.	1.1	17
9155	Selecting Superior De Novo Transcriptome Assemblies: Lessons Learned by Leveraging the Best Plant Genome. <i>PLoS ONE</i> , 2016, 11, e0146062.	1.1	93
9156	Transcriptome Analysis of Salt Stress Responsiveness in the Seedlings of Dongxiang Wild Rice ( <i>Oryza</i> ) Tj ETQq1 1 0,784314 rgBT /Overl 1.1 127	1.1	127
9157	Transcriptome Analysis of Honeybee ( <i>Apis Mellifera</i> ) Haploid and Diploid Embryos Reveals Early Zygotic Transcription during Cleavage. <i>PLoS ONE</i> , 2016, 11, e0146447.	1.1	43
9158	De Novo Transcriptome and Expression Profile Analysis to Reveal Genes and Pathways Potentially Involved in Cantharidin Biosynthesis in the Blister Beetle <i>Mylabris cichorii</i> . <i>PLoS ONE</i> , 2016, 11, e0146953.	1.1	15
9159	Identification and Comparison of Candidate Olfactory Genes in the Olfactory and Non-Olfactory Organs of Elm Pest <i>Ambrostoma quadriimpressum</i> (Coleoptera: Chrysomelidae) Based on Transcriptome Analysis. <i>PLoS ONE</i> , 2016, 11, e0147144.	1.1	32
9160	Transcriptomic Analysis of Tea Plant Responding to Drought Stress and Recovery. <i>PLoS ONE</i> , 2016, 11, e0147306.	1.1	67
9161	Transcriptomic Analysis of Grapevine (cv. Summer Black) Leaf, Using the Illumina Platform. <i>PLoS ONE</i> , 2016, 11, e0147369.	1.1	20
9162	Transcriptome and Expression Patterns of Chemosensory Genes in Antennae of the Parasitoid Wasp <i>Chouioia cunea</i> . <i>PLoS ONE</i> , 2016, 11, e0148159.	1.1	53

#	ARTICLE	IF	CITATIONS
9163	Gene Structures, Evolution and Transcriptional Profiling of the WRKY Gene Family in Castor Bean ( <i>Ricinus communis</i> L.). PLoS ONE, 2016, 11, e0148243.	1.1	33
9164	Transcriptome Analysis for Abnormal Spike Development of the Wheat Mutant dms. PLoS ONE, 2016, 11, e0149287.	1.1	6
9165	Identification of Differentially Expressed Genes Related to Dehydration Resistance in a Highly Drought-Tolerant Pear, <i>Pyrus betulaefolia</i> , as through RNA-Seq. PLoS ONE, 2016, 11, e0149352.	1.1	37
9166	Tolerant and Susceptible Sesame Genotypes Reveal Waterlogging Stress Response Patterns. PLoS ONE, 2016, 11, e0149912.	1.1	42
9167	Liver Transcriptome Analysis of the Large Yellow Croaker ( <i>Larimichthys crocea</i> ) during Fasting by Using RNA-Seq. PLoS ONE, 2016, 11, e0150240.	1.1	25
9168	Transcriptome Analysis Provides Insights into the Mechanisms Underlying Wheat Plant Resistance to Stripe Rust at the Adult Plant Stage. PLoS ONE, 2016, 11, e0150717.	1.1	61
9169	Microglia Transcriptome Changes in a Model of Depressive Behavior after Immune Challenge. PLoS ONE, 2016, 11, e0150858.	1.1	35
9170	Identification of Gene Networks for Residual Feed Intake in Angus Cattle Using Genomic Prediction and RNA-seq. PLoS ONE, 2016, 11, e0152274.	1.1	106
9171	Differential Expression Analysis of Chemoreception Genes in the Striped Flea Beetle <i>Phyllotreta striolata</i> Using a Transcriptomic Approach. PLoS ONE, 2016, 11, e0153067.	1.1	58
9172	Comprehensive Transcriptome Analysis of Response to Nickel Stress in White Birch ( <i>Betula papyrifera</i> ). PLoS ONE, 2016, 11, e0153762.	1.1	28
9173	Genome Assembly of the Fungus <i>Cochliobolus miyabeanus</i> , and Transcriptome Analysis during Early Stages of Infection on American Wildrice ( <i>Zizania palustris</i> L.). PLoS ONE, 2016, 11, e0154122.	1.1	17
9174	An Integrated Bioinformatics Analysis Reveals Divergent Evolutionary Pattern of Oil Biosynthesis in High- and Low-Oil Plants. PLoS ONE, 2016, 11, e0154882.	1.1	21
9175	Midgut Transcriptome of the Cockroach <i>Periplaneta americana</i> and Its Microbiota: Digestion, Detoxification and Oxidative Stress Response. PLoS ONE, 2016, 11, e0155254.	1.1	43
9176	Comparative Transcriptome Analysis of <i>Bombyx mori</i> (Lepidoptera) Larval Midgut Response to BmNPV in Susceptible and Near-Isogenic Resistant Strains. PLoS ONE, 2016, 11, e0155341.	1.1	36
9177	Transcriptome Analysis of the Innate Immunity-Related Complement System in Spleen Tissue of <i>Ctenopharyngodon idella</i> Infected with <i>Aeromonas hydrophila</i> . PLoS ONE, 2016, 11, e0157413.	1.1	85
9178	Deep Sequencing-Based Transcriptome Analysis Reveals the Regulatory Mechanism of <i>Bemisia tabaci</i> (Hemiptera: Aleyrodidae) Nymph Parasitized by <i>Encarsia sophia</i> (Hymenoptera: Aphelinidae). PLoS ONE, 2016, 11, e0157684.	1.1	1
9179	Dissecting the Root Nodule Transcriptome of Chickpea ( <i>Cicer arietinum</i> L.). PLoS ONE, 2016, 11, e0157908.	1.1	20
9180	Proteomic and Transcriptomic Analyses of Swine Pathogen <i>Erysipelothrix rhusiopathiae</i> Reveal Virulence Repertoire. PLoS ONE, 2016, 11, e0159462.	1.1	7

#	ARTICLE	IF	CITATIONS
9181	Targeting Tumor Cells with Anti-CD44 Antibody Triggers Macrophage-Mediated Immune Modulatory Effects in a Cancer Xenograft Model. <i>PLoS ONE</i> , 2016, 11, e0159716.	1.1	18
9182	Deciphering Transcriptome and Complex Alternative Splicing Transcripts in Mammary Gland Tissues from Cows Naturally Infected with <i>Staphylococcus aureus</i> Mastitis. <i>PLoS ONE</i> , 2016, 11, e0159719.	1.1	66
9183	Comparative Analysis of the Chrysanthemum Leaf Transcript Profiling in Response to Salt Stress. <i>PLoS ONE</i> , 2016, 11, e0159721.	1.1	14
9184	Deciphering the Transcriptional Response Mediated by the Redox-Sensing System HbpS-SenS-SenR from <i>Streptomyces</i> . <i>PLoS ONE</i> , 2016, 11, e0159873.	1.1	7
9185	Single Nucleotide Polymorphism Discovery in Bovine Pituitary Gland Using RNA-Seq Technology. <i>PLoS ONE</i> , 2016, 11, e0161370.	1.1	14
9186	IL-31-Driven Skin Remodeling Involves Epidermal Cell Proliferation and Thickening That Lead to Impaired Skin-Barrier Function. <i>PLoS ONE</i> , 2016, 11, e0161877.	1.1	59
9187	Profiling of Small Nucleolar RNAs by Next Generation Sequencing: Potential New Players for Breast Cancer Prognosis. <i>PLoS ONE</i> , 2016, 11, e0162622.	1.1	57
9188	Transcriptome Profile Analysis of Breast Muscle Tissues from High or Low Levels of Atmospheric Ammonia Exposed Broilers ( <i>Gallus gallus</i> ). <i>PLoS ONE</i> , 2016, 11, e0162631.	1.1	18
9189	Identification of Immunity-Related Genes in <i>Dialeurodes citri</i> against Entomopathogenic Fungus <i>Lecanicillium attenuatum</i> by RNA-Seq Analysis. <i>PLoS ONE</i> , 2016, 11, e0162659.	1.1	9
9190	Transcriptomic Study of the Soybean- <i>Fusarium virguliforme</i> Interaction Revealed a Novel Ankyrin-Repeat Containing Defense Gene, Expression of Whose during Infection Led to Enhanced Resistance to the Fungal Pathogen in Transgenic Soybean Plants. <i>PLoS ONE</i> , 2016, 11, e0163106.	1.1	22
9191	MicroRNA Stability in FFPE Tissue Samples: Dependence on GC Content. <i>PLoS ONE</i> , 2016, 11, e0163125.	1.1	43
9192	Transcriptomic Variation during Spermiogenesis in Mouse Germ Cells. <i>PLoS ONE</i> , 2016, 11, e0164874.	1.1	13
9193	Filtration and Normalization of Sequencing Read Data in Whole-Metagenome Shotgun Samples. <i>PLoS ONE</i> , 2016, 11, e0165015.	1.1	22
9194	Antennal Transcriptome and Differential Expression Analysis of Five Chemosensory Gene Families from the Asian Honeybee <i>Apis cerana cerana</i> . <i>PLoS ONE</i> , 2016, 11, e0165374.	1.1	27
9195	Genome-Wide Identification, Characterization, and Stress-Responsive Expression Profiling of Genes Encoding LEA (Late Embryogenesis Abundant) Proteins in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>PLoS ONE</i> , 2016, 11, e0165953.	1.1	38
9196	Sugarcane transcriptome analysis in response to infection caused by <i>Acidovorax avenae</i> subsp. <i>avenae</i> . <i>PLoS ONE</i> , 2016, 11, e0166473.	1.1	41
9197	The Development Of <i>Drosophila Melanogaster</i> under Different Duration Space Flight and Subsequent Adaptation to Earth Gravity. <i>PLoS ONE</i> , 2016, 11, e0166885.	1.1	21
9198	A Hypothesis Testing Based Method for Normalization and Differential Expression Analysis of RNA-Seq Data. <i>PLoS ONE</i> , 2017, 12, e0169594.	1.1	8



#	ARTICLE	IF	CITATIONS
9199	A Gene-Oriented Haplotype Comparison Reveals Recently Selected Genomic Regions in Temperate and Tropical Maize Germplasm. PLoS ONE, 2017, 12, e0169806.	1.1	3
9200	A Screen for Key Genes and Pathways Involved in High-Quality Brush Hair in the Yangtze River Delta White Goat. PLoS ONE, 2017, 12, e0169820.	1.1	16
9201	A novel RNA sequencing data analysis method for cell line authentication. PLoS ONE, 2017, 12, e0171435.	1.1	25
9202	Transcriptome analysis of hexaploid hulless oat in response to salinity stress. PLoS ONE, 2017, 12, e0171451.	1.1	41
9203	Survey of the rubber tree genome reveals a high number of cysteine protease-encoding genes homologous to Arabidopsis SAG12. PLoS ONE, 2017, 12, e0171725.	1.1	13
9204	Comparative transcriptome analysis of the different tissues between the cultivated and wild tomato. PLoS ONE, 2017, 12, e0172411.	1.1	22
9205	Transcriptome using Illumina sequencing reveals the traits of spermatogenesis and developing testes in <i>Eriocheir sinensis</i> . PLoS ONE, 2017, 12, e0172478.	1.1	22
9206	Coevolution with bacteria drives the evolution of aerobic fermentation in <i>Lachancea kluyveri</i> . PLoS ONE, 2017, 12, e0173318.	1.1	25
9207	Transcriptomic profiling of taproot growth and sucrose accumulation in sugar beet ( <i>Beta vulgaris</i> L.) at different developmental stages. PLoS ONE, 2017, 12, e0175454.	1.1	28
9208	Age, gender and UV-exposition related effects on gene expression in in vivo aged short term cultivated human dermal fibroblasts. PLoS ONE, 2017, 12, e0175657.	1.1	29
9209	Gene expression analysis of rocket salad under pre-harvest and postharvest stresses: A transcriptomic resource for <i>Diplotaxis tenuifolia</i> . PLoS ONE, 2017, 12, e0178119.	1.1	35
9210	Genome-wide identification and characterization of microRNAs differentially expressed in fibers in a cotton phytochrome A1 RNAi line. PLoS ONE, 2017, 12, e0179381.	1.1	9
9211	Antennal transcriptome analysis of the piercing moth <i>Oraesia emarginata</i> (Lepidoptera: Noctuidae). PLoS ONE, 2017, 12, e0179433.	1.1	18
9212	Genome-wide identification of pistil-specific genes expressed during fruit set initiation in tomato ( <i>Solanum lycopersicum</i> ). PLoS ONE, 2017, 12, e0180003.	1.1	28
9213	Gene expression allelic imbalance in ovine brown adipose tissue impacts energy homeostasis. PLoS ONE, 2017, 12, e0180378.	1.1	8
9214	Genome-wide analysis of the CCCH zinc finger family identifies tissue specific and stress responsive candidates in chickpea ( <i>Cicer arietinum</i> L.). PLoS ONE, 2017, 12, e0180469.	1.1	32
9215	Transcriptomic and metabolomic profiles of Chinese citrus fly, <i>Bactrocera minax</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td e0181033.	1.1	24
9216	Large-scale identification of <i>Gossypium hirsutum</i> genes associated with <i>Verticillium dahliae</i> by comparative transcriptomic and reverse genetics analysis. PLoS ONE, 2017, 12, e0181609.	1.1	32

#	ARTICLE	IF	CITATIONS
9217	Transcriptome analysis of the tea oil camellia ( <i>Camellia oleifera</i> ) reveals candidate drought stress genes. <i>PLoS ONE</i> , 2017, 12, e0181835.	1.1	41
9218	A comprehensive simulation study on classification of RNA-Seq data. <i>PLoS ONE</i> , 2017, 12, e0182507.	1.1	28
9219	Comparison of alternative approaches for analysing multi-level RNA-seq data. <i>PLoS ONE</i> , 2017, 12, e0182694.	1.1	25
9220	Differential gene expression in leaf tissues between mutant and wild-type genotypes response to late leaf spot in peanut ( <i>Arachis hypogaea</i> L.). <i>PLoS ONE</i> , 2017, 12, e0183428.	1.1	14
9221	Characterization of lincRNA expression in the human retinal pigment epithelium and differentiated induced pluripotent stem cells. <i>PLoS ONE</i> , 2017, 12, e0183939.	1.1	12
9222	Discovery of numerous novel small genes in the intergenic regions of the <i>Escherichia coli</i> O157:H7 Sakai genome. <i>PLoS ONE</i> , 2017, 12, e0184119.	1.1	38
9223	Antifungal defense of probiotic <i>Lactobacillus rhamnosus</i> GG is mediated by blocking adhesion and nutrient depletion. <i>PLoS ONE</i> , 2017, 12, e0184438.	1.1	38
9224	Genome-wide expression analysis of salt-stressed diploid and autotetraploid <i>Paulownia tomentosa</i> . <i>PLoS ONE</i> , 2017, 12, e0185455.	1.1	22
9225	Transcriptome-wide analysis reveals the progress of <i>Cordyceps militaris</i> subculture degeneration. <i>PLoS ONE</i> , 2017, 12, e0186279.	1.1	34
9226	Integrated mRNA and microRNA transcriptome analyses reveal regulation of thermal acclimation in <i>Gymnocypris przewalskii</i> : A case study in Tibetan Schizothoracine fish. <i>PLoS ONE</i> , 2017, 12, e0186433.	1.1	25
9227	Kojic acid-mediated damage responses induce mycelial regeneration in the basidiomycete <i>Hypsizygus marmoreus</i> . <i>PLoS ONE</i> , 2017, 12, e0187351.	1.1	15
9228	RNA-seq reveals transcriptome changes in goats following myostatin gene knockout. <i>PLoS ONE</i> , 2017, 12, e0187966.	1.1	27
9229	Transcriptome analysis of WRKY gene family in <i>Oryza officinalis</i> Wall ex Watt and WRKY genes involved in responses to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> stress. <i>PLoS ONE</i> , 2017, 12, e0188742.	1.1	11
9230	Genome-wide identification of WRKY genes and their expression profiles under different abiotic stresses in <i>Elaeis guineensis</i> . <i>PLoS ONE</i> , 2017, 12, e0189224.	1.1	51
9231	Pheromone expression reveals putative mechanism of unisexuality in a saprobic ascomycete fungus. <i>PLoS ONE</i> , 2018, 13, e0192517.	1.1	16
9232	Ribosome profiling reveals changes in translational status of soybean transcripts during immature cotyledon development. <i>PLoS ONE</i> , 2018, 13, e0194596.	1.1	20
9233	Comparative transcriptome analysis of flower bud transition and functional characterization of <i>EjAGL17</i> involved in regulating floral initiation in loquat. <i>PLoS ONE</i> , 2020, 15, e0239382.	1.1	6
9234	Transcriptome analysis of <i>Curcuma wenyujin</i> from Haikou and Wenzhou, and a comparison of the main constituents and related genes of <i>Rhizoma Curcumae</i> . <i>PLoS ONE</i> , 2020, 15, e0242776.	1.1	4

#	ARTICLE	IF	CITATIONS
9235	Candida albicans Inhibits Pseudomonas aeruginosa Virulence through Suppression of Pyochelin and Pyoverdine Biosynthesis. PLoS Pathogens, 2015, 11, e1005129.	2.1	111
9236	Trehalose-6-Phosphate-Mediated Toxicity Determines Essentiality of OtsB2 in Mycobacterium tuberculosis In Vitro and in Mice. PLoS Pathogens, 2016, 12, e1006043.	2.1	35
9237	Honey can repairing damage of liver tissue due to protein energy malnutrition through induction of endogenous stem cells. Veterinary World, 2017, 10, 711-715.	0.7	12
9238	Estimation of Gene Regulatory Networks. Postdoc Journal, 0, , .	0.4	6
9239	Analysis of Genes with Alternatively Spliced Transcripts in the Leaf, Root, Panicle and Seed of Rice Using a Long Oligomer Microarray and RNA-Seq. Molecules and Cells, 2017, 40, 714-730.	1.0	28
9240	Dissecting Cellular Heterogeneity Using Single-Cell RNA Sequencing. Molecules and Cells, 2019, 42, 189-199.	1.0	45
9241	RNA sequencing data: biases and normalization. EMBnet Journal, 2012, 18, 99.	0.2	1
9242	A strategy to reduce technical variability and bias in RNA sequencing data. EMBnet Journal, 2012, 18, 65.	0.2	2
9243	Androgen receptor enhancer usage and the chromatin regulatory landscape in human prostate cancers. Endocrine-Related Cancer, 2019, 26, R267-R285.	1.6	22
9244	Transcriptome analysis of wheat grain using RNA-Seq. Frontiers of Agricultural Science and Engineering, 2014, 1, 214.	0.9	8
9245	Transcriptome and Proteome Analysis: A Perspective on Correlation. MOJ Proteomics & Bioinformatics, 2014, 1, .	0.1	4
9246	RNA-SEQ: A GLANCE AT TECHNOLOGIES AND METHODOLOGIES. Acta Biologica Colombiana, 2015, 20, .	0.1	9
9247	Pesquisa translacional na era pÃ3s-genÃ3mica: avanÃ7os na Ã7rea da transcriptÃ3mica. SaÃ3de Em Debate, 2019, 43, 169-180.	0.1	2
9249	Genome-wide investigation and expression analysis of AP2-ERF gene family in salt tolerant common bean. EXCLI Journal, 2015, 14, 1187-206.	0.5	24
9250	Molecular Cloning and Characterization of Dmc1 from the Chinese Mitten Crab (Eriocheir sinensis). International Journal of Aquaculture and Fishery Sciences, 0, , 024-029.	0.1	1
9251	RNA-Seq-based analysis of differential gene expression associated with hepatitis C virus infection in cell culture. Acta Biochimica Polonica, 2017, 63, 789-798.	0.3	5
9252	Transcriptome analysis of duck embryo fibroblasts for the dynamic response to duck tembusu virus infection and dual regulation of apoptosis genes. Aging, 2020, 12, 17503-17527.	1.4	10
9253	Comparative transcriptome analysis reveals a regulatory network of microRNA-29b during mouse early embryonic development. Oncotarget, 2016, 7, 53772-53782.	0.8	11

#	ARTICLE	IF	CITATIONS
9254	GADD45 $\beta$ , an anti-tumor gene, inhibits avian leukosis virus subgroup J replication in chickens. <i>Oncotarget</i> , 2016, 7, 68883-68893.	0.8	16
9255	Deregulation of small non-coding RNAs at the <i>DLK1-DIO3</i> imprinted locus predicts lung cancer patient outcome. <i>Oncotarget</i> , 2016, 7, 80957-80966.	0.8	35
9256	New differentially expressed genes and differential DNA methylation underlying refractory epilepsy. <i>Oncotarget</i> , 2016, 7, 87402-87416.	0.8	34
9257	Estimating the effects of transcription factors binding and histone modifications on gene expression levels in human cells. <i>Oncotarget</i> , 2017, 8, 40090-40103.	0.8	15
9258	A subset of microRNAs defining the side population of a human malignant mesothelioma cell line. <i>Oncotarget</i> , 2017, 8, 42847-42856.	0.8	4
9259	Identification of a long non-coding RNA as a novel biomarker and potential therapeutic target for metastatic prostate cancer. <i>Oncotarget</i> , 2014, 5, 764-774.	0.8	215
9260	ATRX mRNA expression combined with IDH1/2 mutational status and Ki-67 expression refines the molecular classification of astrocytic tumors: evidence from the whole transcriptome sequencing of 169 samples. <i>Oncotarget</i> , 2014, 5, 2551-2561.	0.8	61
9261	Melatonin suppresses hepatocellular carcinoma progression via lncRNA-CPS1-IT-mediated HIF-1 $\beta$ inactivation. <i>Oncotarget</i> , 2017, 8, 82280-82293.	0.8	33
9262	Selecting lncRNAs in gastric cancer cells for directed therapy with bioactive peptides and chemotherapy drugs. <i>Oncotarget</i> , 2017, 8, 86082-86097.	0.8	7
9263	Differential regulation of mRNAs and lncRNAs related to lipid metabolism in two pig breeds. <i>Oncotarget</i> , 2017, 8, 87539-87553.	0.8	40
9264	Integrated analysis of mRNA and miRNA expression profiles in livers of Yimeng black pigs with extreme phenotypes for backfat thickness. <i>Oncotarget</i> , 2017, 8, 114787-114800.	0.8	9
9265	IGF2BP3-mediated translation in cell protrusions promotes cell invasiveness and metastasis of pancreatic cancer. <i>Oncotarget</i> , 2014, 5, 6832-6845.	0.8	70
9266	Mutational analysis of genes coding for cell surface proteins in colorectal cancer cell lines reveal novel altered pathways, druggable mutations and mutated epitopes for targeted therapy. <i>Oncotarget</i> , 2014, 5, 9199-9213.	0.8	31
9267	RNA-seq analysis reveals significant effects of EGFR signalling on the secretome of mesenchymal stem cells. <i>Oncotarget</i> , 2014, 5, 10518-10528.	0.8	16
9268	ER $\alpha$ -mediated cell cycle progression is an important requisite for CDK4/6 inhibitor response in HR+ breast cancer. <i>Oncotarget</i> , 2018, 9, 27736-27751.	0.8	11
9269	Novel long non-coding RNAs are specific diagnostic and prognostic markers for prostate cancer. <i>Oncotarget</i> , 2015, 6, 4036-4050.	0.8	42
9270	New somatic mutations and <i>WNK1-B4GALNT3</i> gene fusion in papillary thyroid carcinoma. <i>Oncotarget</i> , 2015, 6, 11242-11251.	0.8	51
9271	Integrated genomic analyses identify frequent gene fusion events and <i>VHL</i> inactivation in gastrointestinal stromal tumors. <i>Oncotarget</i> , 2016, 7, 6538-6551.	0.8	29

#	ARTICLE	IF	CITATIONS
9272	Genome-wide analysis of p53 transcriptional programs in B cells upon exposure to genotoxic stress <i>in vivo</i> . <i>Oncotarget</i> , 2015, 6, 24611-24626.	0.8	31
9273	Genome-wide endogenous DAF-16/FOXO recruitment dynamics during lowered insulin signalling in <i>C. elegans</i> . <i>Oncotarget</i> , 2015, 6, 41418-41433.	0.8	30
9274	Functional networks of aging markers in the glomeruli of IgA nephropathy: a new therapeutic opportunity. <i>Oncotarget</i> , 2016, 7, 33616-33626.	0.8	22
9275	Piwi-interacting RNAs and PIWI genes as novel prognostic markers for breast cancer. <i>Oncotarget</i> , 2016, 7, 37944-37956.	0.8	78
9276	Alterations of androgen receptor-regulated enhancer RNAs (eRNAs) contribute to enzalutamide resistance in castration-resistant prostate cancer. <i>Oncotarget</i> , 2016, 7, 38551-38565.	0.8	36
9277	The new technologies of high-throughput single-cell RNA sequencing. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2019, 23, 508-518.	0.4	1
9278	Transcriptome profiling: methods and applications- A review. <i>Agricultural Reviews</i> , 2017, 38, .	0.1	12
9279	Integration of <i>omics</i> and system biology approaches to study grapevine ( <i>Vitis vinifera</i> L.) response to salt stress: a perspective for functional genomics - A review. <i>Oeno One</i> , 2016, 48, 189.	0.7	7
9280	Analysis of Differentially Expressed Genes in Necrotic Enteritis-infected Fayoumi Chickens using RNA Sequencing. <i>Journal of Poultry Science</i> , 2017, 54, 121-133.	0.7	5
9281	Metabolism of Oxalate in Humans: A Potential Role Kynurenine Aminotransferase/Glutamine Transaminase/Cysteine Conjugate Betalyase Plays in Hyperoxaluria. <i>Current Medicinal Chemistry</i> , 2019, 26, 4944-4963.	1.2	7
9282	Review: Alternative Splicing (AS) of Genes As An Approach for Generating Protein Complexity. <i>Current Genomics</i> , 2013, 14, 182-194.	0.7	80
9283	Transcriptome Profiles of <i>Populus euphratica</i> upon Heat Shock stress. <i>Current Genomics</i> , 2014, 15, 326-340.	0.7	19
9284	An Integrative <i>Omics</i> Approach, for Identification of Bona Fides PLK1 Associated Biomarker in Esophageal Adenocarcinoma. <i>Current Cancer Drug Targets</i> , 2019, 19, 742-755.	0.8	1
9285	The Regulation of Target Genes by Co-occupancy of Transcription Factors, c-Myc and Mxi1 with Max in the Mouse Cell Line. <i>Current Bioinformatics</i> , 2020, 15, 581-588.	0.7	9
9286	Statistical Methods for Overdispersion in mRNA-Seq Count Data. <i>Open Bioinformatics Journal</i> , 2013, 7, 34-40.	1.0	8
9287	Low-cost and High-throughput RNA-seq Library Preparation for Illumina Sequencing from Plant Tissue. <i>Bio-protocol</i> , 2020, 10, e3799.	0.2	5
9288	Mechanisms and Targets Involved in Dissemination of Ovarian Cancer. <i>Cancer Genomics and Proteomics</i> , 2016, 13, 407-424.	1.0	108
9289	Personal Health Information Inference Using Machine Learning on RNA Expression Data from Patients With Cancer: Algorithm Validation Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e18387.	2.1	3

#	ARTICLE	IF	CITATIONS
9290	Exogenous glutamine increases lipid accumulation in developing seeds of castor bean ( <i>Ricinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	0.2	3
9291	De novo characterization of the <i>Lycium ruthenicum</i> transcriptome and analysis of its digital gene expression profiles during fruit development and ripening. <i>Archives of Biological Sciences</i> , 2017, 69, 181-190.	0.2	2
9292	Development of 15 genic-ssr markers in oil-tea tree ( <i>Camellia oleifera</i> ) based on transcriptome sequencing. <i>Genetika</i> , 2014, 46, 789-797.	0.1	11
9293	Transcription profiles of skin and head kidney from goldfish suffering hemorrhagic septicemia with an emphasis on the TLR signaling pathway. <i>Zoological Research</i> , 2019, 40, 337-342.	0.9	4
9294	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. <i>In Silico Biology</i> , 2011, 11, 251-61.	0.4	6
9295	Comparative Transcriptome Analysis of Two <i>Aegilops tauschii</i> with Contrasting Drought Tolerance by RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3595.	1.8	21
9296	Transient Receptor Potential Ankyrin 1 (TRPA1) Is Involved in Upregulating Interleukin-6 Expression in Osteoarthritic Chondrocyte Models. <i>International Journal of Molecular Sciences</i> , 2021, 22, 87.	1.8	21
9297	Recent advances in RNA sequence analysis. <i>F1000 Biology Reports</i> , 2010, 2, 64.	4.0	13
9300	Comparative systems biology between human and animal models based on next-generation sequencing methods. <i>Zoological Research</i> , 2013, 34, E35.	0.6	1
9301	A Review on The Processing and Analysis of Next-generation RNA-seq Data*. <i>Progress in Biochemistry and Biophysics</i> , 2010, 37, 834-846.	0.3	8
9302	Prediction of Long Non-Coding RNAs Based on RNA-Seq*. <i>Progress in Biochemistry and Biophysics</i> , 2013, 39, 1156-1166.	0.3	3
9304	Transcriptome sequencing reveals dynamic changes in matrix metalloproteinases in facet joint osteoarthritis. <i>Experimental and Therapeutic Medicine</i> , 2020, 19, 2475-2482.	0.8	3
9305	The role of myoglobin in epithelial cancers: Insights from transcriptomics. <i>International Journal of Molecular Medicine</i> , 2020, 45, 385-400.	1.8	13
9306	Human cathelicidin antimicrobial peptide suppresses proliferation, migration and invasion of oral carcinoma HSC-3 cells via a novel mechanism involving caspase-3 mediated apoptosis. <i>Molecular Medicine Reports</i> , 2020, 22, 5243-5250.	1.1	11
9307	Transcriptome analysis of dog oral melanoma and its oncogenic analogy with human melanoma. <i>Oncology Reports</i> , 2020, 43, 16-30.	1.2	17
9308	Cloning and Expression Analysis of a Chalcone isomerase (CnCHI) Gene from <i>Chamaemelum nobile</i> . <i>Biotechnology</i> , 2017, 17, 19-25.	0.5	5
9309	Characterization of Novel Chalcone Synthase Gene (CnCHS) from <i>Chamaemelum nobile</i> . <i>Biotechnology</i> , 2018, 17, 54-61.	0.5	3
9310	Comprehensive molecular screening: from the RT-PCR to the RNA-seq. <i>Translational Lung Cancer Research</i> , 2013, 2, 87-91.	1.3	48

#	ARTICLE	IF	CITATIONS
9311	Statistical strategies for microRNAseq batch effect reduction. <i>Translational Cancer Research</i> , 2014, 3, 260-265.	0.4	19
9312	Transcriptomic Analysis of Genes Modulated by Cyclo(L-Phenylalanine-L-Proline) in <i>Vibrio vulnificus</i> . <i>Journal of Microbiology and Biotechnology</i> , 2013, 23, 1791-1801.	0.9	14
9313	Phosphate Solubilization and Gene Expression of Phosphate-Solubilizing Bacterium <i>Burkholderia multivorans</i> WS-FJ9 under Different Levels of Soluble Phosphate. <i>Journal of Microbiology and Biotechnology</i> , 2017, 27, 844-855.	0.9	51
9314	Effective Statistical Methods for Big Data Analytics. <i>Advances in Computational Intelligence and Robotics Book Series</i> , 0, , 280-299.	0.4	11
9315	Transcriptomics to Metabolomics. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2018, , 188-206.	0.2	5
9316	Transcriptomics to Metabolomics. , 2019, , 361-379.		1
9317	Molecular Biology of Protein-Protein Interactions for Computer Scientists. , 2009, , 1-13.		6
9318	Differential temporal expression of matrix metalloproteinases following sciatic nerve crush. <i>Neural Regeneration Research</i> , 2016, 11, 1165.	1.6	37
9319	Methotrexate combined with methylprednisolone for the recovery of motor function and differential gene expression in rats with spinal cord injury. <i>Neural Regeneration Research</i> , 2017, 12, 1507.	1.6	13
9320	Transcriptome analysis of adherens junction pathway-related genes after peripheral nerve injury. <i>Neural Regeneration Research</i> , 2018, 13, 1804.	1.6	10
9321	Analysis of transcriptome sequencing of sciatic nerves in Sprague-Dawley rats of different ages. <i>Neural Regeneration Research</i> , 2018, 13, 2182.	1.6	19
9322	Integrative Analysis of Genome-wide Expression and Methylation Data. <i>Journal of Biometrics &amp; Biostatistics</i> , 2013, 04, .	4.0	3
9323	Cell Wall Degrading Enzymes in <i>Trichoderma asperellum</i> Grown on Wheat Bran. <i>Fungal Genomics &amp; Biology</i> , 2014, 04, .	0.4	5
9324	Genetic Expression Profile Analysis of the Temporal Inhibition of Quercetin and Naringenin on <i>Lactobacillus Rhamnosus</i> GG. <i>Journal of Probiotics &amp; Health</i> , 2016, 04, .	0.6	2
9325	The Quest for More Tolerant Rice: How High Concentrations of Iron Affect Alternative Splicing?. <i>Transcriptomics: Open Access</i> , 2015, 03, .	0.2	3
9326	Enhanced Rice Growth is Conferred by Increased Leaf ADP-Glucose Pyrophosphorylase Activity. <i>Journal of Plant Physiology &amp; Pathology</i> , 2014, 02, .	0.1	7
9327	Transcriptome Analysis of the Chinese Cabbage ( <i>Brassica rapa</i> Ssp. <i>Pekinensis</i> ) Petal Using RNA-Seq. <i>Journal of Horticulture</i> , 2014, 01, .	0.3	2
9328	Management of High-Throughput DNA Sequencing Projects: Alpheus. <i>Journal of Computer Science and Systems Biology</i> , 2008, 01, 132.	0.0	65

#	ARTICLE	IF	CITATIONS
9329	Transcriptome Analysis of Drought Induced Stress in <i>Chenopodium quinoa</i> . American Journal of Plant Sciences, 2014, 05, 338-357.	0.3	43
9330	Transcriptome Analysis of Ten-DPA Fiber in an Upland Cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 American Journal of Plant Sciences, 2017, 08, 2530-2553.	0.3	8
9331	Challenges Analyzing RNA-Seq Gene Expression Data. Open Journal of Statistics, 2016, 06, 628-636.	0.3	4
9332	Gene expression profile analysis of testis and ovary of oriental river prawn, <i>Macrobrachium nipponense</i> , reveals candidate reproduction-related genes. Genetics and Molecular Research, 2015, 14, 2041-2054.	0.3	12
9333	Transcriptome Sequencing and Analysis of Changes Associated with Insecticide Resistance in the Dengue Mosquito ( <i>Aedes aegypti</i> ) in Vietnam. American Journal of Tropical Medicine and Hygiene, 2019, 100, 1240-1248.	0.6	27
9334	Methods for Allocating Ambiguous Short-reads. Communications in Information and Systems, 2010, 10, 69-82.	0.3	15
9335	Single-gene negative binomial regression models for RNA-Seq data with higher-order asymptotic inference. Statistics and Its Interface, 2015, 8, 405-418.	0.2	7
9336	A penalized likelihood approach for robust estimation of isoform expression. Statistics and Its Interface, 2015, 8, 437-445.	0.2	11
9337	Keeping house: evaluation of housekeeping genes for real-time PCR in the red alga, <i>Bostrychia moritziana</i> (Florideophyceae). Algae, 2016, 31, 167-174.	0.9	15
9338	Transcriptome profiling of the coffee ( <i>C. arabica</i> L.) seedlings under salt stress condition. Journal of Plant Biotechnology, 2018, 45, 45-54.	0.1	5
9339	Comparative miRNAome Analysis Revealed Numerous Conserved and Novel Drought Responsive miRNAs in Cotton ( <i>Gossypium</i> spp.). Cotton Genomics and Genetics, 0, , .	0.0	1
9340	De Novo RNA Seq Assembly and Annotation of <i>Phaseolus vulgaris</i> L. (SRR1283084). Genomics and Applied Biology, 0, , .	0.0	1
9341	De Novo RNA Seq Assembly and Annotation of <i>Vicia sativa</i> L. (SRR403901). Genomics and Applied Biology, 0, , .	0.0	1
9342	De Novo RNA Seq Assembly and Annotation of <i>Trigonella foenum-graecum</i> L. (SRR066197). Legume Genomics and Genetics, 0, , .	0.0	1
9343	Differential Expression Analysis for RNA-Seq Data. , 2012, 2012, 1-8.		14
9344	Transcriptome Analysis of the Small Brown Planthopper, <i>Laodelphax striatellus</i> Carrying Rice stripe virus. Plant Pathology Journal, 2013, 29, 330-337.	0.7	17
9345	Suppression of Rice Stripe Virus Replication in <i>Laodelphax striatellus</i> Using Vector Insect-Derived Double-Stranded RNAs. Plant Pathology Journal, 2020, 36, 280-288.	0.7	6
9346	RNAseq-based Transcriptome Analysis of <i>Burkholderia glumae</i> Quorum Sensing. Plant Pathology Journal, 2013, 29, 249-259.	0.7	14



#	ARTICLE	IF	CITATIONS
9347	Statistical modeling for differential transcriptome analysis using RNA-Seq technology. <i>Journal of Solid Tumors</i> , 2012, 2, .	0.1	3
9348	Swedish mutation within amyloid precursor protein modulates global gene expression towards the pathogenesis of Alzheimer's disease. <i>BMB Reports</i> , 2010, 43, 704-709.	1.1	30
9349	De novo sequencing and comparative transcriptome analysis of white petals and red labella in <i>Phalaenopsis</i> for discovery of genes related to flower color and floral differentiation. <i>Acta Societatis Botanicorum Poloniae</i> , 2014, 83, 191-199.	0.8	6
9350	RNA-seq Profiles of Immune Related Genes in the Spleen of Necrotic Enteritis-afflicted Chicken Lines. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 1496-1511.	2.4	44
9351	Novel splice isoforms of pig myoneurin and their diverse mRNA expression patterns. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018, 31, 1581-1590.	2.4	6
9352	Deep Sequencing Data Analysis: Challenges and Solutions. , 0, , .		4
9353	Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins. , 0, , .		7
9354	Analysis of Whole Transcriptome Sequencing Data: Workflow and Software. <i>Genomics and Informatics</i> , 2015, 13, 119.	0.4	58
9355	COEX-Seq: Convert a Variety of Measurements of Gene Expression in RNA-Seq. <i>Genomics and Informatics</i> , 2018, 16, e36.	0.4	10
9356	Gene Expression Study of <i>Arachis Hypogaea</i> L.. <i>International Journal of Agriculture Environment and Biotechnology</i> , 2015, 8, 295.	0.1	1
9357	Suppression subtractive hybridization (SSH) combined with bioinformatics method: an integrated functional annotation approach for analysis of differentially expressed immune-genes in insects. <i>Bioinformation</i> , 2013, 9, 216-221.	0.2	10
9358	BBD454: A database for transcriptome analysis of blueberry using 454 sequences. <i>Bioinformation</i> , 2013, 9, 883-886.	0.2	4
9360	Transcriptome Assembly and Expression Data from Normal and Mantled Oil Palm Fruit. <i>Dataset Papers in Biology</i> , 2013, 2013, 1-7.	0.5	4
9361	Comparison of the Gene Expression Profiles Between Smokers With and Without Lung Cancer Using RNA-Seq. <i>Asian Pacific Journal of Cancer Prevention</i> , 2012, 13, 3605-3609.	0.5	7
9362	SEC24A deficiency lowers plasma cholesterol through reduced PCSK9 secretion. <i>ELife</i> , 2013, 2, e00444.	2.8	104
9363	Global cellular response to chemotherapy-induced apoptosis. <i>ELife</i> , 2013, 2, e01236.	2.8	59
9364	Chromatin signature of widespread monoallelic expression. <i>ELife</i> , 2013, 2, e01256.	2.8	71
9365	Evolution of extreme resistance to ionizing radiation via genetic adaptation of DNA repair. <i>ELife</i> , 2014, 3, e01322.	2.8	80

#	ARTICLE	IF	CITATIONS
9366	Musashi proteins are post-transcriptional regulators of the epithelial-luminal cell state. <i>ELife</i> , 2014, 3, e03915.	2.8	88
9367	Genome-wide regulatory dynamics of translation in the <i>Plasmodium falciparum</i> asexual blood stages. <i>ELife</i> , 2014, 3, .	2.8	115
9368	mTORC1 is necessary but mTORC2 and GSK3 $\beta$ are inhibitory for AKT3-induced axon regeneration in the central nervous system. <i>ELife</i> , 2016, 5, e14908.	2.8	98
9369	The exon junction complex regulates the splicing of cell polarity gene <i>dlg1</i> to control Wingless signaling in development. <i>ELife</i> , 2016, 5, .	2.8	12
9370	Nematophagous fungus <i>Arthrobotrys oligospora</i> mimics olfactory cues of sex and food to lure its nematode prey. <i>ELife</i> , 2017, 6, .	2.8	75
9371	MEF2C regulates cortical inhibitory and excitatory synapses and behaviors relevant to neurodevelopmental disorders. <i>ELife</i> , 2016, 5, .	2.8	138
9372	Expansion of the fatty acyl reductase gene family shaped pheromone communication in Hymenoptera. <i>ELife</i> , 2019, 8, .	2.8	26
9373	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. <i>ELife</i> , 2019, 8, .	2.8	98
9374	Deciphering the regulatory genome of <i>Escherichia coli</i> , one hundred promoters at a time. <i>ELife</i> , 2020, 9, .	2.8	31
9375	Investigation for a multi-silique trait in <i>Brassica napus</i> by alternative splicing analysis. <i>PeerJ</i> , 2020, 8, e10135.	0.9	6
9376	miR-21 is upregulated, promoting fibrosis and blocking G2/M in irradiated rat cardiac fibroblasts. <i>PeerJ</i> , 2020, 8, e10502.	0.9	7
9377	Improving transcriptome assembly through error correction of high-throughput sequence reads. <i>PeerJ</i> , 2013, 1, e113.	0.9	38
9378	Comparative transcriptomics in three <i>Methylophilaceae</i> species uncover different strategies for environmental adaptation. <i>PeerJ</i> , 2013, 1, e115.	0.9	20
9379	Augmenting transcriptome assembly by combining <i>de novo</i> and genome-guided tools. <i>PeerJ</i> , 2013, 1, e133.	0.9	19
9380	Expression patterns of cysteine peptidase genes across the <i>Tribolium castaneum</i> life cycle provide clues to biological function. <i>PeerJ</i> , 2016, 4, e1581.	0.9	20
9381	BD-Func: a streamlined algorithm for predicting activation and inhibition of pathways. <i>PeerJ</i> , 2013, 1, e159.	0.9	10
9382	Characterization of RNA in exosomes secreted by human breast cancer cell lines using next-generation sequencing. <i>PeerJ</i> , 2013, 1, e201.	0.9	187
9383	Predominant intragenic methylation is associated with gene expression characteristics in a bivalve mollusc. <i>PeerJ</i> , 2013, 1, e215.	0.9	132

#	ARTICLE	IF	CITATIONS
9384	Genome-wide identification and characterization of TIFY family genes in Moso Bamboo ( <i>Phyllostachys edulis</i> ) and expression profiling analysis under dehydration and cold stresses. PeerJ, 2016, 4, e2620.	0.9	37
9385	Transcriptomic analysis reveals metabolic switches and surface remodeling as key processes for stage transition in <i>Trypanosoma cruzi</i> . PeerJ, 2017, 5, e3017.	0.9	48
9386	Comparative venom gland transcriptomics of <i>Naja kaouthia</i> (monocled cobra) from Malaysia and Thailand: elucidating geographical venom variation and insights into sequence novelty. PeerJ, 2017, 5, e3142.	0.9	66
9387	Transcriptome analysis reveals the regulation of brassinosteroids on petal growth in <i>Gerbera hybrida</i> . PeerJ, 2017, 5, e3382.	0.9	30
9388	Shot-gun proteome and transcriptome mapping of the jujube floral organ and identification of a pollen-specific S-locus F-box gene. PeerJ, 2017, 5, e3588.	0.9	8
9389	The complete mitochondrial genome of the grooved carpet shell, <i>Ruditapes decussatus</i> (Bivalvia). Tj ETQq1 1,0,784314,rgBT/Ome	0.9	16
9390	Gene expression profiling and functional analysis reveals that p53 pathway-related gene expression is highly activated in cancer cells treated by cold atmospheric plasma-activated medium. PeerJ, 2017, 5, e3751.	0.9	31
9391	Characterisation of the horse transcriptome from immunologically active tissues. PeerJ, 2014, 2, e382.	0.9	6
9392	Alpha-arylphorin is a mitogen in the <i>Heliothis virescens</i> midgut cell secretome upon Cry1Ac intoxication. PeerJ, 2017, 5, e3886.	0.9	13
9393	Global analysis of A-to-I RNA editing reveals association with common disease variants. PeerJ, 2018, 6, e4466.	0.9	21
9394	Transcriptome profiling of anthocyanin-related genes reveals effects of light intensity on anthocyanin biosynthesis in red leaf lettuce. PeerJ, 2018, 6, e4607.	0.9	54
9395	Transcriptome profiling by RNA-Seq reveals differentially expressed genes related to fruit development and ripening characteristics in strawberries ( <i>Fragaria</i> — <i>ananassa</i> ). PeerJ, 2018, 6, e4976.	0.9	29
9396	Genetic analysis reveals candidate genes for activity QTL in the blind Mexican tetra, <i>Astyanax mexicanus</i> . PeerJ, 2018, 6, e5189.	0.9	15
9397	RNA-Seq analysis of differential gene expression in <i>Betula luminifera</i> xylem during the early stages of tension wood formation. PeerJ, 2018, 6, e5427.	0.9	15
9398	The Oyster River Protocol: a multi-assembler and kmer approach for de novo transcriptome assembly. PeerJ, 2018, 6, e5428.	0.9	85
9399	<i>De novo</i> transcriptome sequencing and analysis of genes related to salt stress response in <i>Glehnia littoralis</i> . PeerJ, 2018, 6, e5681.	0.9	21
9400	Error estimates for the analysis of differential expression from RNA-seq count data. PeerJ, 2014, 2, e576.	0.9	61
9401	Genome-wide identification and comparative evolutionary analysis of the Dof transcription factor family in physic nut and castor bean. PeerJ, 2019, 7, e6354.	0.9	16

#	ARTICLE	IF	CITATIONS
9402	Transcriptome sequencing of olfactory-related genes in olfactory transduction of large yellow croaker ( <i>Larimichthys crocea</i> ) in response to bile salts. PeerJ, 2019, 7, e6627.	0.9	5
9403	Genomics analysis of genes encoding respiratory burst oxidase homologs (RBOHs) in jatropha and the comparison with castor bean. PeerJ, 2019, 7, e7263.	0.9	9
9404	Identification of conserved genes involved in nitrogen metabolic activities in wheat. PeerJ, 2019, 7, e7281.	0.9	17
9405	Association of transcription factor WRKY56 gene from <i>Populus simonii</i> Ā— <i>P. nigra</i> with salt tolerance in <i>Arabidopsis thaliana</i> . PeerJ, 2019, 7, e7291.	0.9	6
9406	Different expression pattern of flowering pathway genes contribute to male or female organ development during floral transition in the monoecious weed <i>Ambrosia artemisiifolia</i> L. ( <i>Asteraceae</i> ). PeerJ, 2019, 7, e7421.	0.9	14
9407	Exploration of the effects of a <i>degS</i> mutant on the growth of <i>Vibrio cholerae</i> and the global regulatory function of <i>degS</i> by RNA sequencing. PeerJ, 2019, 7, e7959.	0.9	5
9408	Prediction of clusters of miRNA binding sites in mRNA candidate genes of breast cancer subtypes. PeerJ, 2019, 7, e8049.	0.9	18
9409	A new insight to biomarkers related to resistance in survived-white spot syndrome virus challenged giant tiger shrimp, <i>Penaeus monodon</i> . PeerJ, 2019, 7, e8107.	0.9	11
9410	Transcriptome analysis and transcription factors responsive to drought stress in <i>Hibiscus cannabinus</i> . PeerJ, 2020, 8, e8470.	0.9	11
9411	Characterization of the transcriptional response of <i>Candida parapsilosis</i> to the antifungal peptide MAF-1A. PeerJ, 2020, 8, e9767.	0.9	4
9412	Blood-Based Gene Expression in children with Autism spectrum disorder. BioDiscovery, 2015, , 2.	0.1	8
9413	Framework Based on Relationship to Describe Non-Hierarchical, Boundaryless and Multi-Perspective Phenomena. SICE Journal of Control Measurement and System Integration, 2018, 11, 381-389.	0.4	9
9414	Development of EST-SSR Markers for Cultivar Determination and Genetic Diversity Studies of Commercial Chrysanthemums in the Korean Floral Market. Han'guk Yukchong Hakhoe Chi, 2019, 51, 201-208.	0.2	3
9415	Genome-wide RNA-seq Analysis of Differentially Expressed Transcription Factor Genes Against Bacterial Leaf Pustule in Soybean. Plant Breeding and Biotechnology, 2015, 3, 197-207.	0.3	7
9416	Expression of Heat Shock Proteins by Heat Stress in Soybean. Plant Breeding and Biotechnology, 2017, 5, 344-353.	0.3	8
9417	Identification of lncRNA-mRNA regulatory network associated with isolated systolic hypertension and atherosclerotic cerebral infarction. Annals of Translational Medicine, 2021, 9, 1589-1589.	0.7	1
9418	Status of diagnosis and treatment of esophageal cancer and non-coding RNA correlation research: a narrative review. Translational Cancer Research, 2021, 10, 4532-4552.	0.4	2
9419	Interactions Among Nerve Regeneration, Angiogenesis, and the Immune Response Immediately After Sciatic Nerve Crush Injury in Sprague-Dawley Rats. Frontiers in Cellular Neuroscience, 2021, 15, 717209.	1.8	9

#	ARTICLE	IF	CITATIONS
9421	A major checkpoint for protein expression in <i>Rhodobacter sphaeroides</i> during heat stress response occurs at the level of translation. <i>Environmental Microbiology</i> , 2021, 23, 6483-6502.	1.8	7
9422	Constitutively enhanced genome integrity maintenance and direct stress mitigation characterize transcriptome of extreme stress-adapted <i>Arabidopsis halleri</i> . <i>Plant Journal</i> , 2021, 108, 896-911.	2.8	7
9423	Runx3 regulates iron metabolism via modulation of BMP signalling. <i>Cell Proliferation</i> , 2021, 54, e13138.	2.4	3
9424	A Putative C2H2 Transcription Factor CgTF6, Controlled by CgTF1, Negatively Regulates Chaetoglobosin A Biosynthesis in <i>Chaetomium globosum</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	0
9425	Transcriptome and metabolome analysis of stress tolerance to aluminium in <i>Vitis quinquangularis</i> . <i>Planta</i> , 2021, 254, 105.	1.6	10
9426	Deep characterization of paired chromatin and transcriptomes in four immune cell types from multiple sclerosis patients. <i>Epigenomics</i> , 2021, 13, 1607-1618.	1.0	4
9427	Identification of altered exosomal microRNAs and mRNAs in Alzheimer's disease. <i>Ageing Research Reviews</i> , 2022, 73, 101497.	5.0	38
9428	Transcriptome Analysis Reveals the Complex Molecular Mechanisms of <i>Brassica napus</i> – <i>Sclerotinia sclerotiorum</i> Interactions. <i>Frontiers in Plant Science</i> , 2021, 12, 716935.	1.7	8
9429	Effects of Nitrogen and Phosphorus Limitation on Fatty Acid Contents in <i>Aspergillus oryzae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 739569.	1.5	3
9430	Transcriptomic analysis of blackberry plant ( <i>Rubus</i> spp.) reveals a comprehensive metabolic network involved in fruit ripening process. <i>Biologia (Poland)</i> , 2021, 76, 3827-3840.	0.8	2
9431	Cellulose synthase-like protein OsCSLD4 plays an important role in the response of rice to salt stress by mediating abscisic acid biosynthesis to regulate osmotic stress tolerance. <i>Plant Biotechnology Journal</i> , 2022, 20, 468-484.	4.1	41
9432	Testis transcriptome profiling identified lncRNAs involved in spermatogenic arrest of cattleyak. <i>Functional and Integrative Genomics</i> , 2021, 21, 665-678.	1.4	9
9433	Expression Elements Derived From Plant Sequences Provide Effective Gene Expression Regulation and New Opportunities for Plant Biotechnology Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 712179.	1.7	2
9434	PIC-Me: paralogs and isoforms classifier based on machine-learning approaches. <i>BMC Bioinformatics</i> , 2021, 22, 311.	1.2	0
9435	Depside and Depsidone Synthesis in Lichenized Fungi Comes into Focus through a Genome-Wide Comparison of the Olivetoric Acid and Physodic Acid Chemotypes of <i>Pseudevernia furfuracea</i> . <i>Biomolecules</i> , 2021, 11, 1445.	1.8	27
9436	Advanced Genomics-Based Approaches for Defining Allograft Rejection With Single Cell Resolution. <i>Frontiers in Immunology</i> , 2021, 12, 750754.	2.2	5
9437	Comparative RNA-Seq Analyses of <i>Solenopsis japonica</i> (Hymenoptera: Formicidae) Reveal Gene in Response to Cold Stress. <i>Genes</i> , 2021, 12, 1610.	1.0	10
9438	Research on the release mechanism of glucoraphanin and sulforaphane mediated by methyl jasmonate in broccoli hairy roots. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2021, 57, 831.	0.9	1

#	ARTICLE	IF	CITATIONS
9439	A photoregulatory mechanism of the circadian clock in Arabidopsis. <i>Nature Plants</i> , 2021, 7, 1397-1408.	4.7	76
9440	Transcriptome and de novo analysis of <i>Rosa xanthina</i> f. <i>spontanea</i> in response to cold stress. <i>BMC Plant Biology</i> , 2021, 21, 472.	1.6	7
9441	Annotation depth confounds direct comparison of gene expression across species. <i>BMC Bioinformatics</i> , 2021, 22, 499.	1.2	3
9442	Transcriptomic and Coexpression Network Analyses Revealed Pine Chalcone Synthase Genes Associated with Pine Wood Nematode Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11195.	1.8	11
9443	<i>CARMN</i> Is an Evolutionarily Conserved Smooth Muscle Cell-Specific LncRNA That Maintains Contractile Phenotype by Binding Myocardin. <i>Circulation</i> , 2021, 144, 1856-1875.	1.6	50
9444	Genomic and experimental evidence that <i>ALKATI</i> does not predict single agent sensitivity to ALK inhibitors. <i>IScience</i> , 2021, 24, 103343.	1.9	3
9445	Differential expression analysis using a model-based gene clustering algorithm for RNA-seq data. <i>BMC Bioinformatics</i> , 2021, 22, 511.	1.2	9
9446	Pleiotropic Effects of the P5-Type ATPase SpfA on Stress Response Networks Contribute to Virulence in the Pathogenic Mold <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2021, 12, e0273521.	1.8	4
9447	Integrative transcriptomic and gene co-expression network analysis of host responses upon <i>Verticillium dahliae</i> infection in <i>Gossypium hirsutum</i> . <i>Scientific Reports</i> , 2021, 11, 20586.	1.6	11
9448	A connectome is not enough – what is still needed to understand the brain of <i>Drosophila</i> ?. <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	12
9449	Transcriptome profile of <i>Haemaphysalis longicornis</i> (Acari: Ixodidae) exposed to <i>Cymbopogon citratus</i> essential oil and citronellal suggest a cytotoxic mode of action involving mitochondrial Ca <sup>2+</sup> overload and depolarization. <i>Pesticide Biochemistry and Physiology</i> , 2021, 179, 104971.	1.6	6
9451	Assessing Host-Pathogen Interaction Networks via RNA-Seq Profiling: A Systems Biology Approach. , 0, , .		1
9452	Identification of Transcription Factor Genes and Functional Characterization of <i>PIMYB1</i> From <i>Pueraria lobata</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 743518.	1.7	6
9453	Integrated Transcriptomic and Translatomic Inquiry of the Role of Betaine on Lipid Metabolic Dysregulation Induced by a High-Fat Diet. <i>Frontiers in Nutrition</i> , 2021, 8, 751436.	1.6	10
9454	Host-Microbiota Interactions in the Esophagus During Homeostasis and Allergic Inflammation. <i>Gastroenterology</i> , 2022, 162, 521-534.e8.	0.6	24
9455	Engineering <i>Bacteroides thetaiotaomicron</i> to produce non-native butyrate based on a genome-scale metabolic model-guided design. <i>Metabolic Engineering</i> , 2021, 68, 174-186.	3.6	13
9456	Curc-mPEG454, a PEGylated curcumin derivative, as a multi-target anti-fibrotic prodrug. <i>International Immunopharmacology</i> , 2021, 101, 108166.	1.7	4
9457	Transcriptome analysis of the influence of CPPU application for fruit setting on melon volatile content. <i>Journal of Integrative Agriculture</i> , 2021, 20, 3199-3208.	1.7	2

#	ARTICLE	IF	CITATIONS
9458	Transcriptome aberration associated with altered locomotor behavior of zebrafish ( <i>Danio rerio</i> ) caused by Waterborne Benzo[a]pyrene. <i>Ecotoxicology and Environmental Safety</i> , 2021, 227, 112928.	2.9	2
9459	Transcriptomic analysis reveals innate immune mechanisms of an underlying parasite-resistant grouper hybrid ( <i>Epinephelus fuscogutatus</i> × <i>Epinephelus lanceolatus</i> ). <i>Fish and Shellfish Immunology</i> , 2021, 119, 67-75.	1.6	9
9461	Sequence Based Gene Expression Analysis. , 2009, , 191-207.		2
9463	A Fast and Efficient Algorithm for Mapping Short Sequences to a Reference Genome. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 399-403.	0.8	8
9464	DEVELOPMENT OF A METHOD OF RNA-Seq DATA ANALYSIS. , 2010, , .		0
9466	Outsourcing of Experimental Work. <i>Methods in Molecular Biology</i> , 2011, 703, 319-325.	0.4	0
9468	A Succinct Index for Hypertext. <i>Lecture Notes in Computer Science</i> , 2011, , 209-220.	1.0	0
9470	Maximum Likelihood Estimation of Incomplete Genomic Spectrum from HTS Data. <i>Lecture Notes in Computer Science</i> , 2011, , 213-224.	1.0	2
9471	The Hallmarks of Cancer Revisited Through Systems Biology and Network Modelling. , 2011, , 245-266.		2
9472	Generation of a Large Catalog of Unique Transcripts for Whole-Genome Expression Analysis in Nonmodel Species. <i>Methods in Molecular Biology</i> , 2011, 729, 257-269.	0.4	0
9473	Computational Molecular Biology: an Integration of Experimental Molecular and Genome Biology with Computational Technology. <i>Computational Molecular Biology</i> , 0, , .	0.0	0
9476	Renaissance of the Regulatory RNAs. , 2012, , 3-22.		0
9477	Expression Profiling of ncRNAs Employing RNP Libraries and Custom LNA/DNA Microarray Analysis. , 2012, , 229-251.		0
9478	Identification of lncRNAs Using Computational and Experimental Approaches. , 2012, , 319-340.		0
9479	Novel Methods in the Study of the Breast Cancer Genome: Towards a Better Understanding of the Disease of Breast Cancer. <i>Journal of Cancer Therapy</i> , 2012, 03, 797-809.	0.1	0
9480	The Molecular Cloning and Bioactivity Characterization of Unknown Gene 1C10 from Medicinal Fungus <i>Agrocybe aegerita</i> . <i>Medical Diagnosis</i> , 2012, 02, 1-5.	0.0	0
9481	Characterization of RNA. <i>Springer Protocols</i> , 2012, , 135-160.	0.1	0
9482	Defining Genetic Blueprints “ Kidney and Craniofacial Development. <i>Translational Bioinformatics</i> , 2012, , 335-358.	0.0	0

#	ARTICLE	IF	CITATIONS
9483	An Integrated RNA-seq Atlas of the Murine T-Helper Cell Transcriptome. EMBnet Journal, 2012, 17, 29.	0.2	0
9485	Identification of RNA Editing Sites in Chimpanzee by Transcriptome-wide Sequencing Data*. Progress in Biochemistry and Biophysics, 2012, 39, 282-293.	0.3	0
9486	Slate and Trait Markers of Alcohol Abuse. , 2012, , 47-92.		0
9487	RNA-seq Using Next Generation Sequencing. Materials and Methods, 0, 2, .	0.0	1
9489	INTERPRETING PERSONAL TRANSCRIPTOMES: PERSONALIZED MECHANISM-SCALE PROFILING OF RNA-SEQ DATA. , 2012, , .		6
9490	A Hierarchical Bayesian Model for RNA-Seq Data. Contributions To Statistics, 2013, , 215-227.	0.2	0
9491	Evaluation of RNA-Seq software in gene expression quantification. Journal of Biomedical Science and Engineering, 2013, 06, 473-477.	0.2	0
9492	Pardiff: Inference of Differential Expression at Base-Pair Level from RNA-Seq Experiments. Lecture Notes in Computer Science, 2013, , 418-427.	1.0	0
9493	Mapping and Analysis of Illumina Reads for Transcriptome of Medicago Truncatula During the Early Organogenesis of the Nodule. Bio-protocol, 2013, 3, .	0.2	2
9494	Isoform Inference From RNA-Seq Samples Based on Gene Structures on Chromosomes. Journal of Biosciences and Medicines, 2013, 01, 1-5.	0.1	0
9495	Transcriptome Sequencing. , 2013, , 2259-2259.		0
9496	Next-Generation Sequencing for Cancer Genomics. , 2013, , 55-74.		1
9497	Innovative Technologies in the Molecular Characterization of Pancreatic Cancer. , 2013, , 209-228.		0
9498	Emerging Technologies to Study Long Non-coding RNAs. , 2013, , 163-195.		0
9499	Biological Sequences. SpringerBriefs in Optimization, 2013, , 1-6.	0.3	0
9500	Genome-Wide Analysis of Transcription Factor-Binding Sites in Skeletal Muscle Cells Using ChIP-Seq. Methods in Molecular Biology, 2013, 1067, 51-64.	0.4	0
9502	From Genome to Proteome: Transcriptional and Proteomic Analysis of Cryptosporidium Parasites. , 2014, , 345-359.		0
9503	An Information Integration Approach for Classifying Coding and Non-Coding Genomic Data. Lecture Notes in Electrical Engineering, 2014, , 1085-1093.	0.3	0



#	ARTICLE	IF	CITATIONS
9506	Comparative study of five Legume species based on De Novo Sequence Assembly and Annotation. Computational Molecular Biology, 0, , .	0.0	1
9507	De Novo RNA Seq Assembly and Annotation of <i>Cicer arietinum</i> L. (SRR627764). Legume Genomics and Genetics, 0, , .	0.0	0
9509	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0
9511	RNA-Seq Data Analysis in Prokaryotes: A Review for Non-experts. Acta Biologica Colombiana, 2014, 19, 131.	0.1	1
9512	Transcriptome-Wide Analysis of Regulatory Interactions of the RNA-Binding Protein HuR. Springer Theses, 2014, , 35-54.	0.0	0
9513	Transcriptome Analysis of Tessellated and Green Leaves in Paphiopedilum Orchids Using Illumina Paired-End Sequencing and Discovery Simple Sequence Repeat Markers. Journal of Plant Biochemistry & Physiology, 2014, 02, .	0.5	1
9514	The Bench Scientist's Guide to Statistical Analysis of RNA-Seq Data. , 2014, , 1-20.		0
9515	DEVELOPMENT IN RICE GENOME RESEARCH BASED ON ACCURATE GENOME SEQUENCE. , 2014, , 197-218.		0
9516	Link-Based Quantitative Methods to Identify Differentially Coexpressed Genes and Gene Pairs. , 2014, , 173-196.		0
9517	MOLECULAR MECHANISMS OF EPIGENETIC VARIATION IN PLANTS. , 2014, , 357-386.		0
9518	Identificación de genes relacionados a sequencia en papas nativas empleando RNA-Seq. Revista Peruana De Biología, 2013, 20, 211-214.	0.1	2
9521	DNA Markers in Tree Improvement of Tropical Plantation Species. , 2014, , 568-592.		0
9533	Aspergillus flavus Blast2GO Gene Ontology Database: Elevated Growth Temperature Alters Amino Acid Metabolism. Journal of Genetics and Genome Research, 2014, 1, .	0.3	1
9537	Modeling Expression Plasticity of Genes that Differentiate Drug-sensitive from Drug-resistant Cells to Chemotherapeutic Treatment. Current Genomics, 2014, 15, 349-356.	0.7	1
9540	Annotation Pipelines for Next-Generation Sequencing Projects. Computational Biology, 2015, , 325-367.	0.1	0
9542	Gujarat State Leguminosae Family Database (GLDB): Bioinformatics Database of Leguminosae Family present in Gujarat state of INDIA. Computational Molecular Biology, 0, , .	0.0	0
9543	Mapping RNA Interactions to Proteins in Virions Using CLIP-Seq. Methods in Molecular Biology, 2015, 1297, 213-224.	0.4	0
9544	Developing a Comprehensive Taxonomy for Human Cell Types. , 2015, , 123-151.		0

#	ARTICLE	IF	CITATIONS
9548	How are Bayesian and Non-Parametric Methods Doing a Great Job in RNA-Seq Differential Expression Analysis? : A Review. Communications for Statistical Applications and Methods, 2015, 22, 181-199.	0.1	1
9551	The Analyses of Global Gene Expression and Transcription Factor Regulation. Translational Bioinformatics, 2016, , 1-35.	0.0	2
9554	Use of the pBUTR Reporter System for Scalable Analysis of 3â€² UTR-Mediated Gene Regulation. Methods in Molecular Biology, 2016, 1358, 109-128.	0.4	0
9555	Gene Expression Analysis: Current Methods. , 2016, , 107-136.		2
9558	Identification and Sequence Analysis of Î²-D-Xylosidase Gene from Citrus grandis var. Shatinyu Hort. World Journal of Forestry, 2016, 05, 102-110.	0.0	0
9559	Ribosome Profiling. , 2016, , 175-195.		0
9560	Functional Genomics-Renal Development and Disease. Translational Bioinformatics, 2016, , 421-443.	0.0	0
9561	Gene Expression Analysis: Applications. , 2016, , 137-149.		0
9562	Applications of Non-coding RNA in the Molecular Pathology of Cancer. , 2016, , 177-217.		1
9571	De novo transcriptome sequencing and analysis of Hydrilla verticillata (L.f.) Royle. Plant OMICS, 2016, 9, 270-280.	0.4	4
9579	Omics Approaches to Understand Biotic Stresses: A Case Study on Plant Parasitic Nematodes. SpringerBriefs in Systems Biology, 2017, , 35-54.	0.1	2
9580	Data characterization. , 2017, , 15-43.		0
9581	Comparative Transcriptomics ofBuzura suppressaria(Lepidoptera: Geometridae) Assembled De Novo Yield Insights Into Response AfterBuzura suppressariaNuclear Polyhedrosis Virus Infection. Journal of Economic Entomology, 2017, 110, tow298.	0.8	1
9584	IRIS-TCGA: An Information Retrieval and Integration System for Genomic Data of Cancer. Lecture Notes in Computer Science, 2017, , 160-171.	1.0	1
9586	Sequencing Strategies. , 2017, , 61-80.		0
9587	Alignment and Mapping. , 2017, , 105-125.		0
9590	Applications of Genomics in Weed Science. , 2017, , 185-217.		0
9592	An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Nonuniformity of the Expected Fragment Starting-Point and Coverage Profile. Journal of Computational Biology, 2017, 24, 200-212.	0.8	2

#	ARTICLE	IF	CITATIONS
9596	Potentialities of Proteomics for Generating Abiotic Stress Tolerant Crop Species. , 2017, , 421-442.		0
9603	Applications of Genomics in Weed Science. , 2017, , 185-217.		0
9607	Overview of Next-Generation Sequencing Technologies and Its Application in Chemical Biology. Springer Theses, 2018, , 1-41.	0.0	0
9617	Recent Advances in the Transcriptomic Study of Shrimps. Advances in Marine Sciences, 2018, 05, 9-17.	0.2	0
9618	The Difference Analysis of Histone Modifications in Cancer Cell Line HepG2 and Normal Cell Line Hepatocyte. Hans Journal of Computational Biology, 2018, 08, 49-57.	0.0	0
9619	Transcriptome Analysis of Gene Expression Patterns of Populus tomentosa in Response to Oxidative Stress. Botanical Research, 2018, 07, 186-195.	0.0	0
9622	Transcriptomic Analysis of Flower Development in the Bamboo Phyllostachys violascens (Poaceae:). Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	0
9643	<i>De novo</i> oviduct transcriptome of the moor frog <i>Rana arvalis</i>: a quest for maternal effect candidate genes. PeerJ, 2018, 6, e5452.	0.9	1
9644	Computational Modelling and Pattern Recognition in Bioinformatics. Springer Series on Bio- and Neurosystems, 2019, , 505-543.	0.2	0
9658	Circular RNAs in Human Health and Disease. , 2019, , 119-132.		0
9661	Transcriptomic Approaches for Muscle Biology and Disorders. , 2019, , 79-107.		0
9662	Applications of Genomic Technologies in Retinal Degenerative Diseases. Advances in Experimental Medicine and Biology, 2019, 1185, 281-285.	0.8	0
9663	The Next Generation Sequencing Techniques and Application in Drug Discovery and Development. Advances in Medical Technologies and Clinical Practice Book Series, 2019, , 240-259.	0.3	0
9664	Guidelines for Bioinformatics and the Statistical Analysis of Omic Data. , 2019, , 45-75.		0
9665	Quantitative Analysis of Pathway Enrichment within Faba Bean Seeds RNA-Seq (&lt;i>Vicia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.3	2
9666	ModHMM: A Modular Supra-Bayesian Genome Segmentation Method. Lecture Notes in Computer Science, 2019, , 35-50.	1.0	2
9667	Genomic Applications and Insights in Unravelling Cancer Signalling Pathways. , 2019, , 471-511.		0
9668	Grape Transcriptomics and Viticulture. Compendium of Plant Genomes, 2019, , 275-299.	0.3	0

#	ARTICLE	IF	CITATIONS
9670	Robust and efficient identification of biomarkers from RNA-Seq data using median control chart. <i>F1000Research</i> , 0, 8, 7.	0.8	1
9671	Transcriptome Analysis of <i>Salvia miltiorrhiza</i> . <i>Compendium of Plant Genomes</i> , 2019, , 83-96.	0.3	1
9672	Smart Persistence and Accessibility of Genomic and Clinical Data. <i>Communications in Computer and Information Science</i> , 2019, , 8-14.	0.4	1
9673	Transcriptome Analysis of the Effect of Cutting Age on Adventitious Root Formation of <i>Populus</i> . <i>Botanical Research</i> , 2019, 08, 293-306.	0.0	0
9677	Methods for analyzing next-generation sequencing data XIII.RNA-seq analysis (Part 1). <i>Japanese Journal of Lactic Acid Bacteria</i> , 2019, 30, 38-45.	0.1	0
9678	Blood transcriptome resources of chinstrap ( <i>Pygoscelis antarcticus</i> ) and gentoo ( <i>Pygoscelis papua</i> ) penguins from the South Shetland Islands, Antarctica. <i>Genomics and Informatics</i> , 2019, 17, e5.	0.4	1
9689	Tagging Transcription Starting Sites with CAGE. , 2019, , 7-20.		0
9705	Tumor Sequencing: Enabling Personalized Targeted Treatments with Informatics. <i>Computers in Health Care</i> , 2020, , 161-174.	0.2	0
9708	Normalization in Human Glioma Tissue. <i>Methods in Molecular Biology</i> , 2020, 2065, 175-190.	0.4	2
9710	Exploring Toxin Evolution: Venom Protein Transcript Sequencing and Transcriptome-Guided High-Throughput Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2068, 97-127.	0.4	3
9712	Identification of Chimeric RNAs Using RNA-Seq Reads and Protein-Protein Interactions of Translated Chimeras. <i>Methods in Molecular Biology</i> , 2020, 2079, 27-40.	0.4	0
9715	Molecular Approaches for Analyzing Environmental <i>Chaetomium</i> Diversity and Exploitation of <i>Chaetomium thermophilum</i> for Biochemical Analyses. <i>Fungal Biology</i> , 2020, , 105-142.	0.3	0
9725	Novel Approaches to Profile Functional Long Noncoding RNAs Associated with Stem Cell Pluripotency. <i>Current Genomics</i> , 2020, 21, 37-45.	0.7	2
9726	Studying strands polarity of different viroids and their combinations in infected hop plants. <i>Acta Agriculturae Slovenica</i> , 2020, 115, .	0.2	0
9727	Thyroid Hormone Metabolite 3-Iodothyronamine (T1AM) Alleviates Hypoxia/Reoxygenation-Induced Cardiac Myocyte Apoptosis via Akt/FoxO1 Pathway. <i>Medical Science Monitor</i> , 2020, 26, e923195.	0.5	6
9731	Differential regulatory pathways associated with drought-inhibition and post-drought recuperation of rhizome development in perennial grass. <i>Annals of Botany</i> , 2020, 126, 481-497.	1.4	8
9734	The Clinical Application of RNA Sequencing in Genetic Diagnosis of Mendelian Disorders. <i>Clinics in Laboratory Medicine</i> , 2020, 40, 121-133.	0.7	19
9735	qPCR multiplex detection of microRNA and messenger RNA in a single reaction. <i>PeerJ</i> , 2020, 8, e9004.	0.9	2

#	ARTICLE	IF	CITATIONS
9740	The <i>Wolfiporia cocos</i> Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotium. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 455-467.	3.0	11
9741	Genes for defense response to <i>Plasmodiophora brassicae</i> during late infection in small spheroid galls of <i>Brassica rapa</i> . <i>Biologia Plantarum</i> , 0, 64, 551-560.	1.9	0
9742	RNA sequencing-based identification of potential targets in acute myeloid leukemia: A case report. <i>Biomedical Reports</i> , 2020, 13, 1-1.	0.9	2
9744	Cadmium and zinc uptake and translocation in dwarf Polish wheat seedlings as affected by calcium and potassium combination. <i>Biologia Plantarum</i> , 0, 64, 642-652.	1.9	0
9746	Investigating the Transcriptomic and Expression Presence-Absence Variation Exist in Japanese Eel ( <i>Anguilla japonica</i> ), a Primitive Teleost. <i>Marine Biotechnology</i> , 2021, 23, 943-954.	1.1	3
9747	Fungal effector SIB1 of <i>Colletotrichum orbiculare</i> has unique structural features and can suppress plant immunity in <i>Nicotiana benthamiana</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101370.	1.6	7
9748	Maternal methionine supplementation during gestation alters alternative splicing and DNA methylation in bovine skeletal muscle. <i>BMC Genomics</i> , 2021, 22, 780.	1.2	9
9749	Transcriptome analysis of the effect of a novel human serine protease inhibitor SPINK13 on gene expression in MHCC97-H cells. <i>Translational Cancer Research</i> , 2021, 10, 4464-4477.	0.4	0
9750	Organ-specific, integrated omics data-based study on the metabolic pathways of the medicinal plant <i>Bletilla striata</i> (Orchidaceae). <i>BMC Plant Biology</i> , 2021, 21, 504.	1.6	8
9751	Extracellular chemoreceptor of deca-brominated diphenyl ether and its engineering in the hydrophobic chassis cell for organics biosensing. <i>Chemical Engineering Journal</i> , 2022, 433, 133266.	6.6	8
9752	Comparative Transcriptomic Analysis of Two Rice ( <i>Oryza sativa</i> L.) Male Sterile Line Seed Embryos Under Accelerated Aging. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 282-293.	1.0	4
9757	Improving Maize Trait through Modifying Combination of Genes. <i>Emerging Topics in Statistics and Biostatistics</i> , 2020, , 173-196.	0.1	0
9758	Transcriptome analyses of <i>Ditylenchus destructor</i> in responses to cold and desiccation stress. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180057.	0.6	0
9759	Epigenetic and Transcriptional Regulation of the Reproductive Hypothalamus. <i>Masterclass in Neuroendocrinology</i> , 2020, , 207-235.	0.1	0
9761	Statistical method for modeling sequencing data from different technologies in longitudinal studies with application to Huntington disease. <i>Biometrical Journal</i> , 2021, 63, 745-760.	0.6	1
9763	In-depth secretome analysis of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in infected wheat uncovers effector functions. <i>Bioscience Reports</i> , 2020, 40, .	1.1	6
9764	Transcriptome analysis of Giant grouper ( <i>Epinephelus lanceolatus</i> ) kidney and spleen in response to spotted knifefish iridovirus (SKIV) infection. <i>Aquaculture Research</i> , 2021, 52, 1954-1964.	0.9	2
9765	Residual Effects Caused by a Past Mycovirus Infection in <i>Fusarium circinatum</i> . <i>Forests</i> , 2021, 12, 11.	0.9	3

#	ARTICLE	IF	CITATIONS
9767	Transcriptome Changes in <i>Pseudomonas putida</i> KT2440 during Medium-Chain-Length Polyhydroxyalkanoate Synthesis Induced by Nitrogen Limitation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 152.	1.8	5
9769	Global Lysine Acetylome Analysis of Flower bud Development in <i>Catalpa bungei</i> . <i>Phyton</i> , 2022, 91, 507-524.	0.4	1
9770	Recommendations for pharmacotranscriptomic profiling of drug response in CNS disorders. <i>European Neuropsychopharmacology</i> , 2022, 54, 41-53.	0.3	4
9771	Genome-wide identification and expression analysis of the ASMT gene family reveals their role in abiotic stress tolerance in apple. <i>Scientia Horticulturae</i> , 2022, 293, 110683.	1.7	15
9772	Dietary vitamin A affects growth performance, immunity, antioxidant capacity, and lipid metabolism of juvenile Chinese mitten crab <i>Eriocheir sinensis</i> . <i>Aquaculture</i> , 2022, 548, 737556.	1.7	9
9773	Big Data and Its Emerging Role in Precision Medicine and Therapeutic Response. <i>RSC Detection Science</i> , 2020, , 88-116.	0.0	0
9774	Survey of Methods Used for Differential Expression Analysis on RNA Seq Data. <i>Learning and Analytics in Intelligent Systems</i> , 2020, , 226-239.	0.5	1
9776	De novo sequencing of <i>Bletilla striata</i> (Orchidaceae) transcriptome and identification of genes involved in polysaccharide biosynthesis. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190417.	0.6	13
9781	Digital Gene Expression Profiling Analysis of Self-Incompatibility Styles in <i>Citrus grandis</i> var. Shatinyu. <i>Botanical Research</i> , 2020, 09, 536-544.	0.0	0
9782	Transcription for Protein Biosynthesis. <i>Biological and Medical Physics Series</i> , 2020, , 477-508.	0.3	0
9783	Experimental toolkit to study RNA level regulation. , 2020, , 371-396.		1
9784	Expression Analysis of <i>Apocheima cinerarius</i> Ershoff from Different Geographical Populations through Illumina RNA-seq. <i>Pakistan Journal of Zoology</i> , 2020, 52, .	0.1	0
9787	Feasibility of primary human cell cultures as a model for adamantinomatous craniopharyngioma research: Evidence from RNA-seq analysis. <i>Oncology Letters</i> , 2020, 19, 2346-2354.	0.8	0
9789	Genetic diversity of limonene synthase genes in Rongan kumquat ( <i>Fortunella crassifolia</i> ). <i>Functional Plant Biology</i> , 2020, 47, 425.	1.1	3
9790	Cost effective, experimentally robust differential-expression analysis for human/mammalian, pathogen and dual-species transcriptomics. <i>Microbial Genomics</i> , 2020, 6, .	1.0	0
9791	Current Status and Challenges of DNA Sequencing. , 2020, , 71-80.		2
9797	Differential transcriptome profiling of the diapause and cold-responsive genes in unfed adult <i>Dermacentor silvarum</i> Olenov (Acari: Ixodidae). <i>Systematic and Applied Acarology</i> , 2020, 25, 193-213.	0.5	1
9802	Key protein-coding genes related to microglia in immune regulation and inflammatory response induced by epilepsy. <i>Mathematical Biosciences and Engineering</i> , 2021, 18, 9563-9578.	1.0	5

#	ARTICLE	IF	CITATIONS
9807	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
9812	Integrated analysis of a lncRNA-mRNA network reveals a potential mechanism underlying necrotizing enterocolitis. Molecular Medicine Reports, 2020, 22, 423-435.	1.1	8
9814	Inducible Resistance to $\beta$ -Lactams in Oxacillin-Susceptible mecA1-Positive Staphylococcus sciuri Isolated From Retail Pork. Frontiers in Microbiology, 2021, 12, 721426.	1.5	8
9816	RNA-seq Data Analysis for Differential Expression. Methods in Molecular Biology, 2022, 2391, 45-54.	0.4	15
9817	Joint transcriptomic and metabolomic analysis reveals the mechanism of low-temperature tolerance in <i>Hosta ventricosa</i> . PLoS ONE, 2021, 16, e0259455.	1.1	11
9818	Development of a novel promoter engineering-based strategy for creating an efficient para-nitrophenol-mineralizing bacterium. Journal of Hazardous Materials, 2022, 424, 127672.	6.5	8
9819	Characteristics of the Gut Microbiome and IL-13/TGF- $\beta$ 1 Mediated Fibrosis in Post-Kasai Cholangitis of Biliary Atresia. Frontiers in Pediatrics, 2021, 9, 751204.	0.9	4
9820	Distinct Transcriptional Programs Underlie Differences in Virulence of Isolates on Host Plants in a Fungal Pathogen, <i>Colletotrichum gloeosporioides</i> . Frontiers in Microbiology, 2021, 12, 743776.	1.5	0
9821	Translatomics Probes Into the Role of Lycopene on Improving Hepatic Steatosis Induced by High-Fat Diet. Frontiers in Nutrition, 2021, 8, 727785.	1.6	4
9822	Transcriptome Analysis Reveals Molecular Mechanisms Underlying Methyl Jasmonate-mediated Biosynthesis of Protopanaxadiol-type Saponins in <i>Panax notoginseng</i> Leaves. Journal of Plant Biology, 2022, 65, 29-41.	0.9	5
9823	The Overexpression of Phasin and Regulator Genes Promoting the Synthesis of Polyhydroxybutyrate in <i>Cupriavidus necator</i> H16 under Nonstress Conditions. Applied and Environmental Microbiology, 2022, 88, AEM0145821.	1.4	15
9824	Enzymatic Activities and Gene Transcript Levels Associated with the Augmentation of Antioxidant Constituents during Drought Stress in Lettuce. Horticulturae, 2021, 7, 444.	1.2	1
9827	Comprehensive transcriptome analyses of different Crocus flower tissues uncover genes involved in crocin biosynthesis. Biologia Plantarum, 0, 64, 504-511.	1.9	1
9830	Identification of lncRNAs Using Computational and Experimental Approaches. , 2012, , 319-340.		0
9831	Expression Profiling of ncRNAs Employing RNP Libraries and Custom LNA/DNA Microarray Analysis. , 2012, , 229-251.		0
9839	Modeling metabolic fluxes underlying cassava storage root growth through E-Fmin analysis. , 2020, , .		0
9840	Transcription Analysis of Recombinant <i>Trichoderma reesei</i> HJ-48 to Compare the Molecular Basis for Fermentation of Glucose and Xylose. Journal of Microbiology and Biotechnology, 2020, 30, 1467-1479.	0.9	0
9841	Global assessment of the integrated stress response in CF patient-derived airway and intestinal tissues. Journal of Cystic Fibrosis, 2020, 19, 1021-1026.	0.3	4

#	ARTICLE	IF	CITATIONS
9842	Heat shock proteins and small nucleolar RNAs are dysregulated in a <i>Drosophila</i> model for feline hypertrophic cardiomyopathy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, 1-16.	0.8	6
9843	Gene expression in the mouse eye: an online resource for genetics using 103 strains of mice. <i>Molecular Vision</i> , 2009, 15, 1730-63.	1.1	90
9846	Next-generation sequencing facilitates quantitative analysis of wild-type and <i>Nrl(-/-)</i> retinal transcriptomes. <i>Molecular Vision</i> , 2011, 17, 3034-54.	1.1	89
9847	Transcriptome analysis using next generation sequencing reveals molecular signatures of diabetic retinopathy and efficacy of candidate drugs. <i>Molecular Vision</i> , 2012, 18, 1123-46.	1.1	38
9848	From sequencer to supercomputer: an automatic pipeline for managing and processing next generation sequencing data. <i>AMIA Summits on Translational Science Proceedings</i> , 2012, 2012, 1-10.	0.4	6
9849	Incorporating genomics into the toolkit of nematology. <i>Journal of Nematology</i> , 2012, 44, 191-205.	0.4	12
9850	Interpreting personal transcriptomes: personalized mechanism-scale profiling of RNA-seq data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 159-70.	0.7	6
9853	Kleat: cleavage site analysis of transcriptomes. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 347-58.	0.7	8
9854	EST sequencing and gene expression profiling in <i>Scutellaria baicalensis</i> . <i>EXCLI Journal</i> , 2014, 13, 392-400.	0.5	1
9855	Chromatin features, RNA polymerase II and the comparative expression of lens genes encoding crystallins, transcription factors, and autophagy mediators. <i>Molecular Vision</i> , 2015, 21, 955-73.	1.1	18
9856	Differentially expressed genes and microRNAs in bladder carcinoma cell line 5637 and T24 detected by RNA sequencing. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 12678-87.	0.5	17
9857	Cellular transcriptomics: gelsolin negatively regulates the expression of apoptosis-associated genes and inhibits apoptosis in hepatocarcinoma cells. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 13871-85.	0.5	5
9858	Serum molecular signature for proliferative diabetic retinopathy in Saudi patients with type 2 diabetes. <i>Molecular Vision</i> , 2016, 22, 636-45.	1.1	6
9859	Expression levels of <i>GSTA2</i> and <i>APOD</i> genes might be associated with carotenoid coloration in golden pheasant ( <i>Chrysolophus pictus</i> ) plumage. <i>Zoological Research</i> , 2016, 37, 144-50.	0.6	5
9861	Graphical Models via Univariate Exponential Family Distributions. <i>Journal of Machine Learning Research</i> , 2015, 16, 3813-3847.	62.4	36
9862	Estimation of Gene Regulatory Networks. <i>Postdoc Journal</i> , 2013, 1, 60-69.	0.4	2
9863	Dicer-dependent pathway contribute to the osteogenesis mediated by regulation of <i>Runx2</i> . <i>American Journal of Translational Research (discontinued)</i> , 2016, 8, 5354-5369.	0.0	3
9864	Genome-wide retinal transcriptome analysis of endotoxin-induced uveitis in mice with next-generation sequencing. <i>Molecular Vision</i> , 2017, 23, 395-406.	1.1	5



#	ARTICLE	IF	CITATIONS
9865	Deep Illumina sequencing reveals differential expression of long non-coding RNAs in hyperoxia induced bronchopulmonary dysplasia in a rat model. <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 5696-5707.	0.0	6
9867	Transcriptomic profile analysis of brain microvascular pericytes in spontaneously hypertensive rats by RNA-Seq. <i>American Journal of Translational Research (discontinued)</i> , 2018, 10, 2372-2386.	0.0	13
9868	Molecular mechanisms involved in TGF- $\beta$ 21-induced Muscle-derived stem cells differentiation to smooth muscle cells. <i>American Journal of Translational Research (discontinued)</i> , 2019, 11, 5150-5161.	0.0	3
9869	High-throughput sequencing analysis of lncRNAs in hippocampus tissues with hypoxic-ischemic brain damage. <i>International Journal of Clinical and Experimental Pathology</i> , 2018, 11, 5265-5277.	0.5	1
9870	RNA-seq with RNase H-based ribosomal RNA depletion specifically designed for. <i>MicroPublication Biology</i> , 2020, 2020, .	0.1	2
9871	An optimized protocol for retina single-cell RNA sequencing. <i>Molecular Vision</i> , 2020, 26, 705-717.	1.1	13
9872	Enrichment and identification of differentially expressed genes in hepatocellular carcinoma stem-like cells. <i>Oncology Letters</i> , 2020, 20, 299.	0.8	1
9873	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic lncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	1.8	0
9874	Transcriptomics Analysis Reveals the Immune Response Mechanism of Rabbits with Diarrhea Fed an Antibiotic-Free Diet. <i>Animals</i> , 2021, 11, .	1.0	0
9875	Safety in multi-assembly via paths appearing in all path covers of a DAG. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	3
9876	Transcriptome and metabolome analyses reveal a key role of the anthocyanin biosynthetic pathway cascade in the pigmentation of a <i>Cinnamomum camphora</i> red bark mutant (â€™Gantong 1â€™™). <i>Industrial Crops and Products</i> , 2022, 175, 114236.	2.5	12
9877	Differential immune and metabolic responses underlie differences in the resistance of <i>Siganus oramin</i> and <i>Trachinotus blochii</i> to <i>Cryptocaryon irritans</i> infection. <i>Fish and Shellfish Immunology</i> , 2022, 120, 166-179.	1.6	3
9878	Interactions of Muscovy duck reovirus, gut microbiota, and host innate immunity: Transcriptome and gut microbiota analysis. <i>Veterinary Microbiology</i> , 2022, 264, 109286.	0.8	3
9879	Transcriptomics Analysis Reveals the Immune Response Mechanism of Rabbits with Diarrhea Fed an Antibiotic-Free Diet. <i>Animals</i> , 2021, 11, 2994.	1.0	5
9880	Transcriptome Analysis Molecular Mechanism of Starch Synthesis During Tuber Development in Chinese Yam ( <i>Dioscorea opposita</i> ). <i>Journal of Biobased Materials and Bioenergy</i> , 2021, 15, 589-597.	0.1	3
9881	Transcriptome Analysis of <i>Crassostrea sikamea</i> (â€™™)– <i>Crassostrea gigas</i> (â€™™,) Hybrids Under and After Thermal Stress. <i>Journal of Ocean University of China</i> , 2022, 21, 213-224.	0.6	3
9882	Identification of essential genes involved in metabolismâ€™based resistance mechanism to fenoxapropâ€™ethyl in <i>Polypogon fugax</i> . <i>Pest Management Science</i> , 2022, 78, 1164-1175.	1.7	12
9883	Integrated Physiological, Transcriptomic, and Metabolomic Analyses Revealed Molecular Mechanism for Salt Resistance in Soybean Roots. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12848.	1.8	12

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9884	Transcriptome of the Maize Leafhopper ( <i>Dalbulus maidis</i> ) and Its Transcriptional Response to Maize Rayado Fino Virus (MRFV), Which It Transmits in a Persistent, Propagative Manner. <i>Microbiology Spectrum</i> , 2021, , e0061221.	1.2	2
9885	Gain of Spontaneous <i>clpX</i> Mutations Boosting Motility via Adaption to Environments in <i>Escherichia coli</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 772397.	2.0	3
9886	Transcriptomic Changes in Internode Explants of Stinging Nettle during Callogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12319.	1.8	1
9887	Comparative Genome Analysis of Genes Regulating Compound Inflorescences in Tomato. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12548.	1.8	1
9888	New Autophagy-Ferroptosis Gene Signature Predicts Survival in Glioma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 739097.	1.8	2
9889	Effects of <i>Laccaria bicolor</i> on Gene Expression of <i>Populus trichocarpa</i> Root under Poplar Canker Stress. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1024.	1.5	2
9890	<i>Chloranthus</i> genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	5.8	44
9891	Dual-Transcriptomic, Microscopic, and Biocontrol Analyses of the Interaction Between the Bioeffector <i>Pythium oligandrum</i> and the <i>Pythium</i> Soft-Rot of Ginger Pathogen <i>Pythium myriotylum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 765872.	1.5	8
9893	RNA-seq and Analysis of <i>Argyrosomus japonicus</i> Under Different Salinities. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	4
9894	Major Complex Trait for Early De Novo Programming of CoV-MAC-TED™ Detected in Human Nasal Epithelial Cells Infected by Two SARS-CoV-2 Variants Is Promising to Help in Designing Therapeutic Strategies. <i>Vaccines</i> , 2021, 9, 1399.	2.1	5
9895	Circ-Hdgfrp3 shuttles along neurites and is trapped in aggregates formed by ALS-associated mutant FUS. <i>IScience</i> , 2021, 24, 103504.	1.9	14
9896	Analysis of the long noncoding RNA profiles of RD and SH-SY5Y cells infected with coxsackievirus B5, using RNA sequencing. <i>Archives of Virology</i> , 2022, 167, 367-376.	0.9	4
9897	<i>Tribulus terrestris</i> L. protects glomerular endothelial cells via the miR155-H2AC6 interaction network in hypertensive renal injury. <i>Annals of Translational Medicine</i> , 2021, 9, 1626-1626.	0.7	2
9899	Defence-related pathways, phytohormones and primary metabolism are key players in kiwifruit plant tolerance to <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Plant, Cell and Environment</i> , 2022, 45, 528-541.	2.8	15
9900	Rare Does Not Mean Worthless: How Rare Diseases Have Shaped Neurodevelopment Research in the NGS Era. <i>Biomolecules</i> , 2021, 11, 1713.	1.8	3
9901	Diguanylate Cyclase and Phosphodiesterase Interact To Maintain the Specificity of Cyclic di-GMP Signaling in the Regulation of Antibiotic Synthesis in <i>Lysobacter enzymogenes</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0189521.	1.4	3
9902	Single-cell transcriptome identifies molecular subtype of autism spectrum disorder impacted by de novo loss-of-function variants regulating glial cells. <i>Human Genomics</i> , 2021, 15, 68.	1.4	20
9903	The Antifungal Effects of Citral on <i>Magnaporthe oryzae</i> Occur via Modulation of Chitin Content as Revealed by RNA-Seq Analysis. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1023.	1.5	8

#	ARTICLE	IF	CITATIONS
9904	The first high-quality chromosomal genome assembly of a medicinal and edible plant <i>Arctium lappa</i> . <i>Molecular Ecology Resources</i> , 2021, , .	2.2	11
9905	Between the Devil and the Deep Blue Sea: Non-Coding RNAs Associated with Transmissible Cancers in Tasmanian Devil, Domestic Dog and Bivalves. <i>Non-coding RNA</i> , 2021, 7, 72.	1.3	1
9906	Transcriptome analysis provides insights into the root response of Chinese fir to phosphorus deficiency. <i>BMC Plant Biology</i> , 2021, 21, 525.	1.6	9
9908	Transcriptome analysis in <i>Alcea rosea</i> L. and identification of critical genes involved in stamen petaloid. <i>Scientia Horticulturae</i> , 2022, 293, 110732.	1.7	2
9909	Integrated de novo Analysis of Transcriptional and Metabolic Variations in Salt-Treated <i>Solenostemma argel</i> Desert Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 744699.	1.7	3
9910	Root-associated microbiota drive phytoremediation strategies to lead of <i>Sonchus Asper</i> (L.) Hill as revealed by intercropping-induced modifications of the rhizosphere microbiome. <i>Environmental Science and Pollution Research</i> , 2022, 29, 23026-23040.	2.7	10
9911	Study on the molecular mechanism of <i>Laccaria bicolor</i> helping <i>Populus trichocarpa</i> to resist the infection of <i>Botryosphaeria dothidea</i> . <i>Journal of Applied Microbiology</i> , 2022, 132, 2220-2233.	1.4	2
9912	Integrative genome, transcriptome, microRNA, and degradome analysis of water dropwort ( <i>Oenanthe</i> ) Tj ETQq1 1 0,784314 ggBT /Over	2.9	31
9913	Comprehensive Transcriptome and Metabolic Profiling of Petal Color Development in <i>Lycoris sprengeri</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 747131.	1.7	7
9914	Integrative Transcriptomics and Proteomics Analyses to Reveal the Developmental Regulation of <i>Metorchis orientalis</i> : A Neglected Trematode With Potential Carcinogenic Implications. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 783662.	1.8	1
9915	Isocitrate dehydrogenase mutations are associated with altered IL-1 $\beta$ responses in acute myeloid leukemia. <i>Leukemia</i> , 2022, 36, 923-934.	3.3	3
9916	The cold adaption profiles of <i>Pseudoalteromonas shioyasakiensis</i> D1497 from Yap trench to cope with cold. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021, 32, e00689.	2.1	2
9917	Transcriptome Analysis of Gills Provides Insights Into Translation Changes Under Hypoxic Stress and Reoxygenation in Golden Pompano, <i>Trachinotus ovatus</i> (Linnaeus 1758). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	9
9918	Characterization of Genes Associated with Salt Tolerance Using Transcriptome Analysis and Quantitative Trait Loci Mapping in Rice. <i>Plant Breeding and Biotechnology</i> , 2021, 9, 318-330.	0.3	1
9919	Malignancy and NF- $\kappa$ B signalling strengthen coordination between expression of mitochondrial and nuclear-encoded oxidative phosphorylation genes. <i>Genome Biology</i> , 2021, 22, 328.	3.8	7
9920	Transcriptomics and sequencing analysis of gene expression profiling for major depressive disorder. <i>Indian Journal of Psychiatry</i> , 2021, 63, 549.	0.4	11
9921	Dysplasia of male organs induces apomixis in <i>Malus</i> crabapples. <i>Ornamental Plant Research</i> , 2021, 1, 1-16.	0.2	1
9922	Effects of Gestational Exposure to Bisphenol a on the Hepatic Transcriptome and Lipidome of Rat Dams: Intergenerational Comparison of Effects in the Offspring. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
9923	OUP accepted manuscript. Journal of Experimental Botany, 2022, , .	2.4	4
9924	Differential gene expression prediction by ensemble deep networks on Histone Modification data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	0
9925	An Integrative Sialomic Analysis Reveals Molecules From <i>Triatoma sordida</i> (Hemiptera: Reduviidae). Frontiers in Cellular and Infection Microbiology, 2021, 11, 798924.	1.8	3
9926	Metagenomic analysis of rhizosphere microbiome provides insights into occurrence of iron deficiency chlorosis in field of Asian pears. BMC Microbiology, 2022, 22, 18.	1.3	2
9927	Integrated Application of Multiomics Strategies Provides Insights Into the Environmental Hypoxia Response in <i>Pelteobagrus vachelli</i> Muscle. Molecular and Cellular Proteomics, 2022, 21, 100196.	2.5	10
9928	Molecular evidence to the day length in regulating the short shoot phenomenon during summer in roses ( <i>Rosa</i> sp.). Journal of Plant Interactions, 2022, 17, 140-151.	1.0	0
9929	Robust temporal changes of cellular senescence and proliferation after sciatic nerve injury. Neural Regeneration Research, 2022, 17, 1588.	1.6	7
9930	Allele-aware chromosome-scale assembly of the allopolyploid genome of hexaploid Ma bamboo ( <i>Dendrocalamus latiflorus</i> Munro). Journal of Integrative Plant Biology, 2022, 64, 649-670.	4.1	24
9931	Transcriptome sequencing and flavonoid metabolism analysis in the leaves of three different cultivars of <i>Acer truncatum</i> . Plant Physiology and Biochemistry, 2022, 171, 1-13.	2.8	5
9932	Robust normalization and transformation techniques for constructing gene coexpression networks from RNA-seq data. Genome Biology, 2022, 23, 1.	3.8	69
9933	Comparative Transcriptomic Analyses of Different Jujube Cultivars Reveal the Co-Regulation of Multiple Pathways during Fruit Cracking. Genes, 2022, 13, 105.	1.0	8
9934	Comparative Transcriptome Analyses of Gayal ( <i>Bos frontalis</i> ), Yak ( <i>Bos grunniens</i> ), and Cattle ( <i>Bos Tj</i> ETQq1 1 0.784314 rgBT /Overl	1.1	7
9935	Effect Of XBP1 Deficiency In Cartilage On The Regulatory Network Of LncRNA/circRNA-miRNA-mRNA. International Journal of Biological Sciences, 2022, 18, 315-330.	2.6	9
9936	Developing iterative and quantified transgenic manipulations of non-conventional filamentous fungus <i>Talaromyces pinophilus</i> Li-93. Biochemical Engineering Journal, 2022, 179, 108317.	1.8	0
9937	Integrated application of Iso-seq and RNA-seq provides insights into unsynchronized growth in red swamp crayfish ( <i>Procambarus clarkii</i> ). Aquaculture Reports, 2022, 22, 101008.	0.7	2
9938	Analysis of the resistance of small peptides from <i>Periplaneta americana</i> to hydrogen peroxide-induced apoptosis in human ovarian granular cells based on RNA-seq. Gene, 2022, 813, 146120.	1.0	5
9939	Metabolism response of fasting in <i>Octopus sinensis</i> paralarvae revealed by RNA-seq. Aquaculture, 2022, 550, 737859.	1.7	3
9940	Gene expression patterns of sea urchins ( <i>Strongylocentrotus intermedius</i> ) exposed to different combinations of temperature and hypoxia. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 41, 100953.	0.4	3

#	ARTICLE	IF	CITATIONS
9941	Transcriptomic analysis of pituitary in female and male spotted scat ( <i>Scatophagus argus</i> ) after 17 $\beta$ -estradiol injection. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100949.	0.4	2
9942	Potential receptors in <i>Fenneropenaeus merguensis</i> ovary and role of saxophone, the bone morphogenetic protein receptor, in ovarian development. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2022, 266, 111141.	0.8	0
9943	Salicylate and glutamate mediate different Cd accumulation and tolerance between <i>Brassica napus</i> and <i>B. juncea</i> . <i>Chemosphere</i> , 2022, 292, 133466.	4.2	6
9944	Enrichment and identification of differentially expressed genes in hepatocellular carcinoma stem-like cells. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	1
9945	RNA Sequencing: A Potent Transcription Profiling Tool. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2020, 9, 891-905.	0.0	0
9946	Characterization of Analytic and Experimental Uncertainty of RNA-seq Co-expression Network Determination: Application to SCA2. , 2020, , .		0
9947	Lnc-C2orf63-4-1 Confers VSMC Homeostasis and Prevents Aortic Dissection Formation via STAT3 Interaction. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 792051.	1.8	8
9948	Physiological acclimatization in high-latitude zooplankton. <i>Molecular Ecology</i> , 2022, 31, 1753-1765.	2.0	5
9949	Genome-Wide Identification and Characterization of RNA/DNA Differences Associated with Drought Response in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1405.	1.8	4
9950	Regulation of lignin biosynthesis by an atypical bHLH protein CmHLB in <i>Chrysanthemum</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 2403-2419.	2.4	15
9951	Transcriptomic Insight into Underground Floral Differentiation in <i>Erythronium japonicum</i> . <i>BioMed Research International</i> , 2022, 2022, 1-14.	0.9	3
9952	An Integrated Analysis of Metabolomics and Transcriptomics Reveals Significant Differences in Floral Scents and Related Gene Expression between Two Varieties of <i>Dendrobium loddigesii</i> . <i>Applied Sciences (Switzerland)</i> , 2022, 12, 1262.	1.3	5
9953	Comparative transcriptome analyses reveal genes related to pigmentation in the petals of a flower color variation cultivar of <i>Rhododendron obtusum</i> . <i>Molecular Biology Reports</i> , 2022, 49, 2641-2653.	1.0	10
9954	Spermine Regulates Immune and Signal Transduction Dysfunction in Diabetic Cardiomyopathy. <i>Frontiers in Endocrinology</i> , 2021, 12, 740493.	1.5	3
9955	Genomically Hardwired Regulation of Gene Activity Orchestrates Cellular Iron Homeostasis in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2022, 19, 143-161.	1.5	9
9956	Transcriptomic Analysis Reveals That Rho GTPases Regulate Trap Development and Lifestyle Transition of the Nematode-Trapping Fungus <i>Arthrobotrys oligospora</i> . <i>Microbiology Spectrum</i> , 2022, 10, e0175921.	1.2	36
9957	Intestinal Microbiota and Host Cooperate for Adaptation as a Hologenome. <i>MSystems</i> , 2022, 7, e0126121.	1.7	8
9958	Transcriptome Analysis of Detoxification-Related Genes in <i>Spodoptera frugiperda</i> (Lepidoptera:) Tj ETQq1 1 0.784314 r <sub>g</sub> BT /Over	0.6	11

#	ARTICLE	IF	CITATIONS
9960	The Role of DNA Methylation in Genome Defense in Cnidaria and Other Invertebrates. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
9961	Mechanism of molecules crosstalk and the critical role of jasmonic acid on triterpenoid synthesis in <i>Cyclocarya paliurus</i> cells under <i>Aspergillus niger</i> elicitor. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 864-879.	0.9	1
9962	Integrated transcriptomic and metabolic analyses reveal that ethylene enhances peach susceptibility to <i>Lasiodiplodia theobromae</i> -induced gummosis. <i>Horticulture Research</i> , 2022, 9, .	2.9	13
9963	Lack of xyloglucan in the cell walls of the <i>Arabidopsis xxt1/xt2</i> mutant results in specific increases in homogalacturonan and glucomannan. <i>Plant Journal</i> , 2022, 110, 212-227.	2.8	13
9965	De novo Transcriptome Analysis in <i>Leymus mollis</i> to Unveil Genes Involved in Salt Stress Response Tolerance. <i>Phyton</i> , 2022, 91, 1-14.	0.4	0
9966	RBPM2, as a novel biomarker for predicting lymph node metastasis, guides therapeutic regimens in gastric cancer. <i>Human Cell</i> , 2022, 35, 599-612.	1.2	4
9967	Integrated Metabolomic and Transcriptomic Analysis Reveals Differential Mechanism of Flavonoid Biosynthesis in Two Cultivars of <i>Angelica sinensis</i> . <i>Molecules</i> , 2022, 27, 306.	1.7	10
9968	Explore the effect of LLY-283 on the ototoxicity of auditory cells caused by cisplatin: A bioinformatic analysis based on RNA-seq. <i>Journal of Clinical Laboratory Analysis</i> , 2022, 36, e24176.	0.9	3
9969	Clenbuterol exerts antidiabetic activity through metabolic reprogramming of skeletal muscle cells. <i>Nature Communications</i> , 2022, 13, 22.	5.8	15
9970	Transcriptomic profiling suggests candidate molecular responses to waterlogging in cassava. <i>PLoS ONE</i> , 2022, 17, e0261086.	1.1	11
9971	Gene expression profiles in Malpighian tubules of the vector leafhopper <i>Psammotettix striatus</i> (L.) revealed regional functional diversity and heterogeneity. <i>BMC Genomics</i> , 2022, 23, 67.	1.2	6
9972	A comprehensive comparison of supervised and unsupervised methods for cell type identification in single-cell RNA-seq. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	22
9973	A transcriptomic analysis of neuropathic pain in the anterior cingulate cortex after nerve injury. <i>Bioengineered</i> , 2022, 13, 2058-2075.	1.4	12
9974	Identification of a Ubiquitin Related Genes Signature for Predicting Prognosis of Prostate Cancer. <i>Frontiers in Genetics</i> , 2021, 12, 778503.	1.1	5
9975	Transcriptome profiling reveals that foliar water uptake occurs with C3 and crassulacean acid metabolism facultative photosynthesis in <i>Tamarix ramosissima</i> under extreme drought. <i>AoB PLANTS</i> , 2022, 14, plab060.	1.2	3
9976	Recent developments in genome design and assembly tools. , 2022, , 45-65.		2
9977	Lanthanum Promotes Bahiagrass ( <i>Paspalum notatum</i> ) Roots Growth by Improving Root Activity, Photosynthesis and Respiration. <i>Plants</i> , 2022, 11, 382.	1.6	5
9978	Identification of Novel Candidate Genes Involved in Apple Cuticle Integrity and Russeting-Associated Triterpene Synthesis Using Metabolomic, Proteomic, and Transcriptomic Data. <i>Plants</i> , 2022, 11, 289.	1.6	8

#	ARTICLE	IF	CITATIONS
9981	Transcriptome analysis of genes potentially associated with white and black plumage formation in Chinese indigenous ducks ( <i>Anas platyrhynchos</i> ). <i>British Poultry Science</i> , 2022, 63, 466-474.	0.8	3
9982	Pathogen resistance in <i>Sphagneticola trilobata</i> (Singapore daisy): molecular associations and differentially expressed genes in response to disease from a widespread fungus. <i>Genetica</i> , 2022, 150, 13.	0.5	2
9983	Mutations in <i>Hcfc1</i> and <i>Ronin</i> result in an inborn error of cobalamin metabolism and ribosomopathy. <i>Nature Communications</i> , 2022, 13, 134.	5.8	16
9984	Deconstructing a Syndrome: Genomic Insights Into PCOS Causal Mechanisms and Classification. <i>Endocrine Reviews</i> , 2022, 43, 927-965.	8.9	75
9985	Accumulation of Anthocyanidins Determines Leaf Color of <i>Liquidambar Formosana</i> as Revealed by Transcriptome Sequencing and Metabolism Analysis. <i>Current Issues in Molecular Biology</i> , 2022, 44, 242-256.	1.0	1
9986	Cuticular lipids and associated gene expression analysis under NaCl stress in <i>Thellungiella salsuginea</i> . <i>Physiologia Plantarum</i> , 2022, 174, e13625.	2.6	1
9987	Exploring the genetic potential of Pakistani soybean cultivars through RNA-seq based transcriptome analysis. <i>Molecular Biology Reports</i> , 2022, 49, 2889-2897.	1.0	2
9988	Long-distance control of the scion by the rootstock under drought stress as revealed by transcriptome sequencing and mobile mRNA identification. <i>Horticulture Research</i> , 2022, 9, .	2.9	15
9989	Genome Recombination-Mediated tRNA Up-Regulation Conducts General Antibiotic Resistance of Bacteria at Early Stage. <i>Frontiers in Microbiology</i> , 2021, 12, 793923.	1.5	0
9990	Differentially Expressed Hepatic Genes Revealed by Transcriptomics in Pigs with Different Liver Lipid Contents. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-16.	1.9	6
9991	Advances in sarcoma molecular diagnostics. <i>Genes Chromosomes and Cancer</i> , 2022, 61, 332-345.	1.5	7
9992	Integrated transcriptomic and metabolomic analyses of Caucasian clover ( <i>Trifolium ambiguum</i> Bieb.) in response to freezing stress. <i>Revista Brasileira De Botanica</i> , 2022, 45, 573-585.	0.5	2
9993	Nitrogen Uptake and Distribution in Different Chinese Cabbage Genotypes under Low Nitrogen Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1573.	1.8	5
9994	Assembly-free rapid differential gene expression analysis in non-model organisms using DNA-protein alignment. <i>BMC Genomics</i> , 2022, 23, 97.	1.2	2
9995	A rational approach to assess off-target reactivity of a dual-signal integrator for T cell therapy. <i>Toxicology and Applied Pharmacology</i> , 2022, 437, 115894.	1.3	4
9996	Antioxidant properties and transcriptome of cauda epididymis with different levels of fertility in Hu lambs. <i>Theriogenology</i> , 2022, 182, 85-95.	0.9	6
9997	Curcumin attenuates poly(I:C)-induced immune and inflammatory responses in mouse macrophages by inhibiting TLR3/TBK1/IFNB cascade. <i>Journal of Functional Foods</i> , 2022, 89, 104949.	1.6	4
9998	Transcriptomic analysis of interactions between <i>Lymantria dispar</i> larvae and carvacrol. <i>Pesticide Biochemistry and Physiology</i> , 2022, 181, 105012.	1.6	2

#	ARTICLE	IF	CITATIONS
9999	Fruit transcriptional profiling of the contrasting genotypes for shelf life reveals the key candidate genes and molecular pathways regulating post-harvest biology in cucumber. <i>Genomics</i> , 2022, 114, 110273.	1.3	7
10000	Ubiquitin-proteasome pathway plays an essential regulatory role during spermatangium formation in <i>Neopyropia yezoensis</i> . <i>Algal Research</i> , 2022, 62, 102623.	2.4	1
10001	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for gram-scale diosgenin production. <i>Metabolic Engineering</i> , 2022, 70, 115-128.	3.6	18
10002	Sucrose-induced bud outgrowth in <i>Chrysanthemum morifolium</i> involves changes of auxin transport and gene expression. <i>Scientia Horticulturae</i> , 2022, 296, 110904.	1.7	4
10003	VvEIL2 and VvEIL4 regulate ethylene synthesis and carotenoid metabolism during senescence of grape rachis. <i>Postharvest Biology and Technology</i> , 2022, 187, 111853.	2.9	11
10004	Depth normalization of small RNA sequencing: using data and biology to select a suitable method. <i>Nucleic Acids Research</i> , 2022, 50, e56-e56.	6.5	4
10005	RNA-Seq Experiment and Data Analysis. <i>Methods in Molecular Biology</i> , 2022, 2418, 405-424.	0.4	6
10006	Single-cell isoform analysis in human immune cells. <i>Genome Biology</i> , 2022, 23, 47.	3.8	35
10007	CX3CR1-expressing Myeloid Cells Regulate Host-Helminth Interaction and Lung Inflammation. <i>Advanced Biology</i> , 2022, , 2101078.	1.4	2
10008	Nitrogen source as a modulator of the metabolic activity of <i>Pedobacter lusitanus</i> NL19: a transcriptomic approach. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 1583-1597.	1.7	0
10009	Effect of Magnet-Fe <sub>3</sub> O <sub>4</sub> composite structure on methane production during anaerobic sludge digestion: Establishment of direct interspecies electron transfer. <i>Renewable Energy</i> , 2022, 188, 52-60.	4.3	18
10010	Full-length codling moth transcriptome atlas revealed by single-molecule real-time sequencing. <i>Genomics</i> , 2022, 114, 110299.	1.3	2
10011	Screening of Differentially Expressed Genes and Localization Analysis of Female Gametophyte at the Free Nuclear Mitosis Stage in <i>Pinus tabulaeformis</i> Carr.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1915.	1.8	0
10012	Supplementing Sulfate-Based Alginate Polysaccharide Improves Pacific White Shrimp ( <i>Litopenaeus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook Intestinal Health, and Disease Resistance. <i>Aquaculture Nutrition</i> , 2022, 2022, 1-21.	1.1	11
10013	Combined transcriptome and metabolome analysis of strawberry fruits in response to powdery mildew infection. <i>Agronomy Journal</i> , 2022, 114, 1027-1039.	0.9	4
10014	Transcriptome Analysis Revealed a Positive Role of Ethephon on Chlorophyll Metabolism of <i>Zoysia japonica</i> under Cold Stress. <i>Plants</i> , 2022, 11, 442.	1.6	7
10015	Transcriptome analysis of gibberellins and abscisic acid during the flooding response in <i>Fokienia hodginsii</i> . <i>PLoS ONE</i> , 2022, 17, e0263530.	1.1	2
10017	Screening of olfactory genes related to blood-feeding behaviors in <i>Culex pipiens quinquefasciatus</i> and <i>Culex pipiens molestus</i> by transcriptome analysis. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010204.	1.3	7



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10018	Oral Microbiota Changes Contribute to Autism Spectrum Disorder in Mice. <i>Journal of Dental Research</i> , 2022, 101, 821-831.	2.5	3
10019	Anti-microRNA-21 Therapy on Top of ACE Inhibition Delays Renal Failure in Alport Syndrome Mouse Models. <i>Cells</i> , 2022, 11, 594.	1.8	17
10020	Cryptochrome-mediated blue-light signal contributes to lignin biosynthesis in stone cells in pear fruit. <i>Plant Science</i> , 2022, 318, 111211.	1.7	17
10022	ORESARA 15, a PLATZ transcription factor, controls root meristem size through auxin and cytokinin signalling-related pathways. <i>Journal of Experimental Botany</i> , 2022, 73, 2511-2524.	2.4	8
10023	Comparison of Transcriptome Responses between <i>Sogatella furcifera</i> Females That Acquired Southern Rice Black-Streaked Dwarf Virus and Not. <i>Insects</i> , 2022, 13, 182.	1.0	1
10024	Changes in Skeletal Muscle PAK1 Levels Regulate Tissue Crosstalk to Impact Whole Body Glucose Homeostasis. <i>Frontiers in Endocrinology</i> , 2022, 13, 821849.	1.5	10
10025	Comparative de novo transcriptomics reveal the effect of lead on Leech in aquaculture environment. <i>Aquaculture Reports</i> , 2022, 23, 101019.	0.7	0
10026	TT2 controls rice thermotolerance through SCT1-dependent alteration of wax biosynthesis. <i>Nature Plants</i> , 2022, 8, 53-67.	4.7	77
10028	Novel alternatively spliced isoforms of and their mRNA expression patterns in pigs. <i>Journal of Genetics</i> , 2018, 97, 977-985.	0.4	1
10029	Targeting the oncogenic TBX3:nucleolin complex to treat multiple sarcoma subtypes. <i>American Journal of Cancer Research</i> , 2021, 11, 5680-5700.	1.4	0
10030	Modern Approaches for Transcriptome Analyses in Plants. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 11-50.	0.8	0
10031	Hide and Mine in Strings: Hardness, Algorithms, and Experiments. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, , 1-1.	4.0	1
10032	Elucidating Diversity in Obesity-Related Phenotypes Using Longitudinal and Multi-omic Approaches. , 2022, , 63-75.		0
10033	Advances in Breeding Strategies for Improving Stress Tolerance in Brassicas. <i>Compendium of Plant Genomes</i> , 2022, , 439-469.	0.3	2
10034	Cryptochrome-Mediated Blue-Light Signal Contributes to Lignin Biosynthesis in Stone Cells in Pear Fruit. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
10035	LncRNA Biomarkers of Inflammation and Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1363, 121-145.	0.8	15
10036	Multi-View Random-Walk Graph Regularization Low-Rank Representation for Cancer Clustering and Differentially Expressed Gene Selection. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 3578-3589.	3.9	5
10037	Using RNA-Seq for Transcriptome Profiling of <i>Botryllodes</i> sp. Regeneration. <i>Methods in Molecular Biology</i> , 2022, 2450, 599-615.	0.4	3

#	ARTICLE	IF	CITATIONS
10040	Nutrigenomics in Animal Feeding: Digital Gene Expression Analysis in Poultry Fed Tenebrio molitor Larvae Meal. <i>Poultry</i> , 2022, 1, 14-29.	0.5	1
10041	DSDatlas: disorders of sex development atlas for reproductive endocrinological-related gene discovery in integrative omics platforms. <i>F&amp;S Science</i> , 2022, 3, 108-117.	0.5	1
10042	Genome-Wide Analysis of the Banana WRKY Transcription Factor Gene Family Closely Related to Fruit Ripening and Stress. <i>Plants</i> , 2022, 11, 662.	1.6	14
10043	Response to Cold: A Comparative Transcriptomic Analysis in Eight Cold-Adapted Yeasts. <i>Frontiers in Microbiology</i> , 2022, 13, 828536.	1.5	2
10044	Revealing potential anti-fibrotic mechanism of Ganxianfang formula based on RNA sequence. <i>Chinese Medicine</i> , 2022, 17, 23.	1.6	5
10045	Exploration of Potential Roles of m5C-Related Regulators in Colon Adenocarcinoma Prognosis. <i>Frontiers in Genetics</i> , 2022, 13, 816173.	1.1	9
10046	The Verticillium dahliae Spt-Ada-Gcn5 Acetyltransferase Complex Subunit Ada1 Is Essential for Conidia and Microsclerotia Production and Contributes to Virulence. <i>Frontiers in Microbiology</i> , 2022, 13, 852571.	1.5	5
10047	Transcriptional regulation of metal metabolism- and nutrient absorption-related genes in Eucalyptus grandis by arbuscular mycorrhizal fungi at different zinc concentrations. <i>BMC Plant Biology</i> , 2022, 22, 76.	1.6	9
10048	Niche partitioning of the ubiquitous and ecologically relevant NS5 marine group. <i>ISME Journal</i> , 2022, 16, 1570-1582.	4.4	11
10050	Perspectives on Bulk-Tissue RNA Sequencing and Single-Cell RNA Sequencing for Cardiac Transcriptomics. <i>Frontiers in Molecular Medicine</i> , 2022, 2, .	0.6	14
10051	A diffusion MRI-based spatiotemporal continuum of the embryonic mouse brain for probing gene-neuroanatomy connections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
10052	In Silico Genome-Wide Characterisation of the Lipid Transfer Protein Multigenic Family in Sunflower (H. annuus L.). <i>Plants</i> , 2022, 11, 664.	1.6	3
10053	Comprehensive Transcriptome Analysis of Patients With Keratoconus Highlights the Regulation of Immune Responses and Inflammatory Processes. <i>Frontiers in Genetics</i> , 2022, 13, 782709.	1.1	7
10054	Contribution and Future of High-Throughput Transcriptomics in Battling Tuberculosis. <i>Frontiers in Microbiology</i> , 2022, 13, 835620.	1.5	3
10055	Bone Marrow Stroma-Induced Transcriptome and Regulome Signatures of Multiple Myeloma. <i>Cancers</i> , 2022, 14, 927.	1.7	12
10057	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. <i>Sugar Tech</i> , 2022, 24, 1295-1318.	0.9	5
10058	Phosphoryl guanidine oligonucleotides as primers for RNA-dependent DNA synthesis using murine leukemia virus reverse transcriptase. <i>Vavilovskii Zhurnal Genetiki I Selektzii</i> , 2022, 26, 5-13.	0.4	1
10059	Antennal Transcriptome Analysis Reveals Differentially Expressed Olfactory Genes Between Male and Female Citrus Longhorn Beetle Anoplophora chinensis (Forster) (Coleoptera: Cerambycidae). <i>Journal of the Kansas Entomological Society</i> , 2022, 94, .	0.1	0

#	ARTICLE	IF	CITATIONS
10060	The Genome of <i>Rhyzopertha dominica</i> (Fab.) (Coleoptera: Bostrichidae): Adaptation for Success. <i>Genes</i> , 2022, 13, 446.	1.0	10
10061	Melanopsin elevates locomotor activity during the wake state of the diurnal zebrafish. <i>EMBO Reports</i> , 2022, 23, e51528.	2.0	8
10062	RNA sequencing reveals the emerging role of bronchoalveolar lavage fluid exosome lncRNAs in acute lung injury. <i>PeerJ</i> , 2022, 10, e13159.	0.9	3
10063	The role of FYCO1-dependent autophagy in lens fiber cell differentiation. <i>Autophagy</i> , 2022, 18, 2198-2215.	4.3	9
10064	An Integrated Analysis of Transcriptome and miRNA Sequencing Provides Insights into the Dynamic Regulations during Flower Morphogenesis in <i>Petunia</i> . <i>Horticulturae</i> , 2022, 8, 284.	1.2	5
10065	Detection of copy number variants and genes by chromosomal microarray in an Emirati neurodevelopmental disorders cohort. <i>Neurogenetics</i> , 2022, 23, 137-149.	0.7	0
10066	Physiological and Molecular Changes in Cherry Red Tobacco in Response to Iron Deficiency Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 861081.	1.7	1
10067	Profiling of diverse tumor types establishes the broad utility of VHL-based ProTaCs and triages candidate ubiquitin ligases. <i>IScience</i> , 2022, 25, 103985.	1.9	17
10068	Fasulye Genotiplerinde Tuz ve Kuraklık Stresleri Altında VPE Gen Ailesinin Genom Yapısında Analizi ve Karakterizasyonu. <i>European Journal of Science and Technology</i> , 0, , .	0.5	1
10069	Genome-wide maps of nucleolus interactions reveal distinct layers of repressive chromatin domains. <i>Nature Communications</i> , 2022, 13, 1483.	5.8	32
10070	Transcriptome Analysis of <i>Crassostrea sikamea</i> (TM) – <i>Crassostrea gigas</i> (TM) Hybrids Under Hypoxia in Occluded Water. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	2
10071	Developmental Regulation of Transcription in Touriga Nacional Berries under Deficit Irrigation. <i>Plants</i> , 2022, 11, 827.	1.6	1
10072	Antibacterial and anti-virulence effects of furazolidone on <i>Trueperella pyogenes</i> and <i>Pseudomonas aeruginosa</i> . <i>BMC Veterinary Research</i> , 2022, 18, 114.	0.7	4
10073	PvTLP genlerinin genom yapısı tespit ve karakterizasyonu. <i>European Journal of Science and Technology</i> , 0, , .	0.5	0
10074	Transcriptome analysis revealed accumulation and assimilation of selenium and physio-biochemical changes in alfalfa ( <i>Medicago sativa</i> L.) leaves. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 4577-4588.	1.7	3
10075	The Effect of Nitrogen Fertilizer on Rhizome Quality and Starch Physicochemical Properties in <i>Nelumbo nucifera</i> . <i>Agronomy</i> , 2022, 12, 794.	1.3	7
10076	Transcriptome Analysis of Immune Responses and Metabolic Regulations of Chinese Soft-Shelled Turtle ( <i>Pelodiscus sinensis</i> ) against <i>Edwardsiella tarda</i> Infection. <i>Fishes</i> , 2022, 7, 79.	0.7	3
10077	Integrated Analysis of the miRNAome and Transcriptome Reveals miRNA-mRNA Regulatory Networks in <i>Catharanthus roseus</i> Through <i>Cuscuta campestris</i> -Mediated Infection With <i>Candidatus Liberibacter asiaticus</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 799819.	1.5	4

#	ARTICLE	IF	CITATIONS
10078	Small genetic variation affecting mRNA isoforms associated with marbling and meat color in beef cattle. <i>Functional and Integrative Genomics</i> , 2022, , 1.	1.4	0
10080	Identification of an anther-specific promoter from a male sterile AB line in Chinese cabbage ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.1	2
10081	Identification of novel alternative splicing associated with mastitis disease in Holstein dairy cows using large gap read mapping. <i>BMC Genomics</i> , 2022, 23, 222.	1.2	4
10082	Ethylene Response Factor109 Attunes Immunity, Photosynthesis, and Iron Homeostasis in Arabidopsis Leaves. <i>Frontiers in Plant Science</i> , 2022, 13, 841366.	1.7	7
10083	Transcriptome Sequencing Highlights the Regulatory Role of DNA Methylation in Immune-Related Genesâ€™ Expression of Chinese Oak Silkworm, <i>Antheraea pernyi</i> . <i>Insects</i> , 2022, 13, 296.	1.0	2
10084	Genetic variants associated mRNA stability in lung. <i>BMC Genomics</i> , 2022, 23, 196.	1.2	2
10085	Genomic insights into lineage-specific evolution of the oleosin family in Euphorbiaceae. <i>BMC Genomics</i> , 2022, 23, 178.	1.2	5
10086	Molecular taxonomical identification and phylogenetic relationships of some marine dominant algal species during red tide and harmful algal blooms along Egyptian coasts in the Alexandria region. <i>Environmental Science and Pollution Research</i> , 2022, 29, 53403-53419.	2.7	1
10087	Impact of gene annotation choice on the quantification of RNA-seq data. <i>BMC Bioinformatics</i> , 2022, 23, 107.	1.2	8
10088	Transcriptomics analysis of cashmere fineness functional genes. <i>Animal Biotechnology</i> , 2023, 34, 1583-1593.	0.7	4
10089	Differentially expressed genes in <i>Mythimna separata</i> under chlorantraniliprole exposure and functional identification. <i>International Journal of Pest Management</i> , 0, , 1-11.	0.9	1
10090	Interactions between the breast tissue microbiota and host gene regulation in nonpuerperal mastitis. <i>Microbes and Infection</i> , 2022, , 104904.	1.0	1
10091	Genome-wide investigation and functional analysis of RNA editing sites in wheat. <i>PLoS ONE</i> , 2022, 17, e0265270.	1.1	4
10092	Somatic regulation of female germ cell regeneration and development in planarians. <i>Cell Reports</i> , 2022, 38, 110525.	2.9	9
10093	Root Illumination Promotes Seedling Growth and Inhibits Gossypol Biosynthesis in Upland Cotton. <i>Plants</i> , 2022, 11, 728.	1.6	3
10094	State of Knowledge on Molecular Adaptations to Exercise in Humans: Historical Perspectives and Future Directions. , 2022, 12, 3193-3279.		18
10095	Delicate regulation of IL-1 $\beta$ -mediated inflammation by cyclophilin A. <i>Cell Reports</i> , 2022, 38, 110513.	2.9	14
10096	A comparison of transcriptome analysis methods with reference genome. <i>BMC Genomics</i> , 2022, 23, 232.	1.2	18

#	ARTICLE	IF	CITATIONS
10098	Transcriptomic analysis of pea aphids ( <i>Acyrtosiphon pisum</i> ) treated with plant extracts from endophyte-containing drunken horse grass. <i>Journal of Applied Entomology</i> , 0, , .	0.8	0
10099	ADAMTS14, ARHGAP22, and EPDR1 as potential novel targets in acute myeloid leukaemia. <i>Heliyon</i> , 2022, 8, e09065.	1.4	2
10100	Scale Development-Related Genes Identified by Transcriptome Analysis. <i>Fishes</i> , 2022, 7, 64.	0.7	3
10101	Collective effects of human genomic variation on microbiome function. <i>Scientific Reports</i> , 2022, 12, 3839.	1.6	3
10102	The ability to classify patients based on gene-expression data varies by algorithm and performance metric. <i>PLoS Computational Biology</i> , 2022, 18, e1009926.	1.5	6
10105	A specific, non-immune system-related isoform of the human inducible nitric oxide synthase is expressed during differentiation of human stem cells into various cell types. <i>Cell Communication and Signaling</i> , 2022, 20, 47.	2.7	1
10106	Gene-coexpression network analysis identifies specific modules and hub genes related to cold stress in rice. <i>BMC Genomics</i> , 2022, 23, 251.	1.2	17
10108	The medusa of <i>Aurelia coerulea</i> is similar to its polyp in molecular composition and different from the medusa of <i>Stomolophus meleagris</i> in toxicity. <i>Toxicon</i> , 2022, 210, 89-99.	0.8	1
10109	Influenza A pathway analysis of highly pathogenic avian influenza virus (H5N1) infection in genetically disparate Ri chicken lines. <i>Veterinary Immunology and Immunopathology</i> , 2022, 246, 110404.	0.5	7
10110	Differentially expressed genes prediction by multiple self-attention on epigenetics data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	2
10111	Cell environment shapes TDP-43 function with implications in neuronal and muscle disease. <i>Communications Biology</i> , 2022, 5, 314.	2.0	21
10112	Transcriptome-based identification and expression analysis of the glutathione S-transferase (GST) family in tree peony reveals a likely role in anthocyanin transport. <i>Horticultural Plant Journal</i> , 2022, 8, 787-802.	2.3	9
10113	Explore potential disease related metabolites based on latent factor model. <i>BMC Genomics</i> , 2022, 23, 269.	1.2	5
10114	Screening of Genes Related to Growth, Development and Meat Quality of Sahan Crossbred F1 Sheep Based on RNA-Seq Technology. <i>Frontiers in Veterinary Science</i> , 2022, 9, 831519.	0.9	3
10115	Lipidomic and transcriptomic analysis reveals the self-regulation mechanism of <i>Schizochytrium</i> sp. in response to temperature stresses. <i>Algal Research</i> , 2022, 64, 102664.	2.4	6
10116	Transcriptome analysis reveals that cytokinins inhibit adventitious root formation through the MdRR12-MdCRF8 module in apple rootstock. <i>Plant Science</i> , 2022, 318, 111220.	1.7	4
10117	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> : Identification of precocious puberty and slow-growing information. <i>Journal of Invertebrate Pathology</i> , 2022, 190, 107752.	1.5	7
10118	Glia maturation factor-1 <sup>2</sup> induces ferroptosis by impairing chaperone-mediated autophagic degradation of ACSL4 in early diabetic retinopathy. <i>Redox Biology</i> , 2022, 52, 102292.	3.9	48

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10119	Searching and identifying pigmentation genes from <i>Neocaridina denticulate sinensis</i> via comparison of transcriptome in different color strains. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100977.	0.4	0
10120	Effects of gestational exposure to bisphenol A on the hepatic transcriptome and lipidome of rat dams: Intergenerational comparison of effects in the offspring. <i>Science of the Total Environment</i> , 2022, 826, 153990.	3.9	8
10121	Detection of A-to-I RNA Editing in SARS-COV-2. <i>Genes</i> , 2022, 13, 41.	1.0	24
10122	Transcriptomic Analysis of Sex-Associated DEGs in Female and Male Flowers of Kiwifruit ( <i>Actinidia</i> ) Tj ETQq1 1 0.784314 rgBT <sub>0</sub> /Overlook	1.2	0
10123	Transcriptomics Reveals Host-Dependent Differences of Polysaccharides Biosynthesis in <i>Cynomorium songaricum</i> . <i>Molecules</i> , 2022, 27, 44.	1.7	4
10124	Multi-Omics Profiling in Marfan Syndrome: Further Insights into the Molecular Mechanisms Involved in Aortic Disease. <i>International Journal of Molecular Sciences</i> , 2022, 23, 438.	1.8	10
10125	Transcriptomic and Proteomic Characterizations of the Molecular Response to Blue Light and Salicylic Acid in <i>Haematococcus pluvialis</i> . <i>Marine Drugs</i> , 2022, 20, 1.	2.2	20
10126	Analysis of lncRNAs and mRNA Expression in the ZBTB1 Knockout Monoclonal EL4 Cell Line and Combined Analysis With miRNAs and circRNAs. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 806290.	1.8	0
10127	HOPX Plays a Critical Role in Antiretroviral Drugs Induced Epigenetic Modification and Cardiac Hypertrophy. <i>Cells</i> , 2021, 10, 3458.	1.8	2
10128	Transcriptomic Responses of <i>Cordyceps militaris</i> to Salt Treatment During Cordycepins Production. <i>Frontiers in Nutrition</i> , 2021, 8, 793795.	1.6	7
10129	<i>Bacillus amyloliquefaciens</i> SN16-1-Induced Resistance System of the Tomato against <i>Rhizoctonia solani</i> . <i>Pathogens</i> , 2022, 11, 35.	1.2	2
10130	CTLA4-Mediated Immunosuppression in Glioblastoma is Associated with the Infiltration of Macrophages in the Tumor Microenvironment. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 7315-7329.	1.6	15
10131	Comparative Transcriptome Analysis Identifies Key Regulatory Genes Involved in Anthocyanin Metabolism During Flower Development in <i>Lycoris radiata</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 761862.	1.7	12
10132	Transcriptomic analysis provides insights into the immune responses and nutrition in <i>Ostrinia furnacalis</i> larvae parasitized by <i>Macrocentrus cingulum</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2022, 109, e21863.	0.6	6
10134	Autotoxin Rg <sub>1</sub> Induces Degradation of Root Cell Walls and Aggravates Root Rot by Modifying the Rhizospheric Microbiome. <i>Microbiology Spectrum</i> , 2021, 9, e0167921.	1.2	15
10135	Slinker: Visualising novel splicing events in RNA-Seq data. <i>F1000Research</i> , 2021, 10, 1255.	0.8	2
10136	Exploration of Human Lung-Resident Immunity and Response to Respiratory Viral Immunization in a Humanized Mouse Model. <i>Journal of Immunology</i> , 2022, 208, 420-428.	0.4	5
10137	Identification of Genes Related to Cold Tolerance and Novel Genetic Markers for Molecular Breeding in Taiwan Tilapia ( <i>Oreochromis</i> spp.) via Transcriptome Analysis. <i>Animals</i> , 2021, 11, 3538.	1.0	5

#	ARTICLE	IF	CITATIONS
10138	phytanoyl-CoA dioxygenase domain-containing protein 1 plays an important role in egg shell formation of silkworm ( <i>Bombyx mori</i> ). <i>PLoS ONE</i> , 2021, 16, e0261918.	1.1	1
10139	Scenarios for the Integration of Microarray Gene Expression Profiles in COVID-19-Related Studies. <i>Methods in Molecular Biology</i> , 2022, 2401, 195-215.	0.4	0
10142	DNA-Sequenzierung. , 2022, , 863-883.		0
10143	Transcriptome sequencing reveals a lncRNA-mRNA interaction network in extramammary Paget's disease. <i>BMC Medical Genomics</i> , 2021, 14, 291.	0.7	4
10144	Modular control of multiple pathways of <i>Corynebacterium glutamicum</i> for 5-aminolevulinic acid production. <i>AMB Express</i> , 2021, 11, 179.	1.4	11
10145	Neurophysiological and transcriptomic predictors of chronic low back pain: Study protocol for a longitudinal inception cohort study. <i>Research in Nursing and Health</i> , 2022, 45, 11-22.	0.8	3
10146	Single-Cell Sequencing to Unveil the Mystery of Embryonic Development. <i>Advanced Biology</i> , 2022, 6, e2101151.	1.4	2
10147	Fruit and Vegetable Supplemented Diet Modulates the Pig Transcriptome and Microbiome after a Two-Week Feeding Intervention. <i>Nutrients</i> , 2021, 13, 4350.	1.7	3
10149	Interference With ACSL1 Gene in Bovine Adipocytes: Transcriptome Profiling of mRNA and lncRNA Related to Unsaturated Fatty Acid Synthesis. <i>Frontiers in Veterinary Science</i> , 2021, 8, 788316.	0.9	4
10150	DNA, RNA Chemical Properties (Including Sequencing and Next-Generation Sequencing). , 2022, , .		0
10151	Early in vivo transcriptome of <i>Trichoplusia ni</i> ascovirus core genes. <i>Journal of General Virology</i> , 2022, 103, .	1.3	2
10152	The RNA Chaperone Protein Hfq Regulates the Characteristic Sporulation and Insecticidal Activity of <i>Bacillus thuringiensis</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 884528.	1.5	0
10153	Water Stress Differentially Modulates the Expression of Tomato Cell Wall Metabolism-Related Genes in <i>Meloidogyne incognita</i> Feeding Sites. <i>Frontiers in Plant Science</i> , 2022, 13, 817185.	1.7	8
10154	Redistribution of Histone Marks on Inflammatory Genes Associated With Intracerebral Hemorrhage-Induced Acute Brain Injury in Aging Rats. <i>Frontiers in Neuroscience</i> , 2022, 16, 639656.	1.4	2
10155	Transcriptomics Coupled to Proteomics Reveals Novel Targets for the Protective Role of Spermine in Diabetic Cardiomyopathy. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-14.	1.9	0
10156	Microphysiological stem cell models of the human heart. <i>Materials Today Bio</i> , 2022, 14, 100259.	2.6	4
10157	H3K4 demethylase KDM5B regulates cancer cell identity and epigenetic plasticity. <i>Oncogene</i> , 2022, 41, 2958-2972.	2.6	8
10158	Transcriptome Profiling to Dissect the Role of Genome Duplication on Graft Compatibility Mechanisms in Watermelon. <i>Biology</i> , 2022, 11, 575.	1.3	3

#	ARTICLE	IF	CITATIONS
10159	Native RNA or cDNA Sequencing for Transcriptomic Analysis: A Case Study on <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 842299.	2.0	3
10160	Identification and Tissue Expression Profiles of Odorant Receptor Genes in the Green Peach Aphid <i>Myzus persicae</i> . <i>Insects</i> , 2022, 13, 398.	1.0	2
10161	Znhit1 controls meiotic initiation in male germ cells by coordinating with Stra8 to activate meiotic gene expression. <i>Developmental Cell</i> , 2022, 57, 901-913.e4.	3.1	16
10163	Integrative Transcriptomics and Proteomics Elucidate the Regulatory Mechanism of <i>Hydrangea macrophylla</i> Flower-Color Changes Induced by Exogenous Aluminum. <i>Agronomy</i> , 2022, 12, 969.	1.3	3
10850	Interactive and Reproducible Workflows for Exploring and Modeling RNA-seq Data with <i>pcaExplorer</i> , <i>Ideal</i> , and <i>GeneTonic</i> . <i>Current Protocols</i> , 2022, 2, e411.	1.3	9
10851	Characterization of the Myometrial Transcriptome of Long Non-coding RNA Genes in Human Labor by High-Throughput RNA-seq. <i>Reproductive Sciences</i> , 2022, 29, 2885-2893.	1.1	3
10852	Coupling the immunomodulatory properties of the HDAC6 inhibitor ACY241 with Oxaliplatin promotes robust anti-tumor response in non-small cell lung cancer. <i>Oncolmmunology</i> , 2022, 11, 2042065.	2.1	8
10853	Comparative transcriptome analysis of experimental cryptorchidism: Of mice and cynomolgus monkeys. <i>Physiological Genomics</i> , 2022, , .	1.0	0
10854	Tissue-specific expression of IL-15RA alternative splicing transcripts and its regulation by DNA methylation. <i>European Cytokine Network</i> , 2010, 21, 308-18.	1.1	8
10856	Sex-Specific Development in Haplodiploid Honeybee Is Controlled by the Female-Embryo-Specific Activation of Thousands of Intronic LncRNAs. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 690167.	1.8	0
10857	Transcriptomic and Physiological Analysis Reveals the Responses to Auxin and Abscisic Acid Accumulation During <i>Vaccinium corymbosum</i> Flower Bud and Fruit Development. <i>Frontiers in Plant Science</i> , 2022, 13, 818233.	1.7	0
10858	Integrated Metabolomic and Transcriptomic Analysis and Identification of Dammarenediol-II Synthase Involved in Saponin Biosynthesis in <i>Gynostemma longipes</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 852377.	1.7	4
10860	Transcriptomic Analysis of Entomopathogenic Fungus <i>Beauveria Bassiana</i> Infected by a Hypervirulence Polymycovirus BbPmV-4. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
10861	In Silico analysis of <i>Vitis vinifera</i> Cabernet Sauvignon TOR and its responses to sugar and abscisic acid signaling. <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	1
10862	Pan-Cancer Analysis of Tissue and Single-Cell HIF-Pathway Activation Using a Conserved Gene Signature. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
10864	An organ-specific transcriptomic atlas of the medicinal plant <i>Bletilla striata</i> : Protein-coding genes, microRNAs, and regulatory networks. <i>Plant Genome</i> , 2022, 15, e20210.	1.6	5
10865	Root Transcriptional and Metabolic Dynamics Induced by the Plant Growth Promoting Rhizobacterium (PGPR) <i>Bacillus subtilis</i> Mbi600 on Cucumber Plants. <i>Plants</i> , 2022, 11, 1218.	1.6	17
10866	SRTdb: an omnibus for human tissue and cancer-specific RNA transcripts. <i>Biomarker Research</i> , 2022, 10, 27.	2.8	5



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10867	Rosa1, a Transposable Element-Like Insertion, Produces Red Petal Coloration in Rose Through Altering RcMYB114 Transcription. <i>Frontiers in Plant Science</i> , 2022, 13, 857684.	1.7	5
10868	Comparative transcriptome analysis of Ts (Resistant genotype) and Ma (Susceptible genotype) marigold ( <i>Tagetes erecta</i> L.) leaves in response to <i>Alternaria tagetica</i> . <i>Horticultural Plant Journal</i> , 2023, 9, 321-334.	2.3	1
10869	Network Approaches for Charting the Transcriptomic and Epigenetic Landscape of the Developmental Origins of Health and Disease. <i>Genes</i> , 2022, 13, 764.	1.0	1
10870	Differential Epigenetic Effects of BMI Inhibitor PTC-028 on Fusion-Positive Rhabdomyosarcoma Cell Lines from Distinct Metastatic Sites. <i>Regenerative Engineering and Translational Medicine</i> , 2022, 8, 446-455.	1.6	3
10871	Insights into the Molecular Regulation of Lignin Content in Triploid Poplar Leaves. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4603.	1.8	15
10872	In Silico Design Strategies for the Production of Target Chemical Compounds Using Iterative Single-Level Linear Programming Problems. <i>Biomolecules</i> , 2022, 12, 620.	1.8	0
10873	Comparative Analysis of Transcriptome Profiles Reveals the Mechanisms in the Difference of Low Potassium Tolerance among Cultivated and Tibetan Wild Barleys. <i>Agronomy</i> , 2022, 12, 1094.	1.3	2
10874	Overexpression of Human Estrogen Biosynthetic Enzyme Hydroxysteroid (17beta) Dehydrogenase Type 1 Induces Adenomyosis-like Phenotype in Transgenic Mice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4815.	1.8	4
10875	Transcriptome Profiling Provides New Insights into the Molecular Mechanism Underlying the Sensitivity of Cotton Varieties to Mepiquat Chloride. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5043.	1.8	2
10876	Identification and Clarification of VrCYCA1: A Key Genic Male Sterility-Related Gene in Mungbean by Multi-Omics Analysis. <i>Agriculture (Switzerland)</i> , 2022, 12, 686.	1.4	2
10877	Comparative Analysis of rRNA Removal Methods for RNA-Seq Differential Expression in Halophilic Archaea. <i>Biomolecules</i> , 2022, 12, 682.	1.8	11
10878	Antimicrobial Resistance Profile by Metagenomic and Metatranscriptomic Approach in Clinical Practice: Opportunity and Challenge. <i>Antibiotics</i> , 2022, 11, 654.	1.5	7
10879	Expression of matrix metalloproteinase-3 and -10 is up-regulated in the periodontal tissues of aged mice. <i>Journal of Periodontal Research</i> , 2022, 57, 733-741.	1.4	3
10880	The Multi-Omics Analysis Revealed a Metabolic Regulatory System of Cecum in Rabbit with Diarrhea. <i>Animals</i> , 2022, 12, 1194.	1.0	6
10883	Genome-Wide Identification and Expression of MAPK Gene Family in Cultivated Strawberry and Their Involvement in Fruit Developing and Ripening. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5201.	1.8	9
10884	Meta-Omics reveal the metabolic acclimation of freshwater anammox bacteria for saline wastewater treatment. <i>Journal of Cleaner Production</i> , 2022, 362, 132184.	4.6	5
10885	Comparative whole-genome transcriptome analysis in renal cell populations reveals high tissue specificity of MAPK/ERK targets in embryonic kidney. <i>BMC Biology</i> , 2022, 20, 112.	1.7	4
10887	The Mettl3 epitranscriptomic writer amplifies p53 stress responses. <i>Molecular Cell</i> , 2022, 82, 2370-2384.e10.	4.5	22

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10888	Transcriptome Analysis of Antennal Chemosensory Genes in <i>Curculio Dieckmanni</i> Faust. (Coleoptera: Tj ETQq0 0 0,rgBT /Overlock 10 T	1.9	0
10889	Transcriptomes Suggest That Pinniped and Cetacean Brains Have a High Capacity for Aerobic Metabolism While Reducing Energy-Intensive Processes Such as Synaptic Transmission. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, .	1.4	5
10890	Transcriptome analysis of <i>Grapholitha molesta</i> (Busk) (Lepidoptera: Tortricidae) larvae in response to entomopathogenic fungi <i>Beauveria bassiana</i> . <i>Journal of Asia-Pacific Entomology</i> , 2022, 25, 101926.	0.4	2
10891	Diagnostic yield of exome sequencing in congenital vertical talus. <i>European Journal of Medical Genetics</i> , 2022, 65, 104514.	0.7	2
10892	The First Cbk-Like Phage Infecting <i>Erythrobacter</i> , Representing a Novel Siphoviral Genus. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	1
10893	Multiple cells of origin in common with various types of mouse N-Myc acute leukemia. <i>Leukemia Research</i> , 2022, 117, 106843.	0.4	0
10894	Weighted gene Co-expression network analysis (WGCNA) reveals a set of hub genes related to chlorophyll metabolism process in <i>Chlorella vulgaris</i> response androstenedione. <i>Environmental Pollution</i> , 2022, 306, 119360.	3.7	9
10895	Sex-specific extracellular matrix remodeling during early adipogenic differentiation by gestational bisphenol A exposure. <i>Chemosphere</i> , 2022, 302, 134806.	4.2	2
10896	Mutation adaptation and genotoxicity of microalgae induced by Long-Term high CO2 stress. <i>Chemical Engineering Journal</i> , 2022, 445, 136745.	6.6	13
10897	Biglycan as a potential regulator of tumorigenicity and immunogenicity in K-RAS-transformed cells. <i>Oncolmmunology</i> , 2022, 11, 2069214.	2.1	4
10898	Analysis of rhodopsin G protein-coupled receptor orthologs reveals semiochemical peptides for parasite ( <i>Schistosoma mansoni</i> ) and host ( <i>Biomphalaria glabrata</i> ) interplay. <i>Scientific Reports</i> , 2022, 12, 8243.	1.6	5
10899	The effect of BMP4, FGF8 and WNT3a on mouse iPS cells differentiating to odontoblast-like cells. <i>Medical Molecular Morphology</i> , 2022, 55, 199-209.	0.4	1
10900	A model for isoform-level differential expression analysis using RNA-seq data without pre-specifying isoform structure. <i>PLoS ONE</i> , 2022, 17, e0266162.	1.1	3
10901	Genome-wide DNA methylation and gene expression patterns of androgenetic haploid tiger pufferfish ( <i>Takifugu rubripes</i> ) provide insights into haploid syndrome. <i>Scientific Reports</i> , 2022, 12, 8252.	1.6	1
10902	Overexpression of AHL9 accelerates leaf senescence in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2022, 22, 248.	1.6	6
10903	Cold Atmospheric Plasma Boosts Virus Multiplication via EGFR(Tyr1068) Phosphorylation-Mediated Control on Cell Mitophagy. <i>International Journal of Biological Sciences</i> , 2022, 18, 3405-3420.	2.6	1
10904	Gene Expression Profiling. , 2022, , 2882-2887.		0
10906	Biogenesis and Regulatory Roles of Circular RNAs. <i>Annual Review of Cell and Developmental Biology</i> , 2022, 38, 263-289.	4.0	75

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10908	Mycorrhizal symbiosis reprograms ion fluxes and fatty acid metabolism in wild jujube during salt stress. <i>Plant Physiology</i> , 2022, 189, 2481-2499.	2.3	12
10909	The functional activity of donor kidneys is negatively regulated by microribonucleic acid-451 in different perfusion methods to inhibit adenosine triphosphate metabolism and the proliferation of HK2 cells. <i>Bioengineered</i> , 2022, 13, 12706-12717.	1.4	1
10910	Effects of modified clay on the formation of <i>Phaeocystis globosa</i> colony revealed by physiological and transcriptomic analyses. <i>Science of the Total Environment</i> , 2022, 838, 155985.	3.9	3
10911	Transcriptome Analysis and Morphological Changes in Response to Waterlogging in <i>Iris pseudacorus</i> . <i>Phyton</i> , 2022, 91, 2135-2162.	0.4	0
10912	Using biological networks to integrate, visualize and analyze gene-disease interactions. <i>E3S Web of Conferences</i> , 2022, 351, 01034.	0.2	0
10913	Agonist/antagonist compounds' mechanism of action on estrogen receptor-positive breast cancer: A system-level investigation assisted by meta-analysis. <i>Informatics in Medicine Unlocked</i> , 2022, 31, 100985.	1.9	2
10914	Comparing the Transcriptomes of Two Different Tissues in <i>Helicoverpa assulta</i> (Guenée). <i>Journal of Chemistry</i> , 2022, 2022, 1-7.	0.9	0
10915	De novo transcriptome assembly of the cotyledon of <i>Camellia oleifera</i> for discovery of genes regulating seed germination. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
10916	Graph-Based Integration of Histone Modification Profiles. <i>Mathematics</i> , 2022, 10, 1842.	1.1	2
10917	Lessons From Transcriptome Analysis of Autoimmune Diseases. <i>Frontiers in Immunology</i> , 2022, 13, .	2.2	3
10919	Vanadium(IV)-Chlorodipicolinate Protects against Hepatic Steatosis by Ameliorating Lipid Peroxidation, Endoplasmic Reticulum Stress, and Inflammation. <i>Antioxidants</i> , 2022, 11, 1093.	2.2	3
10921	Candidate Chemosensory Genes Identified in the Adult Antennae of <i>Sympiezomias velatus</i> and Binding Property of Odorant-Binding Protein 15. <i>Frontiers in Physiology</i> , 2022, 13, .	1.3	4
10922	Coping with antagonistic predation risks: Predator-dependent unique responses are dominant in <i>Ceriodaphnia cornuta</i> . <i>Molecular Ecology</i> , 2022, 31, 3951-3962.	2.0	10
10924	Pan-Cancer Methylated Dysregulation of Long Non-coding RNAs Reveals Epigenetic Biomarkers. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, .	1.8	3
10925	Applications of Omics Technology for Livestock Selection and Improvement. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	10
10926	Integrated transcriptome and in vitro analysis revealed anti-proliferative effect of sodium perborate on hepatocellular carcinoma cells. <i>Journal of Trace Elements in Medicine and Biology</i> , 2022, , 127011.	1.5	1
10927	Genome and transcriptome analysis of rock-dissolving <i>Pseudomonas</i> sp. NLX-4 strain. <i>Bioresources and Bioprocessing</i> , 2022, 9, .	2.0	5
10928	Rapeseed ( <i>Brassica napus</i> ) Mitogen-Activated Protein Kinase 1 Enhances Shading Tolerance by Regulating the Photosynthesis Capability of Photosystem II. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1

#	ARTICLE	IF	CITATIONS
10929	Physiological and transcription analyses reveal regulatory pathways of 6-benzylaminopurine delaying leaf senescence and maintaining quality in postharvest Chinese flowering cabbage. <i>Food Research International</i> , 2022, 157, 111455.	2.9	9
10930	Low Temperature Stress Tolerance: An Insight Into the Omics Approaches for Legume Crops. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	30
10931	Sensitive and accurate analysis of gene expression signatures enabled by oligonucleotide-labelled cDNA. <i>RNA Biology</i> , 2022, 19, 774-780.	1.5	1
10933	Phylogenetic analysis and expression profiling of nuclear factor-Y gene family in <i>Dendrobium catenatum</i> Lindl. (Orchidaceae). <i>Plant Gene</i> , 2022, , 100365.	1.4	0
10934	Key Role of Heat Shock Protein Expression Induced by Ampicillin in Citrus Defense against Huanglongbing: A Transcriptomics Study. <i>Agronomy</i> , 2022, 12, 1356.	1.3	2
10935	The evolution of <i>pre-mRNA</i> splicing and its machinery revealed by reduced extremophilic red algae. <i>Journal of Eukaryotic Microbiology</i> , 0, , .	0.8	5
10936	Comparative transcriptome analysis reveals the molecular mechanism underlying lily double flowering. <i>Scientia Horticulturae</i> , 2022, 303, 111221.	1.7	1
10943	Full-length transcripts facilitates <i>Portunus trituberculatus</i> genome structure annotation. <i>Journal of Oceanology and Limnology</i> , 2022, 40, 2042-2051.	0.6	3
10944	IR: Regulation of DNA Methylation During the Testicular Development of Shaziling Pigs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
10945	Benzotriazole Uv Stabilizer-Induced Genotoxicity in Freshwater Benthic Clams: A Survey on Apoptosis, Oxidative Stress, Histopathology and Transcriptomics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
10946	Evolution of sexual systems, sex chromosomes and sex-linked gene transcription in flatworms and roundworms. <i>Nature Communications</i> , 2022, 13, .	5.8	6
10947	Microfluidics Facilitates the Development of Single-Cell RNA Sequencing. <i>Biosensors</i> , 2022, 12, 450.	2.3	8
10948	Deletion C-terminal thioesterase abolishes melanin biosynthesis, affects metabolism and reduces the pathogenesis of <i>Fonsecaea monophora</i> . <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010485.	1.3	5
10949	Comparative Transcriptome and Metabolome Analysis of Resistant and Susceptible Piper Species Upon Infection by the Oomycete <i>Phytophthora Capsici</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
10950	Emergence of Resistance to MTI-101 Selects for a MET Genotype and Phenotype in EGFR Driven PC-9 and PTEN Deleted H446 Lung Cancer Cell Lines. <i>Cancers</i> , 2022, 14, 3062.	1.7	1
10951	Acetyl-CoA metabolism drives epigenome change and contributes to carcinogenesis risk in fatty liver disease. <i>Genome Medicine</i> , 2022, 14, .	3.6	12
10952	Transcriptome Analysis Reveals the Regulatory Networks of Cytokinin in Promoting Floral Feminization in <i>Castanea henryi</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6389.	1.8	6
10953	<i>Vibrio cholerae</i> senses human enteric $\hat{\iota}$ -defensin 5 through a CarSR two-component system to promote bacterial pathogenicity. <i>Communications Biology</i> , 2022, 5, .	2.0	6

#	ARTICLE	IF	CITATIONS
10954	Carotenoid Biosynthesis: Genome-Wide Profiling, Pathway Identification in <i>Rhodotorula glutinis</i> X-20, and High-Level Production. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	4
10955	Advancements in Genomic and Behavioral Neuroscience Analysis for the Study of Normal and Pathological Brain Function. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
10956	New Perspectives in Grapevine ( <i>Vitis</i> spp.) Breeding. , 0, , .		4
10957	Critical Role of Osteopontin in Maintaining Urinary Phosphate Solubility in CKD. <i>Kidney360</i> , 0, 3, 10.34067/KID.0007352021.	0.9	3
10958	Transcriptome Analysis of Sugarcane Response to Sugarcane Yellow Leaf Virus Infection Transmitted by the Vector <i>Melanaphis sacchari</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
10959	Gene fusion as an important mechanism to generate new genes in the genus <i>Oryza</i> . <i>Genome Biology</i> , 2022, 23, .	3.8	7
10960	The Molecular Mechanism of Yellow Mushroom ( <i>Floccularia luteovirens</i> ) Response to Strong Ultraviolet Radiation on the Qinghai-Tibet Plateau. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
10961	Comparative transcriptomes and metabolomes reveal different tolerance mechanisms to cold stress in two different catfish species. <i>Aquaculture</i> , 2022, 560, 738543.	1.7	16
10962	Comparative de novo Transcriptome Analysis of Two Cultivars With Contrasting Content of Oil and Fatty Acids During Kernel Development in <i>Torreyia grandis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
10963	PD-L1 blockade restores CAR T cell activity through IFN- $\beta$ -regulation of CD163+ M2 macrophages. , 2022, 10, e004400.		16
10964	Interplay of CodY and CcpA in Regulating Central Metabolism and Biofilm Formation in <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	9
10965	Metabolite Effect on Angiogenesis: Insights from Transcriptome Analysis. <i>Cell Biochemistry and Biophysics</i> , 2022, 80, 519-536.	0.9	2
10966	Exceptional response to combination ipilimumab and nivolumab in metastatic uveal melanoma: Insights from genomic analysis. <i>Melanoma Research</i> , 0, Publish Ahead of Print, .	0.6	4
10967	The XadA Trimeric Autotransporter Adhesins in <i>Xylella fastidiosa</i> Differentially Contribute to Cell Aggregation, Biofilm Formation, Insect Transmission and Virulence to Plants. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 857-866.	1.4	3
10968	Identification of neuropeptides and neuropeptide receptor genes in <i>Phauda flammans</i> (Walker). <i>Scientific Reports</i> , 2022, 12, .	1.6	3
10969	<i>Dwarf and High Tiling1</i> represses rice tillering through mediating the splicing of <i>D14</i> pre-mRNA. <i>Plant Cell</i> , 2022, 34, 3301-3318.	3.1	12
10970	Hierarchical regulation of <i>Burkholderia glumae</i> type III secretion system by <i>GluR</i> response regulator and Lon protease. <i>Molecular Plant Pathology</i> , 0, , .	2.0	1
10971	Polyketide synthases (PKSs) of secondary metabolism: <i>in silico</i> identification and characterization in orchids. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 5486-5498.	2.0	1

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10972	Large-scale comparative transcriptome analysis of <i>Nicotiana tabacum</i> response to <i>Ralstonia solanacearum</i> infection. <i>Plant Biotechnology Reports</i> , 2022, 16, 757-775.	0.9	2
10973	Transcriptome analysis of <i>Stipa purpurea</i> interacted with endophytic <i>Bacillus subtilis</i> in response to temperature and ultraviolet stress. <i>Plant Growth Regulation</i> , 0, , .	1.8	2
10974	Combined High-Throughput Approaches Reveal the Signals Driven by Skin and Blood Environments and Define the Tumor Heterogeneity in SÅ©zary Syndrome. <i>Cancers</i> , 2022, 14, 2847.	1.7	1
10975	Genome-Wide Identification and Characterization of CPR5 Genes in <i>Gossypium</i> Reveals Their Potential Role in Trichome Development. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
10976	Transcriptomic Profile Analysis of <i>Populus talassica</i> Å— <i>Populus euphratica</i> Response and Tolerance under Salt Stress Conditions. <i>Genes</i> , 2022, 13, 1032.	1.0	3
10977	Understanding a defensive response of methicillin-resistant <i>Staphylococcus aureus</i> after exposure to multiple cycles of sub-lethal blue light. <i>FEMS Microbiology Letters</i> , 2022, 369, .	0.7	2
10978	Porcine Circovirus type 2 infected myocardial tissue transcriptome signature. <i>Gene</i> , 2022, 836, 146670.	1.0	7
10979	Genetic analysis and identification of VrFRO8, a salt tolerance-related gene in mungbean. <i>Gene</i> , 2022, 836, 146658.	1.0	5
10980	Riboflavin deficiency leads to irreversible cellular changes in the RPE and disrupts retinal function through alterations in cellular metabolic homeostasis. <i>Redox Biology</i> , 2022, 54, 102375.	3.9	4
10981	Selectively facilitating the electron acceptance of methanogens by riboflavin. <i>Renewable Energy</i> , 2022, 195, 734-741.	4.3	5
10982	Silicon-enhanced tolerance to cadmium toxicity in soybean by enhancing antioxidant defense capacity and changing cadmium distribution and transport. <i>Ecotoxicology and Environmental Safety</i> , 2022, 241, 113766.	2.9	10
10983	RNA-seq analysis of the differential response to low-temperature stress in two morphs of mud crabs ( <i>Scylla paramamosain</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 43, 101010.	0.4	5
10984	Transcriptomic profiling reveals the protection mechanism of bivalent inactivated bacteria vaccine <i>Aeromonas salmonicida</i> and <i>Vibrio scophthalmi</i> in turbot ( <i>Scophthalmus maximus</i> ). <i>Aquaculture</i> , 2022, 560, 738479.	1.7	3
10985	Transcriptome Analysis via RNA Sequencing Reveals the Molecular Mechanisms Underlying the <i>Hedera helix</i> Response to High Temperature. <i>Phyton</i> , 2022, 91, 2403-2417.	0.4	0
10986	Molecular arms race between geminiviruses and host plants during infection cycleâ€”a transcriptomics overview. , 2022, , 471-483.		0
10987	BnKAT2 Positively Regulates the Main Inflorescence Length and Silique Number in <i>Brassica napus</i> by Regulating the Auxin and Cytokinin Signaling Pathways. <i>Plants</i> , 2022, 11, 1679.	1.6	5
10988	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	8
10989	Host Cytoskeleton Gene Expression Is Correlated with the Formation of Ascovirus Reproductive Viral Vesicles. <i>Viruses</i> , 2022, 14, 1444.	1.5	1

#	ARTICLE	IF	CITATIONS
10990	DEVEA: an interactive shiny application for Differential Expression analysis, data Visualization and Enrichment Analysis of transcriptomics data. <i>F1000Research</i> , 0, 11, 711.	0.8	0
10991	Dynamic Transcriptome-Based Weighted Gene Co-expression Network Analysis Reveals Key Modules and Hub Genes Associated With the Structure and Nutrient Formation of Endosperm for Wax Corn. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
10992	The Black Necrotic Lesion Enhanced <i>Fusarium graminearum</i> Resistance in Wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
10993	De novo transcriptome assembly and comprehensive assessment provide insight into fruiting body formation of <i>Sparassis latifolia</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	2
10994	An Equine Model for Vaccination against a Hepacivirus: Insights into Host Responses to E2 Recombinant Protein Vaccination and Subsequent Equine Hepacivirus Inoculation. <i>Viruses</i> , 2022, 14, 1401.	1.5	0
10996	Identification and Expression Analysis of Chemosensory Genes in the Antennal Transcriptome of <i>Chrysanthemum Aphid Macrosiphoniella sanborni</i> . <i>Insects</i> , 2022, 13, 597.	1.0	6
10997	<sc>RNA</sc> sequencing and expression heterogeneity in head and neck cancer. <i>Cancer Cytopathology</i> , 2022, 130, 842-843.	1.4	0
10998	The airway smooth muscle sodium/calcium exchanger NCLX is critical for airway remodeling and hyperresponsiveness in asthma. <i>Journal of Biological Chemistry</i> , 2022, 298, 102259.	1.6	5
11000	Chromosome-level genome assembly defines female-biased genes associated with sex determination and differentiation in the human blood fluke <i>Schistosoma japonicum</i> . <i>Molecular Ecology Resources</i> , 0, , .	2.2	1
11001	Integrated Transcriptome and Metabolomic Analysis Reveal Anti-Angiogenic Properties of Disarib, a Novel Bcl2-Specific Inhibitor. <i>Genes</i> , 2022, 13, 1208.	1.0	0
11002	A RAS-Independent Biomarker Panel to Reliably Predict Response to MEK Inhibition in Colorectal Cancer. <i>Cancers</i> , 2022, 14, 3252.	1.7	1
11003	Expression Patterns Divergence of Reciprocal F1 Hybrids Between <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> Reveals Overdominance Mediating Interspecific Biomass Heterosis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11004	Transcriptome-wide identification of microRNAs in the roots of <i>Pinus massoniana</i> seedlings under Pi stress and Pi recovery. <i>Acta Physiologiae Plantarum</i> , 2022, 44, .	1.0	1
11005	Approaches in Gene Coexpression Analysis in Eukaryotes. <i>Biology</i> , 2022, 11, 1019.	1.3	4
11006	Transcriptome Sequencing of <i>Agave angustifolia</i> Reveals Conservation and Diversification in the Expression of Cinnamyl Alcohol Dehydrogenase Genes in Agave Species. <i>Agriculture (Switzerland)</i> , 2022, 12, 1003.	1.4	3
11007	How candidate genes respond to aluminum toxicity in <i>Citrus x limonia</i> Osbeck?. <i>Theoretical and Experimental Plant Physiology</i> , 0, , .	1.1	1
11008	Changes in the Species and Functional Composition of Activated Sludge Communities Revealed Mechanisms of Partial Nitrification Established by Ultrasonication. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
11009	Genome and Transcriptome Sequencing Analysis of <i>Fusarium commune</i> Provides Insights into the Pathogenic Mechanisms of the Lotus Rhizome Rot. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

#	ARTICLE	IF	CITATIONS
11010	Integrated mRNA and Small RNA Sequencing Reveals a microRNA Regulatory Network Associated with Starch Biosynthesis in Lotus ( <i>Nelumbo nucifera</i> Gaertn.) Rhizomes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7605.	1.8	2
11012	Mitigating sarcoplasmic reticulum stress limits disuse-induced muscle loss in hindlimb unloaded mice. <i>Npj Microgravity</i> , 2022, 8, .	1.9	10
11014	Anti-fungal Activity of <i>Dalbergia retusa</i> Extract on <i>Gloeophyllum trabeum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11015	PNGSeqR: An R Package for Rapid Candidate Gene Selection through Pooled Next-Generation Sequencing. <i>Plants</i> , 2022, 11, 1821.	1.6	0
11016	Comparative Transcriptomics and Gene Knockout Reveal Virulence Factors of <i>Neofusicoccum parvum</i> in Walnut. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
11017	In vivo transcriptional analysis of mice infected with <i>Leishmania major</i> unveils cellular heterogeneity and altered transcriptomic profiling at single-cell resolution. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010518.	1.3	9
11018	SICKLE modulates lateral root development by promoting degradation of lariat intronic RNA. <i>Plant Physiology</i> , 0, , .	2.3	4
11019	scDLC: a deep learning framework to classify large sample single-cell RNA-seq data. <i>BMC Genomics</i> , 2022, 23, .	1.2	5
11020	Comparative Transcriptome Analysis Reveals Regulatory Factors Involved in <i>Vibrio Parahaemolyticus</i> Biofilm Formation. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	4
11021	A Genome-Wide Association Study Coupled With a Transcriptomic Analysis Reveals the Genetic Loci and Candidate Genes Governing the Flowering Time in Alfalfa ( <i>Medicago sativa</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11022	Single-cell transcriptomes identifies characteristic features of mouse macrophages in liver Mallory-Denk bodies formation. <i>Experimental and Molecular Pathology</i> , 2022, 127, 104811.	0.9	4
11023	Effects of air exposure stress on crustaceans: Histopathological changes, antioxidant and immunity of the red swamp crayfish <i>Procambarus clarkii</i> . <i>Developmental and Comparative Immunology</i> , 2022, 135, 104480.	1.0	6
11024	A Phosphoproteomics Study of the Soybean root necrosis 1 Mutant Revealed Type II Metacaspases Involved in Cell Death Pathway. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
11025	The Epigenetic Regulatory Protein CBX2 Promotes mTORC1 Signalling and Inhibits DREAM Complex Activity to Drive Breast Cancer Cell Growth. <i>Cancers</i> , 2022, 14, 3491.	1.7	11
11026	MicroRNA-mediated regulation of lipid metabolism in virus-infected <i>Emiliana huxleyi</i> . <i>ISME Journal</i> , 2022, 16, 2457-2466.	4.4	6
11027	<i>In Vivo</i> Syngeneic Tumor Models with Acquired Resistance to Anti-PD-1/PD-L1 Therapies. <i>Cancer Immunology Research</i> , 2022, 10, 1013-1027.	1.6	6
11028	An apple somatic mutation of delayed fruit maturation date is primarily caused by a retrotransposon insertion-associated large deletion. <i>Plant Journal</i> , 2022, 111, 1609-1625.	2.8	4
11029	GLS2 Is a Tumor Suppressor and a Regulator of Ferroptosis in Hepatocellular Carcinoma. <i>Cancer Research</i> , 2022, 82, 3209-3222.	0.4	42



#	ARTICLE	IF	CITATIONS
11030	A Linarin Derivative Protects against Ischemia-Induced Neuronal Injury in Mice by Promoting Cerebral Blood Flow Recovery via KDELR-Dependent CSPG4 Activation. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-19.	1.9	2
11031	Liver transcriptome analysis reveals changes in energy metabolism, oxidative stress, and apoptosis in pearl gentian grouper exposed to acute hypoxia. <i>Aquaculture</i> , 2022, 561, 738635.	1.7	16
11032	Development of Reference Genes for Horticultural Plants. <i>Critical Reviews in Plant Sciences</i> , 2022, 41, 190-208.	2.7	3
11033	Mining new meroterpenoids from the marine red alga-derived endophytic <i>Penicillium chermesinum</i> EN-480 by comparative transcriptome analysis. <i>Bioorganic Chemistry</i> , 2022, 128, 106021.	2.0	4
11034	Analysis of <i>Cyperus esculentus</i> SMP family genes reveals lineage-specific evolution and seed desiccation-like transcript accumulation during tuber maturation. <i>Industrial Crops and Products</i> , 2022, 187, 115382.	2.5	5
11035	Gene Drive by <i>Fusarium Skc1</i> is Dependent on its Competing Allele. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
11036	Transcriptomics of meat quality. , 2022, , 337-391.		0
11037	Transcriptomics for Drought Stress Mediated by Biological Processes in-relation to Key Regulated Pathways in <i>Gossypium darwinii</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	0
11039	Genome-wide identification and expression pattern of short-wavelength light responsive members of the NAC family in turnip. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 581-594.	0.7	0
11040	Comparative Transcriptomic Analysis of Root and Leaf Transcript Profiles Reveals the Coordinated Mechanisms in Response to Salinity Stress in Common Vetch. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8477.	1.8	5
11041	Postponing development: dormancy in the earliest developmental stages of a high-latitude calanoid copepod. <i>Journal of Plankton Research</i> , 2022, 44, 923-935.	0.8	1
11042	Transcriptome analysis reveals candidate genes related to steroid alkaloid biosynthesis in <i>Fritillaria anhuiensis</i> . <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	2
11043	Sugarcane Genotypes with Contrasting Biological Nitrogen Fixation Efficiencies Differentially Modulate Nitrogen Metabolism, Auxin Signaling, and Microorganism Perception Pathways. <i>Plants</i> , 2022, 11, 1971.	1.6	2
11044	RNA-Seq as an Effective Tool for Modern Transcriptomics, A Review-based Study. <i>Journal of Applied Research in Plant Sciences</i> , 2022, 3, 236-241.	0.4	1
11045	Fetal origin of sex bias brain aging. <i>FASEB Journal</i> , 2022, 36, .	0.2	8
11046	Analysis of transcriptome data and quantitative trait loci enables the identification of candidate genes responsible for fiber strength in <i>Gossypium barbadense</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
11047	TET enzymes regulate skeletal development through increasing chromatin accessibility of RUNX2 target genes. <i>Nature Communications</i> , 2022, 13, .	5.8	12
11048	Downstream Effects of Mutations in SOD1 and TARDBP Converge on Gene Expression Impairment in Patient-Derived Motor Neurons. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9652.	1.8	3

#	ARTICLE	IF	CITATIONS
11049	Drought Stress Stimulates the Terpenoid Backbone and Triterpenoid Biosynthesis Pathway to Promote the Synthesis of Saikosaponin in <i>Bupleurum chinense</i> DC. <i>Roots. Molecules</i> , 2022, 27, 5470.	1.7	4
11050	Ascendancy of semi-synthetic biomaterials from design towards democratization. <i>Nature Materials</i> , 2022, 21, 989-992.	13.3	7
11052	Transcriptome Analysis of Developing Xylem Provides New Insights into Shade Response in Three Poplar Hybrids. <i>Forests</i> , 2022, 13, 1261.	0.9	1
11053	A Comprehensive Transcriptomic Analysis of Arsenic-Induced Bladder Carcinogenesis. <i>Cells</i> , 2022, 11, 2435.	1.8	7
11054	Modulation of sol mRNA expression by the long non-coding RNA Assolrna in <i>Clostridium saccharoperbutylacetonicum</i> affects solvent formation. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
11055	Chromosomal assembly of the flat oyster ( <i>Ostrea edulis</i> L.) genome as a new genetic resource for aquaculture. <i>Evolutionary Applications</i> , 2022, 15, 1730-1748.	1.5	10
11056	Evaluation of the early defoliation trait and identification of resistance genes through a comprehensive transcriptome analysis in pears. <i>Journal of Integrative Agriculture</i> , 2023, 22, 120-138.	1.7	1
11057	DeLTa-Seq: direct-lysate targeted RNA-Seq from crude tissue lysate. <i>Plant Methods</i> , 2022, 18, .	1.9	4
11058	Transcriptomic Analyses Reveal Key Genes Involved in Pigment Biosynthesis Related to Leaf Color Change of <i>Liquidambar formosana</i> Hance. <i>Molecules</i> , 2022, 27, 5433.	1.7	3
11059	Olfactory proteins of <i>Endoclista signifer</i> larvae and their roles in host recognition. <i>Chemical and Biological Technologies in Agriculture</i> , 2022, 9, .	1.9	1
11062	AhrC Negatively Regulates <i>Streptococcus mutans</i> Arginine Biosynthesis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
11063	Systemic RNA Interference Defective (SID) genes modulate dopaminergic neurodegeneration in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2022, 18, e1010115.	1.5	10
11064	The miRNome of canine invasive urothelial carcinoma. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
11065	The Synthesis and Assembly of a Truncated Cyanophage Genome and Its Expression in a Heterogenous Host. <i>Life</i> , 2022, 12, 1234.	1.1	5
11066	Integrative network analysis revealed the molecular function of folic acid on immunological enhancement in a sheep model. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
11067	ASF1B, as an Independent Prognostic Biomarker, Correlates with Immune Infiltrates in Hepatocellular Carcinoma. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2023, 26, 1311-1323.	0.6	1
11068	The Role of Alternative Splicing in Cancer: Regulatory Mechanism, Therapeutic Strategy, and Bioinformatics Application. <i>DNA and Cell Biology</i> , 0, , .	0.9	0
11069	RRAP: RPKM Recruitment Analysis Pipeline. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	7

#	ARTICLE	IF	CITATIONS
11070	Integration of RNA-seq and ATAC-seq identifies muscle-regulated hub genes in cattle. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
11071	Functional characterization of ion channels expressed in kidney organoids derived from human induced pluripotent stem cells. <i>American Journal of Physiology - Renal Physiology</i> , 2022, 323, F479-F491.	1.3	6
11072	Integrated analysis of small RNAs, transcriptome and degradome sequencing reveal the drought stress network in <i>Agropyron mongolicum</i> Keng. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11073	Transcriptome Analyses in a Selected Gene Set Indicate Alternative Oxidase (AOX) and Early Enhanced Fermentation as Critical for Salinity Tolerance in Rice. <i>Plants</i> , 2022, 11, 2145.	1.6	9
11074	Novel Long-Chain Fatty Acid (LCFA)-Degrading Bacteria and Pathways in Anaerobic Digestion Promoted by Hydrochar as Revealed by Genome-Centric Metatranscriptomics Analysis. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	8
11076	PagDET2 promotes cambium cell division and xylem differentiation in poplar stem. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11077	Regulation of DNA methylation during the testicular development of Shaziling pigs. <i>Genomics</i> , 2022, 114, 110450.	1.3	4
11078	Scutellarin Loaded on Ultradeflexible Nanoliposome Scutellarin EDTMP (S-UNL-E) Promotes Osteogenesis in Osteoporotic Rats. <i>Stem Cells International</i> , 2022, 2022, 1-10.	1.2	2
11080	Aquaporin-8 transports hydrogen peroxide to regulate granulosa cell autophagy. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	2
11081	The combination of RNA-seq transcriptomics and data-independent acquisition proteomics reveals the mechanisms underlying enhanced salt tolerance by the ZmPDI gene in <i>Zoysia matrella</i> [L.] Merr.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
11082	Differential analysis of ergosterol function in response to high salt and sugar stress in <i>Zygosaccharomyces rouxii</i> . <i>FEMS Yeast Research</i> , 0, , .	1.1	2
11083	Whole-transcriptome analysis of differentially expressed genes between ray and disc florets and identification of flowering regulatory genes in <i>Chrysanthemum morifolium</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11084	Physiological and transcriptomic analyses revealed the change of main flavor substance of <i>Zygosaccharomyces rouxii</i> under salt treatment. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	5
11085	Metabolic response provides insights into the mechanism of adaption to hypoxia in largemouth bass ( <i>Micropterus salmoides</i> ) under intermittent hypoxic conditions. <i>Ecotoxicology and Environmental Safety</i> , 2022, 242, 113957.	2.9	8
11086	Hypoxia alters glucose and lipid metabolisms in golden pompano ( <i>Trachinotus blochii</i> ). <i>Aquaculture</i> , 2023, 562, 738747.	1.7	6
11088	Single-cell gene regulation network inference by large-scale data integration. <i>Nucleic Acids Research</i> , 2022, 50, e126-e126.	6.5	9
11089	Decoding the olfactory map through targeted transcriptomics links murine olfactory receptors to glomeruli. <i>Nature Communications</i> , 2022, 13, .	5.8	12
11090	Genome-wide analysis of IQD proteins and ectopic expression of watermelon CLIQD24 in tomato suggests its important role in regulating fruit shape. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3

#	ARTICLE	IF	CITATIONS
11091	Effects of N Acetylcysteine on the Expression of Genes Associated with Reproductive Performance in the Goat Uterus during Early Gestation. <i>Animals</i> , 2022, 12, 2431.	1.0	3
11092	Identification of Genes Promoting Growth of <i>Ustilago maydis</i> on Biomolecules Released from Cells Killed by Oxidation. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 957.	1.5	0
11093	Redox imbalance in COVID-19 pathophysiology. <i>Redox Biology</i> , 2022, 56, 102465.	3.9	10
11094	Multi-omics study revealed the genetic basis of beer flavor quality in yeast. <i>LWT - Food Science and Technology</i> , 2022, 168, 113932.	2.5	6
11095	The strategy of arsenic metabolism in an arsenic-resistant bacterium <i>Stenotrophomonas maltophilia</i> SCSIOOM isolated from fish gut. <i>Environmental Pollution</i> , 2022, 312, 120085.	3.7	1
11096	Transcriptome analysis of maize pathogen <i>Fusarium verticillioides</i> revealed FvLcp1, a secreted protein with type-D fungal LysM and chitin-binding domains, that plays important roles in pathogenesis and mycotoxin production. <i>Microbiological Research</i> , 2022, 265, 127195.	2.5	1
11097	Characterization and Pathogenicity of <i>Pseudopestalotiopsis vietnamensis</i> Causing Gray Blight of Wuyi Rock Tea ( <i>Camellia sinensis</i> ) in China and Specific Mechanisms of Disease Infection. <i>Phyton</i> , 2023, 92, 131-147.	0.4	1
11098	Transcriptomic and metabolomic analyses reveal that MYB transcription factors regulate anthocyanin synthesis and accumulation in the disc florets of the anemone form of <i>chrysanthemum morifolium</i> . <i>Scientia Horticulturae</i> , 2023, 307, 110847.	1.7	6
11099	A proposed framework for the identification of indicator genes for monitoring antibiotic resistance in wastewater: Insights from metagenomic sequencing. <i>Science of the Total Environment</i> , 2023, 854, 158698.	3.9	6
11100	Methylome and transcriptome analysis of alters leaf phenotype with autotetraploid in grape. <i>Scientia Horticulturae</i> , 2023, 307, 111534.	1.7	3
11101	Regulation of Podocyte Injury by CircHIPK3/FUS Complex in Diabetic Kidney Disease. <i>International Journal of Biological Sciences</i> , 2022, 18, 5624-5640.	2.6	5
11102	Using genome-wide expression compendia to study microorganisms. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4315-4324.	1.9	0
11103	RNA-seq analysis of alternative pre-mRNA splicing regulation mediated by photoreceptors in <i>Physcomitrium patens</i> . <i>Methods in Enzymology</i> , 2022, , .	0.4	0
11104	The absence of the queuosine tRNA modification leads to pleiotropic phenotypes revealing perturbations of metal and oxidative stress homeostasis in <i>Escherichia coli</i> K12. <i>Metallomics</i> , 2022, 14, .	1.0	9
11105	Multi-Scale Analysis of Nickel Tolerance Mechanism for Thermophilic <i>Sulfobacillus</i> Thermosulfidooxidans in Bioleaching. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
11106	Pacc Mediates Ph and Osmotic Stress, Fruiting Body Development, And Polysaccharide Biosynthesis In <i>Cordyceps Militar</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
11107	Transcriptome Analysis of the Adipose Tissue of Luchuan and Duroc Pigs. <i>Animals</i> , 2022, 12, 2258.	1.0	1
11108	Tissue-Specific Transcriptomes Outline Halophyte Adaptive Strategies in the Gray Mangrove ( <i>Avicennia</i> ) Tj ETQq1 1,0,784314,rgBT /Ove	1.3	3

#	ARTICLE	IF	CITATIONS
11109	Maternal obesity alters methylation level of cytosine in CpG island for epigenetic inheritance in fetal umbilical cord blood. <i>Human Genomics</i> , 2022, 16, .	1.4	2
11110	A Trade-Off for Maintenance of Multidrug-Resistant IncHI2 Plasmids in <i>Salmonella enterica</i> Serovar Typhimurium through Adaptive Evolution. <i>MSystems</i> , 2022, 7, .	1.7	7
11111	Metabolomic and Transcriptomic Analyses Reveal Association of Mature Fruit Pericarp Color Variation with Chlorophyll and Flavonoid Biosynthesis in Wax Gourd ( <i>Benincasa hispida</i> ). <i>Agronomy</i> , 2022, 12, 2045.	1.3	4
11112	Effects of Nutrient Elements on Growth and Expression of Insect-Defense Response Genes in <i>Zanthoxylum bungeanum</i> Maxim. <i>Forests</i> , 2022, 13, 1365.	0.9	2
11113	Characterization and Comparison of Eye Development and Phototransduction Genes in Deep- and Shallow-Water Shrimp <i>Alvinocaris longirostris</i> and <i>Palaemon carinicauda</i> . <i>Diversity</i> , 2022, 14, 653.	0.7	2
11114	Integrative Metabolome and Transcriptome Analysis Reveals the Regulatory Network of Flavonoid Biosynthesis in Response to MeJA in <i>Camellia vietnamensis</i> Huang. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9370.	1.8	7
11115	Location and Identification on Chromosome 3B of Bread Wheat of Genes Affecting Chiasma Number. <i>Plants</i> , 2022, 11, 2281.	1.6	0
11116	Combined transcriptomic and proteomic analysis reveals multiple pathways involved in self-pollen tube development and the potential roles of FviYABBY1 in self-incompatibility in <i>Fragaria viridis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11117	Extremely Low-Frequency Electromagnetic Field Impairs the Development of Honeybee ( <i>Apis cerana</i> ). <i>Animals</i> , 2022, 12, 2420.	1.0	4
11118	Typical Enhancers, Super-Enhancers, and Cancers. <i>Cancers</i> , 2022, 14, 4375.	1.7	9
11119	Decoding brain memory formation by single-cell RNA sequencing. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	6
11120	Benzotriazole UV stabilizer-induced genotoxicity in freshwater benthic clams: A survey on apoptosis, oxidative stress, histopathology and transcriptomics. <i>Science of the Total Environment</i> , 2022, , 159055.	3.9	2
11121	Comparative transcriptome analysis of leaves of sour jujube seedlings under salt stress. <i>Acta Physiologiae Plantarum</i> , 2022, 44, .	1.0	2
11122	Active antibiotic resistome in soils unraveled by single-cell isotope probing and targeted metagenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
11123	Nonparametric single-cell multiomic characterization of trio relationships between transcription factors, target genes, and cis-regulatory regions. <i>Cell Systems</i> , 2022, 13, 737-751.e4.	2.9	16
11124	Applying genetic technologies to combat infectious diseases in aquaculture. <i>Reviews in Aquaculture</i> , 2023, 15, 491-535.	4.6	11
11125	Identification of core genes affecting IMF deposition in bovine. <i>Animal Biotechnology</i> , 2023, 34, 2887-2899.	0.7	2
11126	Incompatible pollen abortion and late-acting self-incompatibility in <i>Schima superba</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	3

#	ARTICLE	IF	CITATIONS
11127	Transcriptome Analysis of Berries of Spine Grape ( <i>Vitis davidii</i> FÃ¶rster) Infected by <i>Colletotrichum viniferum</i> during Symptom Development. <i>Horticulturae</i> , 2022, 8, 843.	1.2	4
11129	Characterization of circular <i>scp</i> RNAs with advanced sequencing technologies in human complex diseases. <i>Wiley Interdisciplinary Reviews RNA</i> , 2023, 14, .	3.2	5
11130	Terpenoids and their gene regulatory networks in <i>Opisthopappus taihangensis</i> "Taihang Mingzhu" as detected by transcriptome and metabolome analyses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11131	Comparative transcriptomics of <i>Pinus massoniana</i> organs provides insights on terpene biosynthesis regulation. <i>Physiologia Plantarum</i> , 0, , .	2.6	2
11132	Transcriptomic and proteomic analyses provide insights into the adaptive responses to the combined impact of salinity and alkalinity in <i>Gymnocypris przewalskii</i> . <i>Bioresources and Bioprocessing</i> , 2022, 9, .	2.0	3
11133	On taming the effect of transcript level intra-condition count variation during differential expression analysis: A story of dogs, foxes and wolves. <i>PLoS ONE</i> , 2022, 17, e0274591.	1.1	1
11134	A multifaceted comparison between the fruit-abscission and fruit-retention cultivars in ornamental crabapple. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
11135	The genetic architecture of phenotypic diversity in the Betta fish ( <i>Betta splendens</i> ). <i>Science Advances</i> , 2022, 8, .	4.7	10
11136	Genome Resequencing and Transcriptome Analysis Reveal the Genetic Diversity of <i>Wolfiporia cocos</i> Germplasm and Genes Related to High Yield. <i>Current Microbiology</i> , 2022, 79, .	1.0	1
11137	Co-overexpression of <i>AtSAT1</i> and <i>EcPAPR</i> improves seed nutritional value in maize. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
11138	Circulating Non-Coding RNAs as Potential Diagnostic Biomarkers in Hepatocellular Carcinoma. <i>Journal of Hepatocellular Carcinoma</i> , 0, Volume 9, 1029-1040.	1.8	10
11142	Comparative physiological analyses and the genetic basis reveal heat stress responses mechanism among different <i>Betula luminifera</i> populations. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11143	Pregestational diabetes alters cardiac structure and function of neonatal rats through developmental plasticity. <i>Frontiers in Cardiovascular Medicine</i> , 0, 9, .	1.1	6
11144	Identification of polyketide synthase genes required for aspinolide biosynthesis in <i>Trichoderma arundinaceum</i> . <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 7153-7171.	1.7	4
11145	Genome-wide association, RNA-seq and iTRAQ analyses identify candidate genes controlling radicle length of wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11146	Using transcriptomic and metabolomic data to investigate the molecular mechanisms that determine protein and oil contents during seed development in soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
11147	Comparative transcriptomics analyses of chemosensory genes of antenna in male red swamp crayfish <i>Procambarus clarkii</i> . <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	3
11148	Biochemical indices, gene expression, and SNPs associated with salinity adaptation in juvenile chum salmon ( <i>Oncorhynchus keta</i> ) as determined by comparative transcriptome analysis. <i>PeerJ</i> , 0, 10, e13585.	0.9	2

#	ARTICLE	IF	CITATIONS
11149	Analyzing RNA posttranscriptional modifications to decipher the epitranscriptomic code. <i>Mass Spectrometry Reviews</i> , 2024, 43, 5-38.	2.8	4
11150	Temporal dysregulation of genes in lamb testis cell during sheeppox virus infection. <i>Letters in Applied Microbiology</i> , 0, , .	1.0	0
11151	Identifying a 6-Gene Prognostic Signature for Lung Adenocarcinoma Based on Copy Number Variation and Gene Expression Data. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-15.	1.9	6
11152	A Pair of Prognostic Biomarkers in Triple-Negative Breast Cancer: KLK10 and KLK11 mRNA Expression. <i>Life</i> , 2022, 12, 1517.	1.1	4
11153	Transcriptome sequencing and DEG analysis in different developmental stages of floral buds induced by potassium chlorate in <i>Dimocarpus longan</i> . <i>Plant Biotechnology</i> , 2022, 39, 259-272.	0.5	0
11154	Effects of Pgam1-mediated glycolysis pathway in Sertoli cells on Spermatogonial stem cells based on transcriptomics and energy metabolomics. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	2
11155	Anlysis and Identification of Hormone Changes and Related Regulatory Genes of <i>Ziziphus jujuba</i> Mill. at the Peak of Abortion. <i>Russian Journal of Plant Physiology</i> , 2022, 69, .	0.5	0
11156	Comparative Transcriptomic Analysis of mRNAs, miRNAs and lncRNAs in the Longissimus dorsi Muscles between Fat-Type and Lean-Type Pigs. <i>Biomolecules</i> , 2022, 12, 1294.	1.8	4
11157	Rapid and sensitive single-cell RNA sequencing with SHERRY2. <i>BMC Biology</i> , 2022, 20, .	1.7	4
11160	Coordinated metabolic transitions and gene expression by NAD <sup>+</sup> during adipogenesis. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	15
11161	Combined transcriptome and metabolite profiling analyses provide insights into the chronic toxicity of carbaryl and acetamidrid to <i>Apis mellifera</i> larvae. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
11162	Transcriptomic analysis provides insight into defensive strategies in response to continuous cropping in strawberry ( <i>Fragaria Å— ananassa</i> Duch.) plants. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
11163	Designation of optimal reference strains representing the infant gut bifidobacterial species through a comprehensive multi-omics approach. <i>Environmental Microbiology</i> , 2022, 24, 5825-5839.	1.8	7
11164	A comprehensive study on ultrasonic deactivation of opportunistic pathogen <i>Saccharomyces cerevisiae</i> in food processing: From transcriptome to phenotype. <i>LWT - Food Science and Technology</i> , 2022, 170, 114069.	2.5	3
11165	Effects of lactic acid bacteria-fermented formula milk supplementation on ileal microbiota, transcriptomic profile, and mucosal immunity in weaned piglets. <i>Journal of Animal Science and Biotechnology</i> , 2022, 13, .	2.1	1
11166	MdMYB52 regulates lignin biosynthesis upon the suberization process in apple. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11167	Astragalus polysaccharides protect against inactivated <i>Vibrio alginolyticus</i> -induced inflammatory injury in macrophages of large yellow croaker. <i>Fish and Shellfish Immunology</i> , 2022, 131, 95-104.	1.6	4
11168	Mixture distribution approach for identifying differentially expressed genes in microarray data of <i>Arabidopsis thaliana</i> . , 2020, 90, 1975-1979.		0

#	ARTICLE	IF	CITATIONS
11169	MiRNAâ€™Gene Activity Interaction Networks (miGAIN): Integrated Joint Models of miRNAâ€™Gene Targeting and Disturbance in Signaling Pathways. ICSA Book Series in Statistics, 2022, , 3-21.	0.0	1
11170	Molecular Phytopathometry. , 2022, , 167-201.		0
11171	Non-coding antisense transcripts: fine regulation of gene expression in cancer. Computational and Structural Biotechnology Journal, 2022, 20, 5652-5660.	1.9	5
11172	RNA Sequencing Reveals the Potential Adaptation Mechanism to Different Hosts of <i>Grapholita molesta</i> . Insects, 2022, 13, 893.	1.0	1
11173	Transcriptomic responses of <i>Saccharum spontaneum</i> roots in response to polyethylene glycol â€™ 6000 stimulated drought stress. Frontiers in Plant Science, 0, 13, .	1.7	0
11175	Attenuation by Time-Restricted Feeding of High-Fat and High-Fructose Diet-Induced NASH in Mice Is Related to Per2 and Ferroptosis. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-20.	1.9	8
11177	Enhanced Hemolytic Activity of Mesophilic <i>Aeromonas salmonicida</i> SRW-OG1 Is Brought about by Elevated Temperatures. Microorganisms, 2022, 10, 2033.	1.6	7
11178	Functional and metabolic alterations of gut microbiota in children with new-onset type 1 diabetes. Nature Communications, 2022, 13, .	5.8	28
11179	Whole genome and transcriptome reveal flavone accumulation in <i>Scutellaria baicalensis</i> roots. Frontiers in Plant Science, 0, 13, .	1.7	4
11180	Differences of macrophages in the tumor microenvironment as an underlying key factor in glioma patients. Frontiers in Immunology, 0, 13, .	2.2	5
11181	Cytochrome P450 BsCYP99A44 and BsCYP704A177 Confer Metabolic Resistance to ALS Herbicides in <i>Beckmannia syzigachne</i> . International Journal of Molecular Sciences, 2022, 23, 12175.	1.8	9
11182	Identification of <i>Schistosoma mansoni</i> miracidia attractant candidates in infected <i>Biomphalaria glabrata</i> using behaviour-guided comparative proteomics. Frontiers in Immunology, 0, 13, .	2.2	2
11183	Regulatory network of ginsenoside biosynthesis under Ro stress in the hairy roots of <i>Panax ginseng</i> revealed by RNA sequencing. Frontiers in Bioengineering and Biotechnology, 0, 10, .	2.0	4
11184	Genome-wide association studies provide genetic insights into natural variation of seed-size-related traits in mungbean. Frontiers in Plant Science, 0, 13, .	1.7	7
11185	Transcriptome analysis reveals different response of resistant and susceptible rice varieties to rice stripe virus infection. Journal of Integrative Agriculture, 2023, 22, 1750-1762.	1.7	4
11187	Identification and characterization of select oxysterols as ligands for GPR17. British Journal of Pharmacology, 0, , .	2.7	3
11188	Transcriptomic analysis of succulent stem development of Chinese kale ( <i>Brassica oleracea</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	1.7	2
11189	Lrpap1 deficiency leads to myopia through TGF-Î²-induced apoptosis in zebrafish. Cell Communication and Signaling, 2022, 20, .	2.7	4



#	ARTICLE	IF	CITATIONS
11190	Jatrorrhizine alleviates ulcerative colitis via regulating gut microbiota and NOS2 expression. <i>Gut Pathogens</i> , 2022, 14, .	1.6	4
11191	Interleukin-33-activated neuropeptide CGRP-producing memory Th2 cells cooperate with somatosensory neurons to induce conjunctival itch. <i>Immunity</i> , 2022, 55, 2352-2368.e7.	6.6	11
11192	Transcriptome analysis of Harumi tangor fruits: Insights into interstock-mediated fruit quality. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
11193	Differentially expressed genes related to plant height and yield in two alfalfa cultivars based on RNA-seq. <i>PeerJ</i> , 0, 10, e14096.	0.9	2
11194	Fasulyede Tuz ve Kuraklık Stresi Altında PIF Gen Ailesinin Genom Açapında Analizi ve Karakterizasyonu. <i>Türkçe Tarımsal Araştırmalar Dergisi</i> , 0, , .	0.5	0
11195	Integrated analysis of miRNA and mRNA expression profiles in testes of Landrace and Hezuo boars. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	5
11196	Transcriptome Analysis Reveals Putative Induction of Floral Initiation by Old Leaves in Tea-Oil Tree ( <i>Camellia oleifera</i> "changlin53"). <i>International Journal of Molecular Sciences</i> , 2022, 23, 13021.	1.8	2
11197	A Transcriptomic Analysis of Tobacco Leaf with the Functional Loss of the Plastid rpoB Operon Caused by TALEN-Mediated Double-Strand Breakage. <i>Plants</i> , 2022, 11, 2860.	1.6	5
11199	Transcriptome Analysis of Protein Kinase MoCK2, which Affects Acetyl-CoA Metabolism and Import of CK2-Interacting Mitochondrial Proteins into Mitochondria in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Microbiology Spectrum</i> , 0, , .	1.2	0
11200	Genome-centric insight into metabolically active microbial population in shallow-sea hydrothermal vents. <i>Microbiome</i> , 2022, 10, .	4.9	2
11201	Effects of Different Rearing Systems on Lueyang Black-Bone Chickens: Meat Quality, Amino Acid Composition, and Breast Muscle Transcriptome. <i>Genes</i> , 2022, 13, 1898.	1.0	5
11202	Trained Immunity Provides Long-Term Protection against Bacterial Infections in Channel Catfish. <i>Pathogens</i> , 2022, 11, 1140.	1.2	2
11203	Multi-Organ Transcriptome Response of Lumpfish ( <i>Cyclopterus lumpus</i> ) to <i>Aeromonas salmonicida</i> Subspecies <i>salmonicida</i> Systemic Infection. <i>Microorganisms</i> , 2022, 10, 2113.	1.6	6
11204	AE-TPGG: a novel autoencoder-based approach for single-cell RNA-seq data imputation and dimensionality reduction. <i>Frontiers of Computer Science</i> , 2023, 17, .	1.6	5
11206	Navigation and Use of Custom Tracks within the Axolotl Genome Browser. <i>Methods in Molecular Biology</i> , 2023, , 273-289.	0.4	0
11207	Comparative transcriptome and proteome analyses of the longissimus dorsi muscle for explaining the difference between donkey meat and other meats. <i>Animal Biotechnology</i> , 2023, 34, 3085-3098.	0.7	1
11208	Role of EmaSR in Ethanol Metabolism by <i>Acinetobacter baumannii</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 12606.	1.8	1
11209	Genome-Wide Analysis and Characterization of SABATH Gene Family in <i>Phaseolus vulgaris</i> Genotypes Subject to Melatonin under Drought and Salinity Stresses. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 242-259.	1.0	5

#	ARTICLE	IF	CITATIONS
11210	Effect of Heat Starvation Stress on Physiological Immunity and Metabolism of Mizuhopecten yessoensis. <i>Sustainability</i> , 2022, 14, 13217.	1.6	1
11211	Emergence of Novel RNA-Editing Sites by Changes in the Binding Affinity of a Conserved PPR Protein. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	8
11212	Recent Advances on Penalized Regression Models for Biological Data. <i>Mathematics</i> , 2022, 10, 3695.	1.1	4
11213	Combined analysis of transcriptome and metabolome reveals the molecular mechanism and candidate genes of Haloxylon drought tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11214	Nitrate and sodium nitroprusside alter the development of Asian black-spined toadsâ€™ embryos by inducing nitric oxide production. <i>Environmental Science and Pollution Research</i> , 2023, 30, 23060-23069.	2.7	1
11215	Transcriptomic analysis of intermuscular bone development in barbel steed ( <i>Hemibarbus labeo</i> ). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 44, 101030.	0.4	0
11216	Molecular Responses and Degradation Mechanisms of the Herbicide Diuron in Rice Crops. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 14352-14366.	2.4	3
11217	Identification of long non-coding RNA using single nucleotide epimutation analysis: a novel gene discovery approach. <i>Cancer Cell International</i> , 2022, 22, .	1.8	2
11218	Callus induction and transcriptomic analysis of in vitro embryos at different developmental stages of peony. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11219	Gene drive by <i>Fusarium SKC1</i> is dependent on its competing allele. <i>Fungal Genetics and Biology</i> , 2022, 163, 103749.	0.9	1
11220	Global Transcriptome Analyses of Cellular and Viral mRNAs during HAdV-C5 Infection Highlight New Aspects of Viral mRNA Biogenesis and Cytoplasmic Viral mRNA Accumulations. <i>Viruses</i> , 2022, 14, 2428.	1.5	3
11221	Nuclear stabilization of p53 requires a functional nucleolar surveillance pathway. <i>Cell Reports</i> , 2022, 41, 111571.	2.9	17
11222	A genome-wide integrated analysis of lncRNA-mRNA in melanocytes from white and brown skin hair boer goats ( <i>Capra aegagrus hircus</i> ). <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
11223	The allelopathic effect of para-hydroxybenzoic acid on the gene expression of photosynthesis and respiration in <i>Solanum lycopersicum</i> . <i>Current Plant Biology</i> , 2022, 32, 100261.	2.3	3
11224	RNA-seq and LC-MS/MS analysis of antiviral effects mediated by cold stress and stress hormone corticosterone in chicken DF-1 cells. <i>Veterinary Microbiology</i> , 2022, 275, 109580.	0.8	1
11225	Toxicity and underlying mechanism of the toxic dinoflagellate <i>Gambierdiscus caribaeus</i> to the fish <i>Oryzias melastigma</i> . <i>Ecotoxicology and Environmental Safety</i> , 2022, 247, 114223.	2.9	5
11226	Short-term exposure to norethisterone affected swimming behavior and antioxidant enzyme activity of medaka larvae, and led to masculinization in the adult population. <i>Chemosphere</i> , 2023, 310, 136844.	4.2	5
11227	Time course gene expression experiments. , 2023, , 85-110.		0

#	ARTICLE	IF	CITATIONS
11228	Transcriptomics and genetic engineering. , 2023, , 43-65.		0
11229	Transcriptomic analysis of genes: expression and regulation. , 2023, , 1-41.		1
11230	Multi-scale analysis of nickel ion tolerance mechanism for thermophilic <i>Sulfobacillus</i> thermosulfidooxidans in bioleaching. <i>Journal of Hazardous Materials</i> , 2023, 443, 130245.	6.5	6
11231	Transcriptome responses to salt stress in roots and leaves of <i>Lilium pumilum</i> . <i>Scientia Horticulturae</i> , 2023, 309, 111622.	1.7	5
11232	Transcriptome profiling revealed salt stress-responsive genes in <i>Lilium pumilum</i> bulbs. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
11235	MINI BODY1, encoding a MATE/DTX family transporter, affects plant architecture in mungbean ( <i>Vigna</i> ) Tj ETQq1 1 0.784314 ggBT /Over	1.7	1
11236	Transcriptome analysis of gills reveals novel insights into the molecular response of stinging catfish ( <i>Heteropneustes fossilis</i> ) to environmental hypertonicity. <i>Gene</i> , 2023, 851, 147044.	1.0	2
11237	The spirotetramat inhibits growth and reproduction of silkworm by interfering with the fatty acid metabolism. <i>Pesticide Biochemistry and Physiology</i> , 2022, 188, 105282.	1.6	4
11238	Whole-genome assembly and annotation for the little yellow croaker ( <i>Larimichthys polyactis</i> ) provide insights into the evolution of hermaphroditism and gonochorism. <i>Molecular Ecology Resources</i> , 2023, 23, 632-658.	2.2	4
11239	Comprehensive understanding of regulatory mechanisms, physiological models and key enzymes in microalgal cells based on various concentrations of CO <sub>2</sub> . <i>Chemical Engineering Journal</i> , 2023, 454, 140233.	6.6	8
11240	High-Throughput Prediction and Design of Novel Conopeptides for Biomedical Research and Development. <i>Biodesign Research</i> , 2022, 2022, .	0.8	0
11242	Sequencing Illumina libraries at high accuracy on the ONT MinION using R2C2. <i>Genome Research</i> , 2022, 32, 2092-2106.	2.4	6
11243	Transcriptome analysis of gonads and brain of giant freshwater prawn ( <i>Macrobrachium rosenbergii</i> ): screening and validation of genes related to germ cell development. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	1
11244	The Mechanisms of Fur Development and Color Formation in American Mink Revealed Using Comparative Transcriptomics. <i>Animals</i> , 2022, 12, 3088.	1.0	1
11245	Comparative phylogenomic analyses and co-expression gene network reveal insights in flowering time and aborted meiosis in woody bamboo, <i>Bambusa oldhamii</i> "Xia Zao"™ ZSX. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
11246	Transcriptome Analysis Revealed Genes Related to <sup>13</sup> Irradiation Induced Emergence Failure in Third-Instar Larvae of <i>Bactrocera dorsalis</i> . <i>Insects</i> , 2022, 13, 1017.	1.0	1
11247	Transcription Analysis of Liver and Muscle Tissues from Landrace Finishing Pigs with Different Feed Conversion Ratios. <i>Genes</i> , 2022, 13, 2067.	1.0	5
11248	Integrated next-generation sequencing and comparative transcriptomic analysis of leaves provides novel insights into the ethylene pathway of <i>Chrysanthemum morifolium</i> in response to a Chinese isolate of chrysanthemum virus B. <i>Virology Journal</i> , 2022, 19, .	1.4	6

#	ARTICLE	IF	CITATIONS
11249	Transcriptome Mining to Identify Molecular Markers for the Diagnosis of Staphylococcus epidermidis Bloodstream Infections. <i>Antibiotics</i> , 2022, 11, 1596.	1.5	1
11250	RNA-Sequencing of Heterorhabditis nematodes to identify factors involved in symbiosis with Photorhabdus bacteria. <i>BMC Genomics</i> , 2022, 23, .	1.2	1
11251	Genome-scale signatures of adaptive gene expression changes in an invasive seaweed <i>Gracilaria vermiculophylla</i> . <i>Molecular Ecology</i> , 2023, 32, 613-627.	2.0	3
11252	KRAB family is involved in network shifts in response to osmotic stress in camels. <i>Animal Cells and Systems</i> , 2022, 26, 348-357.	0.8	0
11253	<i>Pseudomonas koreensis</i> culture filtrate alleviates tomato drought stress: modulation of antioxidant systems coupled with the porphyrin and chlorophyll "photosynthesis" fructose and mannose axis. <i>Plant and Soil</i> , 0, , .	1.8	0
11254	In vivo partial reprogramming by bacteria promotes adult liver organ growth without fibrosis and tumorigenesis. <i>Cell Reports Medicine</i> , 2022, 3, 100820.	3.3	5
11255	Neuroinflammation regulates the balance between hippocampal neuron death and neurogenesis in an ex vivo model of thiamine deficiency. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	4
11256	RNA-Sequencing Reveals Upregulation and a Beneficial Role of Autophagy in Myoblast Differentiation and Fusion. <i>Cells</i> , 2022, 11, 3549.	1.8	2
11257	Transcription level differences in <i>Taxus wallichiana</i> var. <i>mairei</i> elicited by Ce3+, Ce4+ and methyl jasmonate. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
11258	The Role of the Exonic lncRNA PRKDC-210 in Transcription Regulation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13783.	1.8	1
11260	Priority changes between biofilm exopolysaccharides synthesis and rhamnolipids production are mediated by a c-di-GMP-specific phosphodiesterase NbdA in <i>Pseudomonas aeruginosa</i> . <i>IScience</i> , 2022, 25, 105531.	1.9	3
11261	Growth, photosynthetic pigment proteins responses and transcriptome analysis provide insights into survival strategies against short-term cold stress in the blue-green algae, <i>Arthrospira</i> . <i>Aquaculture Reports</i> , 2022, 27, 101403.	0.7	1
11264	Biodegradation of MC-LR and its key bioactive moiety Adda by <i>Sphingopyxis</i> sp. YF1: Comprehensive elucidation of the mechanisms and pathways. <i>Water Research</i> , 2023, 229, 119397.	5.3	14
11265	Tyrosine promotes anthocyanin biosynthesis in pansy ( <i>Viola wittrockiana</i> ) by inducing ABA synthesis. , 2022, 1, 1-12.		0
11266	Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 86-98.	1.9	8
11267	Macrophage migration inhibitory factor facilitates astrocytic production of the CCL2 chemokine following spinal cord injury. <i>Neural Regeneration Research</i> , 2023, .	1.6	1
11268	Microfluidics-based single cell analysis: from transcriptomics to spatiotemporal multi-omics. <i>TrAC - Trends in Analytical Chemistry</i> , 2023, 158, 116868.	5.8	6
11269	A transcriptional complex of FtMYB102 and FtbHLH4 coordinately regulates the accumulation of rutin in <i>Fagopyrum tataricum</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 194, 696-707.	2.8	4

#	ARTICLE	IF	CITATIONS
11270	Downregulation of odontogenic ameloblast-associated protein in the progression of periodontal disease affects cell adhesion, proliferation, and migration. <i>Archives of Oral Biology</i> , 2023, 145, 105588.	0.8	1
11271	Hepatopancreatic transcriptome profiles reveal the effects of toxic dietary concentrations of selenium on the immunity and growth of juvenile abalone <i>Haliotis discus hannai</i> . <i>Aquaculture Reports</i> , 2023, 28, 101449.	0.7	0
11272	Allantoin, a purine metabolite, confers saline-alkaline tolerance to sugar beet by triggering a self-amplifying feedback loop comprising jasmonic acid and nitric oxide. <i>Environmental and Experimental Botany</i> , 2023, 206, 105172.	2.0	7
11273	De novo transcriptome assembly of <i>Coffea liberica</i> reveals phylogeny and expression atlas of phenylalanine ammonia-lyase genes in <i>Coffea</i> species. <i>Industrial Crops and Products</i> , 2023, 192, 116029.	2.5	0
11274	Embryogenesis of a calanoid copepod analyzed by transcriptomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101054.	0.4	0
11275	Transcriptome Sequencing and Analysis of Seabuckthorn ( <i>Hippophae</i> Sp.). <i>Compendium of Plant Genomes</i> , 2022, , 231-246.	0.3	0
11276	Approaches to Marker Gene Identification from Single-Cell RNA-Sequencing Data. <i>Springer Handbooks of Computational Statistics</i> , 2022, , 71-84.	0.2	0
11277	Oct4:Sox2 binding is essential for establishing but not maintaining active and silent states of dynamically regulated genes in pluripotent cells. <i>Genes and Development</i> , 2022, 36, 1079-1095.	2.7	8
11278	Genetic dissection of the soybean dwarf mutant <i>dm</i> with integrated genomic, transcriptomic and methylomic analyses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
11279	Transcriptome Profiling to Identify Genes Involved in Non-Target-Site-Based Resistance to Clodinafop-Propargyl in Asia Minor Bluegrass ( <i>Polypogon fugax</i> ). <i>Agronomy</i> , 2022, 12, 2998.	1.3	1
11280	PurN Is Involved in Antibiotic Tolerance and Virulence in <i>Staphylococcus aureus</i> . <i>Antibiotics</i> , 2022, 11, 1702.	1.5	1
11281	Identification of Novel mRNA Isoforms Associated with Acute Heat Stress Response Using RNA Sequencing Data in Sprague Dawley Rats. <i>Biology</i> , 2022, 11, 1740.	1.3	0
11282	Scalable transcriptomics analysis with Dask: applications in data science and machine learning. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
11283	Computational approaches and challenges for identification and annotation of non-coding RNAs using RNA-Seq. <i>Functional and Integrative Genomics</i> , 2022, 22, 1105-1112.	1.4	9
11284	Cancer Segmentation by Entropic Analysis of Ordered Gene Expression Profiles. <i>Entropy</i> , 2022, 24, 1744.	1.1	0
11286	Alfin- like transcription factor VqAL4 regulates a stilbene synthase to enhance powdery mildew resistance in grapevine. <i>Molecular Plant Pathology</i> , 2023, 24, 123-141.	2.0	3
11287	Transcriptomic Analysis Provides Insights into Microplastic and Heavy Metal Challenges in the Line Seahorse ( <i>Hippocampus erectus</i> ). <i>Fishes</i> , 2022, 7, 338.	0.7	2
11288	Group-specific functional patterns of mitochondrion-related organelles shed light on their multiple transitions from mitochondria in ciliated protists. <i>Marine Life Science and Technology</i> , 2022, 4, 609-623.	1.8	11

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11289	An Intestinal Symbiotic Bacterial Strain of <i>Oscheius chongmingensis</i> Modulates Host Viability at Both Global and Post-Transcriptional Levels. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14692.	1.8	0
11290	Reproduction Evaluation and Transcription Analysis of <i>Aphis gossypii</i> under Various Photoperiods. <i>Insects</i> , 2022, 13, 1105.	1.0	2
11292	Molecular and metabolic insights into floral scent biosynthesis during flowering in <i>Dendrobium chrysotoxum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
11293	RNA Sequencing Analysis of Saliva exRNA. <i>Methods in Molecular Biology</i> , 2023, , 3-11.	0.4	0
11294	Strategy for RNA-Seq Experimental Design and Data Analysis. <i>Methods in Molecular Biology</i> , 2023, , 249-278.	0.4	2
11295	Long noncoding RNA study: Genome-wide approaches. <i>Genes and Diseases</i> , 2023, 10, 2491-2510.	1.5	2
11296	Transcriptome Analysis of Genes Involved in Fatty Acid and Lipid Biosynthesis in Developing Walnut ( <i>Juglans regia</i> L.) Seed Kernels from Qinghai Plateau. <i>Plants</i> , 2022, 11, 3207.	1.6	3
11297	Coupling continuous poly(3-hydroxybutyrate) synthesis with piperazine-contained wastewater treatment: Fermentation performance and microbial contamination deciphering. <i>International Journal of Biological Macromolecules</i> , 2023, 226, 1523-1532.	3.6	1
11298	Getting sweeter: new evidence for glucose transporters in specific cell types of the airway?. <i>American Journal of Physiology - Cell Physiology</i> , 2023, 324, C153-C166.	2.1	1
11299	Transcriptome Profiling and TCP Family Analysis of Broomcorn Millet ( <i>Panicum miliaceum</i> L.) Seedlings Under Hyperosmotic Stress. <i>Plant Molecular Biology Reporter</i> , 0, , .	1.0	0
11300	In vitro production of infectious <i>Plasmodium falciparum</i> sporozoites. <i>Nature</i> , 2022, 612, 534-539.	13.7	16
11301	Upcoming progress of transcriptomics studies on plants: An overview. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	19
11302	Comparison of Metagenomics and Metatranscriptomics Tools: A Guide to Making the Right Choice. <i>Genes</i> , 2022, 13, 2280.	1.0	9
11303	Long-term functional regeneration of radiation-damaged salivary glands through delivery of a neurogenic hydrogel. <i>Science Advances</i> , 2022, 8, .	4.7	5
11304	Metabolomic and Transcriptomic Analyses Reveal New Insights into the Role of Metabolites and Genes in Modulating Flower Colour of <i>Clematis tientaiensis</i> . <i>Horticulturae</i> , 2023, 9, 14.	1.2	5
11305	Characterization of the <i>pars tubercalis</i> and hypothalamus transcriptome in female sheep under different reproductive stages. <i>Animal Biotechnology</i> , 0, , 1-14.	0.7	0
11306	Defined Alginate Hydrogels Support Spinal Cord Organoid Derivation, Maturation, and Modeling of Spinal Cord Diseases. <i>Advanced Healthcare Materials</i> , 2023, 12, .	3.9	10
11307	Integration of transcriptomic and metabolomic profiling of encystation in <i>Cryptocaryon irritans</i> regulated by rapamycin. <i>Veterinary Parasitology</i> , 2023, 314, 109868.	0.7	0

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11309	Improving Coconut Using Modern Breeding Technologies: Challenges and Opportunities. <i>Plants</i> , 2022, 11, 3414.	1.6	9
11310	Integrative Application of Transcriptomics and Metabolomics Provides Insights into Unsynchronized Growth in Sea Cucumber ( <i>Stichopus monotuberculatus</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 15478.	1.8	3
11312	Transcriptome analysis of muskmelon ( <i>Cucumis melo</i> ) for moisture stress tolerance. , 2022, 92, .		0
11313	Tomato receptor-like cytoplasmic kinase Fir1 is involved in flagellin signaling and pre-invasion immunity. <i>Plant Physiology</i> , 0, , .	2.3	1
11314	Multi-tissue RNA-Seq Analysis and Long-read-based Genome Assembly Reveal Complex Sex-specific Gene Regulation and Molecular Evolution in the Manila Clam. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
11315	Effects of larval exposure to the insecticide flumethrin on the development of honeybee ( <i>Apis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 107	1.3	0
11316	Discovery of a LuxR-type regulator involved in isoniazid-dependent gene regulation in <i>Mycobacterium smegmatis</i> . <i>Journal of Infection and Chemotherapy</i> , 2023, 29, 322-328.	0.8	1
11317	A General Signal Pathway to Regulate Multiple Detoxification Genes Drives the Evolution of <i>Helicoverpa armigera</i> Adaptation to Xenobiotics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16126.	1.8	3
11318	<scp>PI3K</scp>/<scp>Akt</scp>/<scp>CncC</scp> signaling pathway mediates the response to <scp>EPNâ€t</scp> infection in <i>Holotrichia parallela</i> larvae. <i>Pest Management Science</i> , 2023, 79, 1660-1673.	1.7	2
11319	Therapeutic Effects of Butyrate on Pediatric Obesity. <i>JAMA Network Open</i> , 2022, 5, e2244912.	2.8	16
11320	Proteomic and Transcriptomic Analysis for Identification of Endosymbiotic Bacteria Associated with BYDV Transmission Efficiency by <i>Sitobion miscanthi</i> . <i>Plants</i> , 2022, 11, 3352.	1.6	4
11321	Analyzing Prokaryotic Transcriptomics in the Light of Genome Data with the MicroScope Platform. <i>Methods in Molecular Biology</i> , 2023, , 241-270.	0.4	0
11322	Revealing Causes for False-Positive and False-Negative Calling of Gene Essentiality in <i>Escherichia coli</i> Using Transposon Insertion Sequencing. <i>MSystems</i> , 2023, 8, .	1.7	2
11323	Metabolic analysis of the regulatory mechanism of sugars on secondary flowering in <i>Magnolia</i> . <i>BMC Molecular and Cell Biology</i> , 2022, 23, .	1.0	3
11324	Taurine metabolism is modulated in <i>Vibrio</i> -infected <i>Penaeus vannamei</i> to shape shrimp antibacterial response and survival. <i>Microbiome</i> , 2022, 10, .	4.9	7
11325	Transcriptome analyses of different edible tissues of <i>Clanis bilineata tsingtauca</i> (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 107	2.1	8
11326	Computational Integration of HSV-1 Multi-omics Data. <i>Methods in Molecular Biology</i> , 2023, , 31-48.	0.4	1
11327	A Phylogenetic Framework to Simulate Synthetic Interspecies RNA-Seq Data. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6

#	ARTICLE	IF	CITATIONS
11328	Parallel evolution of opsin visual pigments in hawkmoths by tuning of spectral sensitivities during transition from a nocturnal to a diurnal ecology. <i>Journal of Experimental Biology</i> , 2022, 225, .	0.8	7
11329	Comprehensive Transcriptome Analysis of Different Skin Colors to Evaluate Genes Related to the Production of Pigment in Celestial Goldfish. <i>Biology</i> , 2023, 12, 7.	1.3	1
11330	A Comparative Transcriptomic with UPLC-Q-Exactive MS Reveals Differences in Gene Expression and Components of Iridoid Biosynthesis in Various Parts of <i>Gentiana macrophylla</i> . <i>Genes</i> , 2022, 13, 2372.	1.0	3
11331	A Non-Gradual Development Process of Cicada Eyes at the End of the Fifth-Instar Nymphal Stage to Obtain Visual Ability. <i>Insects</i> , 2022, 13, 1170.	1.0	0
11332	Improving SWATH-MS analysis by deep learning. <i>Proteomics</i> , 2023, 23, .	1.3	3
11333	Transcriptome profiling of male and female <i>Ascaris lumbricoides</i> reproductive tissues. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	2
11334	Comparing the infection biology and gene expression differences of <i>Plasmodiophora brassicae</i> primary and secondary zoospores. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
11335	Plant Omics Databases: an Online Resource Guide. , 2022, , 253-269.		0
11336	Effects of colonization-associated gene <i>yqiC</i> on global transcriptome, cellular respiration, and oxidative stress in <i>Salmonella Typhimurium</i> . <i>Journal of Biomedical Science</i> , 2022, 29, .	2.6	5
11337	Identification and Functional Characterization of CYP4D2 Putatively Associated with Î²-Cypermethrin Detoxification in <i>Phortica okadai</i> . <i>Genes</i> , 2022, 13, 2338.	1.0	0
11338	High-throughput prediction and characterization of antimicrobial peptides from multi-omics datasets of Chinese tubular cone snail ( <i>Conus betulinus</i> ). <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	0
11340	Different perspectives on translational genomics in personalized medicine. <i>Journal of the Turkish German Gynecology Association</i> , 2022, 23, 314-321.	0.2	1
11341	Knowledge mapping of alternative splicing of cancer from 2012 to 2021: A bibliometric analysis. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	0
11342	Comparative Transcriptome Analysis of <i>Pueraria lobata</i> Provides Candidate Genes Involved in Puerarin Biosynthesis and Its Regulation. <i>Biomolecules</i> , 2023, 13, 170.	1.8	2
11343	Transcriptome analysis of critical genes related to flowering in <i>Mikania micrantha</i> at different altitudes provides insights for a potential control. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
11344	Monitoring Mechano-Regulation of Gene Expression by RNA Sequencing. <i>Methods in Molecular Biology</i> , 2023, , 291-296.	0.4	0
11345	Dissecting the Biology of <i>Rafflesia</i> Species: Current Progress and Future Directions Made Possible with High-Throughput Sequencing Data. <i>Plant and Cell Physiology</i> , 2023, 64, 368-377.	1.5	2
11346	Identification of Key Modules and Candidate Genes for Powdery Mildew Resistance of Wheat- <i>AgropyronAcristatum</i> Translocation Line WAT-2020-17-6 by WGCNA. <i>Plants</i> , 2023, 12, 335.	1.6	0



#	ARTICLE	IF	CITATIONS
11347	Combined widely targeted metabolomics and transcriptomics analysis reveals differentially accumulated metabolites and the underlying molecular bases in fleshy taproots of distinct radish genotypes. <i>Plant Physiology and Biochemistry</i> , 2023, 195, 351-361.	2.8	1
11348	Temporal dynamics of the bat wing transcriptome: Insight into gene-expression changes that enable protection against pathogen. <i>Virulence</i> , 2023, 14, .	1.8	1
11349	Spinach ( <i>Spinacia oleracea</i> L.) Breeding: From Classical to Genomics-Centric Approach. , 2023, , 117-142.		0
11350	Differentially expressed genes in head kidney of <i>Pelteobagrus fulvidraco</i> following <i>Vibrio cholerae</i> challenge. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
11352	Comprehensive Analysis of the Longissimus Dorsi Transcriptome and Metabolome Reveals the Regulatory Mechanism of Different Varieties of Meat Quality. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 1234-1245.	2.4	8
11353	A large-scale RNAi screen reveals that mitochondrial function is important for meiotic chromosome organization in oocytes. <i>Chromosoma</i> , 2023, 132, 1-18.	1.0	3
11354	Transcriptome Profiling of Developing Testes and First Wave of Spermatogenesis in the Rat. <i>Genes</i> , 2023, 14, 229.	1.0	1
11355	Transcriptomic analyses of treatment-naïve pediatric ulcerative colitis patients and exploration of underlying disease pathogenesis. <i>Journal of Translational Medicine</i> , 2023, 21, .	1.8	2
11357	Coupling the immunomodulatory properties of the HDAC6 inhibitor ACY241 with Oxaliplatin promotes robust anti-tumor response in Non-small cell lung cancer. <i>Journal of Immunology</i> , 2022, 208, 118.11-118.11.	0.4	2
11358	Responsive Transcriptome Analysis of <i>Senecio vulgaris</i> L. Under Different Drought Stresses. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
11359	Complex of Proline-Specific Peptidases in the Genome and Gut Transcriptomes of Tenebrionidae Insects and Their Role in Gliadin Hydrolysis. <i>International Journal of Molecular Sciences</i> , 2023, 24, 579.	1.8	1
11360	Transcriptomic and Epigenomic Approaches for Epilepsy. , 2022, , 19-40.		0
11361	Transcriptome analysis of the impact of diabetes as a comorbidity on tuberculosis. <i>Medicine (United Tj ETQq0 0 0 ggBT /Overlock 10 Tf</i>	0.4	1
11362	bulkAnalyseR: an accessible, interactive pipeline for analysing and sharing bulk multi-modal sequencing data. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	4
11363	Transcriptome profiling reveals the roles of pigment formation mechanisms in yellow <i>Paeonia delavayi</i> flowers. <i>Molecular Genetics and Genomics</i> , 2023, 298, 375-387.	1.0	4
11364	Genome-Wide Characterization and Analysis of R2R3-MYB Genes Related to Fruit Ripening and Stress Response in Banana ( <i>Musa acuminata</i> L. AAA Group, cv. "Cavendish™"). <i>Plants</i> , 2023, 12, 152.	1.6	1
11365	Integrated Transcriptomics and Functional Characterization Reveals that the Class Iii Peroxidase Gene <i>Taprx-2a</i> Regulates Drought Stress Tolerance in Transgenic Wheat. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
11366	Epigenetic regulation of cis-regulatory elements and transcription factors during development. , 2023, , 71-113.		1

#	ARTICLE	IF	CITATIONS
11367	De Novo Transcriptome Profiling of <i>Naegleria fowleri</i> Trophozoites and Cysts via RNA Sequencing. <i>Pathogens</i> , 2023, 12, 174.	1.2	0
11368	MITE infestation accommodated by genome editing in the germline genome of the ciliate <i>Blepharisma</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
11369	Impact of electro-activated whey on growth, acid and bile resistance of <i>Lactocaseibacillus rhamnosus</i> GG and <i>Lactobacillus acidophilus</i> ATCC 4356. <i>Heliyon</i> , 2023, 9, e13154.	1.4	4
11370	Genome-wide identification and characterization of exapted transposable elements in the large genome of sunflower ( <i>Helianthus annuus</i> L.). <i>Plant Journal</i> , 2023, 113, 734-748.	2.8	3
11371	From Classical to Modern Computational Approaches to Identify Key Genetic Regulatory Components in Plant Biology. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2526.	1.8	2
11377	Global Gene Expression in Cotton Fed Upon by <i>Aphis gossypii</i> and <i>Acyrtosiphon gossypii</i> (Hemiptera: Aphididae). <i>Journal of Entomological Science</i> , 2023, 58, 47-68.	0.2	0
11378	A novel machine learning model based on ubiquitin-related gene pairs and clinical features to predict prognosis and treatment effect in colon adenocarcinoma. <i>European Journal of Medical Research</i> , 2023, 28, .	0.9	0
11379	Beyond Transcript Concentrations: Quantifying Polyploid Expression Responses per Biomass, per Genome, and per Cell with RNA-Seq. <i>Methods in Molecular Biology</i> , 2023, , 227-250.	0.4	1
11380	Differential gene expression profiling in alveolar echinococcosis identifies potential biomarkers associated with angiogenesis. <i>Open Forum Infectious Diseases</i> , 0, , .	0.4	1
11381	Comparison of Four Classification Methods on Small-Sample-Size Synthetic RNA-seq Data. <i>Studies in Computational Intelligence</i> , 2023, , 111-121.	0.7	0
11382	I-CONVEX: Fast and Accurate de Novo Transcriptome Recovery from Long Reads. <i>Communications in Computer and Information Science</i> , 2023, , 339-363.	0.4	0
11383	Self-assembly and self-delivery of the pure nanodrug dihydroartemisinin for tumor therapy and mechanism analysis. <i>Biomaterials Science</i> , 2023, 11, 2478-2485.	2.6	3
11384	Suppression of citrus canker disease mediated by flagellin perception. <i>Molecular Plant Pathology</i> , 2023, 24, 331-345.	2.0	3
11385	Recent Advances and Future Potential of Long Non-Coding RNAs in Insects. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2605.	1.8	2
11386	Revealing the mode of action of Phenylalanine application in inducing fruit resistance to fungal pathogens. <i>Postharvest Biology and Technology</i> , 2023, 199, 112298.	2.9	4
11387	Comparative transcriptomics and co-expression networks reveal cultivar-specific molecular signatures associated with reproductive-stage cold stress in rice. <i>Plant Cell Reports</i> , 2023, 42, 707-722.	2.8	2
11388	Transcriptome-based analysis reveals the key genes of sesquiterpene glycosylation in <i>Dendrobium nobile</i> . <i>Food Science and Technology</i> , 0, 43, .	0.8	0
11389	Identification of long non-coding RNA and circular RNA associated networks in cellular stress responses. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	2

#	ARTICLE	IF	CITATIONS
11390	Time-Course Transcriptome Analysis of the Lungs of Mice Challenged with Aerosols of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 Clone Reveals Inflammatory Balance. <i>Biomolecules</i> , 2023, 13, 347.	1.8	1
11391	Quantitative analysis of high-throughput biological data. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2023, 13, .	6.2	2
11392	Interaction between Microbes and Host in Sow Vaginas in Early Pregnancy. <i>MSystems</i> , 0, , .	1.7	1
11393	Multi-level interaction between HIF and AHR transcriptional pathways in kidney carcinoma. <i>Life Science Alliance</i> , 2023, 6, e202201756.	1.3	1
11394	Establishing Heterologous Production of Microcins J25 and Y in <i>Bacillus subtilis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 5600-5613.	2.4	1
11395	MiRNA-Seq reveals key MicroRNAs involved in fat metabolism of sheep liver. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
11396	Widely targeted metabolomic, transcriptomic, and metagenomic profiling reveal microbe-plant metabolic reprogramming patterns mediated by <i>Streptomyces pactum</i> Act12 enhance the fruit quality of <i>Capsicum annuum</i> L. <i>Food Research International</i> , 2023, 166, 112587.	2.9	6
11397	Manganese and copper additions differently reduced cadmium uptake and accumulation in dwarf Polish wheat ( <i>Triticum polonicum</i> L.). <i>Journal of Hazardous Materials</i> , 2023, 448, 130998.	6.5	2
11398	Effects of heat and hyposalinity on the gene expression in <i>Acropora pruinosa</i> larvae. <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	2
11400	Probe-based bacterial single-cell RNA sequencing predicts toxin regulation. <i>Nature Microbiology</i> , 2023, 8, 934-945.	5.9	14
11401	N6-methyladenosine mRNA methylation is important for the light response in soybean. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
11402	BAG6-A from <i>Fragaria viridis</i> pollen modulates gametophyte development in diploid strawberry. <i>Plant Science</i> , 2023, 330, 111667.	1.7	0
11403	Time-course transcriptomics analysis reveals key responses of populus to salt stress. <i>Industrial Crops and Products</i> , 2023, 194, 116278.	2.5	7
11404	Two different anti-algal control mechanisms in <i>Microcystis aeruginosa</i> induced by robinin or tannin rich plants. <i>Chemosphere</i> , 2023, 323, 138202.	4.2	4
11405	CRISPR-Cas phage defense systems and prophages in <i>Candidatus Accumulibacter</i> . <i>Water Research</i> , 2023, 235, 119906.	5.3	6
11406	Pre-exposure to titanium or iron oxide nanoparticles suppresses the subsequent cellular uptake of gold nanoparticles. <i>Science of the Total Environment</i> , 2023, 875, 162491.	3.9	2
11407	Regulation mechanism and functional verification of key functional genes regulating muscle development in black Tibetan sheep. <i>Gene</i> , 2023, 868, 147375.	1.0	0
11408	Integrated miRNA-mRNA analysis reveals the molecular mechanism in mandarin fish ( <i>Siniperca chuatsi</i> ) in response to fresh baits and artificial diets feeding. <i>Aquaculture Reports</i> , 2023, 30, 101554.	0.7	2

#	ARTICLE	IF	CITATIONS
11409	Genotypic and phenotypic characterization of a Salmonella Typhimurium strain resistant to pulsed electric fields. <i>Food Microbiology</i> , 2023, 113, 104285.	2.1	0
11410	Microglia-containing cerebral organoids derived from induced pluripotent stem cells for the study of neurological diseases. <i>IScience</i> , 2023, 26, 106267.	1.9	13
11411	Differential impact of yeast cell wall products in recovery of porcine intestinal epithelial cell barrier function following Lipopolysaccharide challenge. <i>Porcine Health Management</i> , 2023, 9, .	0.9	0
11412	Integrated microRNA-mRNA analysis reveals a possible molecular mechanism of enteritis susceptibility in <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2023, 136, 108699.	1.6	1
11413	Transcriptome analysis identifies differentially expressed genes involved in lignin biosynthesis in barley. <i>International Journal of Biological Macromolecules</i> , 2023, 236, 123940.	3.6	1
11414	Identification and characterization of ABC proteins in an important rice insect pest, <i>Cnaphalocrocis medinalis</i> unveil their response to Cry1C toxin. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 123949.	3.6	1
11415	Adverse effects of polystyrene nanoplastics on sea cucumber <i>Apostichopus japonicus</i> and their association with gut microbiota dysbiosis. <i>Chemosphere</i> , 2023, 330, 138568.	4.2	8
11418	Transcriptome-Based Identification and Characterization of Genes Associated with Resistance to Beta-Cypermethrin in <i>Rhopalosiphum padi</i> (Hemiptera: Aphididae). <i>Agriculture (Switzerland)</i> , 2023, 13, 235.	1.4	2
11419	Class Discovery, Comparison, and Prediction Methods for RNA-Seq Data. , 2022, , 2060-2084.		0
11420	Pharmacological inhibition of endoplasmic reticulum stress mitigates testicular pathology in a mouse model of simulated microgravity. <i>Acta Astronautica</i> , 2023, 204, 466-476.	1.7	1
11421	Intra-Exon Motif Correlations as a Proxy Measure for Mean Per-Tile Sequence Quality Data in RNA-Seq. <i>Journal of Computational Biology</i> , 2023, 30, 131-148.	0.8	0
11422	HGCA2.0: An RNA-Seq Based Webtool for Gene Coexpression Analysis in <i>Homo sapiens</i> . <i>Cells</i> , 2023, 12, 388.	1.8	1
11423	LysM receptor-like kinases involved in immunity perceive lipo-chitoooligosaccharides in mycotrophic plants. <i>Plant Physiology</i> , 2023, 192, 1435-1448.	2.3	4
11424	Labyrinthin Expression Is Associated with Poor Prognosis in Patients with Non-Small-Cell Lung Cancer. <i>Cancers</i> , 2023, 15, 924.	1.7	1
11425	Differential gene expression analysis and physiological response characteristics of passion fruit ( <i>Passiflora edulis</i> ) buds under high-temperature stress. <i>PeerJ</i> , 0, 11, e14839.	0.9	2
11426	Proteomic and Transcriptomic Responses of the Desiccation-Tolerant Moss <i>Racomitrium canescens</i> in the Rapid Rehydration Processes. <i>Genes</i> , 2023, 14, 390.	1.0	0
11427	The MAX2- <i>KAI2</i> module promotes salicylic acid-mediated immune responses in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1566-1584.	4.1	1
11428	Single-cell RNA sequencing to identify cellular heterogeneity and targets in cardiovascular diseases: from bench to bedside. <i>Basic Research in Cardiology</i> , 2023, 118, .	2.5	8

#	ARTICLE	IF	CITATIONS
11429	Identification of a new QTL underlying seminal root number in a maize-teosinte population. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
11432	Deletion of histone demethylase Lsd1 (Kdm1a) during retinal development leads to defects in retinal function and structure. <i>Frontiers in Cellular Neuroscience</i> , 0, 17, .	1.8	0
11433	Toxicity of herbicide glyphosate to planarian <i>Dugesia japonica</i> and its potential molecular mechanisms. <i>Aquatic Toxicology</i> , 2023, 256, 106425.	1.9	3
11434	Single-cell transcriptomics is revolutionizing the improvement of plant biotechnology research: recent advances and future opportunities. <i>Critical Reviews in Biotechnology</i> , 2024, 44, 202-217.	5.1	1
11435	Revealing the relationship between nitrogen use efficiency-related <scp>QTLs</scp> and carbon and nitrogen metabolism regulation in poplar. <i>GCB Bioenergy</i> , 2023, 15, 575-592.	2.5	0
11436	Suppression of innate and acquired immunity in severe hand foot and mouth disease caused by EV71 infections in children. <i>Clinical Immunology</i> , 2023, 248, 109260.	1.4	0
11437	Comparative transcriptomic analysis and functional characterization reveals that the class III peroxidase gene TaPRX-2A regulates drought stress tolerance in transgenic wheat. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
11438	Transcriptome analysis of putative key signaling pathways and genes in the nidamental gland tissue associated with reproductive regulation of golden cuttlefish ( <i>Sepia esculenta</i> Hoyle). <i>Aquaculture Reports</i> , 2023, 29, 101494.	0.7	0
11440	Comparative transcriptome analysis of non-germinated and germinated spores of <i>Enterocytozoon hepatopenaei</i> (EHP) in vitro. <i>Journal of Invertebrate Pathology</i> , 2023, 197, 107900.	1.5	3
11442	Distinct H3K27me3 and H3K27ac Modifications in Neural Tube Defects Induced by Benzo[a]pyrene. <i>Brain Sciences</i> , 2023, 13, 334.	1.1	1
11444	Changes in annual transcriptome dynamics of a clone of Japanese cedar ( <i>Cryptomeria japonica</i> D. Don) planted under different climate conditions. <i>PLoS ONE</i> , 2023, 18, e0277797.	1.1	1
11445	Study of <i>Camellia sinensis</i> diploid and triploid leaf development mechanism based on transcriptome and leaf characteristics. <i>PLoS ONE</i> , 2023, 18, e0275652.	1.1	3
11446	Interleukin-27-dependent transcriptome signatures during neonatal sepsis. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
11447	Multi-Omics Analysis Reveals the Regulatory and Metabolic Mechanisms Underlying Low-Nitrogen Tolerance at the Flowering Stage in Rice. <i>Agronomy</i> , 2023, 13, 578.	1.3	0
11448	The transcriptomic and epigenetic alterations in type 2 diabetes mellitus patients of Chinese Tibetan and Han populations. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	2
11449	The therapeutic effect of Zhenbao pills on behavioral changes in zebrafish caused by aluminum chloride. <i>Biomedicine and Pharmacotherapy</i> , 2023, 160, 114399.	2.5	0
11450	Transcriptomic analysis of entomopathogenic fungus <i>Beauveria bassiana</i> infected by a hypervirulent polymycovirus BbPmV-4. <i>Fungal Biology</i> , 2023, 127, 958-967.	1.1	2
11451	Comparative Transcriptome Profiling Reveals Key MicroRNAs and Regulatory Mechanisms for Aluminum Tolerance in Olive. <i>Plants</i> , 2023, 12, 978.	1.6	2

#	ARTICLE	IF	CITATIONS
11454	Unveiling the Effect of NCgl0580 Gene Deletion on 5-Aminolevulinic Acid Biosynthesis in <i>Corynebacterium glutamicum</i> . <i>Fermentation</i> , 2023, 9, 213.	1.4	2
11455	IAG Regulates the Expression of Cytoskeletal Protein-Encoding Genes in Shrimp Testis. <i>Genes</i> , 2023, 14, 564.	1.0	2
11456	Transcriptomics explores the potential of flavonoid in non-medicinal parts of <i>Saposhnikovia divaricata</i> (Turcz.) Schischk. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
11457	Revealing the History and Mystery of RNA-Seq. <i>Current Issues in Molecular Biology</i> , 2023, 45, 1860-1874.	1.0	5
11458	Role of alternative splicing in health and diseases. , 2023, , 19-36.		1
11459	Effect of corn straw or corncobs in total mixed ration during peri-puberty on testis development in Hu lambs. <i>Theriogenology</i> , 2023, 201, 106-115.	0.9	0
11460	Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq. <i>Methods in Molecular Biology</i> , 2023, , 187-230.	0.4	0
11461	Full-length transcriptome sequencing reveals extreme incomplete annotation of the goat genome. <i>Animal Genetics</i> , 2023, 54, 421-424.	0.6	2
11462	<sc>RNA-seq</sc> analysis of soybean (<i>Glycine max</i>) responding to <i>Phytophthora sojae</i>. <i>Journal of Phytopathology</i> , 2023, 171, 180-188.	0.5	0
11463	sRNA21, a novel small RNA, protects <sc><i>Mycobacterium abscessus</i></sc> against oxidative stress. <i>Journal of Gene Medicine</i> , 2023, 25, .	1.4	1
11464	Genome-Wide Identification and Characterisation of Abiotic Stress Responsive mTERF Gene Family in <i>Amaranthus hypochondriacus</i> . <i>Phyton</i> , 2023, 92, 1649-1664.	0.4	1
11465	Transcriptomics Insights into Phosphorus Stress Response of <i>Myriophyllum aquaticum</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4874.	1.8	1
11467	Transcriptome profile in <i>Drosophila</i> Kc and S2 embryonic cell lines. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
11468	Different reoxygenation rates induce different metabolic, apoptotic and immune responses in Golden Pompano ( <i>Trachinotus blochii</i> ) after hypoxic stress. <i>Fish and Shellfish Immunology</i> , 2023, 135, 108640.	1.6	1
11469	Investigating the genetic basis of vertebrate dispersal combining <sc>RNA-seq</sc>, <sc>RAD-seq</sc> and quantitative genetics. <i>Molecular Ecology</i> , 2023, 32, 3060-3075.	2.0	3
11471	Random and Natural Non-Coding RNA Have Similar Structural Motif Patterns but Differ in Bulge, Loop, and Bond Counts. <i>Life</i> , 2023, 13, 708.	1.1	3
11472	The Role of Long Noncoding RNAs in Glioblastoma: What the Neurosurgeon Should Know. <i>Neurosurgery</i> , 2023, Publish Ahead of Print, .	0.6	0
11473	Comprehensive analysis of metabolome and transcriptome reveals the mechanism of color formation in different leave of <i>Loropetalum Chinense</i> var. <i>Rubrum</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	7

#	ARTICLE	IF	CITATIONS
11474	Overexpression of GmWRKY172 enhances cadmium tolerance in plants and reduces cadmium accumulation in soybean seeds. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	11
11475	RNAget: an API to securely retrieve RNA quantifications. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
11476	LTA4H extensively associates with mRNAs and lncRNAs indicative of its novel regulatory targets. <i>PeerJ</i> , 0, 11, e14875.	0.9	1
11477	Transcriptome Analysis During Tetrasporogenesis of <i>Gracilariopsis lemaneiformis</i> and Preliminary Study of the Expressions of Its Meiotic Genes. <i>Journal of Ocean University of China</i> , 2023, 22, 541-554.	0.6	0
11478	Hair Follicle Transcriptome Analysis Reveals Differentially Expressed Genes That Regulate Wool Fiber Diameter in Angora Rabbits. <i>Biology</i> , 2023, 12, 445.	1.3	2
11480	Low dissolved oxygen supply functions as a global regulator of the growth and metabolism of <i>Aurantiochytrium</i> sp. PKU#Mn16 in the early stages of docosahexaenoic acid fermentation. <i>Microbial Cell Factories</i> , 2023, 22, .	1.9	1
11481	Atorvastatin-pretreated mesenchymal stem cell-derived extracellular vesicles promote cardiac repair after myocardial infarction via shifting macrophage polarization by targeting microRNA-139-3p/Stat1 pathway. <i>BMC Medicine</i> , 2023, 21, .	2.3	12
11482	Integrative transcriptome and proteome analysis reveals maize responses to <i>Fusarium verticillioides</i> infection inside the stalks. <i>Molecular Plant Pathology</i> , 2023, 24, 693-710.	2.0	7
11483	SCL14 Inhibits the Functions of the NACO43-MYB61 Signaling Cascade to Reduce the Lignin Content in Autotetraploid <i>Populus hopeiensis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 5809.	1.8	6
11484	Transcriptional Regulation of Female and Male Flower Bud Initiation and Development in Pecan ( <i>Carya</i> ) Tj ETQq1 1 0.784314 µgBT /Over	1.6	0
11485	Characterization of MdMYB68, a suberin master regulator in russeted apples. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
11486	Transcriptomic and Metabolomic Profiles Provide Insights into the Red-Stipe Symptom of Morel Fruiting Bodies. <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 373.	1.5	5
11488	Opportunities for High-plex Spatial Transcriptomics in Solid Organ Transplantation. <i>Transplantation</i> , 0, Publish Ahead of Print, .	0.5	1
11489	DNA hypomethylation mediates immune response in pan-cancer. <i>Epigenetics</i> , 2023, 18, .	1.3	3
11490	Small RNAs >26 nt in length associate with AGO1 and are upregulated by nutrient deprivation in the alga <i>Chlamydomonas</i> . <i>Plant Cell</i> , 2023, 35, 1868-1887.	3.1	4
11491	Genomic Analysis of Foxp3 Function in Regulatory T Cells. <i>Journal of Immunology</i> , 2023, 210, 880-887.	0.4	3
11492	Identification and analysis of lignin biosynthesis genes related to fruit ripening and stress response in banana ( <i>Musa acuminata</i> L. AAA group, cv. Cavendish). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
11493	Effect of priming on germination traits and antioxidant enzymes of pumpkin ( <i>Cucurbita pepo</i> L.) seeds with different vigor under drought stress. <i>Tarim Bilimleri Dergisi</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
11494	DEVEA: an interactive shiny application for Differential Expression analysis, data Visualization and Enrichment Analysis of transcriptomics data. <i>F1000Research</i> , 0, 11, 711.	0.8	0
11495	Investigating the Function of Predicted Proteins from RNA-Seq Data in Holstein and Cholistani Cattle Breeds. <i>Research on Animal Production</i> , 2020, 11, 121-135.	0.2	1
11496	Wds-Mediated H3K4me3 Modification Regulates Lipid Synthesis and Transport in <i>Drosophila</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 6125.	1.8	0
11497	Differential Genes Expression of Blood Tissue Related to Pre-Calving Ketosis in Holstein cow using Transcriptomics Data. <i>Research on Animal Production</i> , 2022, 13, 147-153.	0.2	0
11498	Pleiotropic Modulation of Chitooligosaccharides on Inflammatory Signaling in LPS-Induced Macrophages. <i>Polymers</i> , 2023, 15, 1613.	2.0	0
11500	ElasticBLAST: accelerating sequence search via cloud computing. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	14
11501	Mock community as an in situ positive control for amplicon sequencing of microbiotas from the same ecosystem. <i>Scientific Reports</i> , 2023, 13, .	1.6	2
11502	Chromosome-scale <i>de novo</i> genome assembly and annotation of three representative <i>Casuarina</i> species: <i>C. equisetifolia</i> , <i>C. glauca</i> , and <i>C. cunninghamiana</i> . <i>Plant Journal</i> , 2023, 114, 1490-1505.	2.8	2
11503	RNA interference in cytochrome P450 monooxygenase (CYP) gene results in reduced insecticide resistance in <i>Megalurothrips usitatus</i> Bagnall. <i>Frontiers in Physiology</i> , 0, 14, .	1.3	0
11504	Transcriptome Analysis of Auxin Drives Cone Size Regulation in <i>Fokienia hodginsii</i> . <i>Phyton</i> , 2023, 92, 1713-1723.	0.4	0
11505	MEX3B inhibits collagen production in eosinophilic nasal polyps by downregulating epithelial cell TGFBR3 mRNA stability. <i>JCI Insight</i> , 2023, 8, .	2.3	0
11506	The Landscape of Accessible Chromatin and Developmental Transcriptome Maps Reveal a Genetic Mechanism of Skeletal Muscle Development in Pigs. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6413.	1.8	4
11507	Shoot differentiation from <i>Dendrocalamus brandisii</i> callus and the related physiological roles of sugar and hormones during shoot differentiation. <i>Tree Physiology</i> , 2023, 43, 1159-1186.	1.4	2
11508	RNA sequencing revealed the multi-stage transcriptome transformations during the development of gallbladder cancer associated with chronic inflammation. <i>PLoS ONE</i> , 2023, 18, e0283770.	1.1	0
11509	Design of diversified chimeric antigen receptors through rational module recombination. <i>IScience</i> , 2023, 26, 106529.	1.9	3
11510	In Vitro Antibiofilm Activity of Resveratrol against <i>Aeromonas hydrophila</i> . <i>Antibiotics</i> , 2023, 12, 686.	1.5	5
11511	Nuclei on the Rise: When Nuclei-Based Methods Meet Next-Generation Sequencing. <i>Cells</i> , 2023, 12, 1051.	1.8	1
11512	Immuno-Stimulating Activity of 1,25-Dihydroxyvitamin D in Blood Cells from Five Healthy People and in Blasts from Five Patients with Leukemias and Pre-Leukemic States. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6504.	1.8	1



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11513	Litsea Males Are Better Adapted to Pb Stress Than Females by Modulating Photosynthesis and Pb Subcellular Distribution. <i>Forests</i> , 2023, 14, 724.	0.9	0
11514	Antennal transcriptomic analysis of carboxylesterases and glutathione S-transferases associated with odorant degradation in the tea gray geometrid, <i>Ectropis griseascens</i> (Lepidoptera, Geometridae). <i>Frontiers in Physiology</i> , 0, 14, .	1.3	0
11515	Combining GS-assisted GWAS and transcriptome analysis to mine candidate genes for nitrogen utilization efficiency in <i>Populus cathayana</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	1
11516	Standardization and Interpretation of RNA-sequencing for Transplantation. <i>Transplantation</i> , 2023, 107, 2155-2167.	0.5	3
11517	The transcriptome of <i>Litopenaeus vannamei</i> in zoea larvae and adults infected by <i>Vibrio parahaemolyticus</i> . <i>Frontiers in Marine Science</i> , 0, 10, .	1.2	0
11518	Integrated Transcriptome and Small RNA Sequencing Analyses Reveals Insights into the Molecular Mechanism of Seed Germination in Mung Bean. <i>Phyton</i> , 2023, 92, 1793-1812.	0.4	0
11519	Positive selection in cytochrome P450 genes is associated with gonad phenotype and mating strategy in social bees. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
11520	Differential transcript usage analysis incorporating quantification uncertainty via compositional measurement error regression modeling. <i>Biostatistics</i> , 0, , .	0.9	1
11521	Ageing-associated changes in transcriptional elongation influence longevity. <i>Nature</i> , 2023, 616, 814-821.	13.7	39
11522	DNA Demethylation of Myogenic Genes May Contribute to Embryonic Leg Muscle Development Differences between Wuzong and Shitou Geese. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7188.	1.8	3
11523	Identification and Analysis of MADS-Box Genes Expressed in the Mesocarp of Oil Palm Fruit ( <i>Elaeis</i> ). <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	0.8	0
11524	NF- $\kappa$ B is a critical mediator of post-mitotic senescence in oligodendrocytes and subsequent white matter loss. <i>Molecular Neurodegeneration</i> , 2023, 18, .	4.4	11
11525	Differential gene expression patterns between the head and thorax of <i>Gynaephora aureata</i> are associated with high-altitude adaptation. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	1
11527	An ecdysteroid-regulated 16-kDa protein homolog participates in the immune response of the crayfish <i>Procambarus clarkii</i> . <i>Fish and Shellfish Immunology</i> , 2023, 137, 108750.	1.6	1
11528	Venom-gland transcriptomics of the Malayan pit viper ( <i>Calloselasma rhodostoma</i> ) for identification, classification, and characterization of venom proteins. <i>Heliyon</i> , 2023, 9, e15476.	1.4	0
11529	Multiomics Analysis Reveals Novel Genetic Determinants for Lens Differentiation, Structure, and Transparency. <i>Biomolecules</i> , 2023, 13, 693.	1.8	3
11530	Tetramerization of STAT5 regulates monocyte differentiation and the dextran sulfate sodium-induced colitis in mice. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	0
11531	Large-scale long terminal repeat insertions produced a significant set of novel transcripts in cotton. <i>Science China Life Sciences</i> , 2023, 66, 1711-1724.	2.3	3

#	ARTICLE	IF	CITATIONS
11532	Meta-Analysis of RNA-Seq Data Identifies Potent Biomarkers for Intellectual Disability Disorder (IDD). , 0, , .		1
11533	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos ( <i>Anser cygnoides</i> ). <i>Frontiers in Physiology</i> , 0, 13, .	1.3	6
11534	Transcriptome analysis revealed molecular basis of cold response in <i>Prunus mume</i> . <i>Molecular Breeding</i> , 2023, 43, .	1.0	2
11535	Comparative Transcriptome Analysis Reveals the Mechanism Associated With Dynamic Changes in Meat Quality of the <i>Longissimus Thoracis</i> Muscle in Tibetan Sheep at Different Growth Stages. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	4
11541	DNA and RNA Sequencing. , 2022, , 324-349.		0
11565	Non-coding RNAs in glioblastoma at a glance. , 2023, , 477-504.		0
11569	Tissue Classification Using RNA-Seq Transcriptomics with Distribution Analysis and SVM Models<sup>*</sup>. , 2023, , .		0
11604	Transcription Factors and Splice Factorsâ€™ Interconnected Regulators of Stem Cell Differentiation. <i>Current Stem Cell Reports</i> , 0, , .	0.7	1
11637	Bioinformatics and Biostatistics in Precision Medicine. , 2023, , 189-235.		1
11657	Impact of Normalization Techniques in Microarray Data Analysis. , 2023, , .		0
11663	Gene Expression Profiling and Bioinformatics Analysis in Neurodegenerative Diseases. , 2023, , 967-1002.		0
11723	Myokines, Measurement, and Technical Considerations. <i>Neuromethods</i> , 2023, , 215-241.	0.2	0
11742	The chemistry of next-generation sequencing. <i>Nature Biotechnology</i> , 2023, 41, 1709-1715.	9.4	4
11753	Genome-wide transcriptome profiling of crop plants. , 2023, , 145-171.		0
11814	T cell receptor therapeutics: immunological targeting of the intracellular cancer proteome. <i>Nature Reviews Drug Discovery</i> , 2023, 22, 996-1017.	21.5	7
11823	Interrogating epigenetic mechanisms with chemically customized chromatin. <i>Nature Reviews Genetics</i> , 2024, 25, 255-271.	7.7	1
11860	Applications and Future Perspectives of Computational Approaches in Livestock Animals. , 2023, , 279-309.		0
11883	Systems Biology and Inborn Error of Metabolism: Analytical Strategy in Investigating Different Biochemical/Genetic Parameters. <i>Methods in Molecular Biology</i> , 2024, , 191-210.	0.4	0

#	ARTICLE	IF	CITATIONS
11896	Non-Coding RNA-Mediated Gene Regulation in Cardiovascular Disorders: Current Insights and Future Directions. Journal of Cardiovascular Translational Research, 0, , .	1.1	1
11927	Transcriptomic analyses provide insights into plant-viroid interactions. , 2024, , 255-274.		0
11944	Guidelines and important considerations for omics-level studies. , 2024, , 189-209.		0
11945	Rigor and reproducibility of RNA sequencing analyses. , 2024, , 211-245.		0
11946	NrGe-DTL: a computational framework for cancer drug response prediction based on deep transfer learning from combined denoised genomic profiles and chemical structure embedding of drugs. , 2023, , .		0
11947	Comprehensive evaluation of RNA-seq alignment methods based on long-read sequencing data. , 2023, , .		0
11948	Machine learning applications in cancer genomics. , 2024, , 41-72.		0
11950	Transcriptomic profiling-based identification of biomarkers of stem cells. , 2024, , 203-214.		0
12034	Class Discovery, Comparison, and Prediction Methods for RNA-Seq Data. , 2023, , 457-481.		0
12044	smFISH for Plants. Methods in Molecular Biology, 2024, , 87-100.	0.4	0
12045	Machine Learning Perspective in Cancer Research. , 2023, , 1104-1125.		0
12047	Cochlear Changes After Noise Trauma. , 2024, , 115-122.		0