Blast2GO: a universal tool for annotation, visualization
genomics research

Bioinformatics

21, 3674-3676

DOI: 10.1093/bioinformatics/bti610

Citation Report

#	Article	IF	Citations
2	Comparative profiling of the sense and antisense transcriptome of maize lines. Genome Biology, 2006, 7, R22.	13.9	75
3	Development of the GENIPOL European Flounder (Platichthys flesus) Microarray and Determination of Temporal Transcriptional Responses to Cadmium at Low Dose.. Environmental Science & Technology, 2006, 40, 6479-6488.	4.6	81
4	A hitchhiker's guide to expressed sequence tag (EST) analysis. Briefings in Bioinformatics, 2006, 8, 6-21.	3.2	235
5	Identification of differential gene expression in in vitro FSH treated pig granulosa cells using suppression subtractive hybridization. Reproductive Biology and Endocrinology, 2006, 4, 35.	1.4	13
6	Production of full-length cDNA sequences by sequencing and analysis of expressed sequence tags from Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2006, 101, 161-165.	0.8	5
7	Large-Scale Characterization of Introns in the Pneumocystis carinii Genome. Journal of Eukaryotic Microbiology, 2006, 53, S151-S153.	0.8	8
8	Comparative analysis of whole-genome sequences of Streptococcus suis. Science Bulletin, 2006, 51, 1199-1209.	1.7	3
9	Cyanobacterial Contribution to Algal Nuclear Genomes Is Primarily Limited to Plastid Functions. Current Biology, 2006, 16, 2320-2325.	1.8	107
10	Genome comparison using Gene Ontology (GO) with statistical testing. BMC Bioinformatics, 2006, 7, 374.	1.2	15
11	Generation, annotation and analysis of ESTs from Trichoderma harzianum CECT 2413. BMC Genomics, 2006, 7, 193.	1.2	60
12	Identification and analysis of gene families from the duplicated genome of soybean using EST sequences. BMC Genomics, 2006, 7, 204.	1.2	21
13	EST library sequencing of genes expressed during early limb regeneration in the fiddler crab and transcriptional responses to ecdysteroid exposure in limb bud explants. Integrative and Comparative Biology, 2006, 46, 948-964.	0.9	22
14	Quantitative Comparison of Caste Differences in Honeybee Hemolymph. Molecular and Cellular Proteomics, 2006, 5, 2252-2262.	2.5	133
15	Interferon type I and type II responses in an Atlantic salmon (Salmo salar) SHK-1 cell line by the salmon TRAITS/SGP microarray. Physiological Genomics, 2007, 32, 33-44.	1.0	80
16	Proteomics Analysis of Interleukin (IL)-7-induced Signaling Effectors Shows Selective Changes in IL-7RÎ±449F Knock-in T Cell Progenitors. Molecular and Cellular Proteomics, 2007, 6, 1700-1710.	2.5	17
17	Web Services at the European Bioinformatics Institute. Nucleic Acids Research, 2007, 35, W6-W11.	6.5	166
18	White Leaf Sectors in yellow variegated2 Are Formed by Viable Cells with Undifferentiated Plastids. Plant Physiology, 2007, 144, 952-960.	2.3	104
19	Discovering gene expression patterns in time course microarray experiments by ANOVAâ€“SCA. Bioinformatics, 2007, 23, 1792-1800.	1.8	80

#	ARTICLE	IF	CITATIONS
20	Phylogenomic Analysis Supports the Monophyly of Cryptophytes and Haptophytes and the Association of Rhizaria with Chromalveolates. Molecular Biology and Evolution, 2007, 24, 1702-1713.	3.5	218
21	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. Nucleic Acids Research, 2007, 35, W143-W147.	6.5	60
22	In-depth Analysis of the Adipocyte Proteome by Mass Spectrometry and Bioinformatics. Molecular and Cellular Proteomics, 2007, 6, 1257-1273.	2.5	101
23	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium Bacillus subtilis. Molecular and Cellular Proteomics, 2007, 6, 697-707.	2.5	359
24	firestar--prediction of functionally important residues using structural templates and alignment reliability. Nucleic Acids Research, 2007, 35, W573-W577.	6.5	91
25	Comparative Expression Profiling of <i>Nicotiana benthamiana</i> Leaves Systemically Infected with Three Fruit Tree Viruses. Molecular Plant-Microbe Interactions, 2007, 20, 1004-1017.	1.4	99
26	Phytoremediation of chromium using Salix species: Cloning ESTs and candidate genes involved in the Cr response. Gene, 2007, 402, 68-80.	1.0	42
27	LongSAGE analysis of skeletal muscle at three prenatal stages in Tongcheng and Landrace pigs. Genome Biology, 2007, 8, R115.	13.9	123
28	Dothideomyceteâ€“Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i>. Plant Cell, 2007, 19, 3347-3368.	3.1	235
29	Gene expression responses of European flounder (Platichthys flesus) to 17-Î² estradiol. Toxicology Letters, 2007, 168, 236-248.	0.4	86
30	Hepatopancreatic multiâ€transcript expression patterns in the crayfish <i>Cherax quadricarinatus</i> during the moult cycle. Insect Molecular Biology, 2007, 16, 661-674.	1.0	35
31	Adaptive differences in gene expression in European flounder (Platichthys flesus). Molecular Ecology, 2007, 16, 4674-4683.	2.0	111
32	Common genomeâ€wide patterns of transcript accumulation underlying the wing polyphenism and polymorphism in the pea aphid (<i>Acyrthosiphon pisum</i>). Evolution & Development, 2007, 9, 338-346.	1.1	73
33	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	1.2	68
34	Linking microarray reporters with protein functions. BMC Bioinformatics, 2007, 8, 360.	1.2	12
35	An ancient genome duplication contributed to the abundance of metabolic genes in the moss Physcomitrella patens. BMC Evolutionary Biology, 2007, 7, 130.	3.2	171
36	Generation and analysis of ESTs from the eastern oyster, Crassostrea virginica Gmelin and identification of microsatellite and SNP markers. BMC Genomics, 2007, 8, 157.	1.2	65
37	Generation and analysis of expressed sequence tags from the ciliate protozoan parasite Ichthyophthirius multifiliis. BMC Genomics, 2007, 8, 176.	1.2	29

#	ARTICLE	IF	CITATIONS
38	Microarray analysis of gene expression induced by sexual contact in Schistosoma mansoni. BMC Genomics, 2007, 8, 181.	1.2	37
39	Sampling Daphnia's expressed genes: preservation, expansion and invention of crustacean genes with reference to insect genomes. BMC Genomics, 2007, 8, 217.	1.2	25
40	Expressed sequences tags of the anther smut fungus, Microbotryum violaceum, identify mating and pathogenicity genes. BMC Genomics, 2007, 8, 272.	1.2	30
41	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. BMC Genomics, 2007, 8, 31.	1.2	64
42	A transcriptomic analysis of the adult stage of the bovine lungworm, Dictyocaulus viviparus. BMC Genomics, 2007, 8, 311.	1.2	17
43	Analysis and functional annotation of expressed sequence tags (ESTs) from multiple tissues of oil palm (Elaeis guineensis Jacq.). BMC Genomics, 2007, 8, 381.	1.2	47
44	Profiling sex-biased gene expression during parthenogenetic reproduction in Daphnia pulex. BMC Genomics, 2007, 8, 464.	1.2	51
45	Surviving extreme polar winters by desiccation: clues from Arctic springtail (Onychiurus arcticus) EST libraries. BMC Genomics, 2007, 8, 475.	1.2	61
46	Gene response profiles for Daphnia pulex exposed to the environmental stressor cadmium reveals novel crustacean metallothioneins. BMC Genomics, 2007, 8, 477.	1.2	108
47	Transcriptional response of Citrus aurantifolia to infection by Citrus tristeza virus. Virology, 2007, 367, 298-306.	1.1	65
48	Plant Bioinformatics. , 2007, , .		4
49	Generation, annotation, and analysis of ESTs from four different Trichoderma strains grown under conditions related to biocontrol. Applied Microbiology and Biotechnology, 2007, 75, 853-862.	1.7	39
50	Characterization of genes encoding novel peptidases in the biocontrol fungus Trichoderma harzianum CECT 2413 using the TrichoEST functional genomics approach. Current Genetics, 2007, 51, 331-342.	0.8	71
51	Expressed sequence tag analysis and development of gene associated markers in a near-isogenic plant system of Eragrostis curvula. Plant Molecular Biology, 2008, 67, 1-10.	2.0	51
52	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (Phaseolus vulgaris L.) Genome. Tropical Plant Biology, 2008, 1, 40-48.	1.0	70
53	Pollution-Affected Fish Hepatic Transcriptome and Its Expression Patterns on Exposure to Cadmium. Marine Biotechnology, 2008, 10, 250-261.	1.1	26
54	Transcriptome Analyses of Amoebic Gill Disease-affected Atlantic Salmon (Salmo salar) Tissues Reveal Localized Host Gene Suppression. Marine Biotechnology, 2008, 10, 388-403.	1.1	83
55	Exploring the transcriptome of the burrowing nematode Radopholus similis. Molecular Genetics and Genomics, 2008, 280, 1-17.	1.0	53

#	ARTICLE	IF	CITATIONS
56	Duplicate gene expression in allopolyploid Gossypiumreveals two temporally distinct phases of expression evolution. BMC Biology, 2008, 6, 16.	1.7	235
57	The Gene Ontology â€" Providing a Functional Role in Proteomic Studies. Proteomics, 2008, 8, .	1.3	29
58	A cDNA microarray for the three-spined stickleback, Gasterosteus aculeatus L., and analysis of the interactive effects of oestradiol and dibenzanthracene exposures. Journal of Fish Biology, 2008, 72, 2133-2153.	0.7	34
59	A description of the origins, design and performance of the TRAITSâ€"SGP Atlantic salmon <i>Salmo salar </i>L. cDNA microarray. Journal of Fish Biology, 2008, 72, 2071-2094.	0.7	60
60	The GENIPOL European flounder Platichthys flesus L. toxicogenomics microarray: application for investigation of the response to furunculosis vaccination. Journal of Fish Biology, 2008, 72, 2154-2169.	0.7	19
61	Identification of development and tissue-specific gene expression in the fathead minnow Pimephales promelas, Rafinesque using computational and DNA microarray methods. Journal of Fish Biology, 2008, 72, 2341-2353.	0.7	13
62	Global analysis of gene expression in cotton fibers from wild and domesticated <i>Gossypium barbadense</i>. Evolution & Development, 2008, 10, 567-582.	1.1	77
63	Mining an <i>Ostrinia nubilalis</i> midgut expressed sequence tag (EST) library for candidate genes and single nucleotide polymorphisms (SNPs). Insect Molecular Biology, 2008, 17, 607-620.	1.0	38
64	annot8r: GO, EC and KEGG annotation of EST datasets. BMC Bioinformatics, 2008, 9, 180.	1.2	87
65	A comparison of common programming languages used in bioinformatics. BMC Bioinformatics, 2008, 9, 82.	1.2	88
66	In silico analysis of expressed sequence tags from Trichostrongylus vitrinus (Nematoda): comparison of the automated ESTExplorer workflow platform with conventional database searches. BMC Bioinformatics, 2008, 9, S10.	1.2	17
67	Transferability of the EST-SSRs developed on Nules clementine (Citrus clementina Hort ex Tan) to other Citrus species and their effectiveness for genetic mapping. BMC Genomics, 2008, 9, 287.	1.2	173
68	Proteomic profile of dormant Trichophyton Rubrum conidia. BMC Genomics, 2008, 9, 303.	1.2	36
69	Large-scale Gene Ontology analysis of plant transcriptome-derived sequences retrieved by AFLP technology. BMC Genomics, 2008, 9, 347.	1.2	22
70	Development of genomic resources for Citrus clementina: Characterization of three deep-coverage BAC libraries and analysis of 46,000 BAC end sequences. BMC Genomics, 2008, 9, 423.	1.2	81
71	Genomic resources for a commercial flatfish, the Senegalese sole (Solea senegalensis): EST sequencing, oligo microarray design, and development of the bioinformatic platform Soleamold. BMC Genomics, 2008, 9, 508.	1.2	70
72	Towards the understanding of the cocoa transcriptome: Production and analysis of an exhaustive dataset of ESTs of Theobroma cacao L. generated from various tissues and under various conditions. BMC Genomics, 2008, 9, 512.	1.2	112
73	Analyses of expressed sequence tags from the maize foliar pathogen Cercospora zeae-maydis identify novel genes expressed during vegetative, infectious, and reproductive growth. BMC Genomics, 2008, 9, 523.	1.2	12

#	Article	IF	Citations
74	Oil palm (Elaeis guineensisJacq.) tissue culture ESTs: Identifying genes associated with callogenesis and embryogenesis. BMC Plant Biology, 2008, 8, 62.	1.6	83
75	Transcriptional profiling of the pea shoot apical meristem reveals processes underlying its function and maintenance. BMC Plant Biology, 2008, 8, 73.	1.6	22
76	Schistosoma mansoni: Microarray analysis of gene expression induced by host sex. Experimental Parasitology, 2008, 120, 357-363.	0.5	11
77	A cDNA-AFLP approach to study ochratoxin A production in Aspergillus carbonarius. International Journal of Food Microbiology, 2008, 127, 105-115.	2.1	18
78	Toxicogenomic analysis of immune system-related genes in Japanese flounder (Paralichthys olivaceus) exposed to heavy oil. Marine Pollution Bulletin, 2008, 57, 445-452.	2.3	63
79	Microarray based analysis of temperature and oxidative stress induced messenger RNA in Schistosoma mansoni. Molecular and Biochemical Parasitology, 2008, 162, 134-141.	0.5	30
80	Transcriptional responses of the black-chinned tilapia Sarotherodon melanotheron to salinity extremes. Marine Genomics, 2008, 1, 37-46.	0.4	34
81	Dramatic down-regulation of oxidoreductases in human hepatocellular carcinoma hepG2 cells: proteomics and gene ontology unveiling new frontiers in cancer enzymology. Proteome Science, 2008, 6, 29.	0.7	19
82	Sample prep for proteomics of breast cancer: proteomics and gene ontology reveal dramatic differences in protein solubilization preferences of radioimmunoprecipitation assay and urea lysis buffers. Proteome Science, 2008, 6, 30.	0.7	75
83	Molecular Physiology of Development and Quality of Citrus. Advances in Botanical Research, 2008, , 147-223.	0.5	96
84	Changes in protein expression during honey bee larval development. Genome Biology, 2008, 9, R156.	13.9	60
85	Proteomic analysis of the secretome of Leishmania donovani. Genome Biology, 2008, 9, R35.	13.9	262
86	High-throughput functional annotation and data mining with the Blast2GO suite. Nucleic Acids Research, 2008, 36, 3420-3435.	6.5	3,905
87	Analysis of transcriptome data in the red flour beetle, Tribolium castaneum. Insect Biochemistry and Molecular Biology, 2008, 38, 380-386.	1.2	46
88	Construction of subtracted EST and normalised cDNA libraries from liver of chemical-exposed three-spined stickleback (Gasterosteus aculeatus) containing pollutant-responsive genes as a resource for transcriptome analysis. Marine Environmental Research, 2008, 66, 127-130.	1.1	17
89	Comparative ORESTES-sampling of transcriptomes of immune-challenged Biomphalaria glabrata snails. Journal of Invertebrate Pathology, 2008, 99, 192-203.	1.5	44
90	Microarray analysis of gene expression in the blue catfish liver reveals early activation of the MHC class I pathway after infection with Edwardsiella ictaluri. Molecular Immunology, 2008, 45, 553-566.	1.0	129
91	Transcriptomic responses of European flounder (Platichthys flesus) to model toxicants. Aquatic Toxicology, 2008, 90, 83-91.	1.9	54

#	Article	IF	Citations
92	Hepatic transcriptomic profiles of European flounder (Platichthys flesus) from field sites and computational approaches to predict site from stress gene responses following exposure to model toxicants. Aquatic Toxicology, 2008, 90, 92-101.	1.9	70
93	Direct functional assessment of the composite phenotype through multivariate projection strategies. Genomics, 2008, 92, 373-383.	1.3	9
94	Protein glycosylation pathways in filamentous fungi. Glycobiology, 2008, 18, 626-637.	1.3	157
95	Effects of calorie restriction on the zebrafish liver proteome. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2008, 3, 275-282.	0.4	14
96	Resistance to amoebic gill disease (AGD) is characterised by the transcriptional dysregulation of immune and cell cycle pathways. Developmental and Comparative Immunology, 2008, 32, 1539-1560.	1.0	46
97	Mapping the Integrin-Linked Kinase Interactome Using SILAC. Journal of Proteome Research, 2008, 7, 1740-1749.	1.8	90
98	Network integration and graph analysis in mammalian molecular systems biology. IET Systems Biology, 2008, 2, 206-221.	0.8	42
99	ESTplus: An Integrative System for Comprehensive and Customized EST Analysis and Proteomic Data Matching. , 2008, , .		2
100	Effects of fluoxetine on the reproductive axis of female goldfish (<i>Carassius auratus</i>). Physiological Genomics, 2008, 35, 273-282.	1.0	124
101	ClusFCM: AN ALGORITHM FOR PREDICTING PROTEIN FUNCTIONS USING HOMOLOGIES AND PROTEIN INTERACTIONS. Journal of Bioinformatics and Computational Biology, 2008, 06, 203-222.	0.3	8
102	Whole-genome analysis reveals molecular innovations and evolutionary transitions in chromalveolate species. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3427-3432.	3.3	53
103	Local Function Conservation in Sequence and Structure Space. PLoS Computational Biology, 2008, 4, e1000105.	1.5	20
104	Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. Nucleic Acids Research, 2008, 36, W341-W346.	6.5	73
105	GOfetcher: a database with complex searching facility for gene ontology. Bioinformatics, 2008, 24, 2561-2563.	1.8	9
106	Physiological and Transcriptomic Evidence for a Close Coupling between Chloroplast Ontogeny and Cell Cycle Progression in the Pennate Diatom<i>Seminavis robusta</i>Â Â Â Â. Plant Physiology, 2008, 148, 1394-1411.	2.3	65
107	Bioinformatics of Protein Function. , 2008, , 79-119.		0
108	The F-Box Gene Family Is Expanded in Herbaceous Annual Plants Relative to Woody Perennial Plants Â. Plant Physiology, 2008, 148, 1189-1200.	2.3	125
109	Transcriptional Changes in the Hookworm, Ancylostoma caninum, during the Transition from a Free-Living to a Parasitic Larva. PLoS Neglected Tropical Diseases, 2008, 2, e130.	1.3	72

#	Article	IF	Citations
110	Blast2GO: A Comprehensive Suite for Functional Analysis in Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-12.	2.2	1,866
111	Bioinformatics Tools for Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-2.	2.2	4
112	Analysis of <i>PHOTOPERIOD SENSITIVITY5</i> Sheds Light on the Role of Phytochromes in Photoperiodic Flowering in Rice Â. Plant Physiology, 2009, 151, 681-690.	2.3	73
113	Transcriptome analysis of<i>Schistosoma mansoni</i>larval development using serial analysis of gene expression (SAGE). Parasitology, 2009, 136, 469-485.	0.7	32
114	Genomic Analysis of the Basal Lineage Fungus Rhizopus oryzae Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	1.5	332
115	Crustacean Ecdysteroids and Their Receptors. , 2009, , 73-97.		13
116	Towards an understanding of the mechanism of action of praziquantel. Molecular and Biochemical Parasitology, 2009, 164, 57-65.	0.5	113
117	Generation and analysis of expressed sequence tags from a cDNA library of Moniezia expansa. Molecular and Biochemical Parasitology, 2009, 164, 80-85.	0.5	13
118	Expressed sequence tags of the peanut pod nematode Ditylenchus africanus: The first transcriptome analysis of an Anguinid nematode. Molecular and Biochemical Parasitology, 2009, 167, 32-40.	0.5	50
119	Incremental generation of an EST set for the analysis of scrapie pathogenesis. Small Ruminant Research, 2009, 81, 75-78.	0.6	0
120	The High Throughput Sequence Annotation Service (HT-SAS) â€“ the shortcut from sequence to true Medline words. BMC Bioinformatics, 2009, 10, 148.	1.2	4
121	Functional assessment of time course microarray data. BMC Bioinformatics, 2009, 10, S9.	1.2	19
122	An EST screen from the annelid Pomatoceros lamarckii reveals patterns of gene loss and gain in animals. BMC Evolutionary Biology, 2009, 9, 240.	3.2	40
123	Transcriptomics reveals extensive inducible biotransformation in the soil-dwelling invertebrate Folsomia candida exposed to phenanthrene. BMC Genomics, 2009, 10, 236.	1.2	64
124	A White Campion (Silene latifolia) floral expressed sequence tag (EST) library: annotation, EST-SSR characterization, transferability, and utility for comparative mapping. BMC Genomics, 2009, 10, 243.	1.2	45
125	Gene expression profiling in peanut using high density oligonucleotide microarrays. BMC Genomics, 2009, 10, 265.	1.2	52
126	Expressed sequence tags from larval gut of the European corn borer (Ostrinia nubilalis): Exploring candidate genes potentially involved in Bacillus thuringiensis toxicity and resistance. BMC Genomics, 2009, 10, 286.	1.2	42
127	A BAC-based physical map of the Hessian fly genome anchored to polytene chromosomes. BMC Genomics, 2009, 10, 293.	1.2	20

#	ARTICLE	IF	CITATIONS
128	Generation, annotation, and analysis of ESTs from midgut tissue of adult female Anopheles stephensi mosquitoes. BMC Genomics, 2009, 10, 386.	1.2	8
129	An expressed sequence tag (EST) library for Drosophila serrata, a model system for sexual selection and climatic adaptation studies. BMC Genomics, 2009, 10, 40.	1.2	26
130	Comparative EST transcript profiling of peach fruits under different post-harvest conditions reveals candidate genes associated with peach fruit quality. BMC Genomics, 2009, 10, 423.	1.2	63
131	New insights into molecular pathways associated with flatfish ovarian development and atresia revealed by transcriptional analysis. BMC Genomics, 2009, 10, 434.	1.2	60
132	Characterization of full-length sequenced cDNA inserts (FLIcs) from Atlantic salmon (Salmo salar). BMC Genomics, 2009, 10, 502.	1.2	29
133	Analysis of expressed sequence tags and identification of genes encoding cell-wall-degrading enzymes from the fungivorous nematode Aphelenchus avenae. BMC Genomics, 2009, 10, 525.	1.2	32
134	Transcriptional profiling of trait deterioration in the insect pathogenic nematode Heterorhabditis bacteriophora. BMC Genomics, 2009, 10, 609.	1.2	23
135	Desiccation survival in an Antarctic nematode: molecular analysis using expressed sequenced tags. BMC Genomics, 2009, 10, 69.	1.2	76
136	Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. BMC Genomics, 2009, 10, S11.	1.2	31
137	Computational annotation of genes differentially expressed along olive fruit development. BMC Plant Biology, 2009, 9, 128.	1.6	88
138	Characterization of microsatellites and gene contents from genome shotgun sequences of mungbean (Vigna radiata (L.) Wilczek). BMC Plant Biology, 2009, 9, 137.	1.6	128
139	Construction of 12 EST libraries and characterization of a 12,226 EST dataset for chicory (Cichorium) Tj ETQq1 1 0.784314 rgBT /Overl Biology, 2009, 9, 14.	1.6	12
140	Transcriptomic analysis of tomato carpel development reveals alterations in ethylene and gibberellin synthesis during pat3/pat4 parthenocarpic fruit set. BMC Plant Biology, 2009, 9, 67.	1.6	40
141	Parallel changes in gene expression in peripheral blood mononuclear cells and the brain after maternal separation in the mouse. BMC Research Notes, 2009, 2, 195.	0.6	36
142	Characterization of an Atlantic cod (Gadus morhua) embryonic stem cell cDNA library. BMC Research Notes, 2009, 2, 74.	0.6	4
143	Improved insights into the transcriptomes of the human hookworm Necator americanus â€" Fundamental and biotechnological implications. Biotechnology Advances, 2009, 27, 122-132.	6.0	17
144	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance â€" Fundamental insights toward biotechnological outcomes. Biotechnology Advances, 2009, 27, 439-448.	6.0	29
145	Bioinformatics analysis of mass spectrometryâ€based proteomics data sets. FEBS Letters, 2009, 583, 1703-1712.	1.3	147

#	Article	IF	Citations
146	GenoMass â€•a computer software for automated identification of oligonucleotide DNA adducts from LCâ€MS analysis of DNA digests. Journal of Mass Spectrometry, 2009, 44, 549-560.	0.7	19
147	Addressing drought tolerance in maize by transcriptional profiling and mapping. Molecular Genetics and Genomics, 2009, 281, 163-179.	1.0	65
148	Membrane transporters and carbon metabolism implicated in chloride homeostasis differentiate salt stress responses in tolerant and sensitive Citrus rootstocks. Functional and Integrative Genomics, 2009, 9, 293-309.	1.4	80
149	Isolation of genes from female sterile flowers in Medicago sativa. Sexual Plant Reproduction, 2009, 22, 97-107.	2.2	6
150	Construction, Characterization, and Expressed Sequence Tag (EST) Analysis of Normalized cDNA Library of Thermo-Photoperiod-Sensitive Genic Male Sterile (TPGMS) Wheat from Spike Developmental Stages. Plant Molecular Biology Reporter, 2009, 27, 117-125.	1.0	10
151	Rapid transcriptional response of apple to fire blight disease revealed by cDNA suppression subtractive hybridization analysis. Tree Genetics and Genomes, 2009, 5, 27-40.	0.6	59
152	An EST-SSR-based linkage map for Persea americana Mill. (avocado). Tree Genetics and Genomes, 2009, 5, 553-560.	0.6	20
153	Proteomic analysis of heparin-binding proteins from human seminal plasma: a step towards identification of molecular markers of male fertility. Journal of Biosciences, 2009, 34, 899-908.	0.5	61
154	In Silico Prediction of Two Classes of Honeybee Genes with CpG Deficiency or CpG Enrichment and Sorting According to Gene Ontology Classes. Journal of Molecular Evolution, 2009, 68, 700-705.	0.8	21
155	Hypoxia Promotes Efficient Differentiation of Human Embryonic Stem Cells to Functional Endothelium. Stem Cells, 2010, 28, 407-418.	1.4	92
156	Genomic expression dominance in allopolyploids. BMC Biology, 2009, 7, 18.	1.7	232
157	Transcriptome analysis of the synganglion from the brown dog tick, <i>Rhipicephalus sanguineus</i>. Insect Molecular Biology, 2010, 19, 273-282.	1.0	23
158	Identification and functional characterization of effectors in expressed sequence tags from various life cycle stages of the potato cyst nematode <i>Globodera pallida</i>. Molecular Plant Pathology, 2009, 10, 815-828.	2.0	96
159	A study on genomic distribution and sequence features of human long inverted repeats reveals speciesâ€specific intronic inverted repeats. FEBS Journal, 2009, 276, 1986-1998.	2.2	19
160	A combined subtractive suppression hybridization and expression profiling strategy to identify novel desiccation response transcripts from <i>Tortula ruralis</i> gametophytes. Physiologia Plantarum, 2009, 136, 437-460.	2.6	33
161	Comparative day/night metatranscriptomic analysis of microbial communities in the North Pacific subtropical gyre. Environmental Microbiology, 2009, 11, 1358-1375.	1.8	285
162	Global and cellâ€type gene expression profiles in tomato plants colonized by an arbuscular mycorrhizal fungus. New Phytologist, 2009, 184, 975-987.	3.5	187
163	Hepatic Transcriptomic and Metabolomic Responses in the Stickleback (<i>Gasterosteus aculeatus</i>) Exposed to Environmentally Relevant Concentrations of Dibenzanthracene. Environmental Science & Technology, 2009, 43, 6341-6348.	4.6	71

#	ARTICLE	IF	CITATIONS
164	Transcriptome analysis of a spontaneous mutant in sweet orange [Citrus sinensis (L.) Osbeck] during fruit development. Journal of Experimental Botany, 2009, 60, 801-813.	2.4	68
165	Quantitative Proteomic Profiles of Androgen Receptor Signaling in the Liver of Fathead Minnows (<i>Pimephales promelas</i>). Journal of Proteome Research, 2009, 8, 2186-2200.	1.8	49
166	Molecular dissection of the pea shoot apical meristem*. Journal of Experimental Botany, 2009, 60, 4201-4213.	2.4	13
167	Immune- and stress-related transcriptomic responses of Solea senegalensis stimulated with lipopolysaccharide and copper sulphate using heterologous cDNA microarrays. Fish and Shellfish Immunology, 2009, 26, 699-706.	1.6	41
168	Genome-wide analysis reveals increased levels of transcripts related with infectivity in peanut lectin non-agglutinated promastigotes of Leishmania infantum. Genomics, 2009, 93, 551-564.	1.3	50
169	Dosage analysis of Z chromosome genes using microarray in silkworm, Bombyx mori. Insect Biochemistry and Molecular Biology, 2009, 39, 315-321.	1.2	88
170	Bioinformatic analysis of abundant, gender-enriched transcripts of adult Ascaris suum (Nematoda) using a semi-automated workflow platform. Molecular and Cellular Probes, 2009, 23, 205-217.	0.9	16
171	Nickel and binary metal mixture responses in Daphnia magna: Molecular fingerprints and (sub)organismal effects. Aquatic Toxicology, 2009, 92, 18-29.	1.9	84
172	15-P003 An EST screen from the annelid Pomatoceros lamarckii reveals patterns of gene loss and gain in animals. Mechanisms of Development, 2009, 126, S247-S248.	1.7	1
173	Genome-Wide Transcriptome Analyses of Silicon Metabolism in Phaeodactylum tricornutum Reveal the Multilevel Regulation of Silicic Acid Transporters. PLoS ONE, 2009, 4, e7458.	1.1	101
174	Genetics and Genomics of Cotton. , 2009, , .		23
175	Software Tool for Researching Annotations of Proteins: Open-Source Protein Annotation Software with Data Visualization. Analytical Chemistry, 2009, 81, 9819-9823.	3.2	207
176	Ecdysone: Structures and Functions. , 2009, , .		30
177	Effect of Wheat Roots Infected with the Pathogenic Fungus <i>Gaeumannomyces graminis</i> var. <i>tritici</i> on Gene Expression of the Biocontrol Bacterium <i>Pseudomonas fluorescens</i> Pf29Arp. Molecular Plant-Microbe Interactions, 2009, 22, 1611-1623.	1.4	41
178	Filarial parasites in the postgenomic era. Expert Review of Anti-Infective Therapy, 2009, 7, 189-192.	2.0	1
179	Shotgun proteomics: Tools for analysis of marine particulate proteins. Limnology and Oceanography: Methods, 2009, 7, 865-874.	1.0	11
180	Comparative Analysis of Expression Profiles in Shoots and Roots of Tomato Systemically Infected by Tomato spotted wilt virus Reveals Organ-Specific Transcriptional Responses. Molecular Plant-Microbe Interactions, 2009, 22, 1504-1513.	1.4	64
181	Constitutive Expression of <i>OsGH3.1</i> Reduces Auxin Content and Enhances Defense Response and Resistance to a Fungal Pathogen in Rice. Molecular Plant-Microbe Interactions, 2009, 22, 201-210.	1.4	179

#	Article	IF	Citations
182	Characterization of particulate organic matter in the water column of the South China Sea using a shotgun proteomic approach. Limnology and Oceanography, 2010, 55, 1565-1578.	1.6	29
183	The <i>Ustilago maydis</i> Forkhead Transcription Factor Fox1 Is Involved in the Regulation of Genes Required for the Attenuation of Plant Defenses During Pathogenic Development. Molecular Plant-Microbe Interactions, 2010, 23, 1118-1129.	1.4	40
184	Gene ontology study of methyl jasmonate-treated and non-treated hairy roots of Panax ginseng to identify genes involved in secondary metabolic pathway. Russian Journal of Genetics, 2010, 46, 828-835.	0.2	9
185	Near-isogenic cotton germplasm lines that differ in fiber-bundle strength have temporal differences in fiber gene expression patterns as revealed by comparative high-throughput profiling. Theoretical and Applied Genetics, 2010, 120, 1347-1366.	1.8	48
186	EST analysis and annotation of transcripts derived from a trichome-specific cDNA library from Salvia fruticosa. Plant Cell Reports, 2010, 29, 523-534.	2.8	33
187	Comparative Analysis of Expressed Sequence Tags from the White-Rot Fungi (Phanerochaete) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.0	1
188	Characterization of expressed sequence tags (ESTs) of pigeonpea (Cajanus cajan L.) and functional validation of selected genes for abiotic stress tolerance in Arabidopsis thaliana. Molecular Genetics and Genomics, 2010, 283, 273-287.	1.0	43
189	Gene expression profiling during the byssogenesis of zebra mussel (Dreissena polymorpha). Molecular Genetics and Genomics, 2010, 283, 327-339.	1.0	8
190	Regulation of gene expression by chromosome 5A during cold hardening in wheat. Molecular Genetics and Genomics, 2010, 283, 351-363.	1.0	31
191	Differential Gene Expression During Smoltification of Atlantic Salmon (Salmo salar L.): a First Large-Scale Microarray Study. Marine Biotechnology, 2010, 12, 126-140.	1.1	59
192	Microarray-Based Identification of Gonad Transcripts Differentially Expressed Between Lines of Pacific Oyster Selected to Be Resistant or Susceptible to Summer Mortality. Marine Biotechnology, 2010, 12, 326-339.	1.1	53
193	Generation and analysis of expressed sequence tags from the medicinal plant Salvia miltiorrhiza. Science China Life Sciences, 2010, 53, 273-285.	2.3	33
194	Generation and analysis of expressed sequence tags from leaf and root of Withania somnifera (Ashwgandha). Molecular Biology Reports, 2010, 37, 893-902.	1.0	33
195	Transcription of <i>LINE</i>â€derived sequences in exerciseâ€induced stress in horses. Animal Genetics, 2010, 41, 23-27.	0.6	22
196	Transcripts analysis of the entomopathogenic nematode Steinernema carpocapsae induced in vitro with insect haemolymph. Molecular and Biochemical Parasitology, 2010, 169, 79-86.	0.5	35
197	Transcript analysis of parasitic females of the sedentary semi-endoparasitic nematode Rotylenchulus reniformis. Molecular and Biochemical Parasitology, 2010, 172, 31-40.	0.5	24
198	Transcriptomic analyses of the avirulent protozoan parasite Trypanosoma rangeli. Molecular and Biochemical Parasitology, 2010, 174, 18-25.	0.5	32
199	Molecular and cellular aspects of amphibian lens regeneration. Progress in Retinal and Eye Research, 2010, 29, 543-555.	7.3	89

#	ARTICLE	IF	CITATIONS
200	Transcriptomic and proteomic effects of a neonicotinoid insecticide mixture in the marine mussel (Mytilus galloprovincialis, Lam.). Science of the Total Environment, 2010, 408, 3775-3786.	3.9	80
201	A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate Lepidodinium chlorophorum. BMC Evolutionary Biology, 2010, 10, 191.	3.2	62
202	The Potential for pathogenicity was present in the ancestor of the Ascomycete subphylum Pezizomycotina. BMC Evolutionary Biology, 2010, 10, 318.	3.2	4
203	TobEA: an atlas of tobacco gene expression from seed to senescence. BMC Genomics, 2010, 11, 142.	1.2	55
204	Transcriptome sequencing in an ecologically important tree species: assembly, annotation, and marker discovery. BMC Genomics, 2010, 11, 180.	1.2	374
205	Use of microarray technology to assess the time course of liver stress response after confinement exposure in gilthead sea bream (Sparus aurata L.). BMC Genomics, 2010, 11, 193.	1.2	92
206	Differences in transcription between free-living and CO2-activated third-stage larvae of Haemonchus contortus. BMC Genomics, 2010, 11, 266.	1.2	47
207	An EST resource for tilapia based on 17 normalized libraries and assembly of 116,899 sequence tags. BMC Genomics, 2010, 11, 278.	1.2	39
208	Temperature increase prevails over acidification in gene expression modulation of amastigote differentiation in Leishmania infantum. BMC Genomics, 2010, 11, 31.	1.2	55
209	Transcriptome analysis reveals nuclear-encoded proteins for the maintenance of temporary plastids in the dinoflagellate Dinophysis acuminata. BMC Genomics, 2010, 11, 366.	1.2	94
210	Transcriptome analysis of the oil-rich seed of the bioenergy crop Jatropha curcas L. BMC Genomics, 2010, 11, 462.	1.2	118
211	Generation and analysis of ESTs from strawberry (Fragaria xananassa) fruits and evaluation of their utility in genetic and molecular studies. BMC Genomics, 2010, 11, 503.	1.2	75
212	Differential gene expression during the moult cycle of Antarctic krill (Euphausia superba). BMC Genomics, 2010, 11, 582.	1.2	43
213	A sweetpotato gene index established by de novo assembly of pyrosequencing and Sanger sequences and mining for gene-based microsatellite markers. BMC Genomics, 2010, 11, 604.	1.2	86
214	Transcriptome and proteome analysis of Pinctada margaritifera calcifying mantle and shell: focus on biomineralization. BMC Genomics, 2010, 11, 613.	1.2	208
215	Analyses of genome architecture and gene expression reveal novel candidate virulence factors in the secretome of Phytophthora infestans. BMC Genomics, 2010, 11, 637.	1.2	188
216	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.	1.2	82
217	De novo assembled expressed gene catalog of a fast-growing Eucalyptus tree produced by Illumina mRNA-Seq. BMC Genomics, 2010, 11, 681.	1.2	150

#	ARTICLE	IF	CITATIONS
218	The venom composition of the parasitic wasp Chelonus inanitus resolved by combined expressed sequence tags analysis and proteomic approach. BMC Genomics, 2010, 11, 693.	1.2	102
219	Gene discovery in the horned beetle Onthophagus taurus. BMC Genomics, 2010, 11, 703.	1.2	40
220	De novo assembly and characterization of root transcriptome using Illumina paired-end sequencing and development of cSSR markers in sweetpotato (Ipomoea batatas). BMC Genomics, 2010, 11, 726.	1.2	386
221	Transcriptome analysis of the Cryptocaryon irritans tomont stage identifies potential genes for the detection and control of cryptocaryonosis. BMC Genomics, 2010, 11, 76.	1.2	38
222	Generation, analysis and functional annotation of expressed sequence tags from the sheepshead minnow (Cyprinodon variegatus). BMC Genomics, 2010, 11, S4.	1.2	3
223	In vitro homology search array comprehensively reveals highly conserved genes and their functional characteristics in non-sequenced species. BMC Genomics, 2010, 11, S9.	1.2	3
224	Computational prediction of the Crc regulon identifies genus-wide and species-specific targets of catabolite repression control in Pseudomonas bacteria. BMC Microbiology, 2010, 10, 300.	1.3	34
225	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass (Lolium spp.). BMC Plant Biology, 2010, 10, 177.	1.6	42
226	Transcriptional profile of maize roots under acid soil growth. BMC Plant Biology, 2010, 10, 196.	1.6	51
227	A molecular recombination map of Antirrhinum majus. BMC Plant Biology, 2010, 10, 275.	1.6	16
228	Identification and characterization of NAGNAG alternative splicing in the moss Physcomitrella patens. BMC Plant Biology, 2010, 10, 76.	1.6	13
229	Large impact of the apoplast on somatic embryogenesis in Cyclamen persicum offers possibilities for improved developmental control in vitro. BMC Plant Biology, 2010, 10, 77.	1.6	30
230	Dating and functional characterization of duplicated genes in the apple (Malus domestica Borkh.) by analyzing EST data. BMC Plant Biology, 2010, 10, 87.	1.6	20
231	Uncovering the evolutionary origin of plant molecular processes: comparison of Coleochaete (Coleochaetales) and Spirogyra (Zygnematales) transcriptomes. BMC Plant Biology, 2010, 10, 96.	1.6	91
232	Gene expression responses of paper birch (Betula papyrifera) to elevated CO2 and O3 during leaf maturation and senescence. Environmental Pollution, 2010, 158, 959-968.	3.7	39
233	Gene transcription profiles, global DNA methylation and potential transgenerational epigenetic effects related to Zn exposure history in Daphnia magna. Environmental Pollution, 2010, 158, 3323-3329.	3.7	42
234	Gene transcription and higher-level effects of multigenerational Zn exposure in Daphnia magna. Chemosphere, 2010, 80, 1014-1020.	4.2	39
235	Transcriptomics throughout the life cycle of Leishmania infantum: High down-regulation rate in the amastigote stage. International Journal for Parasitology, 2010, 40, 1497-1516.	1.3	77

#	Article	IF	Citations
236	Analysis of expressed sequence tags from a significant livestock pest, the stable fly (<i>Stomoxys) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Archives of Insect Biochemistry and Physiology, 2010, 74, 179-204.	0.6	17
237	First transcriptomic analysis of the economically important parasitic nematode, Trichostrongylus colubriformis, using a next-generation sequencing approach. Infection, Genetics and Evolution, 2010, 10, 1199-1207.	1.0	55
238	Analysis of expressed sequence tags from a NaHCO3-treated alkali-tolerant plant, Chloris virgata. Plant Physiology and Biochemistry, 2010, 48, 247-255.	2.8	18
239	Gene expression in developing fibres of Upland cotton (Gossypium hirsutum L.) was massively altered by domestication. BMC Biology, 2010, 8, 139.	1.7	87
240	Identification of <i>Leishmaniaâ€</i>specific protein phosphorylation sites by LCâ€ESIâ€MS/MS and comparative genomics analyses. Proteomics, 2010, 10, 3868-3883.	1.3	35
241	CHARACTERIZATION AND EXPRESSION OF NUCLEARâ€ENCODED POLYKETIDE SYNTHASES IN THE BREVETOXINâ€PRODUCING DINOFLAGELLATE <i>KARENIA BREVIS</i>¹. Journal of Phycology, 2010, 46, 541-552.	1.0	40
242	Comparative ecophysiology and genomics of the toxic unicellular alga <i>Fibrocapsa japonica</i>. New Phytologist, 2010, 185, 446-458.	3.5	7
243	Comprehensive Analysis of Expressed Sequence Tags from the Pulp of the Red Mutant â€˜Cara Caraâ€™ Navel Orange (<i>Citrus sinensis</i> Osbeck). Journal of Integrative Plant Biology, 2010, 52, 856-867.	4.1	12
244	Discovery of host defence genes in the Japanese scallop Mizuhopecten yessoensis Jay by expressed sequence tag analysis of kidney tissue. Aquaculture Research, 2010, 41, 1602-1613.	0.9	18
245	Differential gene expression in senescing leaves of two silver birch genotypes in response to elevated CO₂ and tropospheric ozone. Plant, Cell and Environment, 2010, 33, 1016-1028.	2.8	37
246	Pyrosequencing the <i>Manduca sexta</i> larval midgut transcriptome: messages for digestion, detoxification and defence. Insect Molecular Biology, 2010, 19, 61-75.	1.0	148
247	Gene expression associated with changes in cold tolerance levels of the Antarctic springtail, <i>Cryptopygus antarcticus</i>. Insect Molecular Biology, 2010, 19, 113-120.	1.0	92
248	Comparative analysis of the <i>Acyrthosiphon pisum</i> genome and expressed sequence tagâ€based gene sets from other aphid species. Insect Molecular Biology, 2010, 19, 33-45.	1.0	27
249	Variation in gene expression of<i>Andropogon gerardii</i>in response to altered environmental conditions associated with climate change. Journal of Ecology, 2010, 98, 374-383.	1.9	29
250	Finding candidate genes under positive selection in Non-model species: examples of genes involved in host specialization in pathogens. Molecular Ecology, 2010, 19, 292-306.	2.0	44
251	Rapid evolution and selection inferred from the transcriptomes of sympatric crater lake cichlid fishes. Molecular Ecology, 2010, 19, 197-211.	2.0	203
252	Bayesian analysis of molecular variance in pyrosequences quantifies population genetic structure across the genome of Lycaeides butterflies. Molecular Ecology, 2010, 19, no-no.	2.0	87
253	Non-additive gene regulation in a citrus allotetraploid somatic hybrid between C. reticulata Blanco and C. limon (L.) Burm. Heredity, 2010, 105, 299-308.	1.2	34

#	ARTICLE	IF	CITATIONS
254	High bicarbonate assimilation in the dark by Arctic bacteria. ISME Journal, 2010, 4, 1581-1590.	4.4	131
255	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	13.7	1,442
256	Generation and analysis of 10 000 ESTs from the halfâ€smooth tongue sole <i>Cynoglossus semilaevis</i> and identification of microsatellite and SNP markers. Journal of Fish Biology, 2010, 76, 1190-1204.	0.7	27
257	Annotation and overview of the <i>Pseudomonas savastanoi</i> pv. savastanoi NCPPB 3335 draft genome reveals the virulence gene complement of a tumourâ€inducing pathogen of woody hosts. Environmental Microbiology, 2010, 12, 1604-1620.	1.8	80
258	An ESTâ€based genome scan using 454 sequencing in the marine snail <i>Littorina saxatilis</i>. Journal of Evolutionary Biology, 2010, 23, 2004-2016.	0.8	71
260	A Transcript Accounting from Diverse Tissues of a Cultivated Strawberry. Plant Genome, 2010, 3, .	1.6	22
261	The Circadian Clockâ€controlled Transcriptome of Developing Soybean Seeds. Plant Genome, 2010, 3, .	1.6	38
262	In silico identification of coffee genome expressed sequences potentially associated with resistance to diseases. Genetics and Molecular Biology, 2010, 33, 795-806.	0.6	13
263	Combining Next-Generation Sequencing Strategies for Rapid Molecular Resource Development from an Invasive Aphid Species, Aphis glycines. PLoS ONE, 2010, 5, e11370.	1.1	77
264	Identification and Characterization of Full-Length cDNAs in Channel Catfish (Ictalurus punctatus) and Blue Catfish (Ictalurus furcatus). PLoS ONE, 2010, 5, e11546.	1.1	40
265	Tissue-Specific Transcriptomics of the Exotic Invasive Insect Pest Emerald Ash Borer (Agrilus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 T	1.1	87
266	De Novo Transcriptome Sequencing in Anopheles funestus Using Illumina RNA-Seq Technology. PLoS ONE, 2010, 5, e14202.	1.1	132
267	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
268	Isolation and characterization of genes functionally involved in ovarian development of the giant tiger shrimp Penaeus monodon by suppression subtractive hybridization (SSH). Genetics and Molecular Biology, 2010, 33, 676-685.	0.6	18
269	Gene expression profiling of genetically determined growth variation in bivalve larvae (<i>Crassostrea gigas</i>). Journal of Experimental Biology, 2010, 213, 749-758.	0.8	64
270	Computational Analysis of Ciona intestinalis Operons. Integrative and Comparative Biology, 2010, 50, 75-85.	0.9	8
271	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. Nucleic Acids Research, 2010, 38, e171-e171.	6.5	62
272	Identification of genes associated with bud dormancy release in Prunus persica by suppression subtractive hybridization. Tree Physiology, 2010, 30, 655-666.	1.4	102

#	ARTICLE	IF	CITATIONS
273	Transcriptomic Insights into the Physiology of Aspergillus niger Approaching a Specific Growth Rate of Zero. Applied and Environmental Microbiology, 2010, 76, 5344-5355.	1.4	52
274	ESTs from Seeds to Assist the Selective Breeding of <i>Jatropha curcas</i> L. for Oil and Active Compounds. Genomics Insights, 2010, 3, GEI.S4340.	3.0	26
275	SIMAPâ€"a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. Nucleic Acids Research, 2010, 38, D223-D226.	6.5	40
276	High-throughput sequence analysis of <i>Ciona intestinalis</i> SL <i>trans</i>-spliced mRNAs: Alternative expression modes and gene function correlates. Genome Research, 2010, 20, 636-645.	2.4	40
277	Massively parallel sequencing and analysis of expressed sequence tags in a successful invasive plant. Annals of Botany, 2010, 106, 1009-1017.	1.4	33
278	Hyperexpression of the X Chromosome in Both Sexes Results in Extensive Female Bias of X-Linked Genes in the Flour Beetle. Genome Biology and Evolution, 2010, 2, 336-346.	1.1	103
279	A Protein Involved in the Assembly of an Extracellular Calcium Storage Matrix. Journal of Biological Chemistry, 2010, 285, 12831-12839.	1.6	42
280	Generation and Analysis of Expressed Sequence Tags from<i>Olea europaea</i>L.. Comparative and Functional Genomics, 2010, 2010, 1-9.	2.0	16
281	Gene Expression Analysis Reveals a Gene Set Discriminatory to Different Metals in Soil. Toxicological Sciences, 2010, 115, 34-40.	1.4	31
282	Molecular authentication of the traditional Chinese medicinal plant Angelica sinensis based on internal transcribed spacer of nrDNA. Electronic Journal of Biotechnology, 2010, 13, .	1.2	2
283	Analyses of an Expressed Sequence Tag Library from Taenia solium, Cysticerca. PLoS Neglected Tropical Diseases, 2010, 4, e919.	1.3	12
284	The Transcription Factor Rbf1 Is the Master Regulator for b-Mating Type Controlled Pathogenic Development in Ustilago maydis. PLoS Pathogens, 2010, 6, e1001035.	2.1	114
285	Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Nucleic Acids Research, 2010, 38, W210-W213.	6.5	283
286	De novo Assembly of a 40 Mb Eukaryotic Genome from Short Sequence Reads: Sordaria macrospora, a Model Organism for Fungal Morphogenesis. PLoS Genetics, 2010, 6, e1000891.	1.5	169
287	Massively Parallel Sequencing and Analysis of the Necator americanus Transcriptome. PLoS Neglected Tropical Diseases, 2010, 4, e684.	1.3	66
288	Serial Expression Analysis: a web tool for the analysis of serial gene expression data. Nucleic Acids Research, 2010, 38, W239-W245.	6.5	12
289	Practical Applications of the Gene Ontology Resource. , 2010, , 319-339.		0
290	Transcriptional responses to thermal acclimation in the eurythermal fish Gillichthys mirabilis (Cooper 1864). American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2010, 299, R843-R852.	0.9	62

#	ARTICLE	IF	CITATIONS
291	Does an expressed sequence tag (EST) library ofSalsola iberica(tumbleweed) help to understand plant responses to environmental stresses?. Plant Signaling and Behavior, 2010, 5, 1330-1335.	1.2	2
292	Exploring molecular signaling in plant-fungal symbioses using high throughput RNA sequencing. Plant Signaling and Behavior, 2010, 5, 1353-1358.	1.2	8
293	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. Genome Research, 2010, 20, 837-846.	2.4	155
294	Generation and Analysis of ESTs from the Grass Carp,Ctenopharyngodon idellus. Animal Biotechnology, 2010, 21, 217-225.	0.7	5
295	Integrated Metabonomicâ˜'Proteomic Analysis of an Insectâ˜'Bacterial Symbiotic System. Journal of Proteome Research, 2010, 9, 1257-1267.	1.8	47
296	<i>Thermus thermophilus</i> Proteins That Are Differentially Expressed in Response to Growth Temperature and Their Implication in Thermoadaptation. Journal of Proteome Research, 2010, 9, 855-864.	1.8	18
298	Transcriptomic response of the Pacific oyster Crassostrea gigas to hypoxia. Marine Genomics, 2010, 3, 133-143.	0.4	83
299	The ascorbic acid content of tomato fruits is associated with the expression of genes involved in pectin degradation. BMC Plant Biology, 2010, 10, 163.	1.6	103
300	SSHscreen and SSHdb, generic software for microarray based gene discovery: application to the stress response in cowpea. Plant Methods, 2010, 6, 10.	1.9	15
301	Proteomic and Phosphoproteomic Analysis at Diapause Initiation in the Cotton Bollworm, <i>Helicoverpa armigera</i>. Journal of Proteome Research, 2010, 9, 5053-5064.	1.8	71
302	Novel Ser/Thr Protein Phosphatase 5 (PP5) Regulated Targets during DNA Damage Identified by Proteomics Analysis. Journal of Proteome Research, 2010, 9, 945-953.	1.8	18
303	The effect of tert-butyl hydroperoxide on hepatic transcriptome expression patterns in the striped sea bream (Lithognathus mormyrus;<i>Teleostei</i>). Free Radical Research, 2010, 44, 991-1003.	1.5	2
304	Effects of acute dieldrin exposure on neurotransmitters and global gene transcription in largemouth bass (Micropterus salmoides) hypothalamus. NeuroToxicology, 2010, 31, 356-366.	1.4	42
305	Gene expression analysis of volatile-rich male flowers of dioecious Pandanus fascicularis using expressed sequence tags. Journal of Plant Physiology, 2010, 167, 914-919.	1.6	6
306	Differentially expressed genes following persistent infection with infectious pancreatic necrosis virus in vitro and in vivo. Fish and Shellfish Immunology, 2010, 28, 845-853.	1.6	35
307	Assembled catalog of immune-related genes from allogeneic challenged corals that unveils the participation of vWF-like transcript. Developmental and Comparative Immunology, 2010, 34, 630-637.	1.0	8
308	Mixtures of similarly acting compounds in Daphnia magna: From gene to metabolite and beyond. Environment International, 2010, 36, 254-268.	4.8	83
309	Multi-transcript expression patterns in the gastrolith disk and the hypodermis of the crayfish Cherax quadricarinatus at premolt. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2010, 5, 171-177.	0.4	11

#	Article	IF	Citations
310	Analysis and functional annotation of expressed sequence tags from in vitro cell lines of elasmobranchs: Spiny dogfish shark (Squalus acanthias) and little skate (Leucoraja erinacea). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2010, 5, 199-206.	0.4	11
311	Identification and mapping of genes related to caffeoylquinic acid synthesis in Cynara cardunculus L.. Plant Science, 2010, 179, 338-347.	1.7	54
312	Hepatic transcriptomic and metabolomic responses in the Stickleback (Gasterosteus aculeatus) exposed to ethinyl-estradiol. Aquatic Toxicology, 2010, 97, 174-187.	1.9	71
313	Can metal stress induce transferable changes in gene transcription in Daphnia magna?. Aquatic Toxicology, 2010, 97, 188-195.	1.9	32
314	Gene expression profiling of the fathead minnow (Pimephales promelas) neuroendocrine brain in response to pulp and paper mill effluents. Aquatic Toxicology, 2010, 99, 379-388.	1.9	21
315	Digital expression profiling of novel diatom transcripts provides insight into their biological functions. Genome Biology, 2010, 11, R85.	13.9	97
316	agriGO: a GO analysis toolkit for the agricultural community. Nucleic Acids Research, 2010, 38, W64-W70.	6.5	2,289
317	Survey of the transcriptome of Aspergillus oryzae via massively parallel mRNA sequencing. Nucleic Acids Research, 2010, 38, 5075-5087.	6.5	189
318	Introduction to Marine Genomics. , 2010, , .		6
319	A first genome assembly of the barley fungal pathogen Pyrenophora teres f. teres. Genome Biology, 2010, 11, R109.	3.8	90
320	Assembly of 500,000 inter-specific catfish expressed sequence tags and large scale gene-associated marker development for whole genome association studies. Genome Biology, 2010, 11, R8.	13.9	83
321	Discovery and characterization of nutritionally regulated genes associated with muscle growth in Atlantic salmon. Physiological Genomics, 2010, 42A, 114-130.	1.0	63
323	Large changes in anatomy and physiology between diploid Rangpur lime (Citrus limonia) and its autotetraploid are not associated with large changes in leaf gene expression. Journal of Experimental Botany, 2011, 62, 2507-2519.	2.4	146
324	Metabolomics of Microliter Hemolymph Samples Enables an Improved Understanding of the Combined Metabolic and Transcriptional Responses of <i>Daphnia magna</i> to Cadmium. Environmental Science & Technology, 2011, 45, 3710-3717.	4.6	83
325	Toxicity evaluation of benzo[a]pyrene on the polychaete Perinereis nuntia using subtractive cDNA libraries. Aquatic Toxicology, 2011, 105, 279-291.	1.9	15
326	Construction and characterization of Japanese medaka (Oryzias latipes) hepatic cDNA library and its implementation to biomarker screening in aquatic toxicology. Aquatic Toxicology, 2011, 105, 569-575.	1.9	8
327	Heartworm Genomics: Unprecedented Opportunities for Fundamental Molecular Insights and New Intervention Strategies. Topics in Companion Animal Medicine, 2011, 26, 193-199.	0.4	5
328	The General Transcriptional Repressor Tup1 Is Required for Dimorphism and Virulence in a Fungal Plant Pathogen. PLoS Pathogens, 2011, 7, e1002235.	2.1	52

#	ARTICLE	IF	CITATIONS
329	Transcriptomics of the Bed Bug (Cimex lectularius). PLoS ONE, 2011, 6, e16336.	1.1	120
330	ABA-Dependent and -Independent G-Protein Signaling in <i>Arabidopsis</i> Roots Revealed through an iTRAQ Proteomics Approach. Journal of Proteome Research, 2011, 10, 3107-3122.	1.8	38
331	The tale of a resting gland: Transcriptome of a replete venom gland from the scorpion Hottentotta judaicus. Toxicon, 2011, 57, 695-703.	0.8	82
332	A transcriptomic scan for positively selected genes in two closely related marine fishes: Sebastes caurinus and S. rastrelliger. Marine Genomics, 2011, 4, 93-98.	0.4	11
333	Transcriptome sequencing of a highly salt tolerant mangrove species Sonneratia alba using Illumina platform. Marine Genomics, 2011, 4, 129-136.	0.4	49
334	Expressed sequence tags from heat-shocked seagrass Zostera noltii (Hornemann) from its southern distribution range. Marine Genomics, 2011, 4, 181-188.	0.4	29
335	Functional annotation of an expressed sequence tag library from Haliotis diversicolor and analysis of its plant-like sequences. Marine Genomics, 2011, 4, 189-196.	0.4	10
336	Transcriptome analysis in Concholepas concholepas (Gastropoda, Muricidae): Mining and characterization of new genomic and molecular markers. Marine Genomics, 2011, 4, 197-205.	0.4	22
337	In silico whole-genome EST analysis reveals 2322 novel microsatellites for the silver-lipped pearl oyster, Pinctada maxima. Marine Genomics, 2011, 4, 287-290.	0.4	11
338	Cabomba as a model for studies of early angiosperm evolution. Annals of Botany, 2011, 108, 589-598.	1.4	30
340	Novel male-biased expression in paralogs of the aphid slimfast nutrient amino acid transporter expansion. BMC Evolutionary Biology, 2011, 11, 253.	3.2	11
341	Fortunella margarita Transcriptional Reprogramming Triggered by Xanthomonas citri subsp. citri. BMC Plant Biology, 2011, 11, 159.	1.6	21
342	Transcriptome characterization of the South African abalone Haliotis midae using sequencing-by-synthesis. BMC Research Notes, 2011, 4, 59.	0.6	65
343	<i>Pectobacterium carotovorum</i>Elicits Plant Cell Death with DspE/F but the<i>P. carotovorum</i>DspE Does Not Suppress Callose or Induce Expression of Plant Genes Early in Plantâ€"Microbe Interactions. Molecular Plant-Microbe Interactions, 2011, 24, 773-786.	1.4	60
344	Predicted Effector Molecules in the Salivary Secretome of the Pea Aphid (<i>Acyrthosiphon pisum</i>): A Dual Transcriptomic/Proteomic Approach. Journal of Proteome Research, 2011, 10, 1505-1518.	1.8	219
345	Development of Expressed Sequence Tag (EST)-Based Cleaved Amplified Polymorphic Sequence (CAPS) Markers of Tea Plant and Their Application to Cultivar Identification. Journal of Agricultural and Food Chemistry, 2011, 59, 1557-1564.	2.4	19
347	The head-regeneration transcriptome of the planarian Schmidtea mediterranea. Genome Biology, 2011, 12, R76.	13.9	109
348	NaÃ¯ve Atlantic salmon (Salmo Salar L.) surviving a lethal challenge with infectious pancreatic necrosis virus (IPNV) shows upregulation of antiviral genes in head-kidney, including Vig-2. Aquaculture, 2011, 318, 300-308.	1.7	8

#	Article	IF	Citations
349	Transcriptional responses in neonate and adult Daphnia magna in relation to relative susceptibility to genotoxicants. Aquatic Toxicology, 2011, 104, 192-204.	1.9	27
350	Integrative assessment of potential effects of dioxins and related compounds in wild Baikal seals (Pusa sibirica): Application of microarray and biochemical analyses. Aquatic Toxicology, 2011, 105, 89-99.	1.9	13
351	Development and assessment of oligonucleotide microarrays for Atlantic salmon (Salmo salar L.). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 31-38.	0.4	86
352	Analysis of expressed sequence tags from the liver and ovary of the euryhaline hermaphroditic fish, Kryptolebias marmoratus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 244-255.	0.4	14
353	Nickel response in function of temperature differences: Effects at different levels of biological organization in Daphnia magna. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 271-281.	0.4	13
354	Gene expression profiling of a fish parasite Ichthyophthirius multifiliis: Insights into development and senescence-associated avirulence. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 382-392.	0.4	11
355	Metazoan Operons Accelerate Recovery from Growth-Arrested States. Cell, 2011, 145, 981-992.	13.5	53
356	Transcriptome analysis of rainbow trout infected with high and low virulence strains of Infectious hematopoietic necrosis virus. Fish and Shellfish Immunology, 2011, 30, 84-93.	1.6	62
357	Suppression subtractive hybridization coupled with microarray analysis to examine differential expression of genes in Japanese flounder Paralichthys olivaceus leucocytes during Edwardsiella tarda and viral hemorrhagic septicemia virus infection. Fish and Shellfish Immunology, 2011, 31, 524-532.	1.6	11
358	Expressed sequence tags reveal genetic diversity and putative virulence factors of the pathogenic oomycete Pythium insidiosum. Fungal Biology, 2011, 115, 683-696.	1.1	53
359	EST analysis on adipose tissue of rainbow trout Oncorhynchus mykiss and tissue distribution of adiponectin. Gene, 2011, 485, 40-45.	1.0	28
360	Distribution and localization of microsatellites in the Perigord black truffle genome and identification of new molecular markers. Fungal Genetics and Biology, 2011, 48, 592-601.	0.9	67
361	Transcriptomes of Plant-Parasitic Nematodes. , 2011, , 119-138.		7
362	Improving reverse vaccinology with a machine learning approach. Vaccine, 2011, 29, 8156-8164.	1.7	52
363	De novo transcriptome sequencing in Salvia miltiorrhiza to identify genes involved in the biosynthesis of active ingredients. Genomics, 2011, 98, 272-279.	1.3	181
364	Bacterial Phosphoproteomic Analysis Reveals the Correlation Between Protein Phosphorylation and Bacterial Pathogenicity. Genomics, Proteomics and Bioinformatics, 2011, 9, 119-127.	3.0	58
365	Arbuscular Mycorrhizal Symbiosis Limits Foliar Transcriptional Responses to Viral Infection and Favors Long-Term Virus Accumulation. Molecular Plant-Microbe Interactions, 2011, 24, 1562-1572.	1.4	33
366	<i>De novo</i> transcriptome characterization and development of genomic tools for <i>Scabiosa columbaria</i> L. using nextâ€generation sequencing techniques. Molecular Ecology Resources, 2011, 11, 662-674.	2.2	44

#	ARTICLE	IF	CITATIONS
367	Discovery of singleâ€nucleotide polymorphisms (SNPs) in the uncharacterized genome of the ascomycete <i>Ophiognomonia clavigignentiâ€juglandacearum</i> from 454 sequence data. Molecular Ecology Resources, 2011, 11, 693-702.	2.2	19
368	Genetic diversity in cultivated carioca common beans based on molecular marker analysis. Genetics and Molecular Biology, 2011, 34, 88-102.	0.6	32
370	Gene Expression Analysis Using RNA-Seq from Organisms Lacking Substantial Genomic Resources. , 2011, , .		0
371	Expressed sequenced tags profiling of resistant and susceptible Gyr x Holstein cattle infested with the tick Rhipicephalus (Boophilus) microplus. Genetics and Molecular Research, 2011, 10, 3803-3816.	0.3	7
372	Lumiestrone is Photochemically Derived from Estrone and may be Released to the Environment without Detection. Frontiers in Endocrinology, 2011, 2, 83.	1.5	29
373	Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: the StRAnGER web application. Frontiers in Neuroscience, 2011, 5, 8.	1.4	30
374	Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont Piriformospora indica. PLoS Pathogens, 2011, 7, e1002290.	2.1	361
375	Transcriptomic Signatures of Ash (Fraxinus spp.) Phloem. PLoS ONE, 2011, 6, e16368.	1.1	54
376	Transcriptome Analysis of the Desert Locust Central Nervous System: Production and Annotation of a Schistocerca gregaria EST Database. PLoS ONE, 2011, 6, e17274.	1.1	90
377	The First Insight into the Tissue Specific Taxus Transcriptome via Illumina Second Generation Sequencing. PLoS ONE, 2011, 6, e21220.	1.1	169
378	Transcriptome Sequencing, and Rapid Development and Application of SNP Markers for the Legume Pod Borer Maruca vitrata (Lepidoptera: Crambidae). PLoS ONE, 2011, 6, e21388.	1.1	30
379	Transcriptome Sequencing and De Novo Analysis for Yesso Scallop (Patinopecten yessoensis) Using 454 GS FLX. PLoS ONE, 2011, 6, e21560.	1.1	204
380	The Fat Body Transcriptomes of the Yellow Fever Mosquito Aedes aegypti, Pre- and Post- Blood Meal. PLoS ONE, 2011, 6, e22573.	1.1	77
381	Generation, Annotation and Analysis of First Large-Scale Expressed Sequence Tags from Developing Fiber of Gossypium barbadense L. PLoS ONE, 2011, 6, e22758.	1.1	25
382	Identifying Schistosoma japonicum Excretory/Secretory Proteins and Their Interactions with Host Immune System. PLoS ONE, 2011, 6, e23786.	1.1	20
383	Sequence and Role in Virulence of the Three Plasmid Complement of the Model Tumor-Inducing Bacterium Pseudomonas savastanoi pv. savastanoi NCPPB 3335. PLoS ONE, 2011, 6, e25705.	1.1	43
384	Transcriptomics of a Giant Freshwater Prawn (Macrobrachium rosenbergii): De Novo Assembly, Annotation and Marker Discovery. PLoS ONE, 2011, 6, e27938.	1.1	94
385	Comparative Transcriptomics of Eastern African Cichlid Fishes Shows Signs of Positive Selection and a Large Contribution of Untranslated Regions to Genetic Diversity. Genome Biology and Evolution, 2011, 3, 443-455.	1.1	56

#	Article	IF	Citations
386	Development and characterization of microsatellite markers for caladiums (<i>Caladium</i> Vent.). Plant Breeding, 2011, 130, 591-595.	1.0	9
387	Narrowing down the apricot <i>Plum pox virus</i> resistance locus and comparative analysis with the peach genome syntenic region. Molecular Plant Pathology, 2011, 12, 535-547.	2.0	28
388	Synganglion transcriptome and developmental global gene expression in adult females of the American dog tick, Dermacentor variabilis (Acari: Ixodidae). Insect Molecular Biology, 2011, 20, 465-491.	1.0	44
389	Transcriptomic response of red grouse to gastroâ€intestinal nematode parasites and testosterone: implications for population dynamics. Molecular Ecology, 2011, 20, 920-931.	2.0	23
390	Interpopulation patterns of divergence and selection across the transcriptome of the copepod Tigriopus californicus. Molecular Ecology, 2011, 20, 560-572.	2.0	61
391	Two linked genes encoding a secreted effector and a membrane protein are essential for <i>Ustilago maydis</i>â€induced tumour formation. Molecular Microbiology, 2011, 81, 751-766.	1.2	138
392	Deep RNA sequencing improved the structural annotation of the <i>Tuber melanosporum</i> transcriptome. New Phytologist, 2011, 189, 883-891.	3.5	54
393	Transcriptome analysis reveals coordinated spatiotemporal regulation of hemoglobin and nitrate reductase in response to nitrate in maize roots. New Phytologist, 2011, 192, 338-352.	3.5	66
394	Active bacteria and archaea cells fixing bicarbonate in the dark along the water column of a stratified eutrophic lagoon. FEMS Microbiology Ecology, 2011, 77, 370-384.	1.3	31
395	Effects of soil properties and time of exposure on gene expression of Enchytraeus albidus (Oligochaeta). Soil Biology and Biochemistry, 2011, 43, 2078-2084.	4.2	13
396	A transcriptomic study on the pepsin-activated infective larvae of Angiostrongylus cantonensis. Molecular and Biochemical Parasitology, 2011, 179, 47-50.	0.5	9
397	Molecular profiling of the gilthead sea bream (Sparus aurata L.) response to chronic exposure to the myxosporean parasite Enteromyxum leei. Molecular Immunology, 2011, 48, 2102-2112.	1.0	57
398	Dynamic gene expression profiles during arm regeneration in the brittle star Amphiura filiformis. Journal of Experimental Marine Biology and Ecology, 2011, 407, 315-322.	0.7	28
399	Transcript profiling of the meiotic drive phenotype in testis of Aedes aegypti using suppressive subtractive hybridization. Journal of Insect Physiology, 2011, 57, 1220-1226.	0.9	6
400	Physiological and Molecular Evidence that Environmental Changes Elicit Morphological Interconversion in the Model Diatom Phaeodactylum tricornutum. Protist, 2011, 162, 462-481.	0.6	84
401	Integration of biochemical, histochemical and toxicogenomic indices for the assessment of health status of mussels from the Tamar Estuary, U.K.. Marine Environmental Research, 2011, 72, 13-24.	1.1	43
402	A proteomics approach to decipher the molecular nature of planarian stem cells. BMC Genomics, 2011, 12, 133.	1.2	33
403	De novo sequence assembly and characterization of the floral transcriptome in cross- and self-fertilizing plants. BMC Genomics, 2011, 12, 298.	1.2	86

#	Article	IF	Citations
404	De novo assembly and characterization of a maternal and developmental transcriptome for the emerging model crustacean Parhyale hawaiensis. BMC Genomics, 2011, 12, 581.	1.2	85
405	Analysis of expression sequence tags from a full-length-enriched cDNA library of developing sesame seeds (Sesamum indicum). BMC Plant Biology, 2011, 11, 180.	1.6	25
406	Comparative analysis of expressed sequence tags (ESTs) between drought-tolerant and -susceptible genotypes of chickpea under terminal drought stress. BMC Plant Biology, 2011, 11, 70.	1.6	86
407	Humic substances affect Arabidopsis physiology by altering the expression of genes involved in primary metabolism, growth and development. Environmental and Experimental Botany, 2011, 74, 45-55.	2.0	110
408	Construction of a cDNA library from female adult of Toxocara canis, and analysis of EST and immune-related genes expressions. Experimental Parasitology, 2011, 129, 120-126.	0.5	9
409	Differential Gene Expression in <i>Daphnia magna</i> Suggests Distinct Modes of Action and Bioavailability for ZnO Nanoparticles and Zn Ions. Environmental Science & Technology, 2011, 45, 762-768.	4.6	176
410	Contrasting cDNA-AFLP profiles between crown and leaf tissues of cold-acclimated wheat plants indicate differing regulatory circuitries for low temperature tolerance. Plant Molecular Biology, 2011, 75, 379-398.	2.0	19
411	Molecular cloning and functional characterization of genes associated with flowering in citrus using an early-flowering trifoliate orange (Poncirus trifoliata L. Raf.) mutant. Plant Molecular Biology, 2011, 76, 187-204.	2.0	19
412	RNA-Seq analysis and de novo transcriptome assembly of Hevea brasiliensis. Plant Molecular Biology, 2011, 77, 299-308.	2.0	131
413	EST Analysis Predicts Putatively Causative Genes Underlying the Pharmaceutical Application of Glycyrrhiza uralensis Fisch. Plant Molecular Biology Reporter, 2011, 29, 814-824.	1.0	6
414	Unraveling new genes associated with seed development and metabolism in Bixa orellana L. by expressed sequence tag (EST) analysis. Molecular Biology Reports, 2011, 38, 1329-1340.	1.0	29
415	Structural characterization and mapping of functional EST-SSR markers in Theobroma cacao. Tree Genetics and Genomes, 2011, 7, 799-817.	0.6	21
416	Expressed sequence tags from Eimeria brunettiâ€"preliminary analysis and functional annotation. Parasitology Research, 2011, 108, 1059-1062.	0.6	5
417	In silico prediction of drug targets in Vibrio cholerae. Protoplasma, 2011, 248, 799-804.	1.0	11
418	Differential Growth-Related Gene Expression in Abalone (Haliotis midae). Marine Biotechnology, 2011, 13, 1125-1139.	1.1	36
419	Proteins involved in biotic and abiotic stress responses as the most significant biomarkers in the ripening of Pinot Noir skins. Functional and Integrative Genomics, 2011, 11, 341-355.	1.4	31
420	Major chimpanzee-specific structural changes in sperm development-associated genes. Functional and Integrative Genomics, 2011, 11, 507-517.	1.4	6
421	PR-10, defensin and cold dehydrin genes are among those over expressed in Oxytropis (Fabaceae) species adapted to the arctic. Functional and Integrative Genomics, 2011, 11, 497-505.	1.4	40

#	Article	IF	Citations
422	Influence of mitochondria on gene expression in a citrus cybrid. Plant Cell Reports, 2011, 30, 1077-1085.	2.8	16
423	Genetic mapping of DArT markers in the Festucaâ€"Lolium complex and their use in freezing tolerance association analysis. Theoretical and Applied Genetics, 2011, 122, 1133-1147.	1.8	27
424	Comparative analysis of putative pathogenesis-related gene expression in two Rhizoctonia solani pathosystems. Current Genetics, 2011, 57, 391-408.	0.8	21
425	Identification of differentially expressed genes during bud stage of cotton boll development using suppression subtractive hybridization and cDNA macroarray. Journal of Plant Biochemistry and Biotechnology, 2011, 20, 12-19.	0.9	0
426	Development of fifty-one novel EST-SSR loci for use in rockfish (genus Sebastes). Conservation Genetics Resources, 2011, 3, 335-340.	0.4	1
427	Gene expression analysis of â€œgreen tideâ€•alga Ulva prolifera (Chlorophyta) in China. Genes and Genomics, 2011, 33, 173-178.	0.5	9
428	Toxicogenomic investigation of Tetrahymena thermophila exposed to dichlorodiphenyltrichloroethane (DDT), tributyltin (TBT), and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). Science China Life Sciences, 2011, 54, 617-625.	2.3	9
429	Profiling of the transcriptome of Porphyra yezoensis with Solexa sequencing technology. Science Bulletin, 2011, 56, 2119-2130.	1.7	32
430	A cDNA microarray, UniShrimpChip, for identification of genes relevant to testicular development in the black tiger shrimp (Penaeus monodon). BMC Molecular Biology, 2011, 12, 15.	3.0	23
431	Transcriptional analysis of cell growth and morphogenesis in the unicellular green alga Micrasterias(Streptophyta), with emphasis on the role of expansin. BMC Plant Biology, 2011, 11, 128.	1.6	34
432	From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC Plant Biology, 2011, 11, 131.	1.6	109
433	Transcriptomics of shading-induced and NAA-induced abscission in apple (Malus domestica) reveals a shared pathway involving reduced photosynthesis, alterations in carbohydrate transport and signaling and hormone crosstalk. BMC Plant Biology, 2011, 11, 138.	1.6	104
434	Chemical and transcriptional responses of Norway spruce genotypes with different susceptibility to Heterobasidion spp. infection. BMC Plant Biology, 2011, 11, 154.	1.6	82
435	Identification and analysis of phosphorylation status of proteins in dormant terminal buds of poplar. BMC Plant Biology, 2011, 11, 158.	1.6	22
436	Maize microarray annotation database. Plant Methods, 2011, 7, 31.	1.9	9
437	Gene expression pattern in swine neutrophils after lipopolysaccharide exposure: a time course comparison. BMC Proceedings, 2011, 5, S11.	1.8	3
438	mRNA sequencing of Eucalyptus urograndistrees supplemented with flavonoids shows changes on metabolic process and decrease of lignification. BMC Proceedings, 2011, 5, .	1.8	0
439	Functional markers development and genetic diversity analysis in Eucalyptus globuluswith emphasis in wood quality candidate genes. BMC Proceedings, 2011, 5, .	1.8	2

#	Article	IF	Citations
440	Comparative transcriptome analysis of tree Eucalyptusspecies using RNAseq technology: analysis of genes interfering in wood quality aspects. BMC Proceedings, 2011, 5, .	1.8	3
441	Expressed sequence tags from Atta laevigata and identification of candidate genes for the control of pest leaf-cutting ants. BMC Research Notes, 2011, 4, 203.	0.6	3
442	Comparison of RNA expression profiles on generations of Porphyra yezoensis (Rhodophyta), based on suppression subtractive hybridization (SSH). BMC Research Notes, 2011, 4, 428.	0.6	9
443	Generation, analysis and functional annotation of expressed sequence tags from the ectoparasitic mite Psoroptes ovis. Parasites and Vectors, 2011, 4, 145.	1.0	12
444	Gene discovery in Triatoma infestans. Parasites and Vectors, 2011, 4, 39.	1.0	7
445	Major prospects for exploring canine vector borne diseases and novel intervention methods using 'omic technologies. Parasites and Vectors, 2011, 4, 53.	1.0	2
446	Comparative analyses of Campylobacter concisus strains reveal the genome of the reference strain BAA-1457 is not representative of the species. Gut Pathogens, 2011, 3, 15.	1.6	23
447	Reptilian-transcriptome v1.0, a glimpse in the brain transcriptome of five divergent Sauropsida lineages and the phylogenetic position of turtles. EvoDevo, 2011, 2, 19.	1.3	52
448	GOmotif: A web server for investigating the biological role of protein sequence motifs. BMC Bioinformatics, 2011, 12, 379.	1.2	0
449	AIGO: Towards a unified framework for the Analysis and the Inter-comparison of GO functional annotations. BMC Bioinformatics, 2011, 12, 431.	1.2	12
450	iGepros: an integrated gene and protein annotation server for biological nature exploration. BMC Bioinformatics, 2011, 12, S6.	1.2	11
451	Genetic mechanisms involved in the evolution of the cephalopod camera eye revealed by transcriptomic and developmental studies. BMC Evolutionary Biology, 2011, 11, 180.	3.2	17
452	Generation and analysis of expressed sequence tags (ESTs) for marker development in yam (Dioscorea) Tj ETQq0 0 0 rgBT /Overlock 10	1.2	34
453	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
454	Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC1 population between gossypium hirsutum and G. barbadense. BMC Genomics, 2011, 12, 15.	1.2	153
455	A high-density transcript linkage map with 1,845 expressed genes positioned by microarray-based Single Feature Polymorphisms (SFP) in Eucalyptus. BMC Genomics, 2011, 12, 189.	1.2	23
456	Interactions of a pesticide/heavy metal mixture in marine bivalves: a transcriptomic assessment. BMC Genomics, 2011, 12, 195.	1.2	83
457	Identification of ovule transcripts from the Apospory-Specific Genomic Region (ASGR)-carrier chromosome. BMC Genomics, 2011, 12, 206.	1.2	18

#	Article	IF	Citations
458	Profiling the venom gland transcriptomes of Costa Rican snakes by 454 pyrosequencing. BMC Genomics, 2011, 12, 259.	1.2	96
459	Microarray analysis and scale-free gene networks identify candidate regulators in drought-stressed roots of loblolly pine (P. taeda L.). BMC Genomics, 2011, 12, 264.	1.2	110
460	A honey bee (Apis mellifera L.) PeptideAtlas crossing castes and tissues. BMC Genomics, 2011, 12, 290.	1.2	15
461	De novo sequencing and characterization of floral transcriptome in two species of buckwheat (Fagopyrum). BMC Genomics, 2011, 12, 30.	1.2	132
462	Short read Illumina data for the de novo assembly of a non-model snail species transcriptome (Radix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 2011, 12, 317.	1.2	137
463	Transcriptomic response of the red tide dinoflagellate, Karenia brevis, to nitrogen and phosphorus depletion and addition. BMC Genomics, 2011, 12, 346.	1.2	111
464	Comparative high-throughput transcriptome sequencing and development of SiESTa, the Silene EST annotation database. BMC Genomics, 2011, 12, 376.	1.2	25
465	The mosaicism of plasmids revealed by atypical genes detection and analysis. BMC Genomics, 2011, 12, 403.	1.2	16
466	Differential gene expression in male and female rainbow trout embryos prior to the onset of gross morphological differentiation of the gonads. BMC Genomics, 2011, 12, 404.	1.2	48
467	A combined functional and structural genomics approach identified an EST-SSR marker with complete linkage to the Ligon lintless-2 genetic locus in cotton (Gossypium hirsutum L.). BMC Genomics, 2011, 12, 445.	1.2	49
468	Characterization of the sesame (Sesamum indicum L.) global transcriptome using Illumina paired-end sequencing and development of EST-SSR markers. BMC Genomics, 2011, 12, 451.	1.2	354
469	New resources for functional analysis of omics data for the genus Aspergillus. BMC Genomics, 2011, 12, 486.	1.2	28
470	The transcriptome of the novel dinoflagellate Oxyrrhis marina (Alveolata: Dinophyceae): response to salinity examined by 454 sequencing. BMC Genomics, 2011, 12, 519.	1.2	38
471	Development of a novel multiplex DNA microarray for Fusarium graminearum and analysis of azole fungicide responses. BMC Genomics, 2011, 12, 52.	1.2	108
472	Generation of genome-scale gene-associated SNPs in catfish for the construction of a high-density SNP array. BMC Genomics, 2011, 12, 53.	1.2	122
473	The maternal and early embryonic transcriptome of the milkweed bug Oncopeltus fasciatus. BMC Genomics, 2011, 12, 61.	1.2	110
474	An Expressed Sequence Tag collection from the male antennae of the Noctuid moth Spodoptera littoralis: a resource for olfactory and pheromone detection research. BMC Genomics, 2011, 12, 86.	1.2	145
475	De novo characterization of the gametophyte transcriptome in bracken fern, Pteridium aquilinum. BMC Genomics, 2011, 12, 99.	1.2	113

#	Article	IF	Citations
476	Anti-inflammatory effects of tetradecylthioacetic acid (TTA) in macrophage-like cells from Atlantic salmon (Salmo salar L.). BMC Immunology, 2011, 12, 41.	0.9	3
477	Transcriptional and proteomic profiling of flatfish (<i>Solea senegalensis</i>) spermatogenesis. Proteomics, 2011, 11, 2195-2211.	1.3	29
478	Phosphoproteome analysis of the pathogenic bacterium <i>Helicobacter pylori</i> reveals overâ€representation of tyrosine phosphorylation and multiply phosphorylated proteins. Proteomics, 2011, 11, 1449-1461.	1.3	59
479	Purification and characterization of a native zincâ€binding high molecular weight multiprotein complex from human seminal plasma. Journal of Separation Science, 2011, 34, 1076-1083.	1.3	8
480	Characterization of the human serum depletome by labelâ€free shotgun proteomics. Journal of Separation Science, 2011, 34, 1621-1626.	1.3	36
481	Development of a microarray for <i>Enchytraeus albidus</i> (Oligochaeta): preliminary tool with diverse applications. Environmental Toxicology and Chemistry, 2011, 30, 1395-1402.	2.2	17
482	Identification of molecular motors in the Woods Hole squid, <i>Loligo pealei</i>: An expressed sequence tag approach. Cytoskeleton, 2011, 68, 566-577.	1.0	9
483	Network-based function prediction and interactomics: The case for metabolic enzymes. Metabolic Engineering, 2011, 13, 1-10.	3.6	43
484	Non-random sharing of Plantae genes. Communicative and Integrative Biology, 2011, 4, 361-363.	0.6	1
485	Global Transcriptome Analysis of Constitutive Resistance to the White Pine Weevil in Spruce. Genome Biology and Evolution, 2011, 3, 851-867.	1.1	27
486	DNA methylation in liver tumorigenesis in fish from the environment. Epigenetics, 2011, 6, 1319-1333.	1.3	54
487	Comparative study of transcriptional and physiological responses to salinity stress in two contrasting Populus alba L. genotypes. Tree Physiology, 2011, 31, 1335-1355.	1.4	44
488	Genome Economization in the Endosymbiont of the Wood Roach Cryptocercus punctulatus Due to Drastic Loss of Amino Acid Synthesis Capabilities. Genome Biology and Evolution, 2011, 3, 1437-1448.	1.1	35
489	Physiology and gene expression of the rice landrace Horkuch under salt stress. Functional Plant Biology, 2011, 38, 282.	1.1	20
490	B2G-FAR, a species-centered GO annotation repository. Bioinformatics, 2011, 27, 919-924.	1.8	137
491	Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells. Human Molecular Genetics, 2011, 20, 4932-4946.	1.4	16
492	Transcriptome Sequencing of Hevea brasiliensis for Development of Microsatellite Markers and Construction of a Genetic Linkage Map. DNA Research, 2011, 18, 471-482.	1.5	117
493	Transcriptomics of Actinorhizal Symbioses Reveals Homologs of the Whole Common Symbiotic Signaling Cascade Â. Plant Physiology, 2011, 156, 700-711.	2.3	156

#	ARTICLE	IF	CITATIONS
494	mRNA/microRNA Profile at the Metamorphic Stage of Olive Flounder (<i>Paralichthys olivaceus</i>). Comparative and Functional Genomics, 2011, 2011, 1-12.	2.0	16
495	Transcriptome Analysis of Sarracenia, an Insectivorous Plant. DNA Research, 2011, 18, 253-261.	1.5	28
496	Modulation of behavioral phase changes of the migratory locust by the catecholamine metabolic pathway. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3882-3887.	3.3	175
497	miR-124 function during <i>Ciona intestinalis</i> neuronal development includes extensive interaction with the Notch signaling pathway. Development (Cambridge), 2011, 138, 4943-4953.	1.2	46
498	Prediction and Validation of Promoters Involved in the Abscisic Acid Response in Physcomitrella patens. Molecular Plant, 2011, 4, 713-729.	3.9	30
499	Analysis of Sexually Dimorphic Expression of Genes at Early Gonadogenesis of Pejerrey <i>Odontesthes bonariensis</i> Using a Heterologous Microarray. Sexual Development, 2011, 5, 89-101.	1.1	36
500	Identification of differentially expressed genes in a spontaneous mutant of â€˜Nanguoliâ€™ pear (<i>Pyrus) Tj ETQq0 0 0 rgBT /Overlock 595-602.	0.9	11
501	NOA: a novel Network Ontology Analysis method. Nucleic Acids Research, 2011, 39, e87-e87.	6.5	101
502	Analysis of Expressed Sequence Tags from the Placenta of the Live-Bearing Fish Poeciliopsis (Poeciliidae). Journal of Heredity, 2011, 102, 352-361.	1.0	16
503	Transcriptional Effects of Dietary Exposure of Oil-Contaminated<i>Calanus finmarchicus</i>in Atlantic Herring (<i>Clupea harengus</i>). Journal of Toxicology and Environmental Health - Part A: Current Issues, 2011, 74, 508-528.	1.1	8
504	Antennal transcriptome of <i>Manduca sexta</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7449-7454.	3.3	269
505	Analysis of the Asian Seabass Transcriptome Based on Expressed Sequence Tags. DNA Research, 2011, 18, 513-522.	1.5	29
506	Reconciling Gene and Genome Duplication Events: Using Multiple Nuclear Gene Families to Infer the Phylogeny of the Aquatic Plant Family Pontederiaceae. Molecular Biology and Evolution, 2011, 28, 3009-3018.	3.5	48
507	Effects of thermal acclimation on transcriptional responses to acute heat stress in the eurythermal fish Gillichthys mirabilis (Cooper). American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2011, 300, R1373-R1383.	0.9	107
508	Transcriptome analyses of Populus x euramericana clone I-214 leaves exposed to excess zinc. Tree Physiology, 2011, 31, 1293-1308.	1.4	54
509	Towards a System Level Understanding of Non-Model Organisms Sampled from the Environment: A Network Biology Approach. PLoS Computational Biology, 2011, 7, e1002126.	1.5	83
510	Generation of expressed sequence tags, development of microsatellite and single nucleotide polymorphism markers in Primula sieboldii E. Morren (Primulaceae) for analysis of genetic diversity in natural and horticultural populations. Breeding Science, 2011, 61, 234-243.	0.9	4
511	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. PLoS Genetics, 2011, 7, e1002345.	1.5	164

#	ARTICLE	IF	CITATIONS
512	Gene Atlasing of Digestive and Reproductive Tissues in Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2011, 5, e1043.	1.3	69
513	AgBase: supporting functional modeling in agricultural organisms. Nucleic Acids Research, 2011, 39, D497-D506.	6.5	56
514	Tripal: a construction toolkit for online genome databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar044-bar044.	1.4	60
515	Whole Transcriptome Profiling of Successful Immune Response to Vibrio Infections in the Oyster Crassostrea gigas by Digital Gene Expression Analysis. PLoS ONE, 2011, 6, e23142.	1.1	115
516	Baculovirus Induced Transcripts in Hemocytes from the Larvae of Heliothis virescens. Viruses, 2011, 3, 2047-2064.	1.5	39
517	CycADS: an annotation database system to ease the development and update of BioCyc databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar008-bar008.	1.4	16
518	The Salivary Secretome of the Tsetse Fly Glossina pallidipes (Diptera: Glossinidae) Infected by Salivary Gland Hypertrophy Virus. PLoS Neglected Tropical Diseases, 2011, 5, e1371.	1.3	21
519	Proteomic Analysis of Excretory-Secretory Products of Heligmosomoides polygyrus Assessed with Next-Generation Sequencing Transcriptomic Information. PLoS Neglected Tropical Diseases, 2011, 5, e1370.	1.3	80
520	Natural Selection on Functional Modules, a Genome-Wide Analysis. PLoS Computational Biology, 2011, 7, e1001093.	1.5	12
521	Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga Nannochloropsis oceanica CCMP1779. PLoS Genetics, 2012, 8, e1003064.	1.5	376
522	Assembly and Characterization of the European Hazelnut â€˜Jeffersonâ€™ Transcriptome. Crop Science, 2012, 52, 2679-2686.	0.8	35
523	Understanding the Role of Host Hemocytes in a Squid/Vibrio Symbiosis Using Transcriptomics and Proteomics. Frontiers in Immunology, 2012, 3, 91.	2.2	56
524	Transcriptomic Analysis of Phenotypic Changes in Birch (Betula platyphylla) Autotetraploids. International Journal of Molecular Sciences, 2012, 13, 13012-13029.	1.8	52
525	The Transcriptome Analysis of Strongyloides stercoralis L3i Larvae Reveals Targets for Intervention in a Neglected Disease. PLoS Neglected Tropical Diseases, 2012, 6, e1513.	1.3	29
526	Mobilizing the Genome of Lepidoptera through Novel Sequence Gains and End Creation by Non-autonomous Lep1 Helitrons. DNA Research, 2012, 19, 11-21.	1.5	17
527	Discovery of High-Confidence Single Nucleotide Polymorphisms from Large-Scale De Novo Analysis of Leaf Transcripts of Aegilops tauschii, A Wild Wheat Progenitor. DNA Research, 2012, 19, 487-497.	1.5	29
528	Expressed sequence tags from organ-specific cDNA libraries of tea (<i>Camellia sinensis</i>) and polymorphisms and transferability of EST-SSRs across <i>Camellia</i> species. Breeding Science, 2012, 62, 186-195.	0.9	23
529	Gene Amplification, ABC Transporters and Cytochrome P450s: Unraveling the Molecular Basis of Pyrethroid Resistance in the Dengue Vector, Aedes aegypti. PLoS Neglected Tropical Diseases, 2012, 6, e1692.	1.3	163

#	Article	IF	Citations
530	Genome Sequence of Hydrogenophaga sp. Strain PBC, a 4-Aminobenzenesulfonate-Degrading Bacterium. Journal of Bacteriology, 2012, 194, 4759-4760.	1.0	25
531	Genome Sequence of Methylobacterium sp. Strain GXF4, a Xylem-Associated Bacterium Isolated from Vitis vinifera L. Grapevine. Journal of Bacteriology, 2012, 194, 5157-5158.	1.0	17
532	Overexpression of <i>ShCYP51B</i> and <i>ShatrD</i> in Sclerotinia homoeocarpa Isolates Exhibiting Practical Field Resistance to a Demethylation Inhibitor Fungicide. Applied and Environmental Microbiology, 2012, 78, 6674-6682.	1.4	85
533	Genome Sequence of Aureobasidium pullulans AY4, an Emerging Opportunistic Fungal Pathogen with Diverse Biotechnological Potential. Eukaryotic Cell, 2012, 11, 1419-1420.	3.4	17
534	Gene expression changes governing extreme dehydration tolerance in an Antarctic insect. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20744-20749.	3.3	118
535	Global Transcriptional Analysis of Dehydrated Salmonella enterica Serovar Typhimurium. Applied and Environmental Microbiology, 2012, 78, 7866-7875.	1.4	97
536	Genome Sequence and Comparative Pathogenomics Analysis of a Salmonella enterica Serovar Typhi Strain Associated with a Typhoid Carrier in Malaysia. Journal of Bacteriology, 2012, 194, 5970-5971.	1.0	22
537	Comparison of Gene Repertoires and Patterns of Evolutionary Rates in Eight Aphid Species That Differ by Reproductive Mode. Genome Biology and Evolution, 2012, 4, 155-167.	1.1	22
538	Genomics of adaptation and speciation in cichlid fishes: recent advances and analyses in African and Neotropical lineages. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 385-394.	1.8	46
539	Complete Genome Sequence of Burkholderia sp. Strain GG4, a Betaproteobacterium That Reduces 3-Oxo- <i>N</i> -Acylhomoserine Lactones and Produces Different <i>N</i> -Acylhomoserine Lactones. Journal of Bacteriology, 2012, 194, 6317-6317.	1.0	14
540	Genome Sequence of Novosphingobium sp. Strain Rr 2-17, a Nopaline Crown Gall-Associated Bacterium Isolated from Vitis vinifera L. Grapevine. Journal of Bacteriology, 2012, 194, 5137-5138.	1.0	18
541	The Or Gene Enhances Carotenoid Accumulation and Stability During Post-Harvest Storage of Potato Tubers. Molecular Plant, 2012, 5, 339-352.	3.9	120
542	High-Throughput Transcriptome Sequencing for Snp and Gene Discovery in a Moth. Environmental Entomology, 2012, 41, 997-1007.	0.7	5
543	The Transcriptome Analysis and Comparison Explorerâ€"T-ACE: a platform-independent, graphical tool to process large RNAseq datasets of non-model organisms. Bioinformatics, 2012, 28, 777-783.	1.8	10
544	Transcriptomics and Comparative Analysis of Three Antarctic Notothenioid Fishes. PLoS ONE, 2012, 7, e43762.	1.1	85
545	The heterogeneous levels of linkage disequilibrium in white spruce genes and comparative analysis with other conifers. Heredity, 2012, 108, 273-284.	1.2	61
546	A survey of sRNA families in Î±-proteobacteria. RNA Biology, 2012, 9, 119-129.	1.5	32
547	Construction and analysis of an SSH cDNA library of early heat-induced genes of<i>Vigna aconitifolia</i>variety RMO-40. Genome, 2012, 55, 783-796.	0.9	12

#	ARTICLE	IF	CITATIONS
548	In Silico Prediction of Drug Targets in Phytopathogenic Pseudomonas syringae pv. phaseolicola: Charting a Course for Agrigenomics Translation Research. OMICS A Journal of Integrative Biology, 2012, 16, 700-706.	1.0	8
549	Genome Sequence of Enterococcus sp. Strain C1, an Azo Dye Decolorizer. Journal of Bacteriology, 2012, 194, 5716-5717.	1.0	7
550	Genome Sequence of Citrobacter sp. Strain A1, a Dye-Degrading Bacterium. Journal of Bacteriology, 2012, 194, 5485-5486.	1.0	13
551	Draft Genome Sequence of an Aeromonas sp. Strain 159 Clinical Isolate That Shows Quorum-Sensing Activity. Journal of Bacteriology, 2012, 194, 6350-6350.	1.0	21
552	System Response of Metabolic Networks in Chlamydomonas reinhardtii to Total Available Ammonium. Molecular and Cellular Proteomics, 2012, 11, 973-988.	2.5	93
553	Reconstruction of Oomycete Genome Evolution Identifies Differences in Evolutionary Trajectories Leading to Present-Day Large Gene Families. Genome Biology and Evolution, 2012, 4, 199-211.	1.1	44
554	Genome Sequence of the Biocontrol Strain Pseudomonas fluorescens F113. Journal of Bacteriology, 2012, 194, 1273-1274.	1.0	69
555	Whole-Genome Sequence of <i>N</i> -Acylhomoserine Lactone-Synthesizing and -Degrading Acinetobacter sp. Strain GG2. Journal of Bacteriology, 2012, 194, 6318-6318.	1.0	7
556	De Novo Sequencing and Characterization of the Floral Transcriptome of Dendrocalamus latiflorus (Poaceae: Bambusoideae). PLoS ONE, 2012, 7, e42082.	1.1	111
557	Whole-Genome Sequence of Enterobacter sp. Strain SST3, an Endophyte Isolated from Jamaican Sugarcane (Saccharum sp.) Stalk Tissue. Journal of Bacteriology, 2012, 194, 5981-5982.	1.0	5
558	Genome Sequence of Ralstonia sp. Strain PBA, a Bacterium Involved in the Biodegradation of 4-Aminobenzenesulfonate. Journal of Bacteriology, 2012, 194, 5139-5140.	1.0	9
559	Effects of Slow Freezing Procedure on Late Blastocyst Gene Expression and Survival Rate in Rabbit1. Biology of Reproduction, 2012, 87, 91.	1.2	22
560	Microsatellite markers in candidate genes for wood properties and its application in functional diversity assessment in Eucalyptus globulus. Electronic Journal of Biotechnology, 2012, 15, .	1.2	8
561	Global Transcriptional Analysis of Olfactory Genes in the Head of Pine Shoot Beetle,<i>Tomicus yunnanensis</i>. Comparative and Functional Genomics, 2012, 2012, 1-10.	2.0	22
562	Metabolic routes affecting rubber biosynthesis in Hevea brasiliensis latex. Journal of Experimental Botany, 2012, 63, 1863-1871.	2.4	103
563	ASGARD: an open-access database of annotated transcriptomes for emerging model arthropod species. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas048-bas048.	1.4	21
564	Transcriptome Analysis of a North American Songbird, Melospiza melodia. DNA Research, 2012, 19, 325-333.	1.5	16
565	Genome Sequence of Pichia kudriavzevii M12, a Potential Producer of Bioethanol and Phytase. Eukaryotic Cell, 2012, 11, 1300-1301.	3.4	59

#	Article	IF	Citations
566	Genome Sequence of Acinetobacter baumannii AC12, a Polymyxin-Resistant Strain Isolated from Terengganu, Malaysia. Journal of Bacteriology, 2012, 194, 5979-5980.	1.0	3
567	Whole-Genome Sequence of Cupriavidus sp. Strain BIS7, a Heavy-Metal-Resistant Bacterium. Journal of Bacteriology, 2012, 194, 6324-6324.	1.0	17
568	Insights from the Genome Sequence of Quorum-Quenching Staphylococcus sp. Strain AL1, Isolated from Traditional Chinese Soy Sauce Brine Fermentation. Journal of Bacteriology, 2012, 194, 6611-6612.	1.0	8
569	Genome sequencing of the lizard parasite Leishmania tarentolae reveals loss of genes associated to the intracellular stage of human pathogenic species. Nucleic Acids Research, 2012, 40, 1131-1147.	6.5	135
570	Transcriptome sequencing of black grouse (Tetrao tetrix) for immune gene discovery and microsatellite development. Open Biology, 2012, 2, 120054.	1.5	26
571	Genome Sequence of Roseomonas sp. Strain B5, a Quorum-Quenching <i>N</i> -Acylhomoserine Lactone-Degrading Bacterium Isolated from Malaysian Tropical Soil. Journal of Bacteriology, 2012, 194, 6681-6682.	1.0	15
572	Genome Sequence of Dyella japonica Strain A8, a Quorum-Quenching Bacterium That Degrades N -Acylhomoserine Lactones, Isolated from Malaysian Tropical Soil. Journal of Bacteriology, 2012, 194, 6331-6331.	1.0	7
573	Generation and analysis of expressed sequence tags in the extreme large genomes Lilium and Tulipa. BMC Genomics, 2012, 13, 640.	1.2	62
574	Genomics of estradiol-3-sulfate action in the ovine fetal hypothalamus. Physiological Genomics, 2012, 44, 669-677.	1.0	23
575	The First Illumina-Based De Novo Transcriptome Sequencing and Analysis of Safflower Flowers. PLoS ONE, 2012, 7, e38653.	1.1	128
576	Isolation and Identification of miRNAs in <i>Jatropha curcas</i>. International Journal of Biological Sciences, 2012, 8, 418-429.	2.6	26
577	Transcriptional changes inTeladorsagia circumcinctaupon encountering host tissue of differing immune status. Parasitology, 2012, 139, 387-405.	0.7	9
579	Insect Genomics. , 2012, , 1-29.		0
580	Nextâ€generation sequencingâ€based transcriptomic and proteomic analysis of the common reed, <i>Phragmites australis</i> (Poaceae), reveals genes involved in invasiveness and rhizome specificity. American Journal of Botany, 2012, 99, 232-247.	0.8	49
581	Modulation of Protein Phosphorylation, N-Glycosylation and Lys-Acetylation in Grape (Vitis vinifera) Mesocarp and Exocarp Owing to Lobesia botrana Infection. Molecular and Cellular Proteomics, 2012, 11, 945-956.	2.5	118
582	Genome scans reveal candidate regions involved in the adaptation to host plant in the pea aphid complex. Molecular Ecology, 2012, 21, 5251-5264.	2.0	73
583	Gene expression associated with apogamy commitment in Ceratopteris richardii. Sexual Plant Reproduction, 2012, 25, 293-304.	2.2	17
584	<i>De novo</i> assembly of the transcriptome of an invasive snail and its multiple ecological applications. Molecular Ecology Resources, 2012, 12, 1133-1144.	2.2	32

#	ARTICLE	IF	CITATIONS
585	Largeâ€scale transcriptome characterization and mass discovery of SNPs in globe artichoke and its related taxa. Plant Biotechnology Journal, 2012, 10, 956-969.	4.1	33
586	Gene expression profiling of the plant pathogenic basidiomycetous fungus Rhizoctonia solani AG 4 reveals putative virulence factors. Mycologia, 2012, 104, 1020-1035.	0.8	22
587	Analysis of Porphyra Membrane Transporters Demonstrates Gene Transfer among Photosynthetic Eukaryotes and Numerous Sodium-Coupled Transport Systems Â Â Â. Plant Physiology, 2012, 158, 2001-2012.	2.3	35
588	<i>Porphyra</i> (Bangiophyceae) Transcriptomes Provide Insights Into Red Algal Development And Metabolism. Journal of Phycology, 2012, 48, 1328-1342.	1.0	56
589	Comprehensive structural annotation of Pichia pastoris transcriptome and the response to various carbon sources using deep paired-end RNA sequencing. BMC Genomics, 2012, 13, 738.	1.2	59
590	Digital Marine Bioprospecting: Mining New Neurotoxin Drug Candidates from the Transcriptomes of Cold-Water Sea Anemones. Marine Drugs, 2012, 10, 2265-2279.	2.2	20
591	Comparative Analysis of Transcriptomic and Hormonal Responses to Compatible and Incompatible Plant-Virus Interactions that Lead to Cell Death. Molecular Plant-Microbe Interactions, 2012, 25, 709-723.	1.4	53
592	In Silico Identification and Characterization of Effector Catalogs. Methods in Molecular Biology, 2012, 835, 415-425.	0.4	11
593	Oxygen Response of the Wine Yeast Saccharomyces cerevisiae EC1118 Grown under Carbon-Sufficient, Nitrogen-Limited Enological Conditions. Applied and Environmental Microbiology, 2012, 78, 8340-8352.	1.4	59
594	Comparison of toxicity and transcriptomic profiles in a diatom exposed to oil, dispersants, dispersed oil. Aquatic Toxicology, 2012, 124-125, 139-151.	1.9	68
595	Apple miRNAs and tasiRNAs with novel regulatory networks. Genome Biology, 2012, 13, R47.	13.9	272
596	Transcriptome profiling and in silico analysis of somatic embryos in Japanese larch (Larix leptolepis). Plant Cell Reports, 2012, 31, 1637-1657.	2.8	44
597	De novo assembly and characterization of the garlic (Allium sativum) bud transcriptome by Illumina sequencing. Plant Cell Reports, 2012, 31, 1823-1828.	2.8	76
598	EgRBP42 encoding an hnRNP-like RNA-binding protein from Elaeis guineensis Jacq. is responsive to abiotic stresses. Plant Cell Reports, 2012, 31, 1829-1843.	2.8	18
599	Additive multiple k-mer transcriptome of the keelworm Pomatoceros lamarckii (Annelida; Serpulidae) reveals annelid trochophore transcription factor cassette. Development Genes and Evolution, 2012, 222, 325-339.	0.4	11
600	Building an mRNA transcriptome from the shoots of Betula platyphylla by using Solexa technology. Tree Genetics and Genomes, 2012, 8, 1031-1040.	0.6	10
601	Transcriptome profiling of female alates and egg-laying queens of the Formosan subterranean termite. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2012, 7, 14-27.	0.4	15
603	Proteomic profiles of soluble proteins from the esophageal gland in female Meloidogyne incognita. International Journal for Parasitology, 2012, 42, 1177-1183.	1.3	15

#	Article	IF	Citations
604	De novo transcriptome sequencing of Momordica cochinchinensis to identify genes involved in the carotenoid biosynthesis. Plant Molecular Biology, 2012, 79, 413-427.	2.0	66
605	Mining of EST-SSR from 454 pyrosequencing in the surf clam Mesodesma donacium (Lamark, 1818). Conservation Genetics Resources, 2012, 4, 829-832.	0.4	5
606	Expressed sequence tags (ESTs) from young leaves of Metroxylon sagu. 3 Biotech, 2012, 2, 211-218.	1.1	4
607	Comparative transcriptomics of the bacteriome and the spermalege of the bedbug Cimex lectularius (Hemiptera: Cimicidae). Applied Entomology and Zoology, 2012, 47, 233-243.	0.6	12
608	Comprehensive Comparison of iTRAQ and Label-free LC-Based Quantitative Proteomics Approaches Using Two <i>Chlamydomonas reinhardtii</i> Strains of Interest for Biofuels Engineering. Journal of Proteome Research, 2012, 11, 487-501.	1.8	128
609	Validation of Reference Genes for Gene Expression Studies in <I>Aphis glycines</I> (Hemiptera: Aphididae). Journal of Economic Entomology, 2012, 105, 1432-1438.	0.8	54
610	Proteomics: A new tool in bovine claw disease research. Veterinary Journal, 2012, 193, 694-700.	0.6	7
611	Analysis of expressed sequence tags derived from a compatiblePlasmodiophora brassicaeâ€“canola interaction. Canadian Journal of Plant Pathology, 2012, 34, 562-574.	0.8	11
612	Clarifying Omics Concepts, Challenges, and Opportunities for<i>Prunus</i>Breeding in the Postgenomic Era. OMICS A Journal of Integrative Biology, 2012, 16, 268-283.	1.0	32
613	Identification of Representative Genes of the Central Nervous System of the Locust,<i>locusta migratoria manilensis</i>by Deep Sequencing. Journal of Insect Science, 2012, 12, 1-15.	0.9	9
614	Physiological and Molecular Effect Assessment versus Physico-Chemistry Based Mode of Action Schemes: <i>Daphnia magna</i> Exposed to Narcotics and Polar Narcotics. Environmental Science & Technology, 2012, 46, 10-18.	4.6	15
615	Draft Genome Sequence of Streptomyces acidiscabies 84-104, an Emergent Plant Pathogen. Journal of Bacteriology, 2012, 194, 1847-1847.	1.0	19
616	Transcriptome Characterization and Sequencing-Based Identification of Salt-Responsive Genes in Millettia pinnata, a Semi-Mangrove Plant. DNA Research, 2012, 19, 195-207.	1.5	68
617	Genomics in Eels â€” Towards Aquaculture and Biology. Marine Biotechnology, 2012, 14, 583-590.	1.1	14
618	Proteomic and Transcriptomic Analyses of Rigid and Membranous Cuticles and Epidermis from the Elytra and Hindwings of the Red Flour Beetle, <i>Tribolium castaneum</i>. Journal of Proteome Research, 2012, 11, 269-278.	1.8	76
619	Comparative transcriptome analysis of Paracoccidioides brasiliensis during inÂvitro adhesion to type I collagen and fibronectin: identification of potential adhesins. Research in Microbiology, 2012, 163, 182-191.	1.0	19
620	Developmental and insecticide-resistant insights from the de novo assembled transcriptome of the diamondback moth, Plutella xylostella. Genomics, 2012, 99, 169-177.	1.3	75
621	Peculiar patterns of amino acid substitution and conservation in the fast evolving tunicate Oikopleura dioica. Molecular Phylogenetics and Evolution, 2012, 62, 708-717.	1.2	10

#	ARTICLE	IF	CITATIONS
622	Dinoflagellate tandem array gene transcripts are highly conserved and not polycistronic. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15793-15798.	3.3	73
623	Identification of in vivo protein phosphorylation sites in human pathogen Schistosoma japonicum by a phosphoproteomic approach. Journal of Proteomics, 2012, 75, 868-877.	1.2	16
624	Label-free quantitative proteomics reveals differentially regulated proteins in the latex of sticky diseased Carica papaya L. plants. Journal of Proteomics, 2012, 75, 3191-3198.	1.2	31
625	Transcriptome analysis of enriched Golovinomyces orontii haustoria by deep 454 pyrosequencing. Fungal Genetics and Biology, 2012, 49, 470-482.	0.9	44
626	Gene expression analysis of clams Ruditapes philippinarum and Ruditapes decussatus following bacterial infection yields molecular insights into pathogen resistance and immunity. Developmental and Comparative Immunology, 2012, 36, 140-149.	1.0	51
627	Identification of differentially transcribed genes in shrimp Litopenaeus vannamei exposed to osmotic stress and challenged with WSSV virus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2012, 7, 73-81.	0.4	8
628	Functional genomics resources for the North Atlantic copepod, Calanus finmarchicus: EST database and physiological microarray. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2012, 7, 110-123.	0.4	26
629	Effects of short read quality and quantity on a de novo vertebrate transcriptome assembly. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2012, 155, 95-101.	1.3	26
630	Immune gene mining by pyrosequencing in the rockshell, Thais clavigera. Fish and Shellfish Immunology, 2012, 32, 700-710.	1.6	11
631	Comparative transcriptomics and gene expression in larval tiger salamander (Ambystoma tigrinum) gill and lung tissues as revealed by pyrosequencing. Gene, 2012, 492, 329-338.	1.0	23
632	EST-based identification of immune-relevant genes from spleen of Indian catfish, Clarias batrachus (Linnaeus, 1758). Gene, 2012, 502, 53-59.	1.0	8
633	Reference Genes for the Normalization of Gene Expression in Eucalyptus Species. Plant and Cell Physiology, 2012, 53, 405-422.	1.5	69
634	Transcriptional responses in <i>Enchytraeus albidus</i> (Oligochaeta): Comparison between cadmium and zinc exposure and linkage to reproduction effects. Environmental Toxicology and Chemistry, 2012, 31, 2289-2299.	2.2	21
635	Quantitative proteomics of <i>Trypanosoma cruzi</i> during metacyclogenesis. Proteomics, 2012, 12, 2694-2703.	1.3	71
636	Predicting the outer membrane proteome of Pasteurella multocida based on consensus prediction enhanced by results integration and manual confirmation. BMC Bioinformatics, 2012, 13, 63.	1.2	18
637	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. BMC Bioinformatics, 2012, 13, S14.	1.2	137
638	Investigating the molecular basis of local adaptation to thermal stress: population differences in gene expression across the transcriptome of the copepod Tigriopus californicus. BMC Evolutionary Biology, 2012, 12, 170.	3.2	150
639	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. BMC Genomics, 2012, 13, 120.	1.2	80

#	ARTICLE	IF	CITATIONS
640	De novo assembly and characterization of the root transcriptome of Aegilops variabilis during an interaction with the cereal cyst nematode. BMC Genomics, 2012, 13, 133.	1.2	63
641	A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, Cryptomeria japonica. BMC Genomics, 2012, 13, 136.	1.2	69
642	A transcriptome map of perennial ryegrass (Lolium perenne L.). BMC Genomics, 2012, 13, 140.	1.2	60
643	Identification and expression analysis of methyl jasmonate responsive ESTs in paclitaxel producing Taxus cuspidata suspension culture cells. BMC Genomics, 2012, 13, 148.	1.2	37
644	The Physalis peruviana leaf transcriptome: assembly, annotation and gene model prediction. BMC Genomics, 2012, 13, 151.	1.2	52
645	Phylogenomic analysis of UDP glycosyltransferase 1 multigene family in Linum usitatissimum identified genes with varied expression patterns. BMC Genomics, 2012, 13, 175.	1.2	102
646	Genome wide response to dietary tetradecylthioacetic acid supplementation in the heart of Atlantic Salmon (Salmo salar L). BMC Genomics, 2012, 13, 180.	1.2	2
647	Genetic and genome-wide transcriptomic analyses identify co-regulation of oxidative response and hormone transcript abundance with vitamin C content in tomato fruit. BMC Genomics, 2012, 13, 187.	1.2	33
648	Transcriptomic analysis of Chinese bayberry (Myrica rubra) fruit development and ripening using RNA-Seq. BMC Genomics, 2012, 13, 19.	1.2	199
649	De novo assembly and characterization of bark transcriptome using Illumina sequencing and development of EST-SSR markers in rubber tree (Hevea brasiliensis Muell. Arg.). BMC Genomics, 2012, 13, 192.	1.2	228
650	Developing the anemone Aiptasia as a tractable model for cnidarian-dinoflagellate symbiosis: the transcriptome of aposymbiotic A. pallida. BMC Genomics, 2012, 13, 271.	1.2	99
651	Transcriptional profiling by cDNA-AFLP analysis showed differential transcript abundance in response to water stress in Populus hopeiensis. BMC Genomics, 2012, 13, 286.	1.2	29
652	Transcriptome characterization via 454 pyrosequencing of the annelid Pristina leidyi, an emerging model for studying the evolution of regeneration. BMC Genomics, 2012, 13, 287.	1.2	22
653	Transcriptome analysis reveals novel patterning and pigmentation genes underlying Heliconius butterfly wing pattern variation. BMC Genomics, 2012, 13, 288.	1.2	56
654	Transcriptome survey of Patagonian southern beech Nothofagus nervosa (= N. Alpina): assembly, annotation and molecular marker discovery. BMC Genomics, 2012, 13, 291.	1.2	18
655	Transcriptional profile of Taxus chinensis cells in response to methyl jasmonate. BMC Genomics, 2012, 13, 295.	1.2	87
656	RAD tag sequencing as a source of SNP markers in Cynara cardunculus L. BMC Genomics, 2012, 13, 3.	1.2	82
657	De novo transcriptome sequencing in a songbird, the dark-eyed junco (Junco hyemalis): genomic tools for an ecological model system. BMC Genomics, 2012, 13, 305.	1.2	35

#	ARTICLE	IF	CITATIONS
658	The venom-gland transcriptome of the eastern diamondback rattlesnake (Crotalus adamanteus). BMC Genomics, 2012, 13, 312.	1.2	250
659	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	1.2	84
660	Profiling the resting venom gland of the scorpion Tityus stigmurus through a transcriptomic survey. BMC Genomics, 2012, 13, 362.	1.2	74
661	A moderate increase in ambient temperature modulates the Atlantic cod (Gadus morhua) spleen transcriptome response to intraperitoneal viral mimic injection. BMC Genomics, 2012, 13, 431.	1.2	60
662	A draft of the genome and four transcriptomes of a medicinal and pesticidal angiosperm Azadirachta indica. BMC Genomics, 2012, 13, 464.	1.2	80
663	Dietary vegetable oils do not alter the intestine transcriptome of gilthead sea bream (Sparus aurata), but modulate the transcriptomic response to infection with Enteromyxum leei. BMC Genomics, 2012, 13, 470.	1.2	73
664	RNA-Seq reveals complex genetic response to deepwater horizon oil release in Fundulus grandis. BMC Genomics, 2012, 13, 474.	1.2	66
665	Combining laser microdissection and RNA-seq to chart the transcriptional landscape of fungal development. BMC Genomics, 2012, 13, 511.	1.2	73
666	Annotated genetic linkage maps of Pinus pinaster Ait. from a Central Spain population using microsatellite and gene based markers. BMC Genomics, 2012, 13, 527.	1.2	13
667	Analysis of a native whitefly transcriptome and its sequence divergence with two invasive whitefly species. BMC Genomics, 2012, 13, 529.	1.2	54
668	Toward allotetraploid cotton genome assembly: integration of a high-density molecular genetic linkage map with DNA sequence information. BMC Genomics, 2012, 13, 539.	1.2	95
669	Evolutionary force in confamiliar marine vertebrates of different temperature realms: adaptive trends in zoarcid fish transcriptomes. BMC Genomics, 2012, 13, 549.	1.2	17
670	The genome sequence of Propionibacterium acidipropionici provides insights into its biotechnological and industrial potential. BMC Genomics, 2012, 13, 562.	1.2	74
671	De novo assembly of the pepper transcriptome (Capsicum annuum): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. BMC Genomics, 2012, 13, 571.	1.2	109
672	Characterization of a transcriptome from a non-model organism, Cladonia rangiferina, the grey reindeer lichen, using high-throughput next generation sequencing and EST sequence data. BMC Genomics, 2012, 13, 575.	1.2	26
673	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, Botryococcus braunii race B (Showa)*. BMC Genomics, 2012, 13, 576.	1.2	52
674	Toward understanding the genetic basis of adaptation to high-elevation life in poikilothermic species: A comparative transcriptomic analysis of two ranid frogs, Rana chensinensis and R. kukunoris. BMC Genomics, 2012, 13, 588.	1.2	55
675	RNA-Seq and molecular docking reveal multi-level pesticide resistance in the bed bug. BMC Genomics, 2012, 13, 6.	1.2	126

#	ARTICLE	IF	CITATIONS
676	Comparative genomics of bacteria in the genus Providencia isolated from wild Drosophila melanogaster. BMC Genomics, 2012, 13, 612.	1.2	32
677	De Novo characterization of the banana root transcriptome and analysis of gene expression under Fusarium oxysporum f. sp. Cubense tropical race 4 infection. BMC Genomics, 2012, 13, 650.	1.2	74
678	Rapid transcriptome characterization and parsing of sequences in a non-model host-pathogen interaction; pea-Sclerotinia sclerotiorum. BMC Genomics, 2012, 13, 668.	1.2	27
679	Orthologous genes identified by transcriptome sequencing in the spider genus Stegodyphus. BMC Genomics, 2012, 13, 70.	1.2	34
680	High-throughput SNP genotyping in Cucurbita pepo for map construction and quantitative trait loci mapping. BMC Genomics, 2012, 13, 80.	1.2	110
681	De novo assembly and Characterisation of the Transcriptome during seed development, and generation of genic-SSR markers in Peanut (Arachis hypogaea L.). BMC Genomics, 2012, 13, 90.	1.2	231
682	Characterization of resistance to pine wood nematode infection in Pinus thunbergiiusing suppression subtractive hybridization. BMC Plant Biology, 2012, 12, 13.	1.6	92
683	Comparative mapping in the Fagaceae and beyond with EST-SSRs. BMC Plant Biology, 2012, 12, 153.	1.6	54
684	A putative role for amino acid permeases in sink-source communication of barley tissues uncovered by RNA-seq. BMC Plant Biology, 2012, 12, 154.	1.6	46
685	Olive phenolic compounds: metabolic and transcriptional profiling during fruit development. BMC Plant Biology, 2012, 12, 162.	1.6	171
686	Identification of novel microRNAs in Hevea brasiliensis and computational prediction of their targets. BMC Plant Biology, 2012, 12, 18.	1.6	47
687	Transcriptional profile analysis of E3 ligase and hormone-related genes expressed during wheat grain development. BMC Plant Biology, 2012, 12, 35.	1.6	29
688	The arbuscular mycorrhizal status has an impact on the transcriptome profile and amino acid composition of tomato fruit. BMC Plant Biology, 2012, 12, 44.	1.6	98
689	Generation and analysis of blueberry transcriptome sequences from leaves, developing fruit, and flower buds from cold acclimation through deacclimation. BMC Plant Biology, 2012, 12, 46.	1.6	139
690	Transcriptome analysis of stem development in the tumourous stem mustard Brassica juncea var. tumida Tsen et Lee by RNA sequencing. BMC Plant Biology, 2012, 12, 53.	1.6	49
691	RNAi-mediated silencing of the HD-Zip gene HD20 in Nicotiana attenuata affects benzyl acetone emission from corollas via ABA levels and the expression of metabolic genes. BMC Plant Biology, 2012, 12, 60.	1.6	16
692	Molecular interactions between the olive and the fruit fly Bactrocera oleae. BMC Plant Biology, 2012, 12, 86.	1.6	65
693	Efficient recovery of whole blood RNA - a comparison of commercial RNA extraction protocols for high-throughput applications in wildlife species. BMC Biotechnology, 2012, 12, 33.	1.7	36

#	Article	IF	Citations
694	Comparative analysis of hemolymph proteome maps in diapausing and non-diapausing larvae of Sesamia nonagrioides. Proteome Science, 2012, 10, 58.	0.7	8
695	Comparative description of ten transcriptomes of newly sequenced invertebrates and efficiency estimation of genomic sampling in non-model taxa. Frontiers in Zoology, 2012, 9, 33.	0.9	114
696	Transcriptome analysis of head kidney in grass carp and discovery of immune-related genes. BMC Veterinary Research, 2012, 8, 108.	0.7	65
697	Transcriptomic analysis of the oleaginous microalga Neochloris oleoabundans reveals metabolic insights into triacylglyceride accumulation. Biotechnology for Biofuels, 2012, 5, 74.	6.2	178
698	Genetic mapping and identification of QTL for earliness in the globe artichoke/cultivated cardoon complex. BMC Research Notes, 2012, 5, 252.	0.6	39
699	First analysis of the secretome of the canine heartworm, Dirofilaria immitis. Parasites and Vectors, 2012, 5, 140.	1.0	41
700	A comprehensive cDNA library of light- and temperature-stressed<i>Saccharina latissima</i>(Phaeophyceae). European Journal of Phycology, 2012, 47, 83-94.	0.9	22
701	The changes of microRNA expression profiles and tyrosinase related proteins in MITF knocked down melanocytes. Molecular BioSystems, 2012, 8, 2924.	2.9	28
702	COMPARATIVE POPULATION GENOMICS INCOLLINSIASISTER SPECIES REVEALS EVIDENCE FOR REDUCED EFFECTIVE POPULATION SIZE, RELAXED SELECTION, AND EVOLUTION OF BIASED GENE CONVERSION WITH AN ONGOING MATING SYSTEM SHIFT. Evolution; International Journal of Organic Evolution, 2012, 67, no-no.	1.1	36
703	Transcriptome analysis of the entomopathogenic fungus Beauveria bassiana grown on cuticular extracts of the coffee berry borer (Hypothenemus hampei). Microbiology (United Kingdom), 2012, 158, 1826-1842.	0.7	36
704	Treatment with the Proteasome Inhibitor MG132 during the End of Oocyte Maturation Improves Oocyte Competence for Development after Fertilization in Cattle. PLoS ONE, 2012, 7, e48613.	1.1	27
705	Analysis of expressed sequence tags derived from pea leaves infected by <i>Peronospora viciae</i> f. sp. <i>pisi</i>. Annals of Applied Biology, 2012, 161, 214-222.	1.3	2
706	The Absence of Heat Shock Protein HSP101 Affects the Proteome of Mature and Germinating Maize Embryos. Journal of Proteome Research, 2012, 11, 3246-3258.	1.8	10
707	Large-Scale Proteome Comparative Analysis of Developing Rhizomes of the Ancient Vascular Plant Equisetum Hyemale. Frontiers in Plant Science, 2012, 3, 131.	1.7	16
708	Comparison of the genetic determinism of two key phenological traits, flowering and maturity dates, in three Prunus species: peach, apricot and sweet cherry. Heredity, 2012, 109, 280-292.	1.2	139
709	A Transcriptomic View of the Proteome Variability of Newborn and Adult Bothrops jararaca Snake Venoms. PLoS Neglected Tropical Diseases, 2012, 6, e1554.	1.3	61
710	Proteome Profiling of Flax (<i>Linum usitatissimum</i>) Seed: Characterization of Functional Metabolic Pathways Operating during Seed Development. Journal of Proteome Research, 2012, 11, 6264-6276.	1.8	25
711	Toxicogenomic Responses of Nanotoxicity in <i>Daphnia magna</i> Exposed to Silver Nitrate and Coated Silver Nanoparticles. Environmental Science & Technology, 2012, 46, 6288-6296.	4.6	159

#	Article	IF	Citations
712	Next Generation Transcriptome Sequencing and Quantitative Real-Time PCR Technologies for Characterisation of the Bemisia tabaci Asia 1 mtCOI Phylogenetic Clade. Journal of Integrative Agriculture, 2012, 11, 281-292.	1.7	10
713	A global view of gene activity at the flowering transition phase in precocious trifoliate orange and its wild-type [Poncirus trifoliata (L.) Raf.] by transcriptome and proteome analysis. Gene, 2012, 510, 47-58.	1.0	12
714	De novo sequencing and comparative analysis of the blueberry transcriptome to discover putative genes related to antioxidants. Gene, 2012, 511, 54-61.	1.0	86
715	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. Genomics, Proteomics and Bioinformatics, 2012, 10, 94-106.	3.0	90
716	EST sequencing and microarray analysis of the floral transcriptome of Eustoma grandiflorum. Scientia Horticulturae, 2012, 144, 230-235.	1.7	7
717	Transcriptome profiling of genes differentially modulated by sulfur and chromium identifies potential targets for phytoremediation and reveals a complex Sâ€“Cr interplay on sulfate transport regulation in B. juncea. Journal of Hazardous Materials, 2012, 239-240, 192-205.	6.5	36
718	Transcriptome analysis of the salivary glands of potato leafhopper, Empoasca fabae. Journal of Insect Physiology, 2012, 58, 1626-1634.	0.9	60
719	Transcriptome remodeling associated with chronological aging in the dinoflagellate, Karenia brevis. Marine Genomics, 2012, 5, 15-25.	0.4	31
720	Gene discovery from a pilot study of the transcriptomes from three diverse microbial eukaryotes: Corallomyxa tenera, Chilodonella uncinata, and Subulatomonas tetraspora. Protist Genomics, 2012, 1, .	1.7	15
721	Genome scanning for detecting adaptive genes along environmental gradients in the Japanese conifer, Cryptomeria japonica. Heredity, 2012, 109, 349-360.	1.2	61
722	Phosphoproteomic Analysis of <i>Rhodopseudomonas palustris</i> Reveals the Role of Pyruvate Phosphate Dikinase Phosphorylation in Lipid Production. Journal of Proteome Research, 2012, 11, 5362-5375.	1.8	37
723	Global gene expression analysis of gill tissues from normal and thermally selected strains of rainbow trout. Fisheries Science, 2012, 78, 1041-1049.	0.7	20
724	Effects of feed restriction on the expression profiles of the glucose and fatty acid metabolism-related genes in rainbow trout Oncorhynchus mykiss muscle. Fisheries Science, 2012, 78, 1205-1211.	0.7	16
725	Ammonium Secretion During <i>Colletotrichum coccodes</i> Infection Modulates Salicylic and Jasmonic Acid Pathways of Ripe and Unripe Tomato Fruit. Molecular Plant-Microbe Interactions, 2012, 25, 85-96.	1.4	38
727	Gene expression patterns of the coral Acropora millepora in response to contact with macroalgae. Coral Reefs, 2012, 31, 1177-1192.	0.9	34
728	Vesicle and Vesicle-Free Extracellular Proteome of <i>Paracoccidioides brasiliensis</i>: Comparative Analysis with Other Pathogenic Fungi. Journal of Proteome Research, 2012, 11, 1676-1685.	1.8	160
729	Identification of differentially expressed genes in potato associated with tuber dormancy release. Molecular Biology Reports, 2012, 39, 11277-11287.	1.0	22
730	Proteomic Profiling of the Influence of Iron Availability on <i>Cryptococcus gattii</i>. Journal of Proteome Research, 2012, 11, 189-205.	1.8	20

#	Article	IF	Citations
731	Structural and Molecular Diversification of the Anguimorpha Lizard Mandibular Venom Gland System in the Arboreal Species Abronia graminea. Journal of Molecular Evolution, 2012, 75, 168-183.	0.8	19
732	In-Depth Analysis of the <i>Magnaporthe oryzae</i> Conidial Proteome. Journal of Proteome Research, 2012, 11, 5827-5835.	1.8	30
733	FastAnnotator- an efficient transcript annotation web tool. BMC Genomics, 2012, 13, S9.	1.2	51
734	An analysis of the transcriptome of Teladorsagia circumcincta: its biological and biotechnological implications. BMC Genomics, 2012, 13, S10.	1.2	18
735	Transcriptome analysis of Sacha Inchi (Plukenetia volubilis L.) seeds at two developmental stages. BMC Genomics, 2012, 13, 716.	1.2	62
736	A catalogue of putative unique transcripts from Douglas-fir (Pseudotsuga menziesii) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. BMC Genomics, 2012, 13, 673.	1.2	34
737	Genomic resources for a model in adaptation and speciation research: characterization of the Poecilia mexicana transcriptome. BMC Genomics, 2012, 13, 652.	1.2	25
738	Transcriptome characterization and gene expression of Epinephelus spp in endoplasmic reticulum stress-related pathway during betanodavirus infection in vitro. BMC Genomics, 2012, 13, 651.	1.2	54
739	De novo characterization of the Chinese fir (Cunninghamia lanceolata) transcriptome and analysis of candidate genes involved in cellulose and lignin biosynthesis. BMC Genomics, 2012, 13, 648.	1.2	72
740	Reconstructing differentially co-expressed gene modules and regulatory networks of soybean cells. BMC Genomics, 2012, 13, 437.	1.2	21
741	Characterization of the transcriptome of an ecologically important avian species, the Vinous-throated Parrotbill Paradoxornis webbianus bulomachus (Paradoxornithidae; Aves). BMC Genomics, 2012, 13, 149.	1.2	12
742	OPTIMAS-DW: A comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. BMC Plant Biology, 2012, 12, 245.	1.6	47
743	Identification and characterization of gene-based SSR markers in date palm (Phoenix dactylifera L.). BMC Plant Biology, 2012, 12, 237.	1.6	83
744	Deep-sequencing transcriptome analysis of chilling tolerance mechanisms of a subnival alpine plant, Chorispora bungeana. BMC Plant Biology, 2012, 12, 222.	1.6	84
745	Improving N-terminal protein annotation of Plasmodium species based on signal peptide prediction of orthologous proteins. Malaria Journal, 2012, 11, 375.	0.8	3
747	A Powerful Method for Transcriptional Profiling of Specific Cell Types in Eukaryotes: Laser-Assisted Microdissection and RNA Sequencing. PLoS ONE, 2012, 7, e29685.	1.1	104
748	Transcriptome Analysis and SNP Development Can Resolve Population Differentiation of Streblospio benedicti, a Developmentally Dimorphic Marine Annelid. PLoS ONE, 2012, 7, e31613.	1.1	18
749	Transcriptome Profiling of Testis during Sexual Maturation Stages in Eriocheir sinensis Using Illumina Sequencing. PLoS ONE, 2012, 7, e33735.	1.1	83

#	Article	IF	Citations
750	Enchytraeus albidus Microarray: Enrichment, Design, Annotation and Database (EnchyBASE). PLoS ONE, 2012, 7, e34266.	1.1	10
751	Transcriptome Profiling of the Intoxication Response of Tenebrio molitor Larvae to Bacillus thuringiensis Cry3Aa Protoxin. PLoS ONE, 2012, 7, e34624.	1.1	60
752	Transcriptome Responses of Insect Fat Body Cells to Tissue Culture Environment. PLoS ONE, 2012, 7, e34940.	1.1	15
753	Transcriptomics of In Vitro Immune-Stimulated Hemocytes from the Manila Clam Ruditapes philippinarum Using High-Throughput Sequencing. PLoS ONE, 2012, 7, e35009.	1.1	106
754	De Novo Transcriptomic Analysis of an Oleaginous Microalga: Pathway Description and Gene Discovery for Production of Next-Generation Biofuels. PLoS ONE, 2012, 7, e35142.	1.1	19
755	High-Throughput Sequence Analysis of Turbot (Scophthalmus maximus) Transcriptome Using 454-Pyrosequencing for the Discovery of Antiviral Immune Genes. PLoS ONE, 2012, 7, e35369.	1.1	100
756	Gene Expression Responses Linked to Reproduction Effect Concentrations (EC10,20,50,90) of Dimethoate, Atrazine and Carbendazim, in Enchytraeus albidus. PLoS ONE, 2012, 7, e36068.	1.1	26
757	Dufulin Activates HrBP1 to Produce Antiviral Responses in Tobacco. PLoS ONE, 2012, 7, e37944.	1.1	50
758	Transcriptome Sequencing and Comparative Analysis of Saccharina japonica (Laminariales,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 T	1.1	93
759	Developmental Changes in the Metabolic Network of Snapdragon Flowers. PLoS ONE, 2012, 7, e40381.	1.1	72
760	De Novo Sequencing and Transcriptome Analysis of the Central Nervous System of Mollusc Lymnaea stagnalis by Deep RNA Sequencing. PLoS ONE, 2012, 7, e42546.	1.1	92
761	Comparative Transcriptome Analysis of Two Olive Cultivars in Response to NaCl-Stress. PLoS ONE, 2012, 7, e42931.	1.1	39
762	Global Transcriptome Analysis of the Scorpion Centruroides noxius: New Toxin Families and Evolutionary Insights from an Ancestral Scorpion Species. PLoS ONE, 2012, 7, e43331.	1.1	69
763	Transcriptome Analysis of Nicotiana tabacum Infected by Cucumber mosaic virus during Systemic Symptom Development. PLoS ONE, 2012, 7, e43447.	1.1	107
764	Sequencing and de novo Analysis of Crassostrea angulata (Fujian Oyster) from 8 Different Developing Phases Using 454 GSFlx. PLoS ONE, 2012, 7, e43653.	1.1	63
765	Transcriptomic Analysis of Acclimation to Temperature and Light Stress in Saccharina latissima (Phaeophyceae). PLoS ONE, 2012, 7, e44342.	1.1	84
766	Detailed Transcriptome Description of the Neglected Cestode Taenia multiceps. PLoS ONE, 2012, 7, e45830.	1.1	27
767	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
768	Different Transcriptional Response to Xanthomonas citri subsp. citri between Kumquat and Sweet Orange with Contrasting Canker Tolerance. PLoS ONE, 2012, 7, e41790.	1.1	36
769	Distribution and Functions of TonB-Dependent Transporters in Marine Bacteria and Environments: Implications for Dissolved Organic Matter Utilization. PLoS ONE, 2012, 7, e41204.	1.1	97
770	Transcriptional Profiles of Mating-Responsive Genes from Testes and Male Accessory Glands of the Mediterranean Fruit Fly, Ceratitis capitata. PLoS ONE, 2012, 7, e46812.	1.1	40
771	De Novo Assembly, Characterization and Functional Annotation of Pineapple Fruit Transcriptome through Massively Parallel Sequencing. PLoS ONE, 2012, 7, e46937.	1.1	37
772	Ultrastructural Observation and Gene Expression Profiling of Schistosoma japonicum Derived from Two Natural Reservoir Hosts, Water Buffalo and Yellow Cattle. PLoS ONE, 2012, 7, e47660.	1.1	22
773	Transcriptome Analysis of the Asian Honey Bee Apis cerana cerana. PLoS ONE, 2012, 7, e47954.	1.1	32
774	Candidate Olfaction Genes Identified within the Helicoverpa armigera Antennal Transcriptome. PLoS ONE, 2012, 7, e48260.	1.1	163
775	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (Artibeus jamaicensis). PLoS ONE, 2012, 7, e48472.	1.1	77
776	Expression of Small RNA in Aphis gossypii and Its Potential Role in the Resistance Interaction with Melon. PLoS ONE, 2012, 7, e48579.	1.1	40
777	Characterization of Head Transcriptome and Analysis of Gene Expression Involved in Caste Differentiation and Aggression in Odontotermes formosanus (Shiraki). PLoS ONE, 2012, 7, e50383.	1.1	41
778	Transcriptomic Profiling during the Post-Harvest of Heat-Treated Dixiland Prunus persica Fruits: Common and Distinct Response to Heat and Cold. PLoS ONE, 2012, 7, e51052.	1.1	34
779	Transcriptome Profiling of Rabbit Parthenogenetic Blastocysts Developed under In Vivo Conditions. PLoS ONE, 2012, 7, e51271.	1.1	8
780	SNP Detection from De Novo Transcriptome Sequencing in the Bivalve Macoma balthica: Marker Development for Evolutionary Studies. PLoS ONE, 2012, 7, e52302.	1.1	24
781	Application of functional genomic information to develop efficient EST-SSRs for the chicken (Gallus) Tj ETQq1 1 0.784314 rgBT /Overlo	0.3	13
782	Functional Approaches to Study Leaf Senescence in Sunflower. , 0, , .		4
783	Transcript profiling of expressed sequence tags from semimembranosus muscle of commercial and naturalized pig breeds. Genetics and Molecular Research, 2012, 11, 3315-3328.	0.3	4
784	New Insights in the Sugarcane Transcriptome Responding to Drought Stress as Revealed by Supersage. Scientific World Journal, The, 2012, 2012, 1-14.	0.8	44
785	Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress. , 0, , .		16

#	ARTICLE	IF	CITATIONS
786	Microbial diversity of soils on the banks of the SolimÃµes and Negro rivers, state of Amazonas, Brazil. Genetics and Molecular Biology, 2012, 35, 134-141.	0.6	3
787	Candidate chemosensory Genes in Female Antennae of the Noctuid Moth Spodoptera littoralis. International Journal of Biological Sciences, 2012, 8, 1036-1050.	2.6	83
788	Feminizing Wolbachia: a transcriptomics approach with insights on the immune response genes in Armadillidium vulgare. BMC Microbiology, 2012, 12, S1.	1.3	48
789	Host gene response to endosymbiont and pathogen in the cereal weevil Sitophilus oryzae. BMC Microbiology, 2012, 12, S14.	1.3	42
790	Influence of Wolbachia on host gene expression in an obligatory symbiosis. BMC Microbiology, 2012, 12, S7.	1.3	63
791	2â€D DIGE analysis of UVâ€C radiationâ€responsive proteins in globe artichoke leaves. Proteomics, 2012, 12, 448-460.	1.3	11
792	PloGO: Plotting gene ontology annotation and abundance in multiâ€condition proteomics experiments. Proteomics, 2012, 12, 406-410.	1.3	30
793	The subcellular proteome of undifferentiated human embryonic stem cells. Proteomics, 2012, 12, 421-430.	1.3	16
794	Microarray analysis of global gene regulation in the Cry1Abâ€resistant and Cry1Abâ€susceptible strains of <i>Diatraea saccharalis</i>. Pest Management Science, 2012, 68, 718-730.	1.7	27
795	A large scale screen for neural stem cell markers in <i>Xenopus</i> retina. Developmental Neurobiology, 2012, 72, 491-506.	1.5	25
796	High-throughput sequencing discovery of conserved and novel microRNAs in Chinese cabbage (Brassica rapa L. ssp. pekinensis). Molecular Genetics and Genomics, 2012, 287, 555-563.	1.0	47
797	Designing a transcriptome nextâ€generation sequencing project for a nonmodel plant species¹. American Journal of Botany, 2012, 99, 257-266.	0.8	192
798	Molecular and life-history effects of a natural toxin on herbivorous and non-target soil arthropods. Ecotoxicology, 2012, 21, 1084-1093.	1.1	19
799	De novo characterization of the antler tip of Chinese Sika deer transcriptome and analysis of gene expression related to rapid growth. Molecular and Cellular Biochemistry, 2012, 364, 93-100.	1.4	41
800	Development of ESTs and data mining of pineapple EST-SSRs. Molecular Biology Reports, 2012, 39, 5889-5896.	1.0	13
801	Generation, functional analysis and utility of Citrus grandis EST from a flower-derived cDNA library. Molecular Biology Reports, 2012, 39, 7221-7235.	1.0	14
802	Discovery, validation, and in silico functional characterization of EST-SSR markers in Eucalyptus globulus. Tree Genetics and Genomes, 2012, 8, 289-301.	0.6	28
803	De novo characterization of the root transcriptome of a traditional Chinese medicinal plant Polygonum cuspidatum. Science China Life Sciences, 2012, 55, 452-466.	2.3	80

#	ARTICLE	IF	CITATIONS
804	Construction of cDNA library from intestine, mesentery and coelomocyte of Apostichopus japonicus Selenka infected with Vibrio sp. and a preliminary analysis of immunity-related genes. Journal of Ocean University of China, 2012, 11, 187-196.	0.6	3
805	Transcriptome analysis of the roots at early and late seedling stages using Illumina paired-end sequencing and development of EST-SSR markers in radish. Plant Cell Reports, 2012, 31, 1437-1447.	2.8	96
806	De novo sequencing and a comprehensive analysis of purple sweet potato (Impomoea batatas L.) transcriptome. Planta, 2012, 236, 101-113.	1.6	118
807	Transcriptomic Characterization of the Larval Stage in Gilthead Seabream (Sparus aurata) by 454 Pyrosequencing. Marine Biotechnology, 2012, 14, 423-435.	1.1	37
808	Sequencing and de novo analysis of the Chinese Sika deer antler-tip transcriptome during the ossification stage using Illumina RNA-Seq technology. Biotechnology Letters, 2012, 34, 813-822.	1.1	40
809	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. New Phytologist, 2012, 193, 755-769.	3.5	305
810	Characterization of the early response of the orchid, <i>Phalaenopsis amabilis</i>, to <i>Erwinia chrysanthemi</i> infection using expression profiling. Physiologia Plantarum, 2012, 145, 406-425.	2.6	11
811	Species' identification and microarrayâ€based comparative genome analysis of <i>Streptomyces</i> species isolated from potato scab lesions in Norway. Molecular Plant Pathology, 2012, 13, 174-186.	2.0	12
812	Integrated transcriptomic and proteomic profiling of white spruce stems during the transition from active growth to dormancy. Plant, Cell and Environment, 2012, 35, 682-701.	2.8	40
813	Cell and molecular biology of the spiny dogfish <i>Squalus acanthias</i> and little skate <i>Leucoraja erinacea</i>: insights from <i>in vitro</i> cultured cells. Journal of Fish Biology, 2012, 80, 2089-2111.	0.7	4
814	Variable selection for multifactorial genomic data. Chemometrics and Intelligent Laboratory Systems, 2012, 110, 113-122.	1.8	7
815	Combination of de novo assembly of massive sequencing reads with classical repeat prediction improves identification of repetitive sequences in Schistosoma mansoni. Experimental Parasitology, 2012, 130, 470-474.	0.5	15
816	Functional classification of ESTs from vernonia (Vernonia galamensis L.) cDNA library. Industrial Crops and Products, 2012, 36, 370-375.	2.5	0
817	Arbuscular mycorrhizal fungi modulate the leaf transcriptome of a Populus alba L. clone grown on a zinc and copper-contaminated soil. Environmental and Experimental Botany, 2012, 75, 25-35.	2.0	58
818	Key strongylid nematodes of animals â€" Impact of next-generation transcriptomics on systems biology and biotechnology. Biotechnology Advances, 2012, 30, 469-488.	6.0	37
819	Transcriptome analysis of the citrus red mite, <i>Panonychus citri</i>, and its gene expression by exposure to insecticide/acaricide. Insect Molecular Biology, 2012, 21, 422-436.	1.0	30
820	<i>De novo</i> transcriptome assembly and polymorphism detection in the flowering plant <i>Silene vulgaris</i> (Caryophyllaceae). Molecular Ecology Resources, 2012, 12, 333-343.	2.2	60
821	Developing genomic resources in two <i>Linum</i> species via 454 pyrosequencing and genomic reduction. Molecular Ecology Resources, 2012, 12, 492-500.	2.2	35

#	ARTICLE	IF	CITATIONS
822	Genes under positive selection in a model plant pathogenic fungus, Botrytis. Infection, Genetics and Evolution, 2012, 12, 987-996.	1.0	40
823	Identification of water stress genes in Pinus pinaster Ait. by controlled progressive stress and suppression-subtractive hybridization. Plant Physiology and Biochemistry, 2012, 50, 44-53.	2.8	28
824	Expressed sequence tag based identification and expression analysis of some cold inducible elements in seabuckthorn (Hippophae rhamnoides L.). Plant Physiology and Biochemistry, 2012, 51, 123-128.	2.8	25
825	Identification of differentially expressed genes in a spontaneous altered leaf shape mutant of the navel orange [Citrus sinensis (L.) Osbeck]. Plant Physiology and Biochemistry, 2012, 56, 97-103.	2.8	5
826	Intrinsic gene expression during regeneration in arm explants of Amphiura filiformis. Journal of Experimental Marine Biology and Ecology, 2012, 413, 106-112.	0.7	17
827	Transcriptome analysis of <i>Stagonospora nodorum</i>: gene models, effectors, metabolism and pantothenate dispensability. Molecular Plant Pathology, 2012, 13, 531-545.	2.0	40
828	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. Molecular Plant Pathology, 2012, 13, 1120-1134.	2.0	14
829	Disruption of gene expression in hybrids of the fire ants <i>Solenopsis invicta</i> and <i>Solenopsis richteri</i>. Molecular Ecology, 2012, 21, 2488-2501.	2.0	6
830	Differences in transcription levels among wild, domesticated, and hybrid Atlantic salmon (<i>Salmo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	45
831	Transcriptome changes after genomeâ€wide admixture in invasive sculpins (<i>Cottus</i>). Molecular Ecology, 2012, 21, 4797-4810.	2.0	21
832	Bioinformatics meets parasitology. Parasite Immunology, 2012, 34, 265-275.	0.7	23
833	Gene expression in the developing aleurone and starchy endosperm of wheat. Plant Biotechnology Journal, 2012, 10, 668-679.	4.1	75
834	Identification of systemic responses in soybean nodulation by xylem sap feeding and complete transcriptome sequencing reveal a novel component of the autoregulation pathway. Plant Biotechnology Journal, 2012, 10, 680-689.	4.1	30
835	The eroded genome of a <i>Psychotria</i> leaf symbiont: hypotheses about lifestyle and interactions with its plant host. Environmental Microbiology, 2012, 14, 2757-2769.	1.8	60
836	Characterisation of full-length cDNA sequences provides insights into the Eimeria tenella transcriptome. BMC Genomics, 2012, 13, 21.	1.2	20
837	An ovary transcriptome for all maturational stages of the striped bass (Morone saxatilis), a highly advanced perciform fish. BMC Research Notes, 2012, 5, 111.	0.6	47
838	Development of a cDNA microarray for the measurement of gene expression in the sheep scab mite Psoroptes ovis. Parasites and Vectors, 2012, 5, 30.	1.0	15
839	Characterizing the walnut genome through analyses of BAC end sequences. Plant Molecular Biology, 2012, 78, 95-107.	2.0	27

#	ARTICLE	IF	CITATIONS
840	A transcriptomic analysis reveals the nature of salinity tolerance of a wheat introgression line. Plant Molecular Biology, 2012, 78, 159-169.	2.0	58
841	Construction of a Full-Length cDNA Library and Analysis of Expressed Sequence Tags from Inflorescence of Apomictic Sabaigrass (Eulaliopsis binata). Plant Molecular Biology Reporter, 2012, 30, 46-54.	1.0	7
842	Proteomic Analysis of PEG-Fractionated UV-C Stress-Response Proteins in Globe Artichoke. Plant Molecular Biology Reporter, 2012, 30, 111-122.	1.0	7
843	Mining of miRNAs and potential targets from gene oriented clusters of transcripts sequences of the anti-malarial plant, Artemisia annua. Biotechnology Letters, 2012, 34, 737-745.	1.1	23
844	Transcriptome analysis of an invasive weed Mikania micrantha. Biologia Plantarum, 2012, 56, 111-116.	1.9	18
845	Differential gene expression analysis in Enchytraeus albidus exposed to natural and chemical stressors at different exposure periods. Ecotoxicology, 2012, 21, 213-224.	1.1	11
846	Microarray Analysis Highlights Immune Response of Pacific Oysters as a Determinant of Resistance to Summer Mortality. Marine Biotechnology, 2012, 14, 203-217.	1.1	51
847	Molecular imaging of p53 signal pathway in lung cancer cell cycle arrest induced by cisplatin. Molecular Carcinogenesis, 2013, 52, 900-907.	1.3	20
848	Proteomics approach combined with biochemical attributes to elucidate compatible and incompatible plant-virus interactions between Vigna mungo and Mungbean Yellow Mosaic India Virus. Proteome Science, 2013, 11, 15.	0.7	58
849	Gene Ontology consistent protein function prediction: the FALCON algorithm applied to six eukaryotic genomes. Algorithms for Molecular Biology, 2013, 8, 10.	0.3	9
850	Comparative transcriptome analysis to investigate the high starch accumulation of duckweed (Landoltia punctata) under nutrient starvation. Biotechnology for Biofuels, 2013, 6, 72.	6.2	80
851	5-methyl-cytosine and 5-hydroxy-methyl-cytosine in the genome of Biomphalaria glabrata, a snail intermediate host of Schistosoma mansoni. Parasites and Vectors, 2013, 6, 167.	1.0	45
852	Use of expressed sequence tags as an alternative approach for the identification of Taenia solium metacestode excretion/secretion proteins. BMC Research Notes, 2013, 6, 224.	0.6	4
853	De novo transcriptomic resources for two sibling species of moths: Ostrinia nubilalis and O. scapulalis. BMC Research Notes, 2013, 6, 73.	0.6	9
854	A quantitative reference transcriptome for Nematostella vectensis earlyembryonic development: a pipeline for de novo assembly in emergingmodel systems. EvoDevo, 2013, 4, 16.	1.3	57
855	Development of EST-SSR markers through data mining and their use for genetic diversity study in Indian accessions of Jatropha curcas L.: a potential energy crop. Genes and Genomics, 2013, 35, 661-670.	0.5	11
856	Genomic expression responses toward bisphenol-A toxicity in Daphnia magna in terms of reproductive activity. Molecular and Cellular Toxicology, 2013, 9, 149-158.	0.8	37
857	Differential gene expression analysis between anagen and telogen of Capra hircus skin based on the de novo assembled transcriptome sequence. Gene, 2013, 520, 30-38.	1.0	37

#	Article	IF	Citations
858	Molecular mechanisms of desiccation tolerance in the resurrection glacial relic Haberlea rhodopensis. Cellular and Molecular Life Sciences, 2013, 70, 689-709.	2.4	168
859	Use of an expressed sequence tag-based method for single nucleotide polymorphism identification and discrimination of Citrus species and cultivars. Molecular Breeding, 2013, 31, 705-718.	1.0	2
860	Comparative analysis of differentially expressed genes in Sika deer antler at different stages. Molecular Biology Reports, 2013, 40, 1665-1676.	1.0	29
861	Exploring the genome of the salt-marsh Spartina maritima (Poaceae, Chloridoideae) through BAC end sequence analysis. Plant Molecular Biology, 2013, 83, 591-606.	2.0	11
862	Populus euphratica: the transcriptomic response to drought stress. Plant Molecular Biology, 2013, 83, 539-557.	2.0	84
863	SNP discovery and High Resolution Melting Analysis from massive transcriptome sequencing in the California red abalone Haliotis rufescens. Marine Genomics, 2013, 10, 11-16.	0.4	15
864	Environmental regulation of reproductive phase change in Agaricus bisporus by 1-octen-3-ol, temperature and CO2. Fungal Genetics and Biology, 2013, 55, 54-66.	0.9	50
865	Proteomic characterization of larval and adult developmental stages in Echinococcus granulosus reveals novel insight into hostâ€“parasite interactions. Journal of Proteomics, 2013, 84, 158-175.	1.2	90
866	Proteomics Analysis of <i>Psychotria</i> Leaf Nodule Symbiosis: Improved Genome Annotation and Metabolic Predictions. Molecular Plant-Microbe Interactions, 2013, 26, 1325-1333.	1.4	27
867	Genome-wide annotation of genes and noncoding RNAs of foxtail millet in response to simulated drought stress by deep sequencing. Plant Molecular Biology, 2013, 83, 459-473.	2.0	157
868	Dissecting the mechanisms responsible for the multiple insecticide resistance phenotype in Anopheles gambiae s.s., M form, from VallÃ©e du Kou, Burkina Faso. Gene, 2013, 519, 98-106.	1.0	111
869	Transcriptome of an <scp>A</scp>rmillaria root disease pathogen reveals candidate genes involved in host substrate utilization at the hostâ€“pathogen interface. Forest Pathology, 2013, 43, 468-477.	0.5	34
870	Differentially regulated genes in Solanum tuberosum in response to â€œMexican potato purple top phytoplasmaâ€•infection. Physiological and Molecular Plant Pathology, 2013, 81, 33-44.	1.3	5
871	SNP discovery in the marine gastropod Concholepas concholepas by high-throughput transcriptome sequencing. Conservation Genetics Resources, 2013, 5, 1053-1054.	0.4	9
872	Phylogenetic Analysis and Metabolic Potential of Microbial Communities in an Industrial Bagasse Collection Site. Microbial Ecology, 2013, 66, 322-334.	1.4	24
873	Identification of SNP markers for inferring phylogeny in temperate bamboos (P oaceae: B ambusoideae) using RAD sequencing. Molecular Ecology Resources, 2013, 13, 938-945.	2.2	53
874	Transcriptional changes in developing maize kernels in response to fumonisin-producing and nonproducing strains of Fusarium verticillioides. Plant Science, 2013, 210, 183-192.	1.7	20
875	Protein Function Prediction using Text-based Features extracted from the Biomedical Literature: The CAFA Challenge. BMC Bioinformatics, 2013, 14, S14.	1.2	37

#	ARTICLE	IF	CITATIONS
876	Reannotation and extended community resources for the genome of the non-seed plant Physcomitrella patens provide insights into the evolution of plant gene structures and functions. BMC Genomics, 2013, 14, 498.	1.2	170
877	De novo sequencing and transcriptome analysis of the desert shrub, Ammopiptanthus mongolicus, during cold acclimation using Illumina/Solexa. BMC Genomics, 2013, 14, 488.	1.2	80
878	KONAGAbase: a genomic and transcriptomic database for the diamondback moth, Plutella xylostella. BMC Genomics, 2013, 14, 464.	1.2	47
879	Transcriptional profiling of sweetpotato (Ipomoea batatas) roots indicates down-regulation of lignin biosynthesis and up-regulation of starch biosynthesis at an early stage of storage root formation. BMC Genomics, 2013, 14, 460.	1.2	154
880	Global transcriptome profiles of Camellia sinensis during cold acclimation. BMC Genomics, 2013, 14, 415.	1.2	268
881	Comparative transcriptome analysis of microsclerotia development in Nomuraea rileyi. BMC Genomics, 2013, 14, 411.	1.2	38
882	Transcript profiling by microarray and marker analysis of the short cotton (Gossypium hirsutum L.) fiber mutant Ligon lintless-1 (Li 1). BMC Genomics, 2013, 14, 403.	1.2	43
883	RNA-seq analysis reveals extensive transcriptional plasticity to temperature stress in a freshwater fish species. BMC Genomics, 2013, 14, 375.	1.2	152
884	The genome and transcriptome of the pine saprophyte Ophiostoma piceae, and a comparison with the bark beetle-associated pine pathogen Grosmannia clavigera. BMC Genomics, 2013, 14, 373.	1.2	72
885	Comparative transcriptome analysis and marker development of two closely related Primrose species (Primula poissonii and Primula wilsonii). BMC Genomics, 2013, 14, 329.	1.2	62
886	Exploring the larval transcriptome of the common sole (Solea solea L.). BMC Genomics, 2013, 14, 315.	1.2	44
887	Novel genomic resources for a climate change sensitive mammal: characterization of the American pika transcriptome. BMC Genomics, 2013, 14, 311.	1.2	20
888	Transcriptome-wide comparison of sequence variation in divergent ecotypes of kokanee salmon. BMC Genomics, 2013, 14, 308.	1.2	18
889	Unscrambling butterfly oogenesis. BMC Genomics, 2013, 14, 283.	1.2	44
890	Transcriptome analysis of Cymbidium sinense and its application to the identification of genes associated with floral development. BMC Genomics, 2013, 14, 279.	1.2	107
891	Genome analyses of the wheat yellow (stripe) rust pathogen Puccinia striiformis f. sp. triticireveal polymorphic and haustorial expressed secreted proteins as candidate effectors. BMC Genomics, 2013, 14, 270.	1.2	235
892	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. BMC Genomics, 2013, 14, 236.	1.2	82
893	Tyrosine pathway regulation is host-mediated in the pea aphid symbiosis during late embryonic and early larval development. BMC Genomics, 2013, 14, 235.	1.2	51

#	ARTICLE	IF	CITATIONS
894	Xylem transcription profiles indicate potential metabolic responses for economically relevant characteristics of Eucalyptusspecies. BMC Genomics, 2013, 14, 201.	1.2	28
895	Antennal transcriptome analysis of the chemosensory gene families in the tree killing bark beetles, Ips typographus and Dendroctonus ponderosae (Coleoptera: Curculionidae: Scolytinae). BMC Genomics, 2013, 14, 198.	1.2	216
896	Transcriptome-based discovery of pathways and genes related to resistance against Fusariumhead blight in wheat landrace Wangshuibai. BMC Genomics, 2013, 14, 197.	1.2	143
897	Deep sequencing for de novo construction of a marine fish (Sparus aurata)transcriptome database with a large coverage of protein-coding transcripts. BMC Genomics, 2013, 14, 178.	1.2	90
898	De-novo assembly and characterization of the transcriptome of Metschnikowia fructicola reveals differences in gene expression following interaction with Penicillium digitatumand grapefruit peel. BMC Genomics, 2013, 14, 168.	1.2	79
899	De novo assembly and characterization of Camelina sativatranscriptome by paired-end sequencing. BMC Genomics, 2013, 14, 146.	1.2	83
900	De novo assembly and characterization of transcriptome using Illumina paired-end sequencing and identification of CesA gene in ramie (Boehmeria nivea L. Gaud). BMC Genomics, 2013, 14, 125.	1.2	107
901	Characterization of the global transcriptome for Pyropia haitanensis(Bangiales, Rhodophyta) and development of cSSR markers. BMC Genomics, 2013, 14, 107.	1.2	75
902	A hybrid next generation transcript sequencing-based approach to identify allelic and homeolog-specific single nucleotide polymorphisms in allotetraploid white clover. BMC Genomics, 2013, 14, 100.	1.2	18
903	Global analyses of Ceratocystis cacaofunesta mitochondria: from genome to proteome. BMC Genomics, 2013, 14, 91.	1.2	17
904	Comparisons of infant Escherichia coli isolates link genomic profiles with adaptation to the ecological niche. BMC Genomics, 2013, 14, 81.	1.2	12
905	Analysis of the leaf transcriptome of Musa acuminata during interaction with Mycosphaerella musicola: gene assembly, annotation and marker development. BMC Genomics, 2013, 14, 78.	1.2	46
906	Use of digital gene expression to discriminate gene expression differences in early generations of resynthesized Brassica napus and its diploid progenitors. BMC Genomics, 2013, 14, 72.	1.2	36
907	Genome reannotation of the lizard Anolis carolinensis based on 14 adult and embryonic deep transcriptomes. BMC Genomics, 2013, 14, 49.	1.2	55
908	Transcriptomic profiling of the salt-stress response in the wild recretohalophyte Reaumuria trigyna. BMC Genomics, 2013, 14, 29.	1.2	147
909	Evidence of a conserved functional role for <scp>DNA</scp> methylation in termites. Insect Molecular Biology, 2013, 22, 143-154.	1.0	36
910	Isolation, characterization and mapping of genes differentially expressed during fibre development between Gossypium hirsutum and G. barbadense by cDNA-SRAP. Journal of Genetics, 2013, 92, 175-181.	0.4	10
911	Computational identification of conserved microRNAs and their putative targets in the Hypericum perforatum L. flower transcriptome. Plant Reproduction, 2013, 26, 209-229.	1.3	38

#	ARTICLE	IF	CITATIONS
912	Diversity arrays technology (DArT) for studying the genetic polymorphism of flue-cured tobacco (Nicotiana tabacum). Journal of Zhejiang University: Science B, 2013, 14, 570-577.	1.3	7
913	Characterization of the Zhikong Scallop (Chlamys farreri) Mantle Transcriptome and Identification of Biomineralization-Related Genes. Marine Biotechnology, 2013, 15, 706-715.	1.1	49
914	A predicted functional gene network for the plant pathogen Phytophthora infestans as a framework for genomic biology. BMC Genomics, 2013, 14, 483.	1.2	20
915	Genome-Wide SNP Validation and Mantle Tissue Transcriptome Analysis in the Silver-Lipped Pearl Oyster, Pinctada maxima. Marine Biotechnology, 2013, 15, 647-658.	1.1	28
916	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	5.8	244
917	De novo sequencing and assembly of Centella asiatica leaf transcriptome for mapping of structural, functional and regulatory genes with special reference to secondary metabolism. Gene, 2013, 525, 58-76.	1.0	96
918	Contribution of subgenomes to the transcriptome and their intertwined regulation in the allopolyploid <i>Coffea arabica</i> grown at contrasted temperatures. New Phytologist, 2013, 200, 251-260.	3.5	79
919	Comparative metagenomic analysis of microcosm structures and lignocellulolytic enzyme systems of symbiotic biomass-degrading consortia. Applied Microbiology and Biotechnology, 2013, 97, 8941-8954.	1.7	59
920	A transcriptomic investigation of handicap models in sexual selection. Behavioral Ecology and Sociobiology, 2013, 67, 221-234.	0.6	9
921	Genetic mapping of EST-derived simple sequence repeats (EST-SSRs) to identify QTL for leaf morphological characters in a Quercus robur full-sib family. Tree Genetics and Genomes, 2013, 9, 1361-1367.	0.6	16
922	Genetic structure of Quercus rubra L. and Quercus ellipsoidalis E. J. Hill populations at gene-based EST-SSR and nuclear SSR markers. Tree Genetics and Genomes, 2013, 9, 707-722.	0.6	72
923	Transcriptome of oil palm (Elaeis guineensis Jacq.) roots treated with Ganoderma boninense. Tree Genetics and Genomes, 2013, 9, 377-386.	0.6	34
924	An extensive proteome map of tomato (<i>Solanum lycopersicum</i>) fruit pericarp. Proteomics, 2013, 13, 3059-3063.	1.3	28
925	Targeted sequence capture and resequencing implies a predominant role of regulatory regions in the divergence of a sympatric lake whitefish species pair (<i><scp>C</scp>oregonus clupeaformis</i>). Molecular Ecology, 2013, 22, 4896-4914.	2.0	37
926	Complete genome sequence of a novel potato virus S strain infecting Solanum phureja in Colombia. Archives of Virology, 2013, 158, 2205-2208.	0.9	23
927	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. Nature Genetics, 2013, 45, 1092-1096.	9.4	236
928	Vesicular Trafficking and Stress Response Coupled to PI3K Inhibition by LY294002 as Revealed by Proteomic and Cell Biological Analysis. Journal of Proteome Research, 2013, 12, 4435-4448.	1.8	47
929	Correlation between structure, protein composition, morphogenesis and cytopathology of Glossina pallidipes salivary gland hypertrophy virus. Journal of General Virology, 2013, 94, 193-208.	1.3	16

#	ARTICLE	IF	CITATIONS
930	A draft genome sequence of the pulse crop chickpea (<i><scp>C</scp>icer arietinum</i>ÂL.). Plant Journal, 2013, 74, 715-729.	2.8	382
931	Identification of genes associated with fruit ripening in Ziziphus jujuba using suppression subtractive hybridization approach. Acta Physiologiae Plantarum, 2013, 35, 1997-2008.	1.0	2
932	The sarcoplasmic fish proteome: Pathways, metabolic networks and potential bioactive peptides for nutritional inferences. Journal of Proteomics, 2013, 78, 211-220.	1.2	43
933	Effects of exposure to 17Î±-ethynylestradiol during larval development on growth, sexual differentiation, and abundances of transcripts in the liver of the wood frog (Lithobates sylvaticus). Aquatic Toxicology, 2013, 126, 42-51.	1.9	35
934	Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. Scientific Reports, 2013, 3, 1569.	1.6	104
935	Computational identification of microRNAs and their targets in Catharanthus roseus expressed sequence tags. Genomics Data, 2013, 1, 2-6.	1.3	57
936	Illumina-based de novo transcriptome sequencing and analysis of Amanita exitialis basidiocarps. Gene, 2013, 532, 63-71.	1.0	47
937	Silver Nanowire Exposure Results in Internalization and Toxicity to Daphnia magna. ACS Nano, 2013, 7, 10681-10694.	7.3	117
938	Comparative Proteomics Reveal Diverse Functions and Dynamic Changes of <i>Bombyx mori</i> Silk Proteins Spun from Different Development Stages. Journal of Proteome Research, 2013, 12, 5213-5222.	1.8	75
939	Differential expression of American lobster (Homarus americanus) immune related genes during infection of Aerococcus viridans var. homari, the causative agent of Gaffkemia. Journal of Invertebrate Pathology, 2013, 112, 192-202.	1.5	25
940	&lt;i&gt;Pinus taeda&lt;/i&gt; cDNA Microarray as a Tool for Candidate Gene Identification for Local Red/Far-Red Light Adaptive Response in &lt;i&gt;Pinus sylvestris&lt;/i&gt;. American Journal of Plant Sciences, 2013, 04, 479-493.	0.3	6
941	Analysis of the Elodea nuttallii Transcriptome in Response to Mercury and Cadmium Pollution: Development of Sensitive Tools for Rapid Ecotoxicological Testing. Environmental Science & Technology, 2013, 47, 8825-8834.	4.6	41
942	Transcriptome profiling and digital gene expression analysis of Nile tilapia (Oreochromis niloticus) infected by Streptococcus agalactiae. Molecular Biology Reports, 2013, 40, 5657-5668.	1.0	66
943	Analysis of gene expression in Homarus americanus larvae exposed to sublethal concentrations of endosulfan during metamorphosis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 300-308.	0.4	11
944	The High Polyphenol Content of Grapevine Cultivar Tannat Berries Is Conferred Primarily by Genes That Are Not Shared with the Reference Genome. Plant Cell, 2013, 25, 4777-4788.	3.1	138
945	Analysis of the canine brain transcriptome with an emphasis on the hypothalamus and cerebral cortex. Mammalian Genome, 2013, 24, 484-499.	1.0	26
946	Pheromone Evolution, Reproductive Genes, and Comparative Transcriptomics in Mediterranean Earthworms (Annelida, Oligochaeta, Hormogastridae). Molecular Biology and Evolution, 2013, 30, 1614-1629.	3.5	24
947	Suppressive subtractive hybridisation transcriptomics provides a novel insight into the functional role of the hypobranchial gland in a marine mollusc. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 111-122.	0.4	9

#	Article	IF	Citations
948	Transcriptome analysis of a parasitic clade V nematode: Comparative analysis of potential molecular anthelmintic targets in Cylicostephanus goldi. International Journal for Parasitology, 2013, 43, 917-927.	1.3	11
949	The dynamics of functional classes of plant genes in rediploidized ancient polyploids. BMC Bioinformatics, 2013, 14, S19.	1.2	17
950	Pyroptosis and adaptive immunity mechanisms are promptly engendered in mesenteric lymph-nodes during pig infections with Salmonella enterica serovar Typhimurium. Veterinary Research, 2013, 44, 120.	1.1	15
951	Genome sequencing and comparative genomics of honey bee microsporidia, Nosema apis reveal novel insights into host-parasite interactions. BMC Genomics, 2013, 14, 451.	1.2	61
952	Construction and characterization of a forward subtracted library of blue mussels Mytilus edulis for the identification of gene transcription signatures and biomarkers of styrene exposure. Marine Pollution Bulletin, 2013, 71, 230-239.	2.3	11
953	De novo assembly and characterization of spotted seal Phoca largha transcriptome using Illumina paired-end sequencing. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 103-110.	0.4	8
954	The okra (Abelmoschus esculentus) transcriptome as a source for gene sequence information and molecular markers for diversity analysis. Gene, 2013, 517, 27-36.	1.0	45
955	Zebrafish midbrain slow-amplifying progenitors exhibit high levels of transcripts for nucleotide and ribosome biogenesis. Development (Cambridge), 2013, 140, 4860-4869.	1.2	46
956	Development of <scp>EST</scp>â€<scp>SSR</scp> markers for diversity and breeding studies in opium poppy. Plant Breeding, 2013, 132, 344-351.	1.0	24
957	Asexual genome evolution in the apomictic <i><scp>R</scp>anunculus auricomus</i> complex: examining the effects of hybridization and mutation accumulation. Molecular Ecology, 2013, 22, 5908-5921.	2.0	118
958	â€œA draft Musa balbisiana genome sequence for molecular genetics in polyploid, inter- and intra-specific Musa hybridsâ€. BMC Genomics, 2013, 14, 683.	1.2	159
959	Whole transcriptome sequencing reveals genes involved in plastid/chloroplast division and development are regulated by the HP1/DDB1 at an early stage of tomato fruit development. Planta, 2013, 238, 923-936.	1.6	18
960	Histoplasma yeast and mycelial transcriptomes reveal pathogenic-phase and lineage-specific gene expression profiles. BMC Genomics, 2013, 14, 695.	1.2	50
961	Transcriptome analyses of a Chinese hazelnut species Corylus mandshurica. BMC Plant Biology, 2013, 13, 152.	1.6	24
962	Transcriptome profiling of Gossypium barbadense inoculated with Verticillium dahliae provides a resource for cotton improvement. BMC Genomics, 2013, 14, 637.	1.2	93
963	Identification of genes expressed in the sex pheromone gland of the black cutworm Agrotis ipsilon with putative roles in sex pheromone biosynthesis and transport. BMC Genomics, 2013, 14, 636.	1.2	111
964	Transcriptomic analysis highlights epigenetic and transcriptional regulation during zygotic embryo development of Pinus pinaster. BMC Plant Biology, 2013, 13, 123.	1.6	37
965	BSTA: a targeted approach combines bulked segregant analysis with next- generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. BMC Genomics, 2013, 14, 628.	1.2	43

#	Article	IF	Citations
966	De novo transcriptomic analysis of hydrogen production in the green alga Chlamydomonas moewusii through RNA-Seq. Biotechnology for Biofuels, 2013, 6, 118.	6.2	39
967	The predicted secretome and transmembranome of the poultry red mite Dermanyssus gallinae. Parasites and Vectors, 2013, 6, 259.	1.0	32
968	Transcriptome analysis of two buffalograss cultivars. BMC Genomics, 2013, 14, 613.	1.2	12
969	Identification of differential expression genes associated with host selection and adaptation between two sibling insect species by transcriptional profile analysis. BMC Genomics, 2013, 14, 582.	1.2	30
970	Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. BMC Genomics, 2013, 14, 430.	1.2	31
971	Analysis of the global transcriptome of longan (Dimocarpus longan Lour.) embryogenic callus using Illumina paired-end sequencing. BMC Genomics, 2013, 14, 561.	1.2	71
972	Developing molecular tools and insights into the Penstemon genome using genomic reduction and next-generation sequencing. BMC Genetics, 2013, 14, 66.	2.7	14
973	De novo assembly and characterization of fruit transcriptome in Litchi chinensis Sonn and analysis of differentially regulated genes in fruit in response to shading. BMC Genomics, 2013, 14, 552.	1.2	106
974	Analysis of the transcriptome of the Indonesian coelacanth Latimeria menadoensis. BMC Genomics, 2013, 14, 538.	1.2	35
975	Insights into xanthomonas axonopodis pv. citri biofilm through proteomics. BMC Microbiology, 2013, 13, 186.	1.3	40
976	Transcriptomic and proteomic analysis of a compatible tomato-aphid interaction reveals a predominant salicylic acid-dependent plant response. BMC Genomics, 2013, 14, 515.	1.2	103
977	The genome of Romanomermis culicivorax: revealing fundamental changes in the core developmental genetic toolkit in Nematoda. BMC Genomics, 2013, 14, 923.	1.2	43
978	Comparative analyses of two Geraniaceae transcriptomes using next-generation sequencing. BMC Plant Biology, 2013, 13, 228.	1.6	38
979	Uncovering the genetic basis for early isogamete differentiation: a case study of Ectocarpus siliculosus. BMC Genomics, 2013, 14, 909.	1.2	27
980	Whole transcriptome characterization of the effects of dehydration and rehydration on Cladonia rangiferina, the grey reindeer lichen. BMC Genomics, 2013, 14, 870.	1.2	31
981	Analysis of sea-island cotton and upland cotton in response to Verticillium dahliaeinfection by RNA sequencing. BMC Genomics, 2013, 14, 852.	1.2	78
982	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. BMC Genomics, 2013, 14, 843.	1.2	98
983	Midgut transcriptome profiling of Anoplophora glabripennis, a lignocellulose degrading cerambycid beetle. BMC Genomics, 2013, 14, 850.	1.2	65

#	ARTICLE	IF	CITATIONS
984	Genome-wide characterization of microRNA in foxtail millet (Setaria italica). BMC Plant Biology, 2013, 13, 212.	1.6	47
985	De novo characterization of the gene-rich transcriptomes of two color-polymorphic spiders, Theridion grallator and T. californicum (Araneae: Theridiidae), with special reference to pigment genes. BMC Genomics, 2013, 14, 862.	1.2	51
986	Fermentation stage-dependent adaptations of Bacillus licheniformis during enzyme production. Microbial Cell Factories, 2013, 12, 120.	1.9	19
987	Genome sequence and analysis of methylotrophic yeast Hansenula polymorpha DL1. BMC Genomics, 2013, 14, 837.	1.2	81
988	Genome wide gene-expression analysis of facultative reproductive diapause in the two-spotted spider mite Tetranychus urticae. BMC Genomics, 2013, 14, 815.	1.2	92
989	Transcriptional responses to temperature and low oxygen stress in Atlantic salmon studied with next-generation sequencing technology. BMC Genomics, 2013, 14, 817.	1.2	97
990	Identification of phenylpropanoid biosynthetic genes and phenylpropanoid accumulation by transcriptome analysis of Lycium chinense. BMC Genomics, 2013, 14, 802.	1.2	42
991	Comparative transcriptome analysis of tomato (Solanum lycopersicum) in response to exogenous abscisic acid. BMC Genomics, 2013, 14, 841.	1.2	84
992	Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td	1.2	50
993	De novo characterization of the Anthuriumtranscriptome and analysis of its digital gene expression under cold stress. BMC Genomics, 2013, 14, 827.	1.2	78
994	Isolation with differentiation followed by expansion with admixture in the tunicate Pyura chilensis. BMC Evolutionary Biology, 2013, 13, 252.	3.2	21
995	De novo assembly and characterization of tissue specific transcriptomes in the emerald notothen, Trematomus bernacchii. BMC Genomics, 2013, 14, 805.	1.2	54
996	Penicillium decumbens BrlA extensively regulates secondary metabolism and functionally associates with the expression of cellulase genes. Applied Microbiology and Biotechnology, 2013, 97, 10453-10467.	1.7	76
997	Transcriptome generation and analysis from spleen of Indian catfish, Clarias batrachus (Linnaeus,) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	2
998	A genome-wide identification and characterization of mircoRNAs and their targets in â€˜Suliâ€™ pear (Pyrus) Tj ETQq0 0 0 rgBT /Overloc	1.6	19
999	New insights in osteogenic differentiation revealed by mass spectrometric assessment of phosphorylated substrates in murine skin mesenchymal cells. BMC Cell Biology, 2013, 14, 47.	3.0	12
1000	SILAC-Based Proteome Analysis of <i>Starmerella bombicola</i> Sophorolipid Production. Journal of Proteome Research, 2013, 12, 4376-4392.	1.8	22
1001	Tetraploid Rangpur lime rootstock increases drought tolerance via enhanced constitutive root abscisic acid production. Plant, Cell and Environment, 2013, 36, 856-868.	2.8	167

#	ARTICLE	IF	CITATIONS
1002	Attenuation of bone morphogenetic protein signaling during amphibian limb development results in the generation of stageâ€specific defects. Journal of Anatomy, 2013, 223, 474-488.	0.9	13
1003	Application of <i>Cydia pomonella</i> expressed sequence tags: Identification and expression of three general odorant binding proteins in codling moth. Insect Science, 2013, 20, 559-574.	1.5	16
1004	Gender-specific transcriptional profiling of marine medaka (Oryzias melastigma) liver upon BDE-47 exposure. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 255-262.	0.4	8
1005	The regulation of cambial activity in <scp>C</scp>hinese fir (<i><scp>C</scp>unninghamia) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.5	69
1006	Producing more with less: Strategies and novel technologies for plant-based food biofortification. Food Research International, 2013, 54, 961-971.	2.9	153
1007	Genomic divergence between the migratory and stationary ecotypes of <scp>A</scp>tlantic cod. Molecular Ecology, 2013, 22, 5098-5111.	2.0	53
1008	The impact of a moderate chronic temperature increase on spleen immune-relevant gene transcription depends on whether Atlantic cod (<i>Gadus morhua</i>) are stimulated with bacterial versus viral antigens. Genome, 2013, 56, 567-576.	0.9	43
1009	Pyrosequencing of the adult tarnished plant bug, <i><scp>L</scp>ygus lineolaris</i>, and characterization of messages important in metabolism and development. Entomologia Experimentalis Et Applicata, 2013, 146, 364-378.	0.7	11
1010	Deciphering genetic diversity and inheritance of tomato fruit weight and composition through a systems biology approach. Journal of Experimental Botany, 2013, 64, 5737-5752.	2.4	20
1011	Genome-Scale Transcriptomic Insights into Early-Stage Fruit Development in Woodland Strawberry Fragaria vesca. Plant Cell, 2013, 25, 1960-1978.	3.1	268
1012	Annotation and reâ€sequencing of genes from de novo transcriptome assembly of <i>Abies alba</i> (Pinaceae). Applications in Plant Sciences, 2013, 1, 1200179.	0.8	17
1013	Functional Annotation and Comparative Analysis of a Zygopteran Transcriptome. G3: Genes, Genomes, Genetics, 2013, 3, 763-770.	0.8	5
1014	Genomic Divergence during Speciation Driven by Adaptation to Altitude. Molecular Biology and Evolution, 2013, 30, 2553-2567.	3.5	91
1015	Identification of cell wall proteins in the flax (<i>Linum usitatissimum</i>) stem. Proteomics, 2013, 13, 812-825.	1.3	32
1016	Complete mitochondrial genome of Concholepas concholepas inferred by 454 pyrosequencing and mtDNA expression in two mollusc populations. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 17-23.	0.4	3
1017	Proteomic Analysis of <i>Trypanosoma cruzi</i> Secretome: Characterization of Two Populations of Extracellular Vesicles and Soluble Proteins. Journal of Proteome Research, 2013, 12, 883-897.	1.8	235
1018	High SNP density in the blacklegged tick, Ixodes scapularis, the principal vector of Lyme disease spirochetes. Ticks and Tick-borne Diseases, 2013, 4, 63-71.	1.1	22
1019	Transcriptome sequencing of the Antarctic vascular plant Deschampsia antarctica Desv. under abiotic stress. Planta, 2013, 237, 823-836.	1.6	44

#	ARTICLE	IF	CITATIONS
1020	Gene family evolution in green plants with emphasis on the origination and evolution of <i><scp>A</scp>rabidopsis thaliana</i> genes. Plant Journal, 2013, 73, 941-951.	2.8	117
1021	Genomeâ€wide identification of viral and host transcripts targeted by viral <scp>siRNAs</scp> in <i><scp>V</scp>itis vinifera</i>. Molecular Plant Pathology, 2013, 14, 30-43.	2.0	69
1022	Transcriptome de novo assembly from next-generation sequencing and comparative analyses in the hexaploid salt marsh species Spartina maritima and Spartina alterniflora (Poaceae). Heredity, 2013, 110, 181-193.	1.2	50
1023	A genome-wide BAC end-sequence survey of sugarcane elucidates genome composition, and identifies BACs covering much of the euchromatin. Plant Molecular Biology, 2013, 81, 139-147.	2.0	26
1024	A guide to in silico vaccine discovery for eukaryotic pathogens. Briefings in Bioinformatics, 2013, 14, 753-774.	3.2	29
1025	Proteomic analysis of the Cyanophora paradoxa muroplast provides clues on early events in plastid endosymbiosis. Planta, 2013, 237, 637-651.	1.6	33
1026	Identification of cold-responsive genes in a New Zealand alpine stick insect using RNA-Seq. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 24-31.	0.4	32
1027	Comparative bacterial genomics: defining the minimal core genome. Antonie Van Leeuwenhoek, 2013, 103, 385-398.	0.7	14
1028	Transcriptomic analysis of purple leaf determination in birch. Gene, 2013, 526, 251-258.	1.0	13
1029	Identification of reproduction-related genes and SSR-markers through expressed sequence tags analysis of a monsoon breeding carp rohu, Labeo rohita (Hamilton). Gene, 2013, 524, 1-14.	1.0	17
1030	Crosstalk between B16 melanoma cells and B-1 lymphocytes induces global changes in tumor cell gene expression. Immunobiology, 2013, 218, 1293-1303.	0.8	11
1031	Characterization and analysis of a transcriptome from the boreal spider crab Hyas araneus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2013, 8, 344-351.	0.4	14
1032	Low-molecular-mass secretome profiling identifies Câ€"C motif chemokine 5 as a potential plasma biomarker and therapeutic target for nasopharyngeal carcinoma. Journal of Proteomics, 2013, 94, 186-201.	1.2	29
1033	How does exposure to nickel and cadmium affect the transcriptome of yellow perch (Perca) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.9	33
1034	Transcriptome sequencing and phylogenetic analysis of floral and leaf MIKCC MADS-box and R2R3 MYB transcription factors from the monocot Iris fulva. Gene, 2013, 531, 337-346.	1.0	8
1035	Transcriptomic analysis of incised leaf-shape determination in birch. Gene, 2013, 531, 263-269.	1.0	15
1036	A Bioinformatics Approach for Integrated Transcriptomic and Proteomic Comparative Analyses of Model and Non-sequenced Anopheline Vectors of Human Malaria Parasites. Molecular and Cellular Proteomics, 2013, 12, 120-131.	2.5	21
1037	Gene expression and pathologic alterations in juvenile rainbow trout due to chronic dietary TCDD exposure. Aquatic Toxicology, 2013, 140-141, 356-368.	1.9	19

#	ARTICLE	IF	CITATIONS
1038	Genome-wide analysis of endosperm-specific genes in rice. Gene, 2013, 530, 236-247.	1.0	46
1039	Gene expression of the marine copepod Calanus finmarchicus: Responses to small-scale environmental variation in the Gulf of Maine (NW Atlantic Ocean). Journal of Experimental Marine Biology and Ecology, 2013, 446, 76-85.	0.7	11
1040	Transcriptional profiling in burbot (Lota lota) from Lake MjÃ¸saâ€"A Norwegian Lake contaminated by several organic pollutants. Ecotoxicology and Environmental Safety, 2013, 92, 94-103.	2.9	15
1041	A comprehensive analysis of the Manduca sexta immunotranscriptome. Developmental and Comparative Immunology, 2013, 39, 388-398.	1.0	52
1042	Transcriptional responses of male fathead minnows exposed to oil sands process-affected water. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2013, 157, 227-235.	1.3	44
1043	Rapid modulation of gene expression profiles in the telencephalon of male goldfish following exposure to waterborne sex pheromones. General and Comparative Endocrinology, 2013, 192, 204-213.	0.8	16
1044	Transcriptome pyrosequencing of the Antarctic brittle star Ophionotus victoriae. Marine Genomics, 2013, 9, 9-15.	0.4	18
1045	Transcriptome analysis reveals novel genes potentially involved in photoperiodic tuberization in potato. Genomics, 2013, 102, 388-396.	1.3	32
1046	Gene discovery in the tropical scallop Nodipecten nodosus: Construction and sequencing of a normalized cDNA library. Marine Environmental Research, 2013, 91, 34-40.	1.1	3
1047	Transcriptome profile of acibenzolar-S-methyl-induced genes in tomato suggests a complex polygenic effect on resistance to Phytophthora infestans. Physiological and Molecular Plant Pathology, 2013, 81, 97-106.	1.3	14
1048	Ovine subclinical mastitis: Proteomic analysis of whey and milk fat globules unveils putative diagnostic biomarkers in milk. Journal of Proteomics, 2013, 83, 144-159.	1.2	30
1049	A bird's-eye view on the modern genetics workflow and its potential applicability to the locust problem. Comptes Rendus - Biologies, 2013, 336, 375-383.	0.1	6
1050	Phosphoproteome profiling of the sexually transmitted pathogen Trichomonas vaginalis. Journal of Microbiology, Immunology and Infection, 2013, 46, 366-373.	1.5	14
1051	Identification and expression analysis of key enzymes of the terpenoids biosynthesis pathway of a liverwort Plagiochasma appendiculatum by EST analysis. Acta Physiologiae Plantarum, 2013, 35, 107-118.	1.0	14
1052	De-novo characterization of the soft-shelled turtle Pelodiscus sinensis transcriptome using Illumina RNA-Seq technology. Journal of Zhejiang University: Science B, 2013, 14, 58-67.	1.3	18
1053	The fate of duplicated genes in a polyploid plant genome. Plant Journal, 2013, 73, 143-153.	2.8	243
1054	The Maternal Transcriptome of the Crustacean Parhyale hawaiensis Is Inherited Asymmetrically to Invariant Cell Lineages of the Ectoderm and Mesoderm. PLoS ONE, 2013, 8, e56049.	1.1	23
1055	Modeling the zing finger protein SmZF1 from Schistosoma mansoni: Insights into DNA binding and gene regulation. Journal of Molecular Graphics and Modelling, 2013, 39, 29-38.	1.3	4

#	ARTICLE	IF	CITATIONS
1056	Venom gland extract is not required for successful parasitism in the polydnavirus-associated endoparasitoid Hyposoter didymator (Hym. Ichneumonidae) despite the presence of numerous novel and conserved venom proteins. Insect Biochemistry and Molecular Biology, 2013, 43, 292-307.	1.2	70
1057	Differences in gene expression within a striking phenotypic mosaic Eucalyptus tree that varies in susceptibility to herbivory. BMC Plant Biology, 2013, 13, 29.	1.6	43
1058	The molecular basis of invasiveness: differences in gene expression of native and introduced common ragweed (<i><scp>A</scp>mbrosia artemisiifolia</i>) in stressful and benign environments. Molecular Ecology, 2013, 22, 2496-2510.	2.0	70
1059	Quantification and functional analysis of modular protein evolution in a dense phylogenetic tree. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 898-907.	1.1	29
1060	Parsing parallel evolution: ecological divergence and differential gene expression in the adaptive radiations of thickâ€lipped <scp>M</scp>idas cichlid fishes from <scp>N</scp>icaragua. Molecular Ecology, 2013, 22, 650-669.	2.0	82
1061	Differential hippocampal gene expression is associated with climateâ€related natural variation in memory and the hippocampus in foodâ€caching chickadees. Molecular Ecology, 2013, 22, 397-408.	2.0	29
1062	Removal of Retained Introns Regulates Translation in the Rapidly Developing Gametophyte of Marsilea vestita. Developmental Cell, 2013, 24, 517-529.	3.1	121
1063	Going where traditional markers have not gone before: utility of and promise for <scp>RAD</scp> sequencing in marine invertebrate phylogeography and population genomics. Molecular Ecology, 2013, 22, 2953-2970.	2.0	184
1064	Identification and characterization of novel and conserved microRNAs in radish (Raphanus sativus L.) using high-throughput sequencing. Plant Science, 2013, 201-202, 108-114.	1.7	30
1065	Identification of human plasma proteins associated with the cell wall of the pathogenic fungusParacoccidioides brasiliensis. FEMS Microbiology Letters, 2013, 341, 87-95.	0.7	8
1066	A NGS approach to the encrusting Mediterranean sponge C rella elegans (Porifera, Demospongiae,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 along three life cycle stages. Molecular Ecology Resources, 2013, 13, 494-509.	2.2	14
1067	Hyposoter didymator uses a combination of passive and active strategies to escape from the Spodoptera frugiperda cellular immune response. Journal of Insect Physiology, 2013, 59, 500-508.	0.9	18
1068	Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. New Phytologist, 2013, 199, 89-100.	3.5	58
1069	Global transcriptome analysis and identification of a CONSTANS-like gene family in the orchid Erycina pusilla. Planta, 2013, 237, 1425-1441.	1.6	42
1070	<i>De novo</i> transcriptomic analyses for nonâ€model organisms: an evaluation of methods across a multiâ€species data set. Molecular Ecology Resources, 2013, 13, 403-416.	2.2	71
1071	Analysis of RNA-Seq data reveals involvement of JAK/STAT signalling during leg regeneration in the cricket <i>Gryllus bimaculatus</i>. Development (Cambridge), 2013, 140, 959-964.	1.2	65
1072	Proteomic analyses of serous and endometrioid epithelial ovarian cancers â€“ Cases studies â€“ Molecular insights of a possible histological etiology of serous ovarian cancer. Proteomics - Clinical Applications, 2013, 7, 337-354.	0.8	18
1073	Wholeâ€exome targeted sequencing of the uncharacterized pine genome. Plant Journal, 2013, 75, 146-156.	2.8	160

#	ARTICLE	IF	CITATIONS
1074	Transcriptome characterization and detection of gene expression differences in aspen (Populus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	0.6	8
1075	<scp>I</scp>on <scp>T</scp>orrentâ€based transcriptional assessment of a <i><scp>C</scp>orynebacterium pseudotuberculosis</i> equi strain reveals denaturing highâ€performance liquid chromatography a promising <scp>rRNA</scp> depletion method. Microbial Biotechnology, 2013, 6, 168-177.	2.0	11
1076	Effects of Exposure to 17Î±-Ethynylestradiol during Sexual Differentiation on the Transcriptome of the African Clawed Frog (Xenopus laevis). Environmental Science & Technology, 2013, 47, 4822-4828.	4.6	11
1077	Mapping quantitative trait loci associated with resistance to bacterial spot (Xanthomonas arboricola) Tj ETQq1 1 0.784314 rgBT /Overl	0.6	53
1078	Transcriptome Analysis of Newt Lens Regeneration Reveals Distinct Gradients in Gene Expression Patterns. PLoS ONE, 2013, 8, e61445.	1.1	40
1079	<scp>RNA</scp>seqâ€based transcriptome analysis of <i><scp>L</scp>actuca sativa</i> infected by the fungal necrotroph <i><scp>B</scp>otrytis cinerea</i>. Plant, Cell and Environment, 2013, 36, 1992-2007.	2.8	129
1080	De novo characterization of Lentinula edodes C91-3 transcriptome by deep Solexa sequencing. Biochemical and Biophysical Research Communications, 2013, 431, 111-115.	1.0	26
1081	Transcriptomics and <i>in vivo</i> tests reveal novel mechanisms underlying endocrine disruption in an ecological sentinel, <i>Nucella lapillus</i>. Molecular Ecology, 2013, 22, 1589-1608.	2.0	53
1082	Laser microdissection and microarray analysis of <i><scp>T</scp>uber melanosporum</i> ectomycorrhizas reveal functional heterogeneity between mantle and <scp>H</scp>artig net compartments. Environmental Microbiology, 2013, 15, 1853-1869.	1.8	62
1083	Comparison of transcriptome under red and blue light culture of Saccharina japonica (Phaeophyceae). Planta, 2013, 237, 1123-1133.	1.6	58
1084	Combinational effect of mutational bias and translational selection for translation efficiency in tomato (Solanum lycopersicum) cv. Micro-Tom. Genomics, 2013, 101, 290-295.	1.3	7
1085	The proteomic profile of Stichodactyla duerdeni secretion reveals the presence of a novel O-linked glycopeptide. Journal of Proteomics, 2013, 87, 89-102.	1.2	23
1086	Genome of the red alga Porphyridium purpureum. Nature Communications, 2013, 4, 1941.	5.8	204
1087	Mechanistic toxicity study of perfluorooctanoic acid in zebrafish suggests mitochondrial dysfunction to play a key role in PFOA toxicity. Chemosphere, 2013, 91, 844-856.	4.2	90
1088	Comparative Genomics of a Plant-Pathogenic Fungus,<i>Pyrenophora tritici-repentis</i>, Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	0.8	167
1089	Mechanisms of response to silver nanoparticles on Enchytraeus albidus (Oligochaeta): Survival, reproduction and gene expression profile. Journal of Hazardous Materials, 2013, 254-255, 336-344.	6.5	75
1090	The <scp>RNAi</scp> machinery regulates growth and development in the filamentous fungus <i><scp>T</scp>richoderma atroviride</i>. Molecular Microbiology, 2013, 89, 96-112.	1.2	88
1091	Comparative genomic and transcriptomic analyses reveal the hemibiotrophic stage shift of <i>Colletotrichum</i> fungi. New Phytologist, 2013, 197, 1236-1249.	3.5	332

#	ARTICLE	IF	CITATIONS
1092	Cyanobacterial diversity in the hot spring, pelagic and benthic habitats of a tropical soda lake. FEMS Microbiology Ecology, 2013, 85, 389-401.	1.3	71
1093	Comparative RNA-Seq Analysis of Early-Infected Peach Leaves by the Invasive Phytopathogen Xanthomonas arboricola pv. pruni. PLoS ONE, 2013, 8, e54196.	1.1	46
1094	Expressed sequence tags and molecular cloning and characterization of gene encoding pinoresinol/lariciresinol reductase from Podophyllum hexandrum. Protoplasma, 2013, 250, 1239-1249.	1.0	30
1095	A simple genetic basis for complex social behaviour mediates widespread gene expression differences. Molecular Ecology, 2013, 22, 3797-3813.	2.0	21
1096	Horizontal Gene Transfer from Diverse Bacteria to an Insect Genome Enables a Tripartite Nested Mealybug Symbiosis. Cell, 2013, 153, 1567-1578.	13.5	373
1097	Insights on gene expression response of a characterized resistant genotype of Solanum commersonii Dun. against Ralstonia solanacearum. European Journal of Plant Pathology, 2013, 136, 823-835.	0.8	28
1098	Differential Exoproteome Analysis of Two Corynebacterium pseudotuberculosis Biovar Ovis Strains Isolated from Goat (1002) and Sheep (C231). Current Microbiology, 2013, 67, 460-465.	1.0	15
1099	Comparative genomics analysis in <scp>P</scp>runoideae to identify biologically relevant polymorphisms. Plant Biotechnology Journal, 2013, 11, 883-893.	4.1	20
1100	Characterization of differential transcript abundance through time during Nematostella vectensis development. BMC Genomics, 2013, 14, 266.	1.2	85
1101	Genomic and Proteomic Dissection of the Ubiquitous Plant Pathogen, <i>Armillaria mellea</i>: Toward a New Infection Model System. Journal of Proteome Research, 2013, 12, 2552-2570.	1.8	85
1102	Effects of curcumin on the parasite Schistosoma mansoni: A transcriptomic approach. Molecular and Biochemical Parasitology, 2013, 187, 91-97.	0.5	29
1103	The characterization of the <i><scp>P</scp>hlebotomus papatasi</i> transcriptome. Insect Molecular Biology, 2013, 22, 211-232.	1.0	20
1104	Quantitative proteomics of tomato defense against<i>Pseudomonas syringae</i>infection. Proteomics, 2013, 13, 1934-1946.	1.3	40
1105	Using transcriptomic profiles in the diatom Phaeodactylum tricornutum to identify and prioritize stressors. Aquatic Toxicology, 2013, 138-139, 12-25.	1.9	43
1107	Transcriptomic analysis of rice (Oryza sativa) endosperm using the RNA-Seq technique. Plant Molecular Biology, 2013, 81, 363-378.	2.0	82
1108	Functional Annotation of the Human Chromosome 7 â€œMissingâ€•Proteins: A Bioinformatics Approach. Journal of Proteome Research, 2013, 12, 2504-2510.	1.8	17
1110	Transcriptomic analysis of four developmental stages of Strongyloides venezuelensis. Parasitology International, 2013, 62, 57-65.	0.6	15
1111	Identification of miRNAs and their targets in tea (Camellia sinensis). Journal of Zhejiang University: Science B, 2013, 14, 916-923.	1.3	49

#	Article	IF	Citations
1112	Novel aspects of grapevine response to phytoplasma infection investigated by a proteomic and phospho-proteomic approach with data integration into functional networks. BMC Genomics, 2013, 14, 38.	1.2	94
1113	Solanum torvum responses to the root-knot nematode Meloidogyne incognita. BMC Genomics, 2013, 14, 540.	1.2	41
1114	TTG2-regulated development is related to expression of putative AUXIN RESPONSE FACTOR genes in tobacco. BMC Genomics, 2013, 14, 806.	1.2	22
1115	De novo transcriptome sequencing of radish (Raphanus sativus L.) and analysis of major genes involved in glucosinolate metabolism. BMC Genomics, 2013, 14, 836.	1.2	81
1116	Heterologous expression of gentian MYB1R transcription factors suppresses anthocyanin pigmentation in tobacco flowers. Plant Cell Reports, 2013, 32, 1925-1937.	2.8	37
1117	Analysis of a deep transcriptome from the mantle tissue of Patella vulgata Linnaeus (Mollusca:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 230-243.	1.1	53
1118	PcarnBase: Development of a Transcriptomic Database for the Brain Coral Platygyra carnosus. Marine Biotechnology, 2013, 15, 244-251.	1.1	47
1119	Characterizing developmental and inducible differentiation between juvenile and adult plants of Aechmea fasciata treated with ethylene by transcriptomic analysis. Plant Growth Regulation, 2013, 69, 247-257.	1.8	13
1120	TiO₂-Based Phosphoproteomic Analysis of Schistosomes: Characterization of Phosphorylated Proteins in the Different Stages and Sex of <i>Schistosoma japonicum</i>. Journal of Proteome Research, 2013, 12, 729-742.	1.8	13
1121	Patterning and Regulatory Associations of DNA Methylation Are Mirrored by Histone Modifications in Insects. Genome Biology and Evolution, 2013, 5, 591-598.	1.1	91
1122	A Genomic Analysis of<i>Histomonas meleagridis</i>Through Sequencing of a cDNA Library. Journal of Parasitology, 2013, 99, 264-269.	0.3	16
1123	Early changes in the pupal transcriptome of the flesh fly Sarcophagha crassipalpis to parasitization by the ectoparasitic wasp, Nasonia vitripennis. Insect Biochemistry and Molecular Biology, 2013, 43, 1189-1200.	1.2	51
1124	Transcriptome Analysis of Japanese Pear (Pyrus pyrifolia Nakai) Flower Buds Transitioning Through Endodormancy. Plant and Cell Physiology, 2013, 54, 1132-1151.	1.5	147
1125	Ascaris lumbricoides and Ascaris suum: Comparative proteomic studies using 2-DE coupled with mass spectrometry. International Journal of Mass Spectrometry, 2013, 339-340, 1-6.	0.7	4
1126	Frogs and estivation: transcriptional insights into metabolism and cell survival in a natural model of extended muscle disuse. Physiological Genomics, 2013, 45, 377-388.	1.0	31
1127	Proteomic profiling of developing cotton fibers from wild and domesticated <i><scp>G</scp>ossypium barbadense</i>. New Phytologist, 2013, 200, 570-582.	3.5	72
1128	Transcriptome Analysis of Foraminiferan Elphidium margaritaceum Questions the Role of Gene Transfer in Kleptoplastidy. Molecular Biology and Evolution, 2013, 30, 66-69.	3.5	28
1129	Gene expression studies for the analysis of domoic acid production in the marine diatom Pseudo-nitzschia multiseries. BMC Molecular Biology, 2013, 14, 25.	3.0	18

#	Article	IF	Citations
1130	Draft Genome Sequences of Two Multidrug-Resistant Acinetobacter baumannii Strains of Sequence Type ST92 and ST96. Genome Announcements, 2013, 1, .	0.8	1
1131	A Chemical Proteomics Approach to Profiling the ATP-binding Proteome of Mycobacterium tuberculosis. Molecular and Cellular Proteomics, 2013, 12, 1644-1660.	2.5	41
1132	Widespread Selection Across Coding and Noncoding DNA in the Pea Aphid Genome. G3: Genes, Genomes, Genetics, 2013, 3, 993-1001.	0.8	8
1133	Draft Genome Sequence of Shewanella decolorationis S12, a Dye-Degrading Bacterium Isolated from a Wastewater Treatment Plant. Genome Announcements, 2013, 1, .	0.8	8
1134	Draft Genome Sequence of the Opportunistic Marine Pathogen Vibrio harveyi Strain E385. Genome Announcements, 2013, 1, .	0.8	6
1135	High-Quality Draft Genome Sequence of Vagococcus lutrae Strain LBD1, Isolated from the Largemouth Bass <i>Micropterus salmoides</i>. Genome Announcements, 2013, 1, .	0.8	8
1136	Draft Genome Sequence of Bacillus stratosphericus LAMA 585, Isolated from the Atlantic Deep Sea. Genome Announcements, 2013, 1, .	0.8	9
1137	The Transition from a Phytopathogenic Smut Ancestor to an Anamorphic Biocontrol Agent Deciphered by Comparative Whole-Genome Analysis. Plant Cell, 2013, 25, 1946-1959.	3.1	59
1138	Rapid Speciation with Gene Flow Following the Formation of Mt. Etna. Genome Biology and Evolution, 2013, 5, 1704-1715.	1.1	41
1139	Proteomics Approach to the Study of Cattle Tick Adaptation to White Tailed Deer. BioMed Research International, 2013, 2013, 1-8.	0.9	17
1140	Transcriptome-Wide Single Nucleotide Polymorphisms (SNPs) for Abalone (Haliotis midae): Validation and Application Using GoldenGate Medium-Throughput Genotyping Assays. International Journal of Molecular Sciences, 2013, 14, 19341-19360.	1.8	30
1141	Function and Evolution of DNA Methylation in Nasonia vitripennis. PLoS Genetics, 2013, 9, e1003872.	1.5	162
1142	Altered Immunity in Crowded Locust Reduced Fungal (Metarhizium anisopliae) Pathogenesis. PLoS Pathogens, 2013, 9, e1003102.	2.1	79
1143	Impacts of Population Structure and Analytical Models in Genome-Wide Association Studies of Complex Traits in Forest Trees: A Case Study in Eucalyptus globulus. PLoS ONE, 2013, 8, e81267.	1.1	82
1144	Application of D-Crustacean Hyperglycemic Hormone Induces Peptidases Transcription and Suppresses Glycolysis-Related Transcripts in the Hepatopancreas of the Crayfish Pontastacus leptodactylus â€" Results of a Transcriptomic Study. PLoS ONE, 2013, 8, e65176.	1.1	26
1145	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. Genome Research, 2013, 23, 1271-1282.	2.4	338
1146	Acquisition of LURE-Binding Activity at the Pollen Tube Tip of Torenia fournieri. Molecular Plant, 2013, 6, 1074-1090.	3.9	34
1147	Genome Microscale Heterogeneity among Wild Potatoes Revealed by Diversity Arrays Technology Marker Sequences. International Journal of Genomics, 2013, 2013, 1-9.	0.8	14

#	ARTICLE	IF	CITATIONS
1148	De Novo Assembly of the Peanut (Arachis hypogaea L.) Seed Transcriptome Revealed Candidate Unigenes for Oil Accumulation Pathways. PLoS ONE, 2013, 8, e73767.	1.1	64
1149	Differential Evolution and Neofunctionalization of Snake Venom Metalloprotease Domains. Molecular and Cellular Proteomics, 2013, 12, 651-663.	2.5	83
1150	Effects of temperature acclimation on Pacific bluefin tuna (<i>Thunnus orientalis</i>) cardiac transcriptome. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2013, 305, R1010-R1020.	0.9	31
1151	Private Selective Sweeps Identified from Next-Generation Pool-Sequencing Reveal Convergent Pathways under Selection in Two Inbred Schistosoma mansoni Strains. PLoS Neglected Tropical Diseases, 2013, 7, e2591.	1.3	20
1152	Dynamic Expression of Imprinted Genes Associates with Maternally Controlled Nutrient Allocation during Maize Endosperm Development. Plant Cell, 2013, 25, 3212-3227.	3.1	97
1153	Comparative Analysis of Mafriwal (Bos taurus Ã— Bos indicus) and Kedah Kelantan (Bos indicus) Sperm Proteome Identifies Sperm Proteins Potentially Responsible for Higher Fertility in a Tropical Climate. International Journal of Molecular Sciences, 2013, 14, 15860-15877.	1.8	16
1154	A Connected Set of Genes Associated with Programmed Cell Death Implicated in Controlling the Hypersensitive Response in Maize. Genetics, 2013, 193, 609-620.	1.2	50
1155	Effects of Copper and Cadmium Exposure on mRNA Expression of Catalase, Glutamine Synthetase, Cytochrome P450 and Heat Shock Protein 70 in Tambaqui Fish (Colossoma Macropomum). Gene Expression To Genetical Genomics, 2013, , 1.	1.0	7
1156	Genome Sequence of the Polyphosphate-Accumulating Organism <i>Arthrobacter</i> sp. Strain PAO19 Isolated from Maize Rhizosphere Soil. Genome Announcements, 2013, 1, .	0.8	7
1157	Odoriferous Defensive Stink Gland Transcriptome to Identify Novel Genes Necessary for Quinone Synthesis in the Red Flour Beetle, Tribolium castaneum. PLoS Genetics, 2013, 9, e1003596.	1.5	60
1158	Tissue-Specific Transcriptomics in the Field Cricket <i>Teleogryllus oceanicus</i>. G3: Genes, Genomes, Genetics, 2013, 3, 225-230.	0.8	30
1159	Replicon-Dependent Bacterial Genome Evolution: The Case of Sinorhizobium meliloti. Genome Biology and Evolution, 2013, 5, 542-558.	1.1	94
1160	Genetic Control and Comparative Genomic Analysis of Flowering Time in Setaria (Poaceae). G3: Genes, Genomes, Genetics, 2013, 3, 283-295.	0.8	97
1161	The First Chameleon Transcriptome: Comparative Genomic Analysis of the OXPHOS System Reveals Loss of COX8 in Iguanian Lizards. Genome Biology and Evolution, 2013, 5, 1792-1799.	1.1	12
1162	Evolution at Two Levels in Fire Ants: The Relationship between Patterns of Gene Expression and Protein Sequence Evolution. Molecular Biology and Evolution, 2013, 30, 263-271.	3.5	46
1163	Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 1809-1818.	0.8	73
1164	Transcriptome and Proteome Data Reveal Candidate Genes for Pollinator Attraction in Sexually Deceptive Orchids. PLoS ONE, 2013, 8, e64621.	1.1	46
1165	Adult spinal cord ependymal layer: a promising pool of quiescent stem cells to treat spinal cord injury. Frontiers in Physiology, 2013, 4, 340.	1.3	35

#	Article	IF	Citations
1166	Genome-wide transcriptomic analysis of the sporophyte of the moss Physcomitrella patens. Journal of Experimental Botany, 2013, 64, 3567-3581.	2.4	48
1167	Genome-Wide Characterization of Adaptation and Speciation in Tiger Swallowtail Butterflies Using De Novo Transcriptome Assemblies. Genome Biology and Evolution, 2013, 5, 1233-1245.	1.1	29
1168	Squeezers and Leaf-cutters: Differential Diversification and Degeneration of the Venom System in Toxicoferan Reptiles. Molecular and Cellular Proteomics, 2013, 12, 1881-1899.	2.5	52
1169	Thermosensitive ion channel TRPV1 is endogenously expressed in the sperm of a fresh water teleost fish (<i>Labeo rohita</i>) and regulates sperm motility. Channels, 2013, 7, 483-492.	1.5	41
1170	Temporal Analysis of the Magnaporthe Oryzae Proteome During Conidial Germination and Cyclic AMP (cAMP)-mediated Appressorium Formation. Molecular and Cellular Proteomics, 2013, 12, 2249-2265.	2.5	39
1171	Mosaic genome structure of the barley powdery mildew pathogen and conservation of transcriptional programs in divergent hosts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2219-28.	3.3	165
1172	Evolution of the Eye Transcriptome under Constant Darkness in Sinocyclocheilus Cavefish. Molecular Biology and Evolution, 2013, 30, 1527-1543.	3.5	83
1173	dbWFA: a web-based database for functional annotation of Triticum aestivum transcripts. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat014.	1.4	9
1174	Annotated genes and nonannotated genomes: crossâ€species use of Gene Ontology in ecology and evolution research. Molecular Ecology, 2013, 22, 3216-3241.	2.0	77
1175	Transcriptional Profiling of Canker-Resistant Transgenic Sweet Orange (<i>Citrus sinensis</i>Osbeck) Constitutively Overexpressing a Spermidine Synthase Gene. BioMed Research International, 2013, 2013, 1-13.	0.9	15
1176	A Statistical Method without Training Step for the Classification of Coding Frame in Transcriptome Sequences. Bioinformatics and Biology Insights, 2013, 7, BBI.S10053.	1.0	8
1177	De NovoTranscriptome Assembly and Differential Gene Expression Profiling of ThreeCapra hircusSkin Types during Anagen of the Hair Growth Cycle. International Journal of Genomics, 2013, 2013, 1-9.	0.8	11
1178	Target Gene and Function Prediction of Differentially Expressed MicroRNAs in Lactating Mammary Glands of Dairy Goats. International Journal of Genomics, 2013, 2013, 1-13.	0.8	24
1179	Phosphoproteomic Analysis Reveals the Effects of PilF Phosphorylation on Type IV Pilus and Biofilm Formation in Thermus thermophilus HB27. Molecular and Cellular Proteomics, 2013, 12, 2701-2713.	2.5	20
1180	De Novo Assembly and Functional Annotation of the Olive (Olea europaea) Transcriptome. DNA Research, 2013, 20, 93-108.	1.5	84
1181	The Landscape of Nucleotide Polymorphism among 13,500 Genes of the Conifer Picea glauca, Relationships with Functions, and Comparison with Medicago truncatula. Genome Biology and Evolution, 2013, 5, 1910-1925.	1.1	33
1182	Genome-Wide Patterns of Codon Bias Are Shaped by Natural Selection in the Purple Sea Urchin, <i>Strongylocentrotus purpuratus</i>. G3: Genes, Genomes, Genetics, 2013, 3, 1069-1083.	0.8	26
1183	Genetic regulation of cold-induced albinism in the maize inbred line A661. Journal of Experimental Botany, 2013, 64, 3657-3667.	2.4	36

#	ARTICLE	IF	CITATIONS
1184	Glycoproteome of Elongating Cotton Fiber Cells. Molecular and Cellular Proteomics, 2013, 12, 3677-3689.	2.5	53
1185	Novel bioresources for studies of <i><scp>B</scp>rassica oleracea</i>: identification of a kale <scp>MYB</scp> transcription factor responsible for glucosinolate production. Plant Biotechnology Journal, 2013, 11, 1017-1027.	4.1	40
1186	Highly expressed genes in gonads of the bat star <i>Patiria miniata</i>: gene ontology, expression differences, and gamete recognition loci. Invertebrate Biology, 2013, 132, 241-250.	0.3	11
1187	Using Genomeâ€<scp>R</scp>eferenced Expressed Sequence Tag Assembly to Analyze the Origin and Expression Patterns of <i>Gossypium hirsutum</i> Transcripts. Journal of Integrative Plant Biology, 2013, 55, 576-585.	4.1	17
1188	Analysis of the Alfalfa Root Transcriptome in Response to Salinity Stress. Plant and Cell Physiology, 2013, 54, 1041-1055.	1.5	133
1189	Developmental disorders and altered gene expression in the tropical clawed frog (<i>Silurana) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.4	14
1190	Evolutionary analyses of nonâ€family genes in plants. Plant Journal, 2013, 73, 788-797.	2.8	7
1191	Development of highâ€density <scp>SNP</scp> genotyping arrays for white spruce (<i><scp>P</scp>icea) Tj ETQq1 1 0.784314 rgB 2013, 13, 324-336.	2.2	78
1192	Identification of differentially expressed genes in the oviduct of two rabbit lines divergently selected for uterine capacity using suppression subtractive hybridization. Animal Genetics, 2013, 44, 296-304.	0.6	2
1193	Draft genome of the kiwifruit Actinidia chinensis. Nature Communications, 2013, 4, 2640.	5.8	423
1194	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	13.7	468
1195	RNA-Seq reveals expression signatures of genes involved in oxygen transport, protein synthesis, folding, and degradation in response to heat stress in catfish. Physiological Genomics, 2013, 45, 462-476.	1.0	134
1196	Glycyrrhiza uralensis Transcriptome Landscape and Study of Phytochemicals. Plant and Cell Physiology, 2013, 54, 697-710.	1.5	80
1198	Genomics of Loa loa, a Wolbachia-free filarial parasite of humans. Nature Genetics, 2013, 45, 495-500.	9.4	173
1199	A Developmental Transcriptional Network for Maize Defines Coexpression Modules Â Â Â. Plant Physiology, 2013, 161, 1830-1843.	2.3	89
1200	Gene Coexpression Networks Reveal Key Drivers of Phenotypic Divergence in Lake Whitefish. Molecular Biology and Evolution, 2013, 30, 1384-1396.	3.5	115
1201	Transcriptome Analysis to Identify Putative Floral-Specific Genes and Flowering Regulatory-Related Genes of Sweet Potato. Bioscience, Biotechnology and Biochemistry, 2013, 77, 2169-2174.	0.6	33
1202	Large Deletions in the pAtC58 Megaplasmid of Agrobacterium tumefaciens Can Confer Reduced Carriage Cost and Increased Expression of Virulence Genes. Genome Biology and Evolution, 2013, 5, 1353-1364.	1.1	25

#	ARTICLE	IF	CITATIONS
1203	The relative contribution of drift and selection to transcriptional divergence among <scp>B</scp>abine Lake tributary populations of juvenile rainbow trout. Journal of Evolutionary Biology, 2013, 26, 2497-2508.	0.8	3
1204	Aspergillus. , 2013, , 1-51.		5
1205	Development and characterization of 28 polymorphic EST-SSR markers for Cunninghamia lanceolata (Taxodiaceae) based on transcriptome sequences. Silvae Genetica, 2013, 62, 137-141.	0.4	10
1207	De Novo Transcriptome Sequencing in <i>Trigonella foenumâ€graecum</i> L. to Identify Genes Involved in the Biosynthesis of Diosgenin. Plant Genome, 2013, 6, plantgenome2012.08.0021.	1.6	39
1208	High natural gene expression variation in the reef-building coral Acropora millepora: potential for acclimative and adaptive plasticity. BMC Genomics, 2013, 14, 228.	1.2	51
1209	Transcriptomic and phylogenetic analysis of a bacterial cell cycle reveals strong associations between gene co-expression and evolution. BMC Genomics, 2013, 14, 450.	1.2	50
1210	De novo assembly and characterization of leaf transcriptome for the development of functional molecular markers of the extremophile multipurpose tree species Prosopis alba. BMC Genomics, 2013, 14, 705.	1.2	45
1211	Codon usage patterns in Chinese bayberry (Myrica rubra) based on RNA-Seq data. BMC Genomics, 2013, 14, 732.	1.2	42
1212	Probing functional polymorphisms in the dengue vector, Aedes aegypti. BMC Genomics, 2013, 14, 739.	1.2	12
1213	De novo transcriptome analysis using 454 pyrosequencing of the Himalayan Mayapple, Podophyllum hexandrum. BMC Genomics, 2013, 14, 748.	1.2	43
1214	Transcriptome analysis of Pinus monticola primary needles by RNA-seq provides novel insight into host resistance to Cronartium ribicola. BMC Genomics, 2013, 14, 884.	1.2	63
1215	Functional analyses of cotton (Gossypium hirsutum L.) immature fiber (im) mutant infer that fiber cell wall development is associated with stress responses. BMC Genomics, 2013, 14, 889.	1.2	43
1216	Transcriptional profile of Paracoccidioides induced by oenothein B, a potential antifungal agent from the Brazilian Cerrado plant Eugenia uniflora. BMC Microbiology, 2013, 13, 227.	1.3	22
1217	mRNA-Seq and microarray development for the Grooved carpet shell clam, Ruditapes decussatus: a functional approach to unravel host -parasite interaction. BMC Genomics, 2013, 14, 741.	1.2	39
1218	<i><scp>D</scp>e novo</i> assembly of the pennycress (<i><scp>T</scp>hlaspi arvense</i>) transcriptome provides tools for the development of a winter cover crop and biodiesel feedstock. Plant Journal, 2013, 75, 1028-1038.	2.8	73
1219	Isolation and identification of mannose-binding proteins and estimation of their abundance in sera from hepatocellular carcinoma patients. Proteomics, 2013, 13, 878-892.	1.3	21
1220	Transcriptomic Analysis of Paulownia Infected by Paulownia Witches'-Broom Phytoplasma. PLoS ONE, 2013, 8, e77217.	1.1	65
1221	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

#	Article	IF	Citations
1222	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. Current Topics in Medicinal Chemistry, 2013, 13, 526-575.	1.0	13
1223	Candidate Chemosensory Genes in the Stemborer <i>Sesamia nonagrioides</i>. International Journal of Biological Sciences, 2013, 9, 481-495.	2.6	47
1224	Regulated aggregative multicellularity in a close unicellular relative of metazoa. ELife, 2013, 2, e01287.	2.8	139
1225	The ClpP Protease Is Required for the Stress Tolerance and Biofilm Formation in Actinobacillus pleuropneumoniae. PLoS ONE, 2013, 8, e53600.	1.1	49
1226	Next Generation Sequencing Based Transcriptome Analysis of Septic-Injury Responsive Genes in the Beetle Tribolium castaneum. PLoS ONE, 2013, 8, e52004.	1.1	49
1227	Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. PLoS ONE, 2013, 8, e53171.	1.1	62
1228	De Novo Sequencing of Astyanax mexicanus Surface Fish and PachÃ³n Cavefish Transcriptomes Reveals Enrichment of Mutations in Cavefish Putative Eye Genes. PLoS ONE, 2013, 8, e53553.	1.1	93
1229	Transcriptomic Immune Response of Tenebrio molitor Pupae to Parasitization by Scleroderma guani. PLoS ONE, 2013, 8, e54411.	1.1	54
1230	Increasing Sequence Search Sensitivity with Transitive Alignments. PLoS ONE, 2013, 8, e54422.	1.1	3
1231	Genetic Mapping and Characteristics of Genes Specifically or Preferentially Expressed during Fiber Development in Cotton. PLoS ONE, 2013, 8, e54444.	1.1	21
1232	mRNA-seq Analysis of the Gossypium arboreum transcriptome Reveals Tissue Selective Signaling in Response to Water Stress during Seedling Stage. PLoS ONE, 2013, 8, e54762.	1.1	45
1233	Sequencing and De Novo Assembly of the Western Tarnished Plant Bug (Lygus hesperus) Transcriptome. PLoS ONE, 2013, 8, e55105.	1.1	49
1234	Post-Embryonic Transcriptomes of the Prawn Macrobrachium rosenbergii: Multigenic Succession through Metamorphosis. PLoS ONE, 2013, 8, e55322.	1.1	39
1235	Identification of Odor-Processing Genes in the Emerald Ash Borer, Agrilus planipennis. PLoS ONE, 2013, 8, e56555.	1.1	60
1236	Comparative Transcriptional Profiling Provides Insights into the Evolution and Development of the Zygomorphic Flower of Vicia sativa (Papilionoideae). PLoS ONE, 2013, 8, e57338.	1.1	29
1237	Identification of Key Drought Stress-Related Genes in the Hyacinth Bean. PLoS ONE, 2013, 8, e58108.	1.1	28
1238	Transcriptome Analysis of Artificial Hybrid Pufferfish Jiyan-1 and Its Parental Species: Implications for Pufferfish Heterosis. PLoS ONE, 2013, 8, e58453.	1.1	24
1239	First Comparative Transcriptomic Analysis of Wild Adult Male and Female Lutzomyia longipalpis, Vector of Visceral Leishmaniasis. PLoS ONE, 2013, 8, e58645.	1.1	17

#	ARTICLE	IF	CITATIONS
1240	Physical Mapping Integrated with Syntenic Analysis to Characterize the Gene Space of the Long Arm of Wheat Chromosome 1A. PLoS ONE, 2013, 8, e59542.	1.1	26
1241	RNA-Seq Analysis of Cocos nucifera: Transcriptome Sequencing and De Novo Assembly for Subsequent Functional Genomics Approaches. PLoS ONE, 2013, 8, e59997.	1.1	71
1242	A Comparison of the Olfactory Gene Repertoires of Adults and Larvae in the Noctuid Moth Spodoptera littoralis. PLoS ONE, 2013, 8, e60263.	1.1	109
1243	Testosterone Affects Neural Gene Expression Differently in Male and Female Juncos: A Role for Hormones in Mediating Sexual Dimorphism and Conflict. PLoS ONE, 2013, 8, e61784.	1.1	52
1244	Transcriptome Sequencing of Zhikong Scallop (Chlamys farreri) and Comparative Transcriptomic Analysis with Yesso Scallop (Patinopecten yessoensis). PLoS ONE, 2013, 8, e63927.	1.1	45
1245	Transcriptomic Analysis of a Tertiary Relict Plant, Extreme Xerophyte Reaumuria soongorica to Identify Genes Related to Drought Adaptation. PLoS ONE, 2013, 8, e63993.	1.1	55
1246	A Rapid Transcriptome Response Is Associated with Desiccation Resistance in Aerially-Exposed Killifish Embryos. PLoS ONE, 2013, 8, e64410.	1.1	17
1247	Profiling and Quantifying Differential Gene Transcription Provide Insights into Ganoderic Acid Biosynthesis in Ganoderma lucidum in Response to Methyl Jasmonate. PLoS ONE, 2013, 8, e65027.	1.1	41
1248	Global Transcriptome Profiling of Salicornia europaea L. Shoots under NaCl Treatment. PLoS ONE, 2013, 8, e65877.	1.1	38
1249	Global Analysis of mRNA Half-Lives and de novo Transcription in a Dinoflagellate, Karenia brevis. PLoS ONE, 2013, 8, e66347.	1.1	49
1250	The Embryonic Transcriptome of the Red-Eared Slider Turtle (Trachemys scripta). PLoS ONE, 2013, 8, e66357.	1.1	19
1251	Rapidly Evolving Genes and Stress Adaptation of Two Desert Poplars, Populus euphratica and P. pruinosa. PLoS ONE, 2013, 8, e66370.	1.1	52
1252	Context-Dependent Competition in a Model Gut Bacterial Community. PLoS ONE, 2013, 8, e67210.	1.1	25
1253	Transcriptome Characterisation of the Ant Formica exsecta with New Insights into the Evolution of Desaturase Genes in Social Hymenoptera. PLoS ONE, 2013, 8, e68200.	1.1	14
1254	Differential Expression Patterns in Chemosensory and Non-Chemosensory Tissues of Putative Chemosensory Genes Identified by Transcriptome Analysis of Insect Pest the Purple Stem Borer Sesamia inferens (Walker). PLoS ONE, 2013, 8, e69715.	1.1	120
1255	Genome-Wide Analysis of Small RNA and Novel MicroRNA Discovery during Fiber and Seed Initial Development in Gossypium hirsutum. L. PLoS ONE, 2013, 8, e69743.	1.1	17
1256	De Novo Transcriptome Assembly for the Tropical Grass Panicum maximum Jacq. PLoS ONE, 2013, 8, e70781.	1.1	32
1257	Comparative Transcriptomic Analysis of Developing Cotton Cotyledons and Embryo Axis. PLoS ONE, 2013, 8, e71756.	1.1	39

#	ARTICLE	IF	CITATIONS
1258	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
1259	Optimization of De Novo Short Read Assembly of Seabuckthorn (Hippophae rhamnoides L.) Transcriptome. PLoS ONE, 2013, 8, e72516.	1.1	36
1260	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	1.1	125
1261	Systematic Analysis and Prediction of Pupylation Sites in Prokaryotic Proteins. PLoS ONE, 2013, 8, e74002.	1.1	24
1262	Parasitization by Cotesia chilonis Influences Gene Expression in Fatbody and Hemocytes of Chilo suppressalis. PLoS ONE, 2013, 8, e74309.	1.1	29
1263	Signatures of Rapid Evolution in Urban and Rural Transcriptomes of White-Footed Mice (Peromyscus) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	68
1264	Comparative Genomics Reveals Insight into Virulence Strategies of Plant Pathogenic Oomycetes. PLoS ONE, 2013, 8, e75072.	1.1	164
1265	Transcriptome Sequencing and Differential Gene Expression Analysis of Delayed Gland Morphogenesis in Gossypium australe during Seed Germination. PLoS ONE, 2013, 8, e75323.	1.1	26
1266	Comparative Genomic Analysis Indicates that Niche Adaptation of Terrestrial Flavobacteria Is Strongly Linked to Plant Glycan Metabolism. PLoS ONE, 2013, 8, e76704.	1.1	95
1267	Transcriptome Sequencing and Expression Analysis of Terpenoid Biosynthesis Genes in Litsea cubeba. PLoS ONE, 2013, 8, e76890.	1.1	80
1268	Population Differentiation and Species Formation in the Deep Sea: The Potential Role of Environmental Gradients and Depth. PLoS ONE, 2013, 8, e77594.	1.1	52
1269	RNA-Seq Analysis Reveals Candidate Genes for Ontogenic Resistance in Malus-Venturia Pathosystem. PLoS ONE, 2013, 8, e78457.	1.1	57
1270	Using Genes as Characters and a Parsimony Analysis to Explore the Phylogenetic Position of Turtles. PLoS ONE, 2013, 8, e79348.	1.1	26
1271	Transcriptome Comparison Reveals Key Candidate Genes Responsible for the Unusual Reblooming Trait in Tree Peonies. PLoS ONE, 2013, 8, e79996.	1.1	25
1272	De Novo Assembly, Gene Annotation, and Marker Discovery in Stored-Product Pest Liposcelis entomophila (Enderlein) Using Transcriptome Sequences. PLoS ONE, 2013, 8, e80046.	1.1	38
1273	Next-Generation Sequencing-Based Transcriptome Analysis of Helicoverpa armigera Larvae Immune-Primed with Photorhabdus luminescens TT01. PLoS ONE, 2013, 8, e80146.	1.1	32
1274	A First Insight into Pycnoporus sanguineus BAFC 2126 Transcriptome. PLoS ONE, 2013, 8, e81033.	1.1	26
1275	Profiling mRNAs of Two Cuscuta Species Reveals Possible Candidate Transcripts Shared by Parasitic Plants. PLoS ONE, 2013, 8, e81389.	1.1	22

#	ARTICLE	IF	CITATIONS
1276	Caste-Specific Expression Patterns of Immune Response and Chemosensory Related Genes in the Leaf-Cutting Ant, Atta vollenweideri. PLoS ONE, 2013, 8, e81518.	1.1	30
1277	Floral Transcriptome Sequencing for SSR Marker Development and Linkage Map Construction in the Tea Plant (Camellia sinensis). PLoS ONE, 2013, 8, e81611.	1.1	80
1278	Comprehensive Analysis of Gene Expression Profiles of the Beet Armyworm Spodoptera exigua Larvae Challenged with Bacillus thuringiensis Vip3Aa Toxin. PLoS ONE, 2013, 8, e81927.	1.1	50
1279	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
1280	De novo Sequencing, Characterization, and Comparison of Inflorescence Transcriptomes of Cornus canadensis and C. florida (Cornaceae). PLoS ONE, 2013, 8, e82674.	1.1	12
1281	Ecological Adaption Analysis of the Cotton Aphid (Aphis gossypii) in Different Phenotypes by Transcriptome Comparison. PLoS ONE, 2013, 8, e83180.	1.1	30
1282	Global Transcriptome Sequencing Using the Illumina Platform and the Development of EST-SSR Markers in Autotetraploid Alfalfa. PLoS ONE, 2013, 8, e83549.	1.1	70
1283	Dynamic Changes in Mucus Thickness and Ion Secretion during Citrobacter rodentium Infection and Clearance. PLoS ONE, 2013, 8, e84430.	1.1	44
1284	Deep Sequencing-Based Analysis of the CymbidiumÂensifolium Floral Transcriptome. PLoS ONE, 2013, 8, e85480.	1.1	88
1285	Genetically Based Location from Triploid Populations and Gene Ontology of a 3.3-Mb Genome Region Linked to Alternaria Brown Spot Resistance in Citrus Reveal Clusters of Resistance Genes. PLoS ONE, 2013, 8, e76755.	1.1	40
1286	Identification of Differentially Expressed Genes in Shoot Apex of Garlic (Allium sativum L.) Using Illumina Sequencing. Journal of Plant Studies, 2013, 2, .	0.3	5
1287	Expression Analysis of Sugarcane Aquaporin Genes under Water Deficit. Journal of Nucleic Acids, 2013, 2013, 1-14.	0.8	19
1288	Characterization and comparison of key genes involved with flowering time regulation from Arabidopsis thaliana, Oryza sativa and Zea mays. African Journal of Biotechnology, 2013, 12, 353-363.	0.3	0
1289	Bioinformatics for spermatogenesis: annotation of male reproduction based on proteomics. Asian Journal of Andrology, 2013, 15, 594-602.	0.8	32
1290	Development and Characterization of Seashore Paspalum SSR Markers. Crop Science, 2013, 53, 2679-2685.	0.8	7
1291	Inside Arbuscular Mycorrhizal Roots â€“ Molecular Probes to Understand the Symbiosis. Plant Genome, 2013, 6, plantgenome2012.06.0007.	1.6	19
1292	Characterization of Structure, Divergence and Regulation Patterns of Plant Promoters. Journal of Molecular Biology Research, 2013, 3, .	0.1	4
1293	Profiling of Concanavalin A-Binding Glycoproteins in Human Hepatic Stellate Cells Activated with Transforming Growth Factor-Î²1. Molecules, 2014, 19, 19845-19867.	1.7	13

#	Article	IF	Citations
1294	Transcriptome Characterization Analysis of <i>Bactrocera minax</i> and New Insights into Its Pupal Diapause Development with Gene Expression Analysis. International Journal of Biological Sciences, 2014, 10, 1051-1063.	2.6	50
1295	Transcriptome Analysis of the Oil-Rich Tea Plant, Camellia oleifera, Reveals Candidate Genes Related to Lipid Metabolism. PLoS ONE, 2014, 9, e104150.	1.1	73
1296	Characterization of Small Interfering RNAs Derived from Sugarcane Mosaic Virus in Infected Maize Plants by Deep Sequencing. PLoS ONE, 2014, 9, e97013.	1.1	47
1297	Comparative Transcriptomic Characterization of the Early Development in Pacific White Shrimp Litopenaeus vannamei. PLoS ONE, 2014, 9, e106201.	1.1	114
1298	ANALYSIS OF THE TIME-DEPENDENT PROTEIN CHANGES IN WOUNDED APPLES ('GOLDEN DELICIOUS'). Acta Horticulturae, 2014, , 171-176.	0.1	0
1299	De Novo Transcriptome Assembly from Fat Body and Flight Muscles Transcripts to Identify Morph-Specific Gene Expression Profiles in Gryllus firmus. PLoS ONE, 2014, 9, e82129.	1.1	37
1300	Local Adaptation at the Transcriptome Level in Brown Trout: Evidence from Early Life History Temperature Genomic Reaction Norms. PLoS ONE, 2014, 9, e85171.	1.1	49
1301	Identification of Differentially Expressed Proteins in Porcine Alveolar Macrophages Infected with Virulent/Attenuated Strains of Porcine Reproductive and Respiratory Syndrome Virus. PLoS ONE, 2014, 9, e85767.	1.1	18
1302	De novo Genome Assembly of the Fungal Plant Pathogen Pyrenophora semeniperda. PLoS ONE, 2014, 9, e87045.	1.1	25
1303	Transcriptome Analysis in Venom Gland of the Predatory Giant Ant Dinoponera quadriceps: Insights into the Polypeptide Toxin Arsenal of Hymenopterans. PLoS ONE, 2014, 9, e87556.	1.1	64
1304	Comprehensive Transcriptome Analysis of Developing Xylem Responding to Artificial Bending and Gravitational Stimuli in Betula platyphylla. PLoS ONE, 2014, 9, e87566.	1.1	20
1305	De Novo Assembly and Annotation of Salvia splendens Transcriptome Using the Illumina Platform. PLoS ONE, 2014, 9, e87693.	1.1	36
1306	Identification and Differential Expression of microRNAs in Ovaries of Laying and Broody Geese (Anser) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	24
1307	Insights into the Development and Evolution of Exaggerated Traits Using De Novo Transcriptomes of Two Species of Horned Scarab Beetles. PLoS ONE, 2014, 9, e88364.	1.1	15
1308	De Novo Assembly and Transcriptome Analysis of Contrasting Sugarcane Varieties. PLoS ONE, 2014, 9, e88462.	1.1	129
1309	De Novo Assembly of a Transcriptome for Calanus finmarchicus (Crustacea, Copepoda) â€“ The Dominant Zooplankter of the North Atlantic Ocean. PLoS ONE, 2014, 9, e88589.	1.1	99
1310	RNA-Seq Analysis of Transcriptome and Glucosinolate Metabolism in Seeds and Sprouts of Broccoli (Brassica oleracea var. italic). PLoS ONE, 2014, 9, e88804.	1.1	63
1311	Effect of Bodily Fluids from Honey Bee (Apis mellifera) Larvae on Growth and Genome-Wide Transcriptional Response of the Causal Agent of American Foulbrood Disease (Paenibacillus larvae). PLoS ONE, 2014, 9, e89175.	1.1	1

#	ARTICLE	IF	CITATIONS
1312	Analysis of Anoxybacillus Genomes from the Aspects of Lifestyle Adaptations, Prophage Diversity, and Carbohydrate Metabolism. PLoS ONE, 2014, 9, e90549.	1.1	56
1313	Transcriptome Sequencing and De Novo Analysis of Youngia japonica Using the Illumina Platform. PLoS ONE, 2014, 9, e90636.	1.1	24
1314	Identification and Analysis of Differential miRNAs in PK-15 Cells after Foot-and-Mouth Disease Virus Infection. PLoS ONE, 2014, 9, e90865.	1.1	8
1315	Scanning of Transposable Elements and Analyzing Expression of Transposase Genes of Sweet Potato [Ipomoea batatas]. PLoS ONE, 2014, 9, e90895.	1.1	11
1316	Comparative Transcriptome Analysis of Two Races of Heterodera glycines at Different Developmental Stages. PLoS ONE, 2014, 9, e91634.	1.1	11
1317	De Novo Assembly of Auricularia polytricha Transcriptome Using Illumina Sequencing for Gene Discovery and SSR Marker Identification. PLoS ONE, 2014, 9, e91740.	1.1	45
1318	RNA-Seq Analysis Using De Novo Transcriptome Assembly as a Reference for the Salmon Louse Caligus rogercresseyi. PLoS ONE, 2014, 9, e92239.	1.1	67
1319	Analyses of the Xylem Sap Proteomes Identified Candidate Fusarium virguliforme Proteinacious Toxins. PLoS ONE, 2014, 9, e93667.	1.1	31
1320	Analysis of the Salivary Gland Transcriptome of Frankliniella occidentalis. PLoS ONE, 2014, 9, e94447.	1.1	74
1321	Transcriptomic Analysis of Petunia hybrida in Response to Salt Stress Using High Throughput RNA Sequencing. PLoS ONE, 2014, 9, e94651.	1.1	46
1322	Analysis of Insecticide Resistance-Related Genes of the Carmine Spider Mite Tetranychus cinnabarinus Based on a De Novo Assembled Transcriptome. PLoS ONE, 2014, 9, e94779.	1.1	39
1323	De Novo Transcriptome and Small RNA Analyses of Two Amorphophallus Species. PLoS ONE, 2014, 9, e95428.	1.1	14
1324	Comparative Transcriptome Analysis of Short Fiber Mutants Ligon-Lintless 1 And 2 Reveals Common Mechanisms Pertinent to Fiber Elongation in Cotton (Gossypium hirsutum L.). PLoS ONE, 2014, 9, e95554.	1.1	33
1325	Changes in the Organics Metabolism in the Hepatopancreas Induced by Eyestalk Ablation of the Chinese Mitten Crab Eriocheir sinensis Determined via Transcriptome and DGE Analysis. PLoS ONE, 2014, 9, e95827.	1.1	27
1326	De Novo Transcriptome Sequencing and Analysis of the Cereal Cyst Nematode, Heterodera avenae. PLoS ONE, 2014, 9, e96311.	1.1	54
1327	Ovary Transcriptome Profiling via Artificial Intelligence Reveals a Transcriptomic Fingerprint Predicting Egg Quality in Striped Bass, Morone saxatilis. PLoS ONE, 2014, 9, e96818.	1.1	73
1328	De Novo Transcriptome Assembly and Analyses of Gene Expression during Photomorphogenesis in Diploid Wheat Triticum monococcum. PLoS ONE, 2014, 9, e96855.	1.1	55
1329	Analysis of the Central Nervous System Transcriptome of the Eastern Rock Lobster Sagmariasus verreauxi Reveals Its Putative Neuropeptidome. PLoS ONE, 2014, 9, e97323.	1.1	89

#	ARTICLE	IF	CITATIONS
1330	Transcriptome Assembly and Analysis of Tibetan Hulless Barley (Hordeum vulgare L. var. nudum) Developing Grains, with Emphasis on Quality Properties. PLoS ONE, 2014, 9, e98144.	1.1	25
1331	Interactome Profile of the Host Cellular Proteins and the Nonstructural Protein 2 of Porcine Reproductive and Respiratory Syndrome Virus. PLoS ONE, 2014, 9, e99176.	1.1	16
1332	Assessment of Bacterial bph Gene in Amazonian Dark Earth and Their Adjacent Soils. PLoS ONE, 2014, 9, e99597.	1.1	21
1333	In Silico Identification of Plant miRNAs in Mammalian Breast Milk Exosomes â€“ A Small Step Forward?. PLoS ONE, 2014, 9, e99963.	1.1	78
1334	Morphological and Proteomic Analysis Reveal the Role of Pistil under Pollination in Liriodendron chinense (Hemsl.) Sarg. PLoS ONE, 2014, 9, e99970.	1.1	13
1335	Transcriptomic Analysis of Prunus domestica Undergoing Hypersensitive Response to Plum Pox Virus Infection. PLoS ONE, 2014, 9, e100477.	1.1	38
1336	Comparative Transcriptome Profiling of Two Tibetan Wild Barley Genotypes in Responses to Low Potassium. PLoS ONE, 2014, 9, e100567.	1.1	76
1337	Transcriptome Analysis of Dastarcus helophoroides (Coleoptera: Bothrideridae) Using Illumina HiSeq Sequencing. PLoS ONE, 2014, 9, e100673.	1.1	17
1338	Toxin Diversity Revealed by a Transcriptomic Study of Ornithoctonus huwena. PLoS ONE, 2014, 9, e100682.	1.1	15
1339	Hijacking of Host Cellular Functions by an Intracellular Parasite, the Microsporidian Anncaliia algerae. PLoS ONE, 2014, 9, e100791.	1.1	22
1340	De Novo Transcriptome Assembly from Inflorescence of Orchis italica: Analysis of Coding and Non-Coding Transcripts. PLoS ONE, 2014, 9, e102155.	1.1	30
1341	Improving the Safety of Staphylococcus aureus Polyvalent Phages by Their Production on a Staphylococcus xylosus Strain. PLoS ONE, 2014, 9, e102600.	1.1	43
1342	Transcriptome of the Female Synganglion of the Black-Legged Tick Ixodes scapularis (Acari: Ixodidae) with Comparison between Illumina and 454 Systems. PLoS ONE, 2014, 9, e102667.	1.1	51
1343	High-Throughput Sequencing and De Novo Assembly of the Isatis indigotica Transcriptome. PLoS ONE, 2014, 9, e102963.	1.1	32
1344	Transcriptome Profiles Associated to VHSV Infection or DNA Vaccination in Turbot (Scophthalmus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	31
1345	Transcriptome of American Oysters, Crassostrea virginica, in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. PLoS ONE, 2014, 9, e105097.	1.1	74
1346	Transcriptome Analysis of Red Swamp Crawfish Procambarus clarkii Reveals Genes Involved in Gonadal Development. PLoS ONE, 2014, 9, e105122.	1.1	44
1347	De Novo Transcriptome Analysis of Wing Development-Related Signaling Pathways in Locusta migratoria Manilensis and Ostrinia furnacalis (GuenÃ©e). PLoS ONE, 2014, 9, e106770.	1.1	15

#	ARTICLE	IF	CITATIONS
1348	Vernalization Mediated Changes in the Lolium perenne Transcriptome. PLoS ONE, 2014, 9, e107365.	1.1	17
1349	Specific Gene Expression Responses to Parasite Genotypes Reveal Redundancy of Innate Immunity in Vertebrates. PLoS ONE, 2014, 9, e108001.	1.1	23
1350	De Novo Transcriptome Analysis of an Aerial Microalga Trentepohlia jolithus: Pathway Description and Gene Discovery for Carbon Fixation and Carotenoid Biosynthesis. PLoS ONE, 2014, 9, e108488.	1.1	17
1351	Transcriptional Responses of Olive Flounder (Paralichthys olivaceus) to Low Temperature. PLoS ONE, 2014, 9, e108582.	1.1	57
1352	Identification and Characterization of Wilt and Salt Stress-Responsive MicroRNAs in Chickpea through High-Throughput Sequencing. PLoS ONE, 2014, 9, e108851.	1.1	101
1353	De Novo Transcriptome Sequencing Analysis and Comparison of Differentially Expressed Genes (DEGs) in Macrobrachium rosenbergii in China. PLoS ONE, 2014, 9, e109656.	1.1	15
1354	Genome-Wide Identification and Tissue-Specific Expression Analysis of UDP-Glycosyltransferases Genes Confirm Their Abundance in Cicer arietinum (Chickpea) Genome. PLoS ONE, 2014, 9, e109715.	1.1	44
1355	Genome-Scale Transcriptome Analysis of the Alpine â€œGlasshouseâ€• Plant Rheum nobile (Polygonaceae) with Special Translucent Bracts. PLoS ONE, 2014, 9, e110712.	1.1	8
1356	A Transcriptome Analysis Suggests Apoptosis-Related Signaling Pathways in Hemocytes of Spodoptera litura After Parasitization by Microplitis bicoloratus. PLoS ONE, 2014, 9, e110967.	1.1	23
1357	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
1358	The Genome of the Generalist Plant Pathogen Fusarium avenaceum Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	1.1	78
1359	RNA-Seq Reveals Leaf Cuticular Wax-Related Genes in Welsh Onion. PLoS ONE, 2014, 9, e113290.	1.1	24
1360	Transcriptome-Wide Profiling and Expression Analysis of Diploid and Autotetraploid Paulownia tomentosa Ã— Paulownia fortunei under Drought Stress. PLoS ONE, 2014, 9, e113313.	1.1	23
1361	Transcriptome Changes in Eriocheir sinensis Megalopae after Desalination Provide Insights into Osmoregulation and Stress Adaption in Larvae. PLoS ONE, 2014, 9, e114187.	1.1	51
1362	De novo Sequencing, Assembly and Characterization of Antennal Transcriptome of Anomala corpulenta Motschulsky (Coleoptera: Rutelidae). PLoS ONE, 2014, 9, e114238.	1.1	22
1363	Inference of the Oxidative Stress Network in Anopheles stephensi upon Plasmodium Infection. PLoS ONE, 2014, 9, e114461.	1.1	14
1364	High-Throughput Sequencing of MicroRNA Transcriptome and Expression Assay in the Sturgeon, Acipenser schrenckii. PLoS ONE, 2014, 9, e115251.	1.1	19
1365	Identification of Genes Associated with Reproduction in the Mud Crab (Scylla olivacea) and Their Differential Expression following Serotonin Stimulation. PLoS ONE, 2014, 9, e115867.	1.1	20

#	ARTICLE	IF	CITATIONS
1366	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
1367	Comprehensive Transcriptome Study to Develop Molecular Resources of the CopepodCalanus sinicusfor Their Potential Ecological Applications. BioMed Research International, 2014, 2014, 1-12.	0.9	16
1368	De NovoAssembly and Characterization ofSophora japonicaTranscriptome Using RNA-seq. BioMed Research International, 2014, 2014, 1-9.	0.9	15
1369	Isolation and Expression Analysis of Novel Silicon Absorption Gene from Roots of Mangrove<i>(Rhizophora apiculata) via</i>Suppression Subtractive Hybridization. BioMed Research International, 2014, 2014, 1-11.	0.9	18
1370	A Novel Method for Functional Annotation Prediction Based on Combination of Classification Methods. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	0
1371	Transcriptome Sequencing in a Tibetan Barley Landrace with High Resistance to Powdery Mildew. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	28
1372	Identification of Candidate Olfactory Genes in <i>Chilo suppressalis</i> by Antennal Transcriptome Analysis. International Journal of Biological Sciences, 2014, 10, 846-860.	2.6	130
1373	The hermit crab's noseâ€”antennal transcriptomics. Frontiers in Neuroscience, 2013, 7, 266.	1.4	26
1374	Genomic Sequence and Experimental Tractability of a New Decapod Shrimp Model, Neocaridina denticulata. Marine Drugs, 2014, 12, 1419-1437.	2.2	77
1375	Genome Wide Association Mapping of <i>Sclerotinia sclerotiorum</i> Resistance in Soybean with a Genotypingâ€•byâ€•Sequencing Approach. Plant Genome, 2014, 7, plantgenome2013.10.0030.	1.6	135
1376	Custom Microarray Analysis for Transcript Profiling of Dormant Vegetative Buds of Japanese Apricot during Prolonged Chilling Exposure. Japanese Society for Horticultural Science, 2014, 83, 1-16.	0.8	16
1377	Evaluation of four different strategies to characterize plasma membrane proteins from banana roots. Ciencia E Agrotecnologia, 2014, 38, 424-434.	1.5	1
1378	<i>De novo</i> Assembly and Analysis of the Northern Leopard Frog <i>Rana pipiens</i> Transcriptome. Journal of Genomics, 2014, 2, 141-149.	0.6	13
1379	Gene Expression Profiling in Winged and Wingless Cotton Aphids, <i>Aphis gossypii </i>(Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlo	2.6	39
1380	Characterization of the Asian Citrus Psyllid Transcriptome. Journal of Genomics, 2014, 2, 54-58.	0.6	48
1381	Transcriptome Sequencing and Analysis of Leaf Tissue of Avicennia marina Using the Illumina Platform. PLoS ONE, 2014, 9, e108785.	1.1	18
1382	Generation and Characterization of a Sugarbeet Transcriptome and Transcriptâ€•Based SSR Markers. Plant Genome, 2014, 7, plantgenome2013.11.0038.	1.6	24
1383	Deep sequencing analysis of microRNA expression in porcine serum-induced hepatic fibrosis rats. Annals of Hepatology, 2014, 13, 439-449.	0.6	8

#	Article	IF	Citations
1384	The Transcriptome of an Amphioxus, Asymmetron lucayanum, from the Bahamas: A Window into Chordate Evolution. Genome Biology and Evolution, 2014, 6, 2681-2696.	1.1	72
1385	Consequences of Whole-Genome Triplication as Revealed by Comparative Genomic Analyses of the Wild Radish<i>Raphanus raphanistrum</i>and Three Other Brassicaceae Species Â. Plant Cell, 2014, 26, 1925-1937.	3.1	137
1386	Transcriptional profiling of the responses to infection by the false smut fungus<i>Ustilaginoidea virens</i>in resistant and susceptible rice varieties. Canadian Journal of Plant Pathology, 2014, 36, 377-388.	0.8	12
1387	Draft Genome Sequence of Virulent Strain AUSTRAL-005 of Piscirickettsia salmonis, the Etiological Agent of Piscirickettsiosis. Genome Announcements, 2014, 2, .	0.8	25
1388	Construction of an EST-SSR-based interspecific transcriptome linkage map of fibre development in cotton. Journal of Genetics, 2014, 93, 689-697.	0.4	5
1389	Biological process annotation of proteins across the plant kingdom. Current Plant Biology, 2014, 1, 73-82.	2.3	7
1390	The Extent of Genome Flux and Its Role in the Differentiation of Bacterial Lineages. Genome Biology and Evolution, 2014, 6, 1514-1529.	1.1	76
1391	Vernalization of Oriental hybrid lily â€˜Sorbonneâ€™: changes in physiology metabolic activity and molecular mechanism. Molecular Biology Reports, 2014, 41, 6619-6634.	1.0	29
1393	Draft Genome Sequence of Streptomyces iranensis. Genome Announcements, 2014, 2, .	0.8	8
1394	Global gene expression profiling of<i>Homarus americanus</i>(Crustacea) larval stages during development and metamorphosis. Invertebrate Reproduction and Development, 2014, 58, 97-107.	0.3	11
1395	Pleiotropic Mutations Are Subject to Strong Stabilizing Selection. Genetics, 2014, 197, 1051-1062.	1.2	38
1396	Transcriptome-derived ESTâ€"SSR markers and their correlations with growth traits in crucian carp Carassius auratus. Fisheries Science, 2014, 80, 977-984.	0.7	17
1397	Comprehensive analysis of differentially expressed genes and transcriptional regulation induced by salt stress in two contrasting cotton genotypes. BMC Genomics, 2014, 15, 760.	1.2	166
1398	Transcriptome analysis of Gossypium hirsutum flower buds infested by cotton boll weevil (Anthonomus grandis) larvae. BMC Genomics, 2014, 15, 854.	1.2	35
1399	Transcriptome sequencing of two wild barley (Hordeum spontaneum L.) ecotypes differentially adapted to drought stress reveals ecotype-specific transcripts. BMC Genomics, 2014, 15, 995.	1.2	54
1400	Biofilm formation by virulent and non-virulent strains of Haemophilus parasuis. Veterinary Research, 2014, 45, 104.	1.1	24
1401	Adaptive genomic structural variation in the grape powdery mildew pathogen, Erysiphe necator. BMC Genomics, 2014, 15, 1081.	1.2	162
1402	The genome sequence of the Antarctic bullhead notothen reveals evolutionary adaptations to a cold environment. Genome Biology, 2014, 15, 468.	3.8	86

#	ARTICLE	IF	CITATIONS
1403	Involvements of PCD and changes in gene expression profile during self-pruning of spring shoots in sweet orange (Citrus sinensis). BMC Genomics, 2014, 15, 892.	1.2	24
1404	Transcriptomic events associated with internal browning of apple during postharvest storage. BMC Plant Biology, 2014, 14, 328.	1.6	76
1405	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 E. urophylla x E. grandis. BMC Plant Biology, 2014, 14, 301.	1.6	8
1406	De-novo assembly of mango fruit peel transcriptome reveals mechanisms of mango response to hot water treatment. BMC Genomics, 2014, 15, 957.	1.2	58
1407	TRANSCRIPTOME AND TISSUEâ€SPECIFIC EXPRESSION ANALYSIS OF <i>OBP</i> AND <i>CSP</i> GENES IN THE DARK BLACK CHAFER. Archives of Insect Biochemistry and Physiology, 2014, 87, 177-200.	0.6	38
1408	SNP discovery using high-throughput 454 pyrosequencing and validation in the spotted scat, Scatophagus argus. Conservation Genetics Resources, 2014, 6, 817-820.	0.4	5
1409	De novo assembly and characterization of the transcriptome of the toxic dinoflagellate Karenia brevis. BMC Genomics, 2014, 15, 888.	1.2	40
1410	Using phylogenetically-informed annotation (PIA) to search for light-interacting genes in transcriptomes from non-model organisms. BMC Bioinformatics, 2014, 15, 350.	1.2	62
1411	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. BMC Plant Biology, 2014, 14, 329.	1.6	42
1412	Transcriptome analysis highlights changes in the leaves of maize plants cultivated in acidic soil containing toxic levels of Al3+. Molecular Biology Reports, 2014, 41, 8107-8116.	1.0	26
1413	Comparative transcriptomics reveals striking similarities between the bovine and feline isolates of Tritrichomonas foetus: consequences for in silico drug-target identification. BMC Genomics, 2014, 15, 955.	1.2	31
1414	Transcriptional profiling of reproductive development, lipid storage and molting throughout the last juvenile stage of the marine copepod Calanus finmarchicus. Frontiers in Zoology, 2014, 11, 91.	0.9	66
1415	Conserved syntenic clusters of protein coding genes are missing in birds. Genome Biology, 2014, 15, 565.	3.8	123
1416	A deep transcriptomic analysis of pod development in the vanilla orchid (Vanilla planifolia). BMC Genomics, 2014, 15, 964.	1.2	42
1417	RNA-Seq reveals a xenobiotic stress response in the soybean aphid, Aphis glycines, when fed aphid-resistant soybean. BMC Genomics, 2014, 15, 972.	1.2	75
1418	In silico analysis of the core signaling proteome from the barley powdery mildew pathogen (Blumeria) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	36
1419	Genome of the house fly, Musca domestica L., a global vector of diseases with adaptations to a septic environment. Genome Biology, 2014, 15, 466.	3.8	252
1420	At the brink of eusociality: transcriptomic correlates of worker behaviour in a small carpenter bee. BMC Evolutionary Biology, 2014, 14, 260.	3.2	59

#	Article	IF	Citations
1421	Transcriptome profiling shows gene regulation patterns in a flavonoid pathway in response to exogenous phenylalanine in Boesenbergia rotunda cell culture. BMC Genomics, 2014, 15, 984.	1.2	21
1422	Subtractive transcriptomes of fruit and leaf reveal differential representation of transcripts in Azadirachta indica. Tree Genetics and Genomes, 2014, 10, 1331-1351.	0.6	27
1423	Introduction to Statistical Methods for MicroRNA Analysis. Methods in Molecular Biology, 2014, 1107, 129-155.	0.4	6
1424	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. Genome Biology and Evolution, 2014, 6, 76-93.	1.1	200
1425	A transcriptomic analysis of Chrysanthemum nankingense provides insights into the basis of low temperature tolerance. BMC Genomics, 2014, 15, 844.	1.2	79
1426	Contrasting nitrogen fertilization treatments impact xylem gene expression and secondary cell wall lignification in Eucalyptus. BMC Plant Biology, 2014, 14, 256.	1.6	41
1427	Comprehensive characterization and RNA-Seq profiling of the HD-Zip transcription factor family in soybean (Glycine max) during dehydration and salt stress. BMC Genomics, 2014, 15, 950.	1.2	120
1428	Gene expression profiling in gills of the great spider crab Hyas araneus in response to ocean acidification and warming. BMC Genomics, 2014, 15, 789.	1.2	70
1429	Gene expression profiling by cDNA-AFLP reveals potential candidate genes for partial resistance of â€˜PrÃ©sident Roulinâ€™ against Venturia inaequalis. BMC Genomics, 2014, 15, 1043.	1.2	10
1430	De novo characterization of the Rehmannia glutinosa leaf transcriptome and analysis of gene expression associated with replanting disease. Molecular Breeding, 2014, 34, 905-915.	1.0	21
1431	De novo transcriptome of Ischnura elegans provides insights into sensory biology, colour and vision genes. BMC Genomics, 2014, 15, 808.	1.2	46
1432	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	3.8	119
1433	Molecular signatures that correlate with induction of lens regeneration in newts: lessons from proteomic analysis. Human Genomics, 2014, 8, 22.	1.4	16
1434	Impact of analytic provenance in genome analysis. BMC Genomics, 2014, 15, S1.	1.2	13
1435	Genomic Evidence for the Emergence and Evolution of Pathogenicity and Niche Preferences in the Genus Campylobacter. Genome Biology and Evolution, 2014, 6, 2392-2405.	1.1	32
1436	Transcriptome sequencing and analysis of sweet osmanthus (Osmanthus fragrans Lour.). Genes and Genomics, 2014, 36, 777-788.	0.5	22
1437	Gonadal transcriptomic analysis of yellow catfish (Pelteobagrus fulvidraco): identification of sex-related genes and genetic markers. Physiological Genomics, 2014, 46, 798-807.	1.0	46
1438	Eugenol synthase genes in floral scent variation in Gymnadenia species. Functional and Integrative Genomics, 2014, 14, 779-788.	1.4	28

#	ARTICLE	IF	CITATIONS
1439	De novo transcriptome of the desert beetle Microdera punctipennis (Coleoptera: Tenebrionidae) using illumina RNA-seq technology. Molecular Biology Reports, 2014, 41, 7293-7303.	1.0	16
1440	Quantitative Phosphoproteomics Reveals the Role of Protein Arginine Phosphorylation in the Bacterial Stress Response. Molecular and Cellular Proteomics, 2014, 13, 537-550.	2.5	103
1441	RNA-sequencing reveals early, dynamic transcriptome changes in the corollas of pollinated petunias. BMC Plant Biology, 2014, 14, 307.	1.6	41
1442	Transcriptome Expression Profiling in Response to Drought Stress in Paulownia australis. International Journal of Molecular Sciences, 2014, 15, 4583-4607.	1.8	21
1443	Odorant and Gustatory Receptors in the Tsetse Fly Glossina morsitans morsitans. PLoS Neglected Tropical Diseases, 2014, 8, e2663.	1.3	51
1444	Sequencing and de novo assembly of a Dahlia hybrid cultivar transcriptome. Frontiers in Plant Science, 2014, 5, 340.	1.7	8
1445	Genes Involved in the Endoplasmic Reticulum N-Glycosylation Pathway of the Red Microalga Porphyridium sp.: A Bioinformatic Study. International Journal of Molecular Sciences, 2014, 15, 2305-2326.	1.8	30
1446	Extensive Copy-Number Variation of Young Genes across Stickleback Populations. PLoS Genetics, 2014, 10, e1004830.	1.5	70
1447	CZT-1 Is a Novel Transcription Factor Controlling Cell Death and Natural Drug Resistance in <i>Neurospora crassa</i>. G3: Genes, Genomes, Genetics, 2014, 4, 1091-1102.	0.8	16
1448	Draft genomes of Amanita jacksonii, Ceratocystis albifundus, Fusarium circinatum, Huntiella omanensis, Leptographium procerum, Rutstroemia sydowiana, and Sclerotinia echinophila. IMA Fungus, 2014, 5, 472-486.	1.7	56
1449	Comparative RNA-Seq based dissection of the regulatory networks and environmental stimuli underlying Vibrio parahaemolyticus gene expression during infection. Nucleic Acids Research, 2014, 42, 12212-12223.	6.5	38
1450	Transcriptional responses of Medicago truncatula upon sulfur deficiency stress and arbuscular mycorrhizal symbiosis. Frontiers in Plant Science, 2014, 5, 680.	1.7	31
1451	Characterization of a Proposed Dichorhavirus Associated with the Citrus Leprosis Disease and Analysis of the Host Response. Viruses, 2014, 6, 2602-2622.	1.5	34
1452	Developmental regulation of ecdysone receptor (EcR) and EcR-controlled gene expression during pharate-adult development of honeybees (Apis mellifera). Frontiers in Genetics, 2014, 5, 445.	1.1	49
1453	Differential Transcriptome Analysis between Paulownia fortunei and Its Synthesized Autopolyploid. International Journal of Molecular Sciences, 2014, 15, 5079-5093.	1.8	35
1454	<i>Gleditsia sinensis</i>: Transcriptome Sequencing, Construction, and Application of Its Protein-Protein Interaction Network. BioMed Research International, 2014, 2014, 1-9.	0.9	9
1455	Hierarchical Ensemble Methods for Protein Function Prediction. , 2014, 2014, 1-34.		32
1456	Transcriptome Profiles of the Protoscoleces of Echinococcus granulosus Reveal that Excretory-Secretory Products Are Essential to Metabolic Adaptation. PLoS Neglected Tropical Diseases, 2014, 8, e3392.	1.3	28

#	Article	IF	Citations
1457	Transcriptome Analysis of Salt Tolerant Common Bean (Phaseolus vulgaris L.) under Saline Conditions. PLoS ONE, 2014, 9, e92598.	1.1	107
1458	Gene Expansion Shapes Genome Architecture in the Human Pathogen Lichtheimia corymbifera: An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). PLoS Genetics, 2014, 10, e1004496.	1.5	80
1459	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. PLoS Genetics, 2014, 10, e1004078.	1.5	238
1460	Insights into the Trypanosome-Host Interactions Revealed through Transcriptomic Analysis of Parasitized Tsetse Fly Salivary Glands. PLoS Neglected Tropical Diseases, 2014, 8, e2649.	1.3	67
1461	Proteomic Analysis of Adult Ascaris suum Fluid Compartments and Secretory Products. PLoS Neglected Tropical Diseases, 2014, 8, e2939.	1.3	55
1462	Exposure to hycanthone alters chromatin structure around specific gene functions and specific repeats in Schistosoma mansoni. Frontiers in Genetics, 2014, 5, 207.	1.1	13
1463	Insilico analysis of hypothetical proteins unveils putative metabolic pathways and essential genes in Leishmania donovani. Frontiers in Genetics, 2014, 5, 291.	1.1	31
1464	Transcriptional and biochemical responses of monoacylglycerol acyltransferase-mediated oil synthesis and associated senescence-like responses in Nicotiana benthamiana. Frontiers in Plant Science, 2014, 5, 204.	1.7	7
1465	Triterpenoid Saponin Biosynthetic Pathway Profiling and Candidate Gene Mining of the Ilex asprella Root Using RNA-Seq. International Journal of Molecular Sciences, 2014, 15, 5970-5987.	1.8	41
1466	The Structure and Dynamics of BmR1 Protein from Brugia malayi: In Silico Approaches. International Journal of Molecular Sciences, 2014, 15, 11082-11099.	1.8	16
1467	Plant-Pathogen Interaction, Circadian Rhythm, and Hormone-Related Gene Expression Provide Indicators of Phytoplasma Infection in Paulownia fortunei. International Journal of Molecular Sciences, 2014, 15, 23141-23162.	1.8	41
1468	Microbial succession and the functional potential during the fermentation of Chinese soy sauce brine. Frontiers in Microbiology, 2014, 5, 556.	1.5	93
1469	RNA Sequencing Analysis Reveals Transcriptomic Variations in Tobacco (Nicotiana tabacum) Leaves Affected by Climate, Soil, and Tillage Factors. International Journal of Molecular Sciences, 2014, 15, 6137-6160.	1.8	17
1470	Draft Sequencing and Analysis of the Genome of Pufferfish Takifugu flavidus. DNA Research, 2014, 21, 627-637.	1.5	20
1471	De Novo Transcriptome Sequence Assembly and Identification of AP2/ERF Transcription Factor Related to Abiotic Stress in Parsley (Petroselinum crispum). PLoS ONE, 2014, 9, e108977.	1.1	21
1472	The biocontrol endophytic bacterium Pseudomonas fluorescens PICF7 induces systemic defense responses in aerial tissues upon colonization of olive roots. Frontiers in Microbiology, 2014, 5, 427.	1.5	100
1473	A Comparison of Transcriptional Patterns and Mycological Phenotypes following Infection of Fusarium graminearum by Four Mycoviruses. PLoS ONE, 2014, 9, e100989.	1.1	63
1474	Species- and genome-wide dissection of the shoot ionome in Brassica napus and its relationship to seedling development. Frontiers in Plant Science, 2014, 5, 485.	1.7	35

#	ARTICLE	IF	CITATIONS
1475	Evolution of genomic structural variation and genomic architecture in the adaptive radiations of African cichlid fishes. Frontiers in Genetics, 2014, 5, 163.	1.1	29
1476	Comparative Transcriptome Analysis of Leaves and Roots in Response to Sudden Increase in Salinity in<i>Brassica napus</i>by RNA-seq. BioMed Research International, 2014, 2014, 1-19.	0.9	48
1477	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower (Helianthus annuus L.) Genome. Biology, 2014, 3, 295-319.	1.3	16
1478	Transcriptomic Survey of the Midgut of Anthonomus grandis (Coleoptera: Curculionidae). Journal of Insect Science, 2014, 14, 219.	0.6	12
1479	How the Mountain Pine Beetle (Dendroctonus ponderosae) Breached the Canadian Rocky Mountains. Molecular Biology and Evolution, 2014, 31, 1803-1815.	3.5	70
1480	<i>De Novo</i> Assembly of the Quorum-Sensing <i>Pandoraea</i> sp. Strain RB-44 Complete Genome Sequence Using PacBio Single-Molecule Real-Time Sequencing Technology. Genome Announcements, 2014, 2, .	0.8	11
1481	Draft Genome Sequence of Methicillin-Resistant Staphylococcus aureus KT/Y21, a Sequence Type 772 (ST772) Strain Isolated from a Pediatric Blood Sample in Terengganu, Malaysia. Genome Announcements, 2014, 2, .	0.8	6
1482	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. MBio, 2014, 5, e01864.	1.8	82
1483	Identification of genes associated with low furanocoumarin content in grapefruit. Genome, 2014, 57, 537-545.	0.9	5
1484	Western corn rootworm (Diabrotica virgifera virgifera) transcriptome assembly and genomic analysis of population structure. BMC Genomics, 2014, 15, 195.	1.2	25
1485	Genome-wide analysis of the distribution of AP2/ERF transcription factors reveals duplication and CBFs genes elucidate their potential function in Brassica oleracea. BMC Genomics, 2014, 15, 422.	1.2	47
1486	BeMADS1 is a key to delivery MADSs into nucleus in reproductive tissues-De novo characterization of Bambusa edulis transcriptome and study of MADS genes in bamboo floral development. BMC Plant Biology, 2014, 14, 179.	1.6	35
1487	Transcriptome analysis of blood orange (<i>Citrus sinensis</i>) following fruit bagging treatment by digital gene expression profiling. Journal of Horticultural Science and Biotechnology, 2014, 89, 397-407.	0.9	8
1488	Identification of drought-responsive microRNAs in leaf and stem tissues of Oryza sativa by Solexa sequencing. , 2014, , .		1
1489	In absence of local adaptation, plasticity and spatially varying selection rule: a view from genomic reaction norms in a panmictic species (Anguilla rostrata). BMC Genomics, 2014, 15, 403.	1.2	41
1490	Transcriptomic analysis of a psammophyte food crop, sand rice (Agriophyllum squarrosum) and identification of candidate genes essential for sand dune adaptation. BMC Genomics, 2014, 15, 872.	1.2	27
1491	Sex- and tissue-specific profiles of chemosensory gene expression in a herbivorous gall-inducing fly (Diptera: Cecidomyiidae). BMC Genomics, 2014, 15, 501.	1.2	81
1492	A pipeline for the de novo assembly of the Themira biloba (Sepsidae: Diptera) transcriptome using a multiple k-mer length approach. BMC Genomics, 2014, 15, 188.	1.2	14

#	ARTICLE	IF	CITATIONS
1493	Comparative Transcriptomics of Maturity-Associated Color Change in Hawaiian Spiders. Journal of Heredity, 2014, 105, 771-781.	1.0	8
1494	The Potato Tuber Mitochondrial Proteome Â Â. Plant Physiology, 2014, 164, 637-653.	2.3	122
1495	<i>Curtobacterium</i> sp. Genome Sequencing Underlines Plant Growth Promotion-Related Traits. Genome Announcements, 2014, 2, .	0.8	15
1496	De Novo Whole-Genome Sequence and Genome Annotation of Lichtheimia ramosa. Genome Announcements, 2014, 2, .	0.8	27
1497	A Horizontally Acquired Transcription Factor Coordinates <i>Salmonella</i> Adaptations to Host Microenvironments. MBio, 2014, 5, e01727-14.	1.8	19
1498	The Cryptococcus neoformans Transcriptome at the Site of Human Meningitis. MBio, 2014, 5, e01087-13.	1.8	113
1499	Annotation of gene function in citrus using gene expression information and co-expression networks. BMC Plant Biology, 2014, 14, 186.	1.6	38
1500	Comparative Genomics of <i>Pneumocystis</i> Species Suggests the Absence of Genes for <i>myo-</i> Inositol Synthesis and Reliance on Inositol Transport and Metabolism. MBio, 2014, 5, e01834.	1.8	23
1501	Genome-wide analysis reveals divergent patterns of gene expression during zygotic and somatic embryo maturation of Theobroma cacao L., the chocolate tree. BMC Plant Biology, 2014, 14, 185.	1.6	27
1502	Analysis of BAC-end sequences in common bean (Phaseolus vulgaris L.) towards the development and characterization of long motifs SSRs. Plant Molecular Biology, 2014, 86, 455-470.	2.0	14
1503	20â€hydroxyecdysone transcriptionally regulates humoral immunity in the fat body of <i><scp>H</scp>elicoverpa armigera</i>. Insect Molecular Biology, 2014, 23, 842-856.	1.0	35
1504	Deadenylase depletion protects inherited mRNAs in primordial germ cells. Development (Cambridge), 2014, 141, 3134-3142.	1.2	31
1505	Sex-dependent transcriptome analysis and single nucleotide polymorphism (SNP) discovery in the brine shrimp Artemia franciscana. Marine Genomics, 2014, 18, 151-154.	0.4	11
1506	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode Nippostrongylus brasiliensis. Molecular and Cellular Proteomics, 2014, 13, 2736-2751.	2.5	88
1507	Toxicological Assessment of Polychlorinated Biphenyls and Their Metabolites in the Liver of Baikal Seal (<i>Pusa sibirica</i>). Environmental Science & Technology, 2014, 48, 13530-13539.	4.6	25
1508	De novo assembly and analysis of Cassia obtusifolia seed transcriptome to identify genes involved in the biosynthesis of active metabolites. Bioscience, Biotechnology and Biochemistry, 2014, 78, 791-799.	0.6	14
1509	Liver transcriptome characterization of the endangered freshwater silverside Basilichthys microlepidotus (Teleostei: Atherinopsidae) using next generation sequencing. Marine Genomics, 2014, 18, 147-150.	0.4	4
1510	Novel Roles for the Polyphenol Oxidase Enzyme in Secondary Metabolism and the Regulation of Cell Death in Walnut Â Â. Plant Physiology, 2014, 164, 1191-1203.	2.3	183

#	ARTICLE	IF	CITATIONS
1511	Molecular interactions between sugar beet and<i>Polymyxa betae</i>during its life cycle. Annals of Applied Biology, 2014, 164, 244-256.	1.3	10
1512	An RNA-seq transcriptome analysis of floral buds of an interspecific Brassica hybrid between B. carinata and B. napus. Plant Reproduction, 2014, 27, 225-237.	1.3	8
1513	Alternative reproductive tactics and sexâ€biased gene expression: the study of the bulb mite transcriptome. Ecology and Evolution, 2014, 4, 623-632.	0.8	50
1514	Stress response or beneficial temperature acclimation: transcriptomic signatures in <scp>A</scp>ntarctic fish (<i><scp>P</scp>achycara brachycephalum</i>). Molecular Ecology, 2014, 23, 3469-3482.	2.0	72
1515	<i>De novo</i> assembly and characterization of the skeletal muscle and electric organ transcriptomes of the African weakly electric fish <i>Campylomormyrus compressirostris</i> (Mormyridae, Teleostei). Molecular Ecology Resources, 2014, 14, 1222-1230.	2.2	31
1516	Exploring Biotic Interactions Within Protist Cell Populations Using Network Methods. Journal of Eukaryotic Microbiology, 2014, 61, 399-403.	0.8	2
1517	Proteomics analysis of adult testis from <i><scp>B</scp>ombyx mori</i>. Proteomics, 2014, 14, 2345-2349.	1.3	7
1518	Quantitative Peptidomics Study Reveals That a Wound-Induced Peptide from PR-1 Regulates Immune Signaling in Tomato. Plant Cell, 2014, 26, 4135-4148.	3.1	155
1519	Crossâ€species outlier detection reveals different evolutionary pressures between sister species. New Phytologist, 2014, 204, 215-229.	3.5	31
1520	Cloning and expression profiling of odorantâ€binding proteins in the tarnished plant bug, <i><scp>L</scp>ygus lineolaris</i>. Insect Molecular Biology, 2014, 23, 78-97.	1.0	69
1521	Transcriptome resources for the perennial sunflower <i>Helianthus maximiliani</i> obtained from ecologically divergent populations. Molecular Ecology Resources, 2014, 14, 812-819.	2.2	18
1522	The lowâ€recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. Plant Journal, 2014, 79, 981-992.	2.8	30
1523	<i>egr-4</i>, a target of EGFR signaling, is required for the formation of the brain primordia and head regeneration in planarians. Development (Cambridge), 2014, 141, 1835-1847.	1.2	48
1524	RNA-Seq analysis reveals genetic bases of the flowering process in oriental hybrid lily cv. Sorbonne. Russian Journal of Plant Physiology, 2014, 61, 880-892.	0.5	3
1525	The haustorial transcriptomes of <i><scp>U</scp>romyces appendiculatus</i> and <i><scp>P</scp>hakopsora pachyrhizi</i> and their candidate effector families. Molecular Plant Pathology, 2014, 15, 379-393.	2.0	67
1526	<i>Nasonia vitripennis</i> venom causes targeted gene expression changes in its fly host. Molecular Ecology, 2014, 23, 5918-5930.	2.0	63
1527	ESTs in Plants: Where Are We Heading?. , 2014, , 161-170.		0
1528	Analysis of the Skin Transcriptome in Two Oujiang Color Varieties of Common Carp. PLoS ONE, 2014, 9, e90074.	1.1	38

#	Article	IF	Citations
1529	Extensive Differences in Gene Expression Between Symbiotic and Aposymbiotic Cnidarians. G3: Genes, Genomes, Genetics, 2014, 4, 277-295.	0.8	150
1530	Identification of Immunity-Related Genes in Ostrinia furnacalis against Entomopathogenic Fungi by RNA-Seq Analysis. PLoS ONE, 2014, 9, e86436.	1.1	58
1531	The Transcriptome of Nacobbus aberrans Reveals Insights into the Evolution of Sedentary Endoparasitism in Plant-Parasitic Nematodes. Genome Biology and Evolution, 2014, 6, 2181-2194.	1.1	39
1532	The de novo Transcriptome and Its Analysis in the Worldwide Vegetable Pest, Delia antiqua (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	16
1533	Comparative Transcriptomics in East African Cichlids Reveals Sex- and Species-Specific Expression and New Candidates for Sex Differentiation in Fishes. Genome Biology and Evolution, 2014, 6, 2567-2585.	1.1	61
1534	Transcriptome de novo assembly and differentially expressed genes related to cytoplasmic male sterility in kenaf (Hibiscus cannabinus L.). Molecular Breeding, 2014, 34, 1879-1891.	1.0	33
1535	2-D and In Silico Analysis of Some Putative Drought-Induced Differential Boiling Soluble Proteins (hydrophilins) of Triticum aestivum. Agricultural Research, 2014, 3, 386-394.	0.9	0
1536	European sea bass genome and its variation provide insights into adaptation to euryhalinity and speciation. Nature Communications, 2014, 5, 5770.	5.8	382
1537	Comparative genomics of closely related Salmonella enterica serovar Typhi strains reveals genome dynamics and the acquisition of novel pathogenic elements. BMC Genomics, 2014, 15, 1007.	1.2	18
1538	Comparative transcriptomic analyses revealed divergences of two agriculturally important aphid species. BMC Genomics, 2014, 15, 1023.	1.2	10
1539	Development of EST-based SNP and InDel markers and their utilization in tetraploid cotton genetic mapping. BMC Genomics, 2014, 15, 1046.	1.2	27
1540	Emiliania huxleyi endures N-limitation with an efficient metabolic budgeting and effective ATP synthesis. BMC Genomics, 2014, 15, 1051.	1.2	36
1541	Label-free proteomic analysis to confirm the predicted proteome of Corynebacterium pseudotuberculosis under nitrosative stress mediated by nitric oxide. BMC Genomics, 2014, 15, 1065.	1.2	29
1542	Transcriptomic analysis of the lesser spotted catshark (Scyliorhinus canicula) pancreas, liver and brain reveals molecular level conservation of vertebrate pancreas function. BMC Genomics, 2014, 15, 1074.	1.2	34
1543	Genomic characterisation of an endometrial pathogenic Escherichia coli strain reveals the acquisition of genetic elements associated with extra-intestinal pathogenicity. BMC Genomics, 2014, 15, 1075.	1.2	13
1544	Species-specific chemosensory gene expression in the olfactory organs of the malaria vector Anopheles gambiae. BMC Genomics, 2014, 15, 1089.	1.2	15
1545	Intrinsically disordered proteins (IDPs) in trypanosomatids. BMC Genomics, 2014, 15, 1100.	1.2	11
1546	De novo assembly of the desert tree Haloxylon ammodendron (C. A. Mey.) based on RNA-Seq data provides insight into drought response, gene discovery and marker identification. BMC Genomics, 2014, 15, 1111.	1.2	52

#	ARTICLE	IF	CITATIONS
1547	The draft genome of the pest tephritid fruit fly Bactrocera tryoni: resources for the genomic analysis of hybridising species. BMC Genomics, 2014, 15, 1153.	1.2	41
1548	Fine mapping of Rcr1 and analyses of its effect on transcriptome patterns during infection by Plasmodiophora brassicae. BMC Genomics, 2014, 15, 1166.	1.2	133
1549	De novo transcriptome analysis of Perna viridis highlights tissue-specific patterns for environmental studies. BMC Genomics, 2014, 15, 804.	1.2	38
1550	The highly polymorphic CYP6M7 cytochrome P450 gene partners with the directionally selected CYP6P9a and CYP6P9b genes to expand the pyrethroid resistance front in the malaria vector Anopheles funestus in Africa. BMC Genomics, 2014, 15, 817.	1.2	100
1551	Stage-specific differential gene expression in Leishmania infantum: from the foregut of Phlebotomus perniciosus to the human phagocyte. BMC Genomics, 2014, 15, 849.	1.2	27
1552	Transcriptomic analysis of the phytopathogenic oomycete Phytophthora cactorum provides insights into infection-related effectors. BMC Genomics, 2014, 15, 980.	1.2	33
1553	De Novo sequencing and transcriptome analysis for Tetramorium bicarinatum: a comprehensive venom gland transcriptome analysis from an ant species. BMC Genomics, 2014, 15, 987.	1.2	42
1554	Comparative transcriptome analysis of the Asteraceae halophyte Karelinia caspica under salt stress. BMC Research Notes, 2014, 7, 927.	0.6	21
1555	VTBuilder: a tool for the assembly of multi isoform transcriptomes. BMC Bioinformatics, 2014, 15, 389.	1.2	36
1556	APP: an Automated Proteomics Pipeline for the analysis of mass spectrometry data based on multiple open access tools. BMC Bioinformatics, 2014, 15, 441.	1.2	20
1557	Development of Cymbidium ensifoliumgenic-SSR markers and their utility in genetic diversity and population structure analysis in cymbidiums. BMC Genetics, 2014, 15, 124.	2.7	25
1558	Comparative Genomic and Transcriptomic Analysis of <i>Wangiella dermatitidis</i>, A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. G3: Genes, Genomes, Genetics, 2014, 4, 561-578.	0.8	58
1559	Transcriptome analysis reveals novel regulatory mechanisms in a genome-reduced bacterium. Nucleic Acids Research, 2014, 42, 13254-13268.	6.5	43
1560	Chromatin structure and gene expression changes associated with loss of MOP1 activity inZea mays. Epigenetics, 2014, 9, 1047-1059.	1.3	31
1561	Polymorphism Identification and Improved Genome Annotation of <i>Brassica rapa</i> Through Deep RNA Sequencing. G3: Genes, Genomes, Genetics, 2014, 4, 2065-2078.	0.8	29
1562	MulSatDB: a first online database for mulberry microsatellites. Trees - Structure and Function, 2014, 28, 1793-1799.	0.9	11
1563	ChiloDB: a genomic and transcriptome database for an important rice insect pest Chilo suppressalis. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau065-bau065.	1.4	50
1564	The Draft Assembly of the Radically Organized Stylonychia lemnae Macronuclear Genome. Genome Biology and Evolution, 2014, 6, 1707-1723.	1.1	58

#	ARTICLE	IF	CITATIONS
1565	Phylogenomic Study Indicates Widespread Lateral Gene Transfer in Entamoeba and Suggests a Past Intimate Relationship with Parabasalids. Genome Biology and Evolution, 2014, 6, 2350-2360.	1.1	24
1566	Proteome Analysis of Cytoplasmatic and Plastidic <i>Î²</i>-Carotene Lipid Droplets in <i>Dunaliella bardawil</i> Â Â. Plant Physiology, 2014, 167, 60-79.	2.3	89
1567	Genetic Differentiation and Evolutionary Adaptation in<i>Cryptomeria japonica</i>. G3: Genes, Genomes, Genetics, 2014, 4, 2389-2402.	0.8	46
1568	<i>De Novo</i> Assembly and Annotation of the Transcriptome of the Agricultural Weed <i>Ipomoea purpurea</i> Uncovers Gene Expression Changes Associated with Herbicide Resistance. G3: Genes, Genomes, Genetics, 2014, 4, 2035-2047.	0.8	48
1569	Apomictic and Sexual Germline Development Differ with Respect to Cell Cycle, Transcriptional, Hormonal and Epigenetic Regulation. PLoS Genetics, 2014, 10, e1004476.	1.5	68
1570	Methylcrotonyl-CoA Carboxylase Regulates Triacylglycerol Accumulation in the Model Diatom <i>Phaeodactylum tricornutum</i> Â Â Â. Plant Cell, 2014, 26, 1681-1697.	3.1	136
1571	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
1572	Complete Genome Sequence of Vibrio anguillarum Phage CHOED Successfully Used for Phage Therapy in Aquaculture. Genome Announcements, 2014, 2, .	0.8	10
1573	A High-Resolution Genetic Map of Yellow Monkeyflower Identifies Chemical Defense QTLs and Recombination Rate Variation. G3: Genes, Genomes, Genetics, 2014, 4, 813-821.	0.8	33
1574	Extensive Local Gene Duplication and Functional Divergence among Paralogs in Atlantic Salmon. Genome Biology and Evolution, 2014, 6, 1790-1805.	1.1	43
1575	Gene Co-expression Modules Underlying Polymorphic and Monomorphic Zooids in the Colonial Hydrozoan, Hydractinia symbiolongicarpus. Integrative and Comparative Biology, 2014, 54, 276-283.	0.9	11
1576	SIMAPâ€"the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. Nucleic Acids Research, 2014, 42, D279-D284.	6.5	24
1577	De Novo Transcriptome Sequencing of the Octopus vulgaris Hemocytes Using Illumina RNA-Seq Technology: Response to the Infection by the Gastrointestinal Parasite Aggregata octopiana. PLoS ONE, 2014, 9, e107873.	1.1	62
1578	The genome sequence and effector complement of the flax rust pathogen Melampsora lini. Frontiers in Plant Science, 2014, 5, 98.	1.7	126
1579	In tobacco BY-2 cells xyloglucan oligosaccharides alter the expression of genes involved in cell wall metabolism, signalling, stress responses, cell division and transcriptional control. Molecular Biology Reports, 2014, 41, 6803-6816.	1.0	19
1580	Effects of a natural toxin on life history and gene expression of <i>Eisenia andrei</i>. Environmental Toxicology and Chemistry, 2014, 33, 412-420.	2.2	8
1581	Analysis of Expressed Genes of the Bacterium â€˜Candidatus Phytoplasma Maliâ€™ Highlights Key Features of Virulence and Metabolism. PLoS ONE, 2014, 9, e94391.	1.1	29
1582	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

#	ARTICLE	IF	CITATIONS
1583	Phosphoproteomic Analysis of Protein Phosphorylation Networks in Tetrahymena thermophila, a Model Single-celled Organism. Molecular and Cellular Proteomics, 2014, 13, 503-519.	2.5	21
1585	Chromosomal Distribution of Cytonuclear Genes in a Dioecious Plant with Sex Chromosomes. Genome Biology and Evolution, 2014, 6, 2439-2443.	1.1	9
1586	RNA-Seq Analysis and De Novo Transcriptome Assembly of Jerusalem Artichoke (Helianthus tuberosus) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	31
1587	Characterization of the rainbow trout spleen transcriptome and identification of immune-related genes. Frontiers in Genetics, 2014, 5, 348.	1.1	41
1588	De Novo Characterization of a Cephalotaxus hainanensis Transcriptome and Genes Related to Paclitaxel Biosynthesis. PLoS ONE, 2014, 9, e106900.	1.1	29
1589	CarrotDB: a genomic and transcriptomic database for carrot. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau096-bau096.	1.4	87
1590	Evolution and Structural Analyses of Glossina morsitans (Diptera; Glossinidae) Tetraspanins. Insects, 2014, 5, 885-908.	1.0	4
1591	Expression Comparison of Oil Biosynthesis Genes in Oil Palm Mesocarp Tissue Using Custom Array. Microarrays (Basel, Switzerland), 2014, 3, 263-281.	1.4	12
1592	Genome-wide identification and analysis of growth regulating factor genes in Brachypodium distachyon: in silico approaches. Turkish Journal of Biology, 2014, 38, 296-306.	2.1	34
1593	Transcriptomic responses of the aphid Myzus persicae nicotianae Blackman (Hemiptera: Aphididae) to insecticides: Analyses in the single Chilean clone of the tobacco aphid. Chilean Journal of Agricultural Research, 2014, 74, 191-199.	0.4	5
1594	Mapping-by-Sequencing Identifies <i>HvPHYTOCHROME C</i> as a Candidate Gene for the <i>early maturity 5</i> Locus Modulating the Circadian Clock and Photoperiodic Flowering in Barley. Genetics, 2014, 198, 383-396.	1.2	102
1595	Rapid Evolution of Phenotypic Plasticity and Shifting Thresholds of Genetic Assimilation in the Nematode<i>Caenorhabditis remanei</i>. G3: Genes, Genomes, Genetics, 2014, 4, 1103-1112.	0.8	66
1596	Begin at the beginning: A BAC-end view of the passion fruit (Passiflora) genome. BMC Genomics, 2014, 15, 816.	1.2	34
1597	Transcriptome sequencing and analysis of the zoonotic parasite Spirometra erinacei spargana (plerocercoids). Parasites and Vectors, 2014, 7, 368.	1.0	15
1598	Defining the genome structure of `Tongil' rice, an important cultivar in the Korean "Green Revolution". Rice, 2014, 7, 22.	1.7	24
1599	Comparative Genomics Suggests That the Human Pathogenic Fungus Pneumocystis jirovecii Acquired Obligate Biotrophy through Gene Loss. Genome Biology and Evolution, 2014, 6, 1938-1948.	1.1	49
1600	Analysis of changes in protein abundance after wounding in â€˜Golden Deliciousâ€™ apples. Postharvest Biology and Technology, 2014, 87, 51-60.	2.9	23
1601	Proteome responses to nitrate in bioethanol production contaminant Dekkera bruxellensis. Journal of Proteomics, 2014, 104, 104-111.	1.2	18

#	ARTICLE	IF	CITATIONS
1602	Transcriptome sequencing reveals single domain Type I-like polyketide synthases in the toxic dinoflagellate Gambierdiscus polynesiensis. Harmful Algae, 2014, 36, 29-37.	2.2	28
1603	Proteomic analysis of interaction between P7-1 of Southern rice black-streaked dwarf virus and the insect vector reveals diverse insect proteins involved in successful transmission. Journal of Proteomics, 2014, 102, 83-97.	1.2	46
1604	The Dinoflagellate Lingulodinium has Predicted Casein Kinase 2 Sites in Many RNA Binding Proteins. Protist, 2014, 165, 330-342.	0.6	6
1605	Phylogenetic analysis of the GST family in Anopheles (Nyssorhynchus) darlingi. Acta Tropica, 2014, 136, 27-31.	0.9	4
1606	A transcriptomic analysis on gene expressions in the infective third and pathogenic fifth larval stages of Angiostrongylus cantonensis. Parasitology International, 2014, 63, 42-48.	0.6	8
1607	Subtle human impacts on neutral genetic diversity and spatial patterns of genetic variation in European beech (Fagus sylvatica). Forest Ecology and Management, 2014, 319, 138-149.	1.4	50
1608	Localization and proteomic characterization of cholesterol-rich membrane microdomains in the inner ear. Journal of Proteomics, 2014, 103, 178-193.	1.2	20
1609	Insights into the transcriptome of the marine copepod Calanus helgolandicus feeding on the oxylipin-producing diatom Skeletonema marinoi. Harmful Algae, 2014, 31, 153-162.	2.2	31
1610	Immune gene discovery in the crucian carp Carassius auratus. Fish and Shellfish Immunology, 2014, 36, 240-251.	1.6	20
1611	Transcriptome de novo assembly sequencing and analysis of the toxic dinoflagellate Alexandrium catenella using the Illumina platform. Gene, 2014, 537, 285-293.	1.0	53
1612	Multifunctional warheads: Diversification of the toxin arsenal of centipedes via novel multidomain transcripts. Journal of Proteomics, 2014, 102, 1-10.	1.2	36
1613	Improving the identification rate of data independent label-free quantitative proteomics experiments on non-model crops: A case study on apple fruit. Journal of Proteomics, 2014, 105, 31-45.	1.2	44
1614	Profiling transcriptomic response of Enchytraeus albidus to Cu and Ni: Comparison with Cd and Zn. Environmental Pollution, 2014, 186, 75-82.	3.7	14
1615	Transcriptome analysis reveals pathogenicity and evolutionary history of the pathogenic oomycete Pythium insidiosum. Fungal Biology, 2014, 118, 640-653.	1.1	38
1616	Advances in Computational Biology. Advances in Intelligent Systems and Computing, 2014, , .	0.5	1
1617	A Methodology for Optimizing the E-value Threshold in Alignment-Based Gene Ontology Prediction Using the ROC Curve. Advances in Intelligent Systems and Computing, 2014, , 315-320.	0.5	0
1618	Microarray Analysis of Hepatic Gene Expression in Juvenile Japanese Flounder Paralichthys olivaceus Fed Diets Supplemented with Fish or Vegetable Oils. Marine Biotechnology, 2014, 16, 88-102.	1.1	20
1619	Comparative transcriptome analysis of ovules reveals stress related genes associated with nucellar polyembryony in citrus. Tree Genetics and Genomes, 2014, 10, 449-464.	0.6	21

#	Article	IF	Citations
1620	Polyploidy and the petal transcriptome of Gossypium. BMC Plant Biology, 2014, 14, 3.	1.6	35
1621	EST-based microsatellites for northern pike (Esox lucius) and cross-amplification across all Esox species. Conservation Genetics Resources, 2014, 6, 451-454.	0.4	4
1622	Generation of expressed sequence tags under cadmium stress for gene discovery and development of molecular markers in chickpea. Protoplasma, 2014, 251, 955-972.	1.0	3
1623	Proteomics of larval hemolymph in Bombyx mori reveals various nutrient-storage and immunity-related proteins. Amino Acids, 2014, 46, 1021-1031.	1.2	39
1624	Carotenoids gene markers for sweetpotato (Ipomoea batatas L. Lam): applications in genetic mapping, diversity evaluation and cross-species transference. Molecular Genetics and Genomics, 2014, 289, 237-251.	1.0	5
1625	A systematic exploration of high-temperature stress-responsive genes in potato using large-scale yeast functional screening. Molecular Genetics and Genomics, 2014, 289, 185-201.	1.0	34
1626	Phenotypic and genomic characterization of the Antarctic bacterium Gillisia sp. CAL575, a producer of antimicrobial compounds. Extremophiles, 2014, 18, 35-49.	0.9	22
1627	Differential Transcriptional Profiles of Dormancy-Related Genes in Apple Buds. Plant Molecular Biology Reporter, 2014, 32, 796-813.	1.0	51
1628	Comprehensive transcriptional profiling of NaHCO3-stressed Tamarix hispida roots reveals networks of responsive genes. Plant Molecular Biology, 2014, 84, 145-157.	2.0	44
1629	Characterization of the transcriptomes ofHaliotis rufescensreproductive tissues. Aquaculture Research, 2014, 45, 1026-1040.	0.9	22
1630	Mechanisms of Antibacterial Activity of MgO: Nonâ€ROS Mediated Toxicity of MgO Nanoparticles Towards <i>Escherichia coli</i>. Small, 2014, 10, 1171-1183.	5.2	418
1631	Differential gene expression identified by RNA-Seq and qPCR in two sizes of pearl oyster (Pinctada) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	62
1632	Comparative analysis of two phenologically divergent populations of the pine processionary moth (Thaumetopoea pityocampa) by de novo transcriptome sequencing. Insect Biochemistry and Molecular Biology, 2014, 46, 31-42.	1.2	10
1633	Dynamic expression of novel and conserved microRNAs and their targets in diploid and tetraploid of Paulownia tomentosa. Biochimie, 2014, 102, 68-77.	1.3	24
1634	Transcriptome and proteomic analysis of mango (Mangifera indica Linn) fruits. Journal of Proteomics, 2014, 105, 19-30.	1.2	80
1635	The Analysis of Eight Transcriptomes from All Poriferan Classes Reveals Surprising Genetic Complexity in Sponges. Molecular Biology and Evolution, 2014, 31, 1102-1120.	3.5	211
1636	Extracting data from the muck: deriving biological insight from complex microbial communities and non-model organisms with next generation sequencing. Current Opinion in Biotechnology, 2014, 28, 103-110.	3.3	31
1637	Mining of microsatellites using next generation sequencing of seabuckthorn (Hippophae rhamnoides) Tj ETQq1 1 0.784314 rgBT /Overl	1.4	28

#	ARTICLE	IF	CITATIONS
1638	Dual RNA-seq of the plant pathogen Phytophthora ramorum and its tanoak host. Tree Genetics and Genomes, 2014, 10, 489-502.	0.6	45
1639	Dynamics of the chili pepper transcriptome during fruit development. BMC Genomics, 2014, 15, 143.	1.2	54
1640	Patchwork sequencing of tomato San Marzano and Vesuviano varieties highlights genome-wide variations. BMC Genomics, 2014, 15, 138.	1.2	32
1641	Analysis of the floral transcriptome of Tarenaya hassleriana (Cleomaceae), a member of the sister group to the Brassicaceae: towards understanding the base of morphological diversity in Brassicales. BMC Genomics, 2014, 15, 140.	1.2	12
1642	A systems-wide comparison of red rice (Oryza longistaminata) tissues identifies rhizome specific genes and proteins that are targets for cultivated rice improvement. BMC Plant Biology, 2014, 14, 46.	1.6	43
1643	RNA-Seq transcriptome analysis of Spirodela dormancy without reproduction. BMC Genomics, 2014, 15, 60.	1.2	34
1644	Genetic diversity analysis of yellow mustard (Sinapis alba L.) germplasm based on genotyping by sequencing. Genetic Resources and Crop Evolution, 2014, 61, 579-594.	0.8	41
1645	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus Penicillium aurantiogriseum NRRL 62431. BMC Genomics, 2014, 15, 69.	1.2	125
1646	Transcriptomic analysis of Asiatic lily in the process of vernalization via RNA-seq. Molecular Biology Reports, 2014, 41, 3839-3852.	1.0	26
1647	Transcriptome sequencing for high throughput SNP development and genetic mapping in Pea. BMC Genomics, 2014, 15, 126.	1.2	104
1648	Large-scale analysis of differential gene expression in coffee genotypes resistant and susceptible to leaf minerâ€"toward the identification of candidate genes for marker assisted-selection. BMC Genomics, 2014, 15, 66.	1.2	30
1649	Construction and de novo characterization of a transcriptome of Chrysanthemum lavandulifolium: analysis of gene expression patterns in floral bud emergence. Plant Cell, Tissue and Organ Culture, 2014, 116, 297-309.	1.2	36
1650	Analysis of Jatropha curcas transcriptome for oil enhancement and genic markers. Physiology and Molecular Biology of Plants, 2014, 20, 139-142.	1.4	19
1651	Shared genes related to aggression, rather than chemical communication, are associated with reproductive dominance in paper wasps (Polistes metricus). BMC Genomics, 2014, 15, 75.	1.2	82
1652	Characterization of mango (Mangifera indica L.) transcriptome and chloroplast genome. Plant Molecular Biology, 2014, 85, 193-208.	2.0	51
1653	Potential of Bioinformatics as functional genomics tool: an overview. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 1.	1.2	3
1654	Transcriptomic profiling to identify genes involved in Fusarium mycotoxin Deoxynivalenol and Zearalenone tolerance in the mycoparasitic fungus Clonostachys rosea. BMC Genomics, 2014, 15, 55.	1.2	61
1655	Comparative transcripts profiling of fruit mesocarp and endocarp relevant to secondary metabolism by suppression subtractive hybridization in Azadirachta indica (neem). Molecular Biology Reports, 2014, 41, 3147-3162.	1.0	40

#	ARTICLE	IF	CITATIONS
1656	Comparative de novo transcriptome analysis and metabolic pathway studies of Citrus paradisi flavedo from naive stage to ripened stage. Molecular Biology Reports, 2014, 41, 3071-3080.	1.0	9
1657	The transcriptome of the NZ endemic sea urchin Kina (Evechinus chloroticus). BMC Genomics, 2014, 15, 45.	1.2	22
1658	Transcriptomic analysis of cut tree peony with glucose supply using the RNA-Seq technique. Plant Cell Reports, 2014, 33, 111-129.	2.8	34
1659	RNA-Seq revealed complex response to heat stress on transcriptomic level in Saccharina japonica (Laminariales, Phaeophyta). Journal of Applied Phycology, 2014, 26, 1585-1596.	1.5	54
1660	De novo transcriptomic profile in the gonadal tissues of the intertidal whelk Reishia clavigera. Marine Pollution Bulletin, 2014, 85, 499-504.	2.3	14
1661	Discovery of sex-related genes through high-throughput transcriptome sequencing from the salmon louse Caligus rogercresseyi. Marine Genomics, 2014, 15, 85-93.	0.4	32
1662	miRNA profiling in leaf and cork tissues of Quercus suber reveals novel miRNAs and tissue-specific expression patterns. Tree Genetics and Genomes, 2014, 10, 721-737.	0.6	20
1663	First insights into the transcriptome and development of new genomic tools of a widespread circumâ€Mediterranean tree species, <i>Pinus halepensis</i> Mill. Molecular Ecology Resources, 2014, 14, 846-856.	2.2	61
1664	Legumes in the Omic Era. , 2014, , .		12
1665	Exploring the hidden honeybee (Apis mellifera) venom proteome by integrating a combinatorial peptide ligand library approach with FTMS. Journal of Proteomics, 2014, 99, 169-178.	1.2	70
1666	Pyrosequencing the salivary transcriptome of <i>Haemadipsa interrupta</i> (Annelida: Clitellata:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 in leeches. Invertebrate Biology, 2014, 133, 74-98.	0.3	33
1667	The metal transporter PgIREG1 from the hyperaccumulator Psychotria gabriellae is a candidate gene for nickel tolerance and accumulation. Journal of Experimental Botany, 2014, 65, 1551-1564.	2.4	97
1668	BLAST output visualization in the new sequencing era. Briefings in Bioinformatics, 2014, 15, 484-503.	3.2	25
1669	Genomic architecture of ecologically divergent body shape in a pair of sympatric crater lake cichlid fishes. Molecular Ecology, 2014, 23, 1828-1845.	2.0	99
1670	High-resolution analysis of gene activity during the <i>Xenopus</i> mid-blastula transition. Development (Cambridge), 2014, 141, 1927-1939.	1.2	87
1671	Origin and Evolution of B Chromosomes in the Cichlid Fish Astatotilapia latifasciata Based on Integrated Genomic Analyses. Molecular Biology and Evolution, 2014, 31, 2061-2072.	3.5	112
1672	Gene expression in closely related species mirrors local adaptation: consequences for responses to a warming world. Molecular Ecology, 2014, 23, 2686-2698.	2.0	23
1673	Cell wall proteomics of sugarcane cell suspension cultures. Proteomics, 2014, 14, 738-749.	1.3	55

#	Article	IF	Citations
1674	MicroRNA expression profile in the third- and fourth-stage larvae of Angiostrongylus cantonensis. Parasitology Research, 2014, 113, 1883-1896.	0.6	14
1675	Microarray analysis of differentially expressed genes engaged in fruit development between table and wine grape. Molecular Biology Reports, 2014, 41, 4397-4412.	1.0	1
1676	Gene expression in mycorrhizal orchid protocorms suggests a friendly plantâ€“fungus relationship. Planta, 2014, 239, 1337-1349.	1.6	79
1677	Compatible solute, transporter protein, transcription factor, and hormone-related gene expression provides an indicator of drought stress in Paulownia fortunei. Functional and Integrative Genomics, 2014, 14, 479-491.	1.4	32
1678	Transcriptome and metabolome analysis of Citrus fruit to elucidate puffing disorder. Plant Science, 2014, 217-218, 87-98.	1.7	52
1679	Microbial and Carbohydrate Active Enzyme profile of buffalo rumen metagenome and their alteration in response to variation in the diet. Gene, 2014, 545, 88-94.	1.0	90
1680	Development and characterization of a new set of 164 polymorphic <scp>EST</scp>â€<scp>SSR</scp> markers for diversity and breeding studies in rubber tree (<i><scp>H</scp>evea brasiliensis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 497 T	1.0	21
1681	Genomic adaptations of the halophilic Dead Sea filamentous fungus Eurotium rubrum. Nature Communications, 2014, 5, 3745.	5.8	62
1682	Cell-autonomous-like silencing of GFP-partitioned transgenic Nicotiana benthamiana. Journal of Experimental Botany, 2014, 65, 4271-4283.	2.4	6
1683	Genome-wide marker development for the wheat D genome based on single nucleotide polymorphisms identified from transcripts in the wild wheat progenitor Aegilops tauschii. Theoretical and Applied Genetics, 2014, 127, 261-271.	1.8	43
1684	Caspase-like activity during aging and cell death in the toxic dinoflagellate Karenia brevis. Harmful Algae, 2014, 31, 41-53.	2.2	23
1685	Identification of differentially-expressed genes potentially implicated in drought response in pitaya (Hylocereus undatus) by suppression subtractive hybridization and cDNA microarray analysis. Gene, 2014, 533, 322-331.	1.0	36
1686	Differentially Expressed Genes during Flowering and Grain Filling in Common Bean (Phaseolus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 438-451.	1.0	25
1687	Analysis of transcriptomes of three orbâ€web spider species reveals gene profiles involved in silk and toxin. Insect Science, 2014, 21, 687-698.	1.5	13
1688	Deep sequencing of the Camellia chekiangoleosa transcriptome revealed candidate genes for anthocyanin biosynthesis. Gene, 2014, 538, 1-7.	1.0	33
1689	Genome assembly and annotation for red clover (<i>Trifolium pratense</i>; Fabaceae). American Journal of Botany, 2014, 101, 327-337.	0.8	69
1690	Molecular Mechanisms Involved in the Response to Desiccation Stress and Persistence in Acinetobacter baumannii. Journal of Proteome Research, 2014, 13, 460-476.	1.8	90
1691	Immunogenicity of Hypothetical Highly Conserved Proteins as Novel Antigens in Anaplasma marginale. Current Microbiology, 2014, 68, 269-277.	1.0	4

#	Article	IF	Citations
1692	RNA-Seq analysis of the toxicant-induced transcriptome of the marine diatom, Ceratoneis closterium. Marine Genomics, 2014, 16, 45-53.	0.4	20
1693	TLR and IMD signaling pathways from Caligus rogercresseyi (Crustacea: Copepoda): In silico gene expression and SNPs discovery. Fish and Shellfish Immunology, 2014, 36, 428-434.	1.6	28
1694	Transcriptome analysis of the couch potato (CPO) protein reveals an expression pattern associated with early development in the salmon louse Caligus rogercresseyi. Gene, 2014, 536, 1-8.	1.0	8
1695	Unveiling the mechanism by which microsporidian parasites prevent locust swarm behavior. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1343-1348.	3.3	60
1696	The impact of automated filtering of BLAST-determined homologs in the phylogenetic detection of horizontal gene transfer from a transcriptome assembly. Molecular Phylogenetics and Evolution, 2014, 71, 184-192.	1.2	8
1697	Chromosome Scale Genome Assembly and Transcriptome Profiling of Nannochloropsis gaditana in Nitrogen Depletion. Molecular Plant, 2014, 7, 323-335.	3.9	178
1698	Phylogenomics resolves the timing and pattern of insect evolution. Science, 2014, 346, 763-767.	6.0	2,096
1699	High-throughput Sequencing Technology and Its Application. The Journal of Northeast Agricultural University, 2014, 21, 84-96.	0.1	16
1700	Gene expression associated with intersterility in Heterobasidion. Fungal Genetics and Biology, 2014, 73, 104-119.	0.9	5
1701	The nutritionally responsive transcriptome of the polyphenic beetle <i>Onthophagus taurus</i> and the importance of sexual dimorphism and body region. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20142084.	1.2	29
1702	De novo assembly of Eugenia uniflora L. transcriptome and identification of genes from the terpenoid biosynthesis pathway. Plant Science, 2014, 229, 238-246.	1.7	33
1703	Extensive transcriptional response associated with seasonal plasticity of butterfly wing patterns. Molecular Ecology, 2014, 23, 6123-6134.	2.0	37
1704	The Involvement of Cholesterol in Sepsis and Tolerance to Lipopolysaccharide Highlighted by the Transcriptome Analysis of Zebrafish (Danio rerio). Zebrafish, 2014, 11, 421-433.	0.5	20
1705	Spatial Variation in Transcript and Protein Abundance of Atlantic Salmon during Feeding Migration in the Baltic Sea. Environmental Science & Technology, 2014, 48, 13969-13977.	4.6	22
1706	Comparative transcriptome analysis of <i><scp>D</scp>iscosporangium mesarthrocarpum</i> (<scp>P</scp>haeophyceae), <i><scp>S</scp>chizocladia ischiensis</i> (<scp>S</scp>chizocladiophyceae), and <i><scp>P</scp>haeothamnion confervicola</i> (<scp>P</scp>haeothamniophyceae), with special reference to cell wallâ€related genes. Journal of Phycology, 2014, 50, 543-551.	1.0	4
1707	<scp>SNP</scp> development from <scp>RNA</scp>â€seq data in a nonmodel fish: how many individuals are needed for accurate allele frequency prediction?. Molecular Ecology Resources, 2014, 14, 157-165.	2.2	38
1708	FmTFDb: a foxtail millet transcription factors database for expediting functional genomics in millets. Molecular Biology Reports, 2014, 41, 6343-6348.	1.0	23
1709	Copy number variation in <scp>F</scp>ayoumi and <scp>L</scp>eghorn chickens analyzed using array comparative genomic hybridization. Animal Genetics, 2014, 45, 400-411.	0.6	14

#	ARTICLE	IF	CITATIONS
1710	Fineâ€scale population epigenetic structure in relation to gastrointestinal parasite load in red grouse (<i>Lagopus lagopus scotica</i>). Molecular Ecology, 2014, 23, 4256-4273.	2.0	51
1711	Integration of <scp>AFLP</scp>s, <scp>SSR</scp>s and <scp>SNP</scp>s markers into a new genetic map of industrial chicory (<i><scp>C</scp>ichorium intybus </i><scp>L</scp>. var. <i>sativum</i>). Plant Breeding, 2014, 133, 130-137.	1.0	19
1712	Polyphosphate accumulation is driven by transcriptome alterations that lead to nearâ€synchronous and nearâ€equivalent uptake of inorganic cations in an arbuscular mycorrhizal fungus. New Phytologist, 2014, 204, 638-649.	3.5	63
1713	<i>De Novo</i> Transcriptome Sequence Assembly from Coconut Leaves and Seeds with a Focus on Factors Involved in RNA-Directed DNA Methylation. G3: Genes, Genomes, Genetics, 2014, 4, 2147-2157.	0.8	33
1714	Floral Transcriptomes in Woodland Strawberry Uncover Developing Receptacle and Anther Gene Networks. Plant Physiology, 2014, 165, 1062-1075.	2.3	167
1715	Genome-wide comparative analysis of tonoplast intrinsic protein (TIP) genes in plants. Functional and Integrative Genomics, 2014, 14, 617-629.	1.4	29
1716	Lysine Propionylation Is a Prevalent Post-translational Modification in Thermus thermophilus. Molecular and Cellular Proteomics, 2014, 13, 2382-2398.	2.5	49
1717	The Global Phosphoproteome of Chlamydomonas reinhardtii Reveals Complex Organellar Phosphorylation in the Flagella and Thylakoid Membrane. Molecular and Cellular Proteomics, 2014, 13, 2337-2353.	2.5	100
1718	The gene expression profile of Monochamus alternatus in response to deltamethrin exposure. Journal of Asia-Pacific Entomology, 2014, 17, 893-899.	0.4	2
1719	Genome comparison of three serovar 5 pathogenic strains of Haemophilus parasuis: insights into an evolving swine pathogen. Microbiology (United Kingdom), 2014, 160, 1974-1984.	0.7	4
1720	Comparison of distinct transcriptional expression patterns of flavonoid biosynthesis in Cabernet Sauvignon grapes from east andÂwest China. Plant Physiology and Biochemistry, 2014, 84, 45-56.	2.8	26
1721	iTRAQ-Based Quantitative Proteomics of Developing and Ripening Muscadine Grape Berry. Journal of Proteome Research, 2014, 13, 555-569.	1.8	69
1722	Proteomic Analysis of Insect Molting Fluid with a Focus on Enzymes Involved in Chitin Degradation. Journal of Proteome Research, 2014, 13, 2931-2940.	1.8	72
1723	Analysis of expressed sequence tags from a normalized cDNA library of perilla (Perilla frutescens). Journal of Plant Biology, 2014, 57, 312-320.	0.9	4
1724	Zinc Oxide Nanoparticles Cause Inhibition of Microbial Denitrification by Affecting Transcriptional Regulation and Enzyme Activity. Environmental Science & Technology, 2014, 48, 13800-13807.	4.6	148
1725	Molecular impact of juvenile hormone agonists on neonatal <i>Daphnia magna</i>. Journal of Applied Toxicology, 2014, 34, 537-544.	1.4	35
1726	Transcriptional profiling of the oesophageal gland region of male worms of Schistosoma mansoni. Molecular and Biochemical Parasitology, 2014, 196, 82-89.	0.5	17
1727	Quantitative Proteomic and Phosphoproteomic Analysis of Trypanosoma cruzi Amastigogenesis. Molecular and Cellular Proteomics, 2014, 13, 3457-3472.	2.5	39

#	ARTICLE	IF	CITATIONS
1728	Characterization of the global transcriptome for cotton (Gossypium hirsutum L.) anther and development of SSR marker. Gene, 2014, 551, 206-213.	1.0	18
1729	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	6.0	520
1730	Comprehensive gene expression profiling in Japanese flounder kidney after injection with two different formalin-killed pathogenic bacteria. Fish and Shellfish Immunology, 2014, 41, 437-440.	1.6	19
1731	Mining Tissue-specific Contigs from Peanut (Arachis hypogaea L.) for Promoter Cloning by Deep Transcriptome Sequencing. Plant and Cell Physiology, 2014, 55, 1793-1801.	1.5	22
1732	In-silico identification of miRNAs and their regulating target functions in Ocimum basilicum. Gene, 2014, 552, 277-282.	1.0	21
1733	Large-scale development of EST-SSR markers in sponge gourd via transcriptome sequencing. Molecular Breeding, 2014, 34, 1903-1915.	1.0	34
1734	Identification of Mytilus edulis genetic regulators during early development. Gene, 2014, 551, 65-78.	1.0	26
1735	Epigenetic inheritance and genome regulation: is DNA methylation linked to ploidy in haplodiploid insects?. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140411.	1.2	36
1736	Genome-wide identification of housekeeping genes in maize. Plant Molecular Biology, 2014, 86, 543-554.	2.0	68
1737	Genome-wide expression profiling of the transcriptomes of four Paulownia tomentosa accessions in response to drought. Genomics, 2014, 104, 295-305.	1.3	20
1738	Compartment Proteomics Analysis of White Perch (<i>Morone americana</i>) Ovary Using Support Vector Machines. Journal of Proteome Research, 2014, 13, 1515-1526.	1.8	20
1739	Next generation sequence analysis of the transcriptome of Sydney rock oysters (Saccostrea) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.4	7
1740	A Polychaeteâ€™s Powerful Punch: Venom Gland Transcriptomics of Glycera Reveals a Complex Cocktail of Toxin Homologs. Genome Biology and Evolution, 2014, 6, 2406-2423.	1.1	66
1741	Sma3s: A Three-Step Modular Annotator for Large Sequence Datasets. DNA Research, 2014, 21, 341-353.	1.5	80
1742	Hemicellulase production by Aspergillus niger DSM 26641 in hydrothermal palm oil empty fruit bunch hydrolysate and transcriptome analysis. Journal of Bioscience and Bioengineering, 2014, 118, 696-701.	1.1	15
1743	Deep sequencing of the tilapia (Oreochromis niloticus) liver transcriptome response to dietary protein to starch ratio. Aquaculture, 2014, 433, 299-306.	1.7	41
1744	Correlation of transcriptomic responses and metal bioaccumulation in Mytilus edulis L. reveals early indicators of stress. Aquatic Toxicology, 2014, 155, 129-141.	1.9	19
1746	Applicability of RADâ€tag genotyping for interfamilial comparisons: empirical data from two cetaceans. Molecular Ecology Resources, 2014, 14, 597-605.	2.2	25

#	ARTICLE	IF	CITATIONS
1747	Transcriptome survey of the lipid metabolic pathways involved in energy production and ecdysteroid synthesis in the salmon louse Caligus rogercresseyi (Crustacea: Copepoda). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2014, 176, 9-17.	0.7	12
1748	Transcriptome Analysis Reveals the Same 17 <i>S-Locus F-Box</i> Genes in Two Haplotypes of the Self-Incompatibility Locus of <i>Petunia inflata</i>. Plant Cell, 2014, 26, 2873-2888.	3.1	84
1749	Comparative Genomics of Flatworms (Platyhelminthes) Reveals Shared Genomic Features of Ecto- and Endoparastic Neodermata. Genome Biology and Evolution, 2014, 6, 1105-1117.	1.1	73
1750	Clawing through Evolution: Toxin Diversification and Convergence in the Ancient Lineage Chilopoda (Centipedes). Molecular Biology and Evolution, 2014, 31, 2124-2148.	3.5	100
1751	Genome-wide screening of pathogenicity islands in Mycobacterium tuberculosis based on the genomic barcode visualization. Molecular Biology Reports, 2014, 41, 5883-5889.	1.0	6
1752	Transcriptomic Insights into the Life History of Bolidophytes, the Sister Lineage to Diatoms. Journal of Phycology, 2014, 50, 977-983.	1.0	17
1753	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
1754	Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. Nature Communications, 2014, 5, 4611.	5.8	128
1755	<scp>ChIP</scp>â€seq reveals a role for <scp>CrzA</scp> in the <scp><i>A</i></scp><i>spergillus fumigatus</i> highâ€osmolarity glycerol response (<scp>HOG</scp>) signalling pathway. Molecular Microbiology, 2014, 94, 655-674.	1.2	60
1756	Insights into the olfactory system of the ectoparasite Caligus rogercresseyi: Molecular characterization and gene transcription analysis of novel ionotropic receptors. Experimental Parasitology, 2014, 145, 99-109.	0.5	21
1757	A comprehensive assessment of the transcriptome of cork oak (Quercus suber) through EST sequencing. BMC Genomics, 2014, 15, 371.	1.2	53
1758	Transcriptomic analysis of differential host gene expression upon uptake of symbionts: a case study with Symbiodinium and the major bioeroding sponge Cliona varians. BMC Genomics, 2014, 15, 376.	1.2	41
1759	Differential gene expression between functionally specialized polyps of the colonial hydrozoan Hydractinia symbiolongicarpus (Phylum Cnidaria). BMC Genomics, 2014, 15, 406.	1.2	45
1760	De novo assembly and transcriptome characterization: novel insights into the natural resistance mechanisms of Microtus fortis against Schistosoma japonicum. BMC Genomics, 2014, 15, 417.	1.2	10
1761	Infection routes matter in population-specific responses of the red flour beetle to the entomopathogen Bacillus thuringiensis. BMC Genomics, 2014, 15, 445.	1.2	60
1762	Genetic control of functional traits related to photosynthesis and water use efficiency in Pinus pinaster Ait. drought response: integration of genome annotation, allele association and QTL detection for candidate gene identification. BMC Genomics, 2014, 15, 464.	1.2	64
1763	Sequencing and characterization of the transcriptome of half-smooth tongue sole (Cynoglossus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	1.2	24
1764	Identification, characterization, and utilization of single copy genes in 29 angiosperm genomes. BMC Genomics, 2014, 15, 504.	1.2	29

#	Article	IF	Citations
1765	Profiling microRNAs in Eucalyptus grandis reveals no mutual relationship between alterations in miR156 and miR172 expression and adventitious root induction during development. BMC Genomics, 2014, 15, 524.	1.2	38
1766	Transcriptome analysis of the differences in gene expression between testis and ovary in green mud crab (Scylla paramamosain). BMC Genomics, 2014, 15, 585.	1.2	96
1767	The sex-specific transcriptome of the hermaphrodite sparid sharpsnout seabream (Diplodus puntazzo). BMC Genomics, 2014, 15, 655.	1.2	65
1768	Comparative transcriptome profiling of a desert evergreen shrub, Ammopiptanthus mongolicus, in response to drought and cold stresses. BMC Genomics, 2014, 15, 671.	1.2	79
1769	The Babesia bovis gene and promoter model: an update from full-length EST analysis. BMC Genomics, 2014, 15, 678.	1.2	8
1770	Transcriptome sequencing of a chimaera reveals coordinated expression of anthocyanin biosynthetic genes mediating yellow formation in herbaceous peony (Paeonia lactiflora Pall.). BMC Genomics, 2014, 15, 689.	1.2	80
1771	Genome wide SNP identification in chickpea for use in development of a high density genetic map and improvement of chickpea reference genome assembly. BMC Genomics, 2014, 15, 708.	1.2	98
1772	Functional genomic analysis of constitutive and inducible defense responses to Fusarium verticillioides infection in maize genotypes with contrasting ear rot resistance. BMC Genomics, 2014, 15, 710.	1.2	120
1773	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. BMC Genomics, 2014, 15, 717.	1.2	122
1774	Genome-wide sequencing of small RNAs reveals a tissue-specific loss of conserved microRNA families in Echinococcus granulosus. BMC Genomics, 2014, 15, 736.	1.2	67
1775	The American cranberry: first insights into the whole genome of a species adapted to bog habitat. BMC Plant Biology, 2014, 14, 165.	1.6	105
1776	Analysis of age and gender associated N-glycoproteome in human whole saliva. Clinical Proteomics, 2014, 11, 25.	1.1	30
1777	EC2KEGG: a command line tool for comparison of metabolic pathways. Source Code for Biology and Medicine, 2014, 9, 19.	1.7	15
1778	Biological pattern and transcriptomic exploration and phylogenetic analysis in the odd floral architecture tree: Helwingia willd. BMC Research Notes, 2014, 7, 402.	0.6	2
1779	Assembly and annotation of a non-model gastropod (Nerita melanotragus) transcriptome: a comparison of De novo assemblers. BMC Research Notes, 2014, 7, 488.	0.6	27
1780	De novo assembly and characterization of the transcriptome in the desiccation-tolerant moss Syntrichia caninervis. BMC Research Notes, 2014, 7, 490.	0.6	69
1781	De novo transcriptome sequencing and sequence analysis of the malaria vector Anopheles sinensis (Diptera: Culicidae). Parasites and Vectors, 2014, 7, 314.	1.0	29
1782	Identification and computational annotation of genes differentially expressed in pulp development of Cocos nuciferaL. by suppression subtractive hybridization. BMC Plant Biology, 2014, 14, 205.	1.6	27

#	Article	IF	Citations
1783	Overexpression of the soybean transcription factor GmDof4 significantly enhances the lipid content of Chlorella ellipsoidea. Biotechnology for Biofuels, 2014, 7, 128.	6.2	47
1784	In-depth Proteomics Characterization of Embryogenesis of the Honey Bee Worker (Apis mellifera) Tj ETQq1 1 0.784314 rgBT /Overlock	2.5	33
1785	Transcriptome Analysis of the Entomopathogenic Oomycete Lagenidium giganteum Reveals Putative Virulence Factors. Applied and Environmental Microbiology, 2014, 80, 6427-6436.	1.4	14
1786	Genome-wide transcriptional changes of ramie (Boehmeria nivea L. Gaud) in response to root-lesion nematode infection. Gene, 2014, 552, 67-74.	1.0	30
1787	Draft Genome Sequence of the Oleaginous Yeast Yarrowia lipolytica PO1f, a Commonly Used Metabolic Engineering Host. Genome Announcements, 2014, 2, .	0.8	59
1788	Sly-miR166 and Sly-miR319 are components of the cold stress response in Solanum lycopersicum. Plant Biotechnology Reports, 2014, 8, 349-356.	0.9	39
1789	Transcriptome characterization and differential expression analysis of cold-responsive genes in young spikes of common wheat. Journal of Biotechnology, 2014, 189, 48-57.	1.9	17
1790	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. Biofouling, 2014, 30, 169-181.	0.8	51
1791	Transcriptome dynamics of a desert poplar (Populus pruinosa) in response to continuous salinity stress. Plant Cell Reports, 2014, 33, 1565-1579.	2.8	42
1792	Transcriptional Assessment by Microarray Analysis and Large-Scale Meta-analysis of the Metabolic Capacity of Cardiac and Skeletal Muscle Tissues to Cope With Reduced Nutrient Availability in Gilthead Sea Bream (Sparus aurata L.). Marine Biotechnology, 2014, 16, 423-435.	1.1	48
1793	De Novo Transcriptome Sequencing of the Snail Echinolittorina malaccana: Identification of Genes Responsive to Thermal Stress and Development of Genetic Markers for Population Studies. Marine Biotechnology, 2014, 16, 547-559.	1.1	43
1794	C2H2 type of zinc finger transcription factors in foxtail millet define response to abiotic stresses. Functional and Integrative Genomics, 2014, 14, 531-543.	1.4	120
1795	Proteinâ€“protein interaction network of the marine microalga <i>Tetraselmis subcordiformis</i>: prediction and application for starch metabolism analysis. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 1287-1296.	1.4	18
1796	Comparison and development of ESTâ€“SSRs from two 454 sequencing libraries of Gossypium barbadense. Euphytica, 2014, 198, 277-288.	0.6	6
1797	Postprandial molecular responses in the liver of the barramundi, Lates calcarifer. Fish Physiology and Biochemistry, 2014, 40, 427-443.	0.9	31
1798	De novo transcriptome analysis-gained insights into physiological and metabolic characteristics of Sargassum thunbergii (Fucales, Phaeophyceae). Journal of Applied Phycology, 2014, 26, 1519-1526.	1.5	19
1799	Leaf-, panel- and latex-expressed sequenced tags from the rubber tree (Hevea brasiliensis) under cold-stressed and suboptimal growing conditions: the development of gene-targeted functional markers for stress response. Molecular Breeding, 2014, 34, 1035-1053.	1.0	32
1800	An insight into the genes involved in secoiridoid biosynthesis in Gentiana macrophylla by RNA-seq. Molecular Biology Reports, 2014, 41, 4817-4825.	1.0	39

#	ARTICLE	IF	CITATIONS
1801	Secretome of the Biocontrol Agent <i>Metarhizium anisopliae</i> Induced by the Cuticle of the Cotton Pest <i>Dysdercus peruvianus</i> Reveals New Insights into Infection. Journal of Proteome Research, 2014, 13, 2282-2296.	1.8	32
1802	Gene expression differences underlying genotype-by-genotype specificity in a hostâ€“parasite system. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3496-3501.	3.3	109
1803	The genome and life-stage specific transcriptomes of Globodera pallida elucidate key aspects of plant parasitism by a cyst nematode. Genome Biology, 2014, 15, R43.	13.9	212
1804	Transcriptomics assisted proteomic analysis of <i>Nicotiana occidentalis</i> infected by <i>Candidatus</i> Phytoplasma mali strain AT. Proteomics, 2014, 14, 1882-1889.	1.3	39
1805	Secretomic Survey of <i>Trichoderma harzianum</i> Grown on Plant Biomass Substrates. Journal of Proteome Research, 2014, 13, 1810-1822.	1.8	23
1806	A ray of venom: Combined proteomic and transcriptomic investigation of fish venom composition using barb tissue from the blue-spotted stingray (Neotrygon kuhlii). Journal of Proteomics, 2014, 109, 188-198.	1.2	29
1807	Early molecular events involved in<i>Pinus pinaster</i>Ait. somatic embryo development under reduced water availability: transcriptomic and proteomic analyses. Physiologia Plantarum, 2014, 152, 184-201.	2.6	81
1808	Comparative transcriptomic analysis of the regulation of flowering in temperate and tropical lotus (<i>Nelumbo nucifera</i>) by <scp>RNA</scp>â€Seq. Annals of Applied Biology, 2014, 165, 73-95.	1.3	26
1809	Gene Expression Differences between <i>Noccaea caerulescens</i> Ecotypes Help to Identify Candidate Genes for Metal Phytoremediation. Environmental Science & Technology, 2014, 48, 3344-3353.	4.6	106
1810	Rewiring Host Lipid Metabolism by Large Viruses Determines the Fate of <i>Emiliania huxleyi</i>, a Bloom-Forming Alga in the Ocean Â Â. Plant Cell, 2014, 26, 2689-2707.	3.1	132
1811	High-throughput sequencing analysis of common fig (Ficus carica L.) transcriptome during fruit ripening. Tree Genetics and Genomes, 2014, 10, 923-935.	0.6	21
1812	Identification of Heat-Related ESTs in Moth Bean Through Suppression Subtraction Hybridization. Applied Biochemistry and Biotechnology, 2014, 173, 2116-2128.	1.4	7
1813	Differential expression analysis of transcripts related to oil metabolism in maturing seeds of Jatropha curcas L.. Physiology and Molecular Biology of Plants, 2014, 20, 181-190.	1.4	8
1814	Genome and secretome analysis of the hemibiotrophic fungal pathogen, Moniliophthora roreri, which causes frosty pod rot disease of cacao: mechanisms of the biotrophic and necrotrophic phases. BMC Genomics, 2014, 15, 164.	1.2	107
1815	Transcriptome analyses and differential gene expression in a non-model fish species with alternative mating tactics. BMC Genomics, 2014, 15, 167.	1.2	76
1816	Identification of mycoparasitism-related genes against the phytopathogen Sclerotinia sclerotiorum through transcriptome and expression profile analysis in Trichoderma harzianum. BMC Genomics, 2014, 15, 204.	1.2	99
1817	RNA-seq analysis identifies an intricate regulatory network controlling cluster root development in white lupin. BMC Genomics, 2014, 15, 230.	1.2	43
1818	Metatranscriptome analysis of fungal strains Penicillium camemberti and Geotrichum candidumreveal cheese matrix breakdown and potential development of sensory properties of ripened Camembert-type cheese. BMC Genomics, 2014, 15, 235.	1.2	85

#	ARTICLE	IF	CITATIONS
1819	Comparative transcript profiling of the fertile and sterile flower buds of pol CMS in B. napus. BMC Genomics, 2014, 15, 258.	1.2	76
1820	Gene expression profile analysis of Manila clam (Ruditapes philippinarum) hemocytes after a Vibrio alginolyticus challenge using an immune-enriched oligo-microarray. BMC Genomics, 2014, 15, 267.	1.2	41
1821	Transcriptome assembly and microarray construction for Enchytraeus crypticus, a model oligochaete to assess stress response mechanisms derived from soil conditions. BMC Genomics, 2014, 15, 302.	1.2	35
1822	De novo genome assembly of the soil-borne fungus and tomato pathogen Pyrenochaeta lycopersici. BMC Genomics, 2014, 15, 313.	1.2	39
1823	A customized Web portal for the genome of the ctenophore Mnemiopsis leidyi. BMC Genomics, 2014, 15, 316.	1.2	28
1824	Deep mRNA sequencing reveals stage-specific transcriptome alterations during microsclerotia development in the smoke tree vascular wilt pathogen, Verticillium dahliae. BMC Genomics, 2014, 15, 324.	1.2	68
1825	Deep-sequencing transcriptome analysis of low temperature perception in a desert tree, Populus euphratica. BMC Genomics, 2014, 15, 326.	1.2	54
1826	Resistance to Botrytis cinerea in Solanum lycopersicoides involves widespread transcriptional reprogramming. BMC Genomics, 2014, 15, 334.	1.2	66
1827	Secretome analysis reveals effector candidates associated with broad host range necrotrophy in the fungal plant pathogen Sclerotinia sclerotiorum. BMC Genomics, 2014, 15, 336.	1.2	241
1828	Transcriptome differences between two sister desert poplar species under salt stress. BMC Genomics, 2014, 15, 337.	1.2	50
1829	High-throughput capturing and characterization of mutations in essential genes of Caenorhabditis elegans. BMC Genomics, 2014, 15, 361.	1.2	15
1830	Dual RNA-seq transcriptional analysis of wheat roots colonized by Azospirillum brasilense reveals up-regulation of nutrient acquisition and cell cycle genes. BMC Genomics, 2014, 15, 378.	1.2	130
1831	RNA sequencing on Solanum lycopersicum trichomes identifies transcription factors that activate terpene synthase promoters. BMC Genomics, 2014, 15, 402.	1.2	123
1832	Comparative transcriptome analysis of eggplant (Solanum melongena L.) and turkey berry (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	66
1833	Transcriptome profiling of pyrethroid resistant and susceptible mosquitoes in the malaria vector, Anopheles sinensis. BMC Genomics, 2014, 15, 448.	1.2	42
1834	Sequencing of transcriptomes from two Miscanthus species reveals functional specificity in rhizomes, and clarifies evolutionary relationships. BMC Plant Biology, 2014, 14, 134.	1.6	17
1835	A deep survey of alternative splicing in grape reveals changes in the splicing machinery related to tissue, stress condition and genotype. BMC Plant Biology, 2014, 14, 99.	1.6	254
1836	Genome-wide expression profile of the response to spinal cord injury in Xenopus laevis reveals extensive differences between regenerative and non-regenerative stages. Neural Development, 2014, 9, 12.	1.1	61

#	ARTICLE	IF	CITATIONS
1837	The protein-protein interaction network of eyestalk, Y-organ and hepatopancreas in Chinese mitten crab Eriocheir sinensis. BMC Systems Biology, 2014, 8, 39.	3.0	18
1838	Bioinformatic analysis of proteomics data. BMC Systems Biology, 2014, 8, S3.	3.0	131
1839	Divergent transcriptional responses to low temperature among populations of alpine and lowland species of <scp>N</scp>ew <scp>Z</scp>ealand stick insects (<i><scp>M</scp>icrarchus</i>). Molecular Ecology, 2014, 23, 2712-2726.	2.0	37
1840	Proteomic Profile of <i>Cryptococcus neoformans</i> Biofilm Reveals Changes in Metabolic Processes. Journal of Proteome Research, 2014, 13, 1545-1559.	1.8	58
1841	Comparative Quantitative Proteomics Analysis of the ABA Response of Roots of Drought-Sensitive and Drought-Tolerant Wheat Varieties Identifies Proteomic Signatures of Drought Adaptability. Journal of Proteome Research, 2014, 13, 1688-1701.	1.8	108
1842	The first Illumina-based de novo transcriptome sequencing and analysis of pumpkin (Cucurbita) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	44
1843	Characterization of the genomic responses in early Senegalese sole larvae fed diets with different dietary triacylglycerol and total lipids levels. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2014, 12, 61-73.	0.4	33
1844	Transcriptome sequencing of the marine microalga, <i>Chlorella pyrenoidosa</i> (Chlorophyta), and analysis of carbonic anhydrase expression under salt stress. Botanica Marina, 2014, 57, 403-412.	0.6	9
1845	Proteome of cell wall-extracts from pathogenic Paracoccidioides brasiliensis: Comparison among morphological phases, isolates, and reported fungal extracellular vesicle proteins. EuPA Open Proteomics, 2014, 3, 216-228.	2.5	30
1846	Changes in transcript abundance for cuticular proteins and other genes three hours after a blood meal in Anopheles gambiae. Insect Biochemistry and Molecular Biology, 2014, 44, 33-43.	1.2	28
1847	Gene expression patterns associated with caste and reproductive status in ants: workerâ€specific genes are more derived than queenâ€specific ones. Molecular Ecology, 2014, 23, 151-161.	2.0	112
1848	Gene expression profile analysis of Ligon lintless-1 (Li1) mutant reveals important genes and pathways in cotton leaf and fiber development. Gene, 2014, 535, 273-285.	1.0	30
1849	Deep transcriptome sequencing of Pecten maximus hemocytes: A genomic resource for bivalve immunology. Fish and Shellfish Immunology, 2014, 37, 154-165.	1.6	72
1850	Distal expression of sprouty (spry) genes during Xenopus laevis limb development and regeneration. Gene Expression Patterns, 2014, 15, 61-66.	0.3	20
1851	A Chinese jujube (Ziziphus jujuba Mill.) fruit-expressed sequence tag (EST) library: Annotation and EST-SSR characterization. Scientia Horticulturae, 2014, 165, 99-105.	1.7	23
1852	Midgut transcriptome response to a Cry toxin in the diamondback moth, Plutella xylostella (Lepidoptera: Plutellidae). Gene, 2014, 533, 180-187.	1.0	82
1853	Increasing transcriptome response of serpins during the ontogenetic stages in the salmon louse Caligus rogercresseyi (Copepoda: Caligidae). Marine Genomics, 2014, 15, 55-64.	0.4	11
1854	Host responses of Japanese flounder Paralichthys olivaceus withÂlymphocystis cell formation. Fish and Shellfish Immunology, 2014, 38, 406-411.	1.6	20

#	ARTICLE	IF	CITATIONS
1855	Origin, duplication and reshuffling of plasmid genes: Insights from Burkholderia vietnamiensis G4 genome. Genomics, 2014, 103, 229-238.	1.3	6
1856	De novo analysis of the Nilaparvata lugens (StÃ¥l) antenna transcriptome and expression patterns of olfactory genes. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2014, 9, 31-39.	0.4	64
1857	Accessing transcriptomic data for ecologically important genes in the goose barnacle (Pollicipes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.4	2
1858	A bioinformatics-based update on microRNAs and their targets in rainbow trout (Oncorhynchus) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	12
1859	454 pyrosequencing-based analysis of gene expression profiles in the amphipod Melita plumulosa: Transcriptome assembly and toxicant induced changes. Aquatic Toxicology, 2014, 153, 73-88.	1.9	38
1860	Analysis of the bovine plasma proteome by matrix-assisted laser desorption/ionisation time-of-flight tandem mass spectrometry. Veterinary Journal, 2014, 199, 175-180.	0.6	15
1861	Genomic analysis of the aconidial and high-performance protein producer, industrially relevant Aspergillus niger SH2 strain. Gene, 2014, 541, 107-114.	1.0	32
1862	Phosphoproteomic Analysis Provides Novel Insights into Stress Responses in <i>Phaeodactylum tricornutum</i>, a Model Diatom. Journal of Proteome Research, 2014, 13, 2511-2523.	1.8	39
1863	Stochastic specification of primordial germ cells from mesoderm precursors in axolotl embryos. Development (Cambridge), 2014, 141, 2429-2440.	1.2	64
1864	New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology. Journal of Arachnology, 2014, 42, 1-15.	0.3	16
1865	Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in Emiliania huxleyi. BMC Genomics, 2014, 15, 148.	1.2	31
1866	Genetic determinism of phenological traits highly affected by climate change in <i>Prunus avium:</i> flowering date dissected into chilling and heat requirements. New Phytologist, 2014, 202, 703-715.	3.5	104
1867	Nitric oxide is required for determining root architecture and lignin composition in sunflower. Supporting evidence from microarray analyses. Nitric Oxide - Biology and Chemistry, 2014, 39, 20-28.	1.2	43
1868	Transcriptome analysis of grain-filling caryopses reveals the potential formation mechanism of the rice sugary mutant. Gene, 2014, 546, 318-326.	1.0	9
1869	The first set of expressed sequence tags (EST) from the medicinal mushroom Agaricus subrufescens delivers resource for gene discovery and marker development. Applied Microbiology and Biotechnology, 2014, 98, 7879-7892.	1.7	13
1870	Novel and useful genic-SSR markers from de novo transcriptome sequencing of radish (Raphanus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	46
1871	Successful pod infections by <i><scp>M</scp>oniliophthora roreri</i> result in differential <i><scp>T</scp>heobroma cacao</i> gene expression depending on the clone's level of tolerance. Molecular Plant Pathology, 2014, 15, 698-710.	2.0	10
1872	Cold-Induced Cysts of the Photosynthetic Dinoflagellate<i>Lingulodinium polyedrum</i>Have an Arrested Circadian Bioluminescence Rhythm and Lower Levels of Protein Phosphorylation Â Â. Plant Physiology, 2014, 164, 966-977.	2.3	43

#	ARTICLE	IF	CITATIONS
1873	Phosphoproteomics in photosynthetic organisms. Electrophoresis, 2014, 35, 3441-3451.	1.3	3
1874	Methyl jasmonate represses growth and affects cell cycle progression in cultured Taxus cells. Plant Cell Reports, 2014, 33, 1479-1492.	2.8	53
1875	Dual role of the cuttlefish salivary proteome in defense and predation. Journal of Proteomics, 2014, 108, 209-222.	1.2	41
1876	Analysis of chemosensory gene families in the beetle Monochamus alternatus and its parasitoid Dastarcus helophoroides. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2014, 11, 1-8.	0.4	75
1877	RNA-seq Reveals Transcriptomic Shock Involving Transposable Elements Reactivation in Hybrids of Young Lake Whitefish Species. Molecular Biology and Evolution, 2014, 31, 1188-1199.	3.5	112
1878	Large-Scale Development of Gene-Associated Single-Nucleotide Polymorphism Markers for Molluscan Population Genomic, Comparative Genomic, and Genome-Wide Association Studies. DNA Research, 2014, 21, 183-193.	1.5	15
1879	Comparative Genomics of the Pine Pathogens and Beetle Symbionts in the Genus Grosmannia. Molecular Biology and Evolution, 2014, 31, 1454-1474.	3.5	9
1880	De novo transcriptome analysis of the Siberian apricot (Prunus sibirica L.) and search for potential SSR markers by 454 pyrosequencing. Gene, 2014, 544, 220-227.	1.0	30
1881	Metatranscriptome profiling of a harmful algal bloom. Harmful Algae, 2014, 37, 75-83.	2.2	45
1882	Suppression Subtractive Hybridization Reveals Different Responses of Two Varieties of Gossypium arboreum L. Under Apolygus lucorum Stress. Journal of Integrative Agriculture, 2014, 13, 1250-1257.	1.7	1
1883	Thymus cDNA library survey uncovers novel features of immune molecules in Chinese giant salamander Andrias davidianus. Developmental and Comparative Immunology, 2014, 46, 413-422.	1.0	24
1884	Gene duplication followed by exon structure divergence substitutes for alternative splicing in zebrafish. Gene, 2014, 546, 271-276.	1.0	7
1885	Development of a 44K custom oligo microarray using 454 pyrosequencing data for large-scale gene expression analysis of Camellia sinensis. Scientia Horticulturae, 2014, 174, 133-141.	1.7	9
1886	Transcriptome profiling and comparative analysis of Panax ginseng adventitious roots. Journal of Ginseng Research, 2014, 38, 278-288.	3.0	53
1887	Analysis of multiple transcriptomes of the African oil palm (Elaeis guineensis) to identify reference genes for RT-qPCR. Journal of Biotechnology, 2014, 184, 63-73.	1.9	42
1888	LC-MS/MS analysis of visceral and subcutaneous adipose tissue proteomes in young goats with focus on innate immunity and inflammation related proteins. Journal of Proteomics, 2014, 108, 295-305.	1.2	21
1889	Transcriptomic responses to heat stress and nickel in the mussel Mytilus galloprovincialis. Aquatic Toxicology, 2014, 148, 104-112.	1.9	31
1890	The sexâ€linked region in <i><scp>P</scp>opulus tremuloides </i><scp>T</scp>uresson 141 corresponds to a pericentromeric region of about two million base pairs on <i><scp>P</scp>.Âtrichocarpa</i> chromosome 19. Plant Biology, 2014, 16, 411-418.	1.8	52

#	ARTICLE	IF	CITATIONS
1891	Dynamic changes in the date palm fruit proteome during development and ripening. Horticulture Research, 2014, 1, 14039.	2.9	34
1892	tropiTree: An NGS-Based EST-SSR Resource for 24 Tropical Tree Species. PLoS ONE, 2014, 9, e102502.	1.1	12
1893	Comprehensive transcriptome analysis of early male and female Bactrocera jarvisi embryos. BMC Genetics, 2014, 15, S7.	2.7	11
1894	<i>CaDMR1</i> Cosegregates with QTL <i>Pc5.1</i> for Resistance to <i>Phytophthora capsici</i> in Pepper (<i>Capsicum annuum</i>). Plant Genome, 2014, 7, plantgenome2014.03.0011.	1.6	46
1895	Identification of SSRs and differentially expressed genes in two cultivars of celery (Apium graveolens) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.9	116
1896	Transcriptional dynamics of the developing sweet cherry (Prunus avium L.) fruit: sequencing, annotation and expression profiling of exocarp-associated genes. Horticulture Research, 2014, 1, 11.	2.9	82
1897	Comparative exomics of Phalariscultivars under salt stress. BMC Genomics, 2014, 15, S18.	1.2	13
1898	Gene expression and fractionation resistance. BMC Genomics, 2014, 15, S19.	1.2	5
1899	A Large Number of Nuclear Genes in the Human Parasite Blastocystis Require mRNA Polyadenylation to Create Functional Termination Codons. Genome Biology and Evolution, 2014, 6, 1956-1961.	1.1	11
1900	Whole transcriptome analysis of the poultry red mite <i>Dermanyssus gallinae</i> (De Geer, 1778). Parasitology, 2014, 141, 336-346.	0.7	40
1901	An approach to identify the novel miRNA encoded from H. Annuus EST sequences. Genomics Data, 2015, 6, 139-144.	1.3	15
1902	Oakleaf : an S locus â€•linked mutation of P rimula vulgaris that affects leaf and flower development. New Phytologist, 2015, 208, 149-161.	3.5	8
1903	Large-scale transcriptional profiling of lignified tissues in Tectona grandis. BMC Plant Biology, 2015, 15, 221.	1.6	27
1904	Gonadal transcriptomic analysis and differentially expressed genes in the testis and ovary of the Pacific white shrimp (Litopenaeus vannamei). BMC Genomics, 2015, 16, 1006.	1.2	72
1905	Genome-wide variation in the pinewood nematode Bursaphelenchus xylophilus and its relationship with pathogenic traits. BMC Genomics, 2015, 16, 845.	1.2	27
1906	Combined de novo and genome guided assembly and annotation of the Pinus patula juvenile shoot transcriptome. BMC Genomics, 2015, 16, 1057.	1.2	44
1907	Lasting effects of early exposure to temperature on the gonadal transcriptome at the time of sex differentiation in the European sea bass, a fish with mixed genetic and environmental sex determination. BMC Genomics, 2015, 16, 679.	1.2	79
1908	De novo assembly and transcriptome analysis of Plasmodium gallinaceum identifies the Rh5 interacting protein (ripr), and reveals a lack of EBL and RH gene family diversification. Malaria Journal, 2015, 14, 296.	0.8	13

#	Article	IF	Citations
1909	Transcriptome changes in Polygonum multiflorum Thunb. roots induced by methyl jasmonate. Journal of Zhejiang University: Science B, 2015, 16, 1027-1041.	1.3	6
1910	Combined metabolome and transcriptome profiling provides new insights into diterpene biosynthesis in S. pomifera glandular trichomes. BMC Genomics, 2015, 16, 935.	1.2	43
1911	Genomeâ€wide identification of target genes of a matingâ€type Î±â€domain transcription factor reveals functions beyond sexual development. Molecular Microbiology, 2015, 96, 1002-1022.	1.2	45
1912	The transcriptomic and evolutionary signature of social interactions regulating honey bee caste development. Ecology and Evolution, 2015, 5, 4795-4807.	0.8	36
1913	iPFPi: A System for Improving Protein Function Prediction through Cumulative Iterations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 825-836.	1.9	7
1914	Genomic basis of the differences between cider and dessert apple varieties. Evolutionary Applications, 2015, 8, 650-661.	1.5	33
1915	Pyrosequencing and de novo assembly of A ntarctic krill (E uphausia superba) transcriptome to study the adaptability of krill to climateâ€induced environmental changes. Molecular Ecology Resources, 2015, 15, 1460-1471.	2.2	30
1916	Effectiveness of managed gene flow in reducing genetic divergence associated with captive breeding. Evolutionary Applications, 2015, 8, 956-971.	1.5	47
1917	Identifying and Analyzing the Diversity of Resistance Gene Analogs in Colombian Rubus Genotypes. Plant Disease, 2015, 99, 994-1001.	0.7	4
1918	Knock-Down of Heat-Shock Protein 90 and Isocitrate Lyase Gene Expression Reduced Root-Knot Nematode Reproduction. Phytopathology, 2015, 105, 628-637.	1.1	29
1919	Evolutionary rate variation in two conifer species, <i>Taxodium</i> <i>distichum</i> (L.) Rich. var. <i>distichum</i> (baldcypress) and <i>Cryptomeria japonica</i> (Thunb. ex L.f.) D. Don (Sugi, Japanese cedar). Genes and Genetic Systems, 2015, 90, 305-315.	0.2	6
1920	The Plasmodiophora brassicae genome reveals insights in its life cycle and ancestry of chitin synthases. Scientific Reports, 2015, 5, 11153.	1.6	202
1921	Label-free Quantitative Analysis of Changes in Broiler Liver Proteins under Heat Stress using SWATH-MS Technology. Scientific Reports, 2015, 5, 15119.	1.6	44
1922	Transcriptome and gene expression analysis of DHA producer Aurantiochytrium under low temperature conditions. Scientific Reports, 2015, 5, 14446.	1.6	55
1923	Transcriptome analysis provides insights into the regulatory function of alternative splicing in antiviral immunity in grass carp (Ctenopharyngodon idella). Scientific Reports, 2015, 5, 12946.	1.6	73
1924	Rapid genome resequencing of an atoxigenic strain of Aspergillus carbonarius. Scientific Reports, 2015, 5, 9086.	1.6	15
1925	Genome analysis of Excretory/Secretory proteins in Taenia solium reveals their Abundance of Antigenic Regions (AAR). Scientific Reports, 2015, 5, 9683.	1.6	54
1926	A transcriptional reference map of defence hormone responses in potato. Scientific Reports, 2015, 5, 15229.	1.6	28

#	Article	IF	Citations
1927	Regulation of transcription factors on sexual dimorphism of fig wasps. Scientific Reports, 2015, 5, 10696.	1.6	2
1928	An advanced draft genome assembly of a desi type chickpea (Cicer arietinum L.). Scientific Reports, 2015, 5, 12806.	1.6	114
1929	Identification and comparative expression analysis of odorant binding protein genes in the tobacco cutworm Spodoptera litura. Scientific Reports, 2015, 5, 13800.	1.6	75
1930	De novo assembly and characterization of root transcriptome in two distinct morphotypes of vetiver, Chrysopogon zizaniodes (L.) Roberty. Scientific Reports, 2015, 5, 18630.	1.6	18
1931	Transcriptome analysis identifies genes involved in adventitious branches formation of Gracilaria lichenoides in vitro. Scientific Reports, 2015, 5, 17099.	1.6	24
1932	The influence of simulated microgravity on the proteome of Daphnia magna. Npj Microgravity, 2015, 1, 15016.	1.9	14
1933	Direct production of XYDMYâˆ' sex reversal female medaka (Oryzias latipes) by embryo microinjection of TALENs. Scientific Reports, 2015, 5, 14057.	1.6	18
1934	Analysis of key genes of jasmonic acid mediated signal pathway for defense against insect damages by comparative transcriptome sequencing. Scientific Reports, 2015, 5, 16500.	1.6	35
1935	Computational discovery of small open reading frames in Bacillus lehensis. AIP Conference Proceedings, 2015, , .	0.3	0
1936	Identification of mycoparasitism-related genes in Clonostachys rosea 67-1 active against Sclerotinia sclerotiorum. Scientific Reports, 2015, 5, 18169.	1.6	41
1937	Transcriptomic variation of hepatopancreas reveals the energy metabolism and biological processes associated with molting in Chinese mitten crab, Eriocheir sinensis. Scientific Reports, 2015, 5, 14015.	1.6	91
1938	Identification and characterization of secreted proteins in Eimeria tenella. AIP Conference Proceedings, 2015, , .	0.3	0
1939	Lysosome-associated membrane glycoprotein (LAMP) â€" preliminary study on a hidden antigen target for vaccination against schistosomiasis. Scientific Reports, 2015, 5, 15069.	1.6	10
1940	Lactococcus garvieae: a small bacteria and a big data world. Health Information Science and Systems, 2015, 3, S5.	3.4	8
1941	The fate of recent duplicated genes following a fourth-round whole genome duplication in a tetraploid fish, common carp (Cyprinus carpio). Scientific Reports, 2015, 5, 8199.	1.6	60
1942	Construction of a high-density linkage map and fine mapping of QTL for growth in Asian seabass. Scientific Reports, 2015, 5, 16358.	1.6	96
1943	Red clover (Trifolium pratense L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394.	1.6	136
1944	TRANSCRIPTIONAL PROFILE ANALYSIS OF YOUNG AND MATURE LEAVES OF CITRUS TREES ACCLIMATED TO SALINITY. Acta Horticulturae, 2015, , 1359-1369.	0.1	0

#	Article	IF	Citations
1945	Ecological transcriptomics â€“ a nonâ€lethal sampling approach for endangered fire salamanders. Methods in Ecology and Evolution, 2015, 6, 1417-1425.	2.2	16
1946	Gossypium barbadense genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. Scientific Reports, 2015, 5, 14139.	1.6	271
1947	Identification of small open reading frames in the Glaciozyma antarctica genome. AIP Conference Proceedings, 2015, , .	0.3	2
1948	Transcriptome analysis of human OXR1 depleted cells reveals its role in regulating the p53 signaling pathway. Scientific Reports, 2015, 5, 17409.	1.6	43
1949	Genome-wide expression analysis offers new insights into the origin and evolution of Physcomitrella patens stress response. Scientific Reports, 2015, 5, 17434.	1.6	54
1950	An acorn squash (Cucurbita pepo ssp. ovifera) fruit and seed transcriptome as a resource for the study of fruit traits in Cucurbita. Horticulture Research, 2015, 2, 14070.	2.9	32
1951	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. Scientific Reports, 2015, 5, 13517.	1.6	144
1952	Genome Sequence and Architecture of the Tobacco Downy Mildew Pathogen <i>Peronospora tabacina</i>. Molecular Plant-Microbe Interactions, 2015, 28, 1198-1215.	1.4	70
1953	Parallel molecular routes to cold adaptation in eight genera of New Zealand stick insects. Scientific Reports, 2015, 5, 13965.	1.6	45
1954	Redefining metamorphosis in spiny lobsters: molecular analysis of the phyllosoma to puerulus transition in Sagmariasus verreauxi. Scientific Reports, 2015, 5, 13537.	1.6	43
1955	Neuropeptides in the cerebral ganglia of the mud crab, Scylla paramamosain: transcriptomic analysis and expression profiles during vitellogenesis. Scientific Reports, 2015, 5, 17055.	1.6	96
1956	Regulatory RNA at the root of animals: dynamic expression of developmental lincRNAs in the calcisponge <i>Sycon ciliatum</i>. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151746.	1.2	16
1957	Transcriptomes of parents identify parenting strategies and sexual conflict in a subsocial beetle. Nature Communications, 2015, 6, 8449.	5.8	78
1958	Global transcriptional and miRNA insights into bases of heterosis in hybridization of Cyprinidae. Scientific Reports, 2015, 5, 13847.	1.6	25
1959	Revisiting the reference genomes of human pathogenic Cryptosporidium species: reannotation of C. parvum Iowa and a new C. hominis reference. Scientific Reports, 2015, 5, 16324.	1.6	44
1960	TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. Evolutionary Bioinformatics, 2015, 11, EBO.S23873.	0.6	37
1961	RNA-seq Reveals Complicated Transcriptomic Responses to Drought Stress in a Nonmodel Tropic Plant, <i>Bombax ceiba</i> L.. Evolutionary Bioinformatics, 2015, 11s1, EBO.S20620.	0.6	14
1962	Comparative transcriptomics of Central Asian Vitis vinifera accessions reveals distinct defense strategies against powdery mildew. Horticulture Research, 2015, 2, 15037.	2.9	47

#	ARTICLE	IF	CITATIONS
1963	The Cipher Code of Simple Sequence Repeats in â€œVampire Pathogensâ€. Scientific Reports, 2015, 5, 12441.	1.6	0
1964	Spliced leader RNA trans-splicing discovered in copepods. Scientific Reports, 2015, 5, 17411.	1.6	9
1965	Honey bee microRNAs respond to infection by the microsporidian parasite Nosema ceranae. Scientific Reports, 2015, 5, 17494.	1.6	18
1966	De novo transcriptome sequencing and comprehensive analysis of the drought-responsive genes in the desert plant Cynanchum komarovii. BMC Genomics, 2015, 16, 753.	1.2	37
1967	Genome analyses of the sunflower pathogen Plasmopara halstedii provide insights into effector evolution in downy mildews and Phytophthora. BMC Genomics, 2015, 16, 741.	1.2	135
1968	De novo transcriptome sequencing and analysis of Coccinella septempunctata L. in non-diapause, diapause and diapause-terminated states to identify diapause-associated genes. BMC Genomics, 2015, 16, 1086.	1.2	43
1969	Secretome profiling of Cryptococcus neoformans reveals regulation of a subset of virulence-associated proteins and potential biomarkers by protein kinase A. BMC Microbiology, 2015, 15, 206.	1.3	47
1970	AlignWise: a tool for identifying protein-coding sequence and correcting frame-shifts. BMC Bioinformatics, 2015, 16, 376.	1.2	18
1971	Transcriptome sequencing and analysis of major genes involved in calcium signaling pathways in pear plants (Pyrus calleryana Decne.). BMC Genomics, 2015, 16, 738.	1.2	19
1972	Analysis of the agrotis segetum pheromone gland transcriptome in the light of Sex pheromone biosynthesis. BMC Genomics, 2015, 16, 711.	1.2	43
1973	Additive transcriptomic variation associated with reproductive traits suggest local adaptation in a recently settled population of the Pacific oyster, Crassostrea gigas. BMC Genomics, 2015, 16, 808.	1.2	15
1974	Transcriptome profiling of soybean (Glycine max) roots challenged with pathogenic and non-pathogenic isolates of Fusarium oxysporum. BMC Genomics, 2015, 16, 1089.	1.2	82
1975	An integrative analysis of post-translational histone modifications in the marine diatom Phaeodactylum tricornutum. Genome Biology, 2015, 16, 102.	3.8	107
1976	A photorespiratory bypass increases plant growth and seed yield in biofuel crop Camelina sativa. Biotechnology for Biofuels, 2015, 8, 175.	6.2	94
1977	Characterization of early transcriptional responses to cadmium in the root and leaf of Cd-resistant Salix matsudana Koidz. BMC Genomics, 2015, 16, 705.	1.2	52
1978	Substantial genome synteny preservation among woody angiosperm species: comparative genomics of Chinese chestnut (Castanea mollissima) and plant reference genomes. BMC Genomics, 2015, 16, 744.	1.2	33
1979	Genome analysis of Daldinia eschscholtzii strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. BMC Genomics, 2015, 16, 966.	1.2	16
1980	Selection processes in simple sequence repeats suggest a correlation with their genomic location: insights from a fungal model system. BMC Genomics, 2015, 16, 1107.	1.2	21

#	ARTICLE	IF	CITATIONS
1981	Metatranscriptomics reveals metabolic adaptation and induction of virulence factors by Haemophilus parasuis during lung infection. Veterinary Research, 2015, 46, 102.	1.1	13
1982	Ecoâ€genomic analysis of the poleward range expansion of the wasp spider <i><scp>A</scp>rgiope bruennichi</i> shows rapid adaptation and genomic admixture. Global Change Biology, 2015, 21, 4320-4332.	4.2	54
1983	Adaptation of a polyphagous herbivore to a novel host plant extensively shapes the transcriptome of herbivore and host. Molecular Ecology, 2015, 24, 4647-4663.	2.0	131
1984	Draft Genome Sequence and Gene Annotation of <i>Stemphylium lycopersici</i> Strain CIDEFI-216. Genome Announcements, 2015, 3, .	0.8	18
1985	Saprophytic and pathogenic fungi in the Ceratocystidaceae differ in their ability to metabolize plant-derived sucrose. BMC Evolutionary Biology, 2015, 15, 273.	3.2	47
1986	Comparative in silico analysis of SSRs in coding regions of high confidence predicted genes in Norway spruce (Picea abies) and Loblolly pine (Pinus taeda). BMC Genetics, 2015, 16, 149.	2.7	3
1987	RNA-Seq in Mytilus galloprovincialis: comparative transcriptomics and expression profiles among different tissues. BMC Genomics, 2015, 16, 728.	1.2	86
1988	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
1989	Identification of four functionally important microRNA families with contrasting differential expression profiles between drought-tolerant and susceptible rice leaf at vegetative stage. BMC Genomics, 2015, 16, 692.	1.2	85
1990	Transcriptome analysis of the white pine blister rust pathogen Cronartium ribicola: de novo assembly, expression profiling, and identification of candidate effectors. BMC Genomics, 2015, 16, 678.	1.2	42
1991	Gonadal transcriptomics elucidate patterns of adaptive evolution within marine rockfishes (Sebastes). BMC Genomics, 2015, 16, 656.	1.2	8
1992	Asymmetric somatic hybridization induces point mutations and indels in wheat. BMC Genomics, 2015, 16, 807.	1.2	16
1993	Integration of Ixodes ricinus genome sequencing with transcriptome and proteome annotation of the naÃ¯ve midgut. BMC Genomics, 2015, 16, 871.	1.2	41
1994	Transcriptome profiling of wheat glumes in wild emmer, hulled landraces and modern cultivars. BMC Genomics, 2015, 16, 777.	1.2	16
1995	Comparative RNA seq analysis of the New Zealand glowworm Arachnocampa luminosa reveals bioluminescence-related genes. BMC Genomics, 2015, 16, 825.	1.2	18
1996	Large-scale identification of wheat genes resistant to cereal cyst nematode Heterodera avenae using comparative transcriptomic analysis. BMC Genomics, 2015, 16, 801.	1.2	39
1997	In silico hybridization enables transcriptomic illumination of the nature and evolution of Myxozoa. BMC Genomics, 2015, 16, 840.	1.2	22
1998	De novo transcriptome sequencing in Bixa orellana to identify genes involved in methylerythritol phosphate, carotenoid and bixin biosynthesis. BMC Genomics, 2015, 16, 877.	1.2	45

#	ARTICLE	IF	CITATIONS
1999	Transcriptional response to sulfide in the Echiuran Worm Urechis unicinctus by digital gene expression analysis. BMC Genomics, 2015, 16, 829.	1.2	16
2000	Transcriptome profiling reveals that feeding wild zooplankton to larval Atlantic cod (Gadus morhua) influences suites of genes involved in oxidation-reduction, mitosis, and selenium homeostasis. BMC Genomics, 2015, 16, 1016.	1.2	25
2001	Complete depletion of primordial germ cells in an All-female fish leads to Sex-biased gene expression alteration and sterile All-male occurrence. BMC Genomics, 2015, 16, 971.	1.2	44
2002	RNA-seq reveals differentially expressed genes of rice (Oryza sativa) spikelet in response to temperature interacting with nitrogen at meiosis stage. BMC Genomics, 2015, 16, 959.	1.2	27
2003	Transcription analysis of neonicotinoid resistance in Mediterranean (MED) populations of B. tabaci reveal novel cytochrome P450s, but no nAChR mutations associated with the phenotype. BMC Genomics, 2015, 16, 939.	1.2	59
2004	Comparative transcriptome analysis of lufenuron-resistant and susceptible strains of Spodoptera frugiperda (Lepidoptera: Noctuidae). BMC Genomics, 2015, 16, 985.	1.2	52
2005	De novo transcriptome sequence and identification of major bast-related genes involved in cellulose biosynthesis in jute (Corchorus capsularis L.). BMC Genomics, 2015, 16, 1062.	1.2	30
2006	Implications of ethylene biosynthesis and signaling in soybean drought stress tolerance. BMC Plant Biology, 2015, 15, 213.	1.6	110
2007	Horizontal gene transfer in bdelloid rotifers is ancient, ongoing and more frequent in species from desiccating habitats. BMC Biology, 2015, 13, 90.	1.7	76
2008	Deciphering the signaling mechanisms of the plant cell wall degradation machinery in Aspergillus oryzae. BMC Systems Biology, 2015, 9, 77.	3.0	5
2009	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200.	3.8	77
2010	Ixodes scapularis and Ixodes ricinus tick cell lines respond to infection with tick-borne encephalitis virus: transcriptomic and proteomic analysis. Parasites and Vectors, 2015, 8, 599.	1.0	71
2011	Transcriptomic analysis of the host response to an iridovirus infection in Chinese giant salamander, Andrias davidianus. Veterinary Research, 2015, 46, 136.	1.1	31
2012	Genome sequence of a native-feather degrading extremely thermophilic Eubacterium, Fervidobacterium islandicum AW-1. Standards in Genomic Sciences, 2015, 10, 71.	1.5	19
2013	Bacteriophage therapy for membrane biofouling in membrane bioreactors and antibioticâ€resistant bacterial biofilms. Biotechnology and Bioengineering, 2015, 112, 1644-1654.	1.7	65
2014	Reproductive workers show queenlike gene expression in an intermediately eusocial insect, the buffâ€tailed bumble bee <i>Bombus terrestris</i>. Molecular Ecology, 2015, 24, 3043-3063.	2.0	67
2015	Oviposition but Not Sex Allocation Is Associated with Transcriptomic Changes in Females of the Parasitoid Wasp Nasonia vitripennis. G3: Genes, Genomes, Genetics, 2015, 5, 2885-2892.	0.8	11
2016	Genome-wide Snapshot of Chromatin Regulators and States in Xenopus Embryos by ChIP-Seq. Journal of Visualized Experiments, 2015, , .	0.2	13

#	ARTICLE	IF	CITATIONS
2017	Transcriptomic differences between day and night in <i>Acropora millepora</i> provide new insights into metabolite exchange and lightâ€enhanced calcification in corals. Molecular Ecology, 2015, 24, 4489-4504.	2.0	51
2018	A population genomic scan in <i>Chorthippus</i> grasshoppers unveils previously unknown phenotypic divergence. Molecular Ecology, 2015, 24, 3918-3930.	2.0	25
2019	Interclonal proteomic responses to predator exposure in <i>Daphnia magna</i> may depend on predator composition of habitats. Molecular Ecology, 2015, 24, 3901-3917.	2.0	21
2020	Evolutionary suppression of erythropoiesis via the modulation of <scp>TGF</scp>â€Î² signalling in an Antarctic icefish. Molecular Ecology, 2015, 24, 4664-4678.	2.0	27
2021	Unique evolutionary trajectories in repeated adaptation to hydrogen sulphideâ€toxic habitats of a neotropical fish (<i>Poecilia mexicana</i>). Molecular Ecology, 2015, 24, 5446-5459.	2.0	49
2022	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. Plant Journal, 2015, 83, 189-212.	2.8	200
2023	Genome analyses suggest the presence of polyploidy and recent humanâ€driven expansions in eight global populations of the honeybee pathogen <scp><i>N</i></scp><i>osema ceranae</i>. Environmental Microbiology, 2015, 17, 4443-4458.	1.8	66
2024	The transcriptome-wide effects of exposure to a pyrethroid pesticide on the Critically Endangered delta smelt Hypomesus transpacificus. Endangered Species Research, 2015, 28, 43-60.	1.2	29
2025	Patterns of Wnt signaling in the life cycle of Podocoryna carnea and its implications for medusae evolution in Hydrozoa (Cnidaria). Evolution & Development, 2015, 17, 325-336.	1.1	24
2026	PTGBase: an integrated database to study tandem duplicated genes in plants. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	46
2027	Draft Genome Sequence of the Fungus <i>Penicillium brasilianum</i> MG11. Genome Announcements, 2015, 3, .	0.8	11
2028	Proteome of monoclonal antibody-purified haustoria from<i>Puccinia triticina</i>Race-1. Proteomics, 2015, 15, 1307-1315.	1.3	29
2029	Linking transcriptional responses to organismal toleranceÂreveals mechanisms of thermal sensitivity inÂaÂmesothermal endangered fish. Molecular Ecology, 2015, 24, 4960-4981.	2.0	51
2030	Environmental adaptation in Chinook salmon (<i>Oncorhynchus tshawytscha</i>) throughout their North American range. Molecular Ecology, 2015, 24, 5573-5595.	2.0	94
2031	Molecular Differentiation of Gender in Buffalograss. Crop Science, 2015, 55, 1827-1833.	0.8	1
2032	paSNPg: A GBS-Based Pipeline for Protein-Associated SNP Discovery and Genotyping in Non-Model Species. Journal of Proteomics and Bioinformatics, 2015, 08, .	0.4	1
2033	Quantitative assessment of protein function prediction programs. Genetics and Molecular Research, 2015, 14, 17555-17566.	0.3	2
2034	Identification and Expression Analysis of Putative Chemosensory Receptor Genes in <i>Microplitis mediator</i> by Antennal Transcriptome Screening. International Journal of Biological Sciences, 2015, 11, 737-751.	2.6	59

#	Article	IF	Citations
2035	Glycoproteomic Analysis of Human Hepatoblastoma Cell Lines Using Glycopeptide Capture and Mass Spectrometry. Journal of Glycomics & Lipidomics, 2015, 05, .	0.4	1
2036	Transcriptome Sequencing of Lima Bean (Phaseolus lunatus) to Identify Putative Positive Selection in Phaseolus and Legumes. International Journal of Molecular Sciences, 2015, 16, 15172-15187.	1.8	13
2037	Transcriptome Analysis and Discovery of Genes Involved in Immune Pathways from Coelomocytes of Sea Cucumber (Apostichopus japonicus) after Vibrio splendidus Challenge. International Journal of Molecular Sciences, 2015, 16, 16347-16377.	1.8	50
2038	Analysis of alterations to the transcriptome of Loquat (Eriobotrya japonica Lindl.) under low temperature stress via de novo sequencing. Genetics and Molecular Research, 2015, 14, 9423-9436.	0.3	11
2039	EvaluaciÃ³n de las herramientas de secuenciaciÃ³n masiva (NGS) para identificar genes asociados con tolerancia al estrÃ©s hÃdrico en caÃ±a de azÃºcar. Acta Agronomica, 2015, 64, .	0.0	2
2040	In silico characterization of hypothetical proteins from Paracoccidioides lutzii. Genetics and Molecular Research, 2015, 14, 17416-17425.	0.3	15
2041	De novo assembly and characterization of the root transcriptome and development of simple sequence repeat markers in Paphiopedilum concolor. Genetics and Molecular Research, 2015, 14, 6189-6201.	0.3	9
2042	Transcriptional Profiling Reveals Differential Gene Expression of Amur Ide (Leuciscus waleckii) during Spawning Migration. International Journal of Molecular Sciences, 2015, 16, 13959-13972.	1.8	13
2043	Analysis of upland cotton (Gossypium hirsutum) response to Verticillium dahliae inoculation by transcriptome sequencing. Genetics and Molecular Research, 2015, 14, 13120-13130.	0.3	9
2044	Illumina-Based <i>De Novo</i> Transcriptome Analysis and Identifications of Genes Involved in the Monolignol Biosynthesis Pathway in <i>Acacia koa</i>. Current Research in Bioinformatics, 2015, 4, 7-27.	0.1	4
2045	De novo assembly and characterization of skin transcriptome using RNAseq in sheep (Ovis aries). Genetics and Molecular Research, 2015, 14, 1371-1384.	0.3	14
2046	Expression of drought tolerance genes in tropical upland rice cultivars (Oryza sativa). Genetics and Molecular Research, 2015, 14, 8181-8200.	0.3	31
2047	De novo assembly, functional annotation, and marker development of Asian pear (Pyrus pyrifolia) fruit transcriptome through massively parallel sequencing. Genetics and Molecular Research, 2015, 14, 18344-18355.	0.3	1
2048	Deep sequencing revealed molecular signature of horizontal gene transfer of plant like transcripts inÂthe mosquito Anopheles culicifacies: an evolutionary puzzle. F1000Research, 2015, 4, 1523.	0.8	9
2049	Differentially expressed genes in the pituitary of the Amazonian fish Arapaima gigas. International Journal of Fisheries and Aquaculture, 2015, 7, 132-141.	1.1	5
2050	Single nucleotide polymorphism discovery through Illumina-based transcriptome sequencing and mapping in lentil. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2015, 39, 470-488.	0.8	23
2051	A Longâ€Read Transcriptome Assembly of Cotton (Gossypium hirsutum L.) and Intraspecific Single Nucleotide Polymorphism Discovery. Plant Genome, 2015, 8, eplantgenome2014.10.0068.	1.6	12
2052	Transcriptome Changes during the Life Cycle of the Red Sponge, Mycale phyllophila (Porifera,) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	14

#	ARTICLE	IF	CITATIONS
2053	De Novo Characterization of Flower Bud Transcriptomes and the Development of EST-SSR Markers for the Endangered Tree Tapiscia sinensis. International Journal of Molecular Sciences, 2015, 16, 12855-12870.	1.8	28
2054	Molecular Mechanisms Underlying Hull-Caryopsis Adhesion/Separation Revealed by Comparative Transcriptomic Analysis of Covered/Naked Barley (Hordeum vulgare L.). International Journal of Molecular Sciences, 2015, 16, 14181-14193.	1.8	26
2055	Global Reprogramming of Transcription in Chinese Fir (Cunninghamia lanceolata) during Progressive Drought Stress and after Rewatering. International Journal of Molecular Sciences, 2015, 16, 15194-15219.	1.8	11
2056	Comparative Analysis of the Brassica napus Root and Leaf Transcript Profiling in Response to Drought Stress. International Journal of Molecular Sciences, 2015, 16, 18752-18777.	1.8	48
2057	Gene Expression Variations of Redâ€"White Skin Coloration in Common Carp (Cyprinus carpio). International Journal of Molecular Sciences, 2015, 16, 21310-21329.	1.8	36
2058	Identification of Ramie Genes in Response to Pratylenchus coffeae Infection Challenge by Digital Gene Expression Analysis. International Journal of Molecular Sciences, 2015, 16, 21989-22007.	1.8	26
2059	Transcriptome Analysis and Identification of Differentially Expressed Transcripts of Immune-Related Genes in Spleen of Gosling and Adult Goose. International Journal of Molecular Sciences, 2015, 16, 22904-22926.	1.8	19
2060	Quantitative Proteomics Analysis of Herbaceous Peony in Response to Paclobutrazol Inhibition of Lateral Branching. International Journal of Molecular Sciences, 2015, 16, 24332-24352.	1.8	9
2061	Morphological Characters and Transcriptome Profiles Associated with Black Skin and Red Skin in Crimson Snapper (Lutjanus erythropterus). International Journal of Molecular Sciences, 2015, 16, 26991-27004.	1.8	21
2062	De Novo Transcriptome Sequencing Analysis of cDNA Library and Large-Scale Unigene Assembly in Japanese Red Pine (Pinus densiflora). International Journal of Molecular Sciences, 2015, 16, 29047-29059.	1.8	22
2063	De Novo Transcriptome Sequencing of Oryza officinalis Wall ex Watt to Identify Disease-Resistance Genes. International Journal of Molecular Sciences, 2015, 16, 29482-29495.	1.8	21
2064	Transcriptome Characterization for Non-Model Endangered Lycaenids, Protantigius superans and Spindasis takanosis, Using Illumina HiSeq 2500 Sequencing. International Journal of Molecular Sciences, 2015, 16, 29948-29970.	1.8	13
2065	Development and Characterization of Transcription Factor Gene-Derived Microsatellite (TFGM) Markers in Medicago truncatula and Their Transferability in Leguminous and Non-Leguminous Species. Molecules, 2015, 20, 8759-8771.	1.7	24
2066	Characterization of Global Transcriptome Using Illumina Paired-End Sequencing and Development of EST-SSR Markers in Two Species of Gynostemma (Cucurbitaceae). Molecules, 2015, 20, 21214-21231.	1.7	12
2067	Identification of candidate olfactory genes in Leptinotarsa decemlineata by antennal transcriptome analysis. Frontiers in Ecology and Evolution, 2015, 3, .	1.1	31
2068	Unravelling the genome of long chain N-acylhomoserine lactone-producing Acinetobacter sp. strain GG2 and identification of its quorum sensing synthase gene. Frontiers in Microbiology, 2015, 6, 240.	1.5	16
2069	Gene expression in the mixotrophic prymnesiophyte, Prymnesium parvum, responds to prey availability. Frontiers in Microbiology, 2015, 6, 319.	1.5	37
2070	Changes in gene expression of Prymnesium parvum induced by nitrogen and phosphorus limitation. Frontiers in Microbiology, 2015, 6, 631.	1.5	46

#	ARTICLE	IF	CITATIONS
2071	Transcriptome analysis of Enterococcus faecalis in response to alkaline stress. Frontiers in Microbiology, 2015, 6, 795.	1.5	48
2072	Systemic responses in a tolerant olive (Olea europaea L.) cultivar upon root colonization by the vascular pathogen Verticillium dahliae. Frontiers in Microbiology, 2015, 6, 928.	1.5	39
2073	Whole genome resequencing of Botrytis cinerea isolates identifies high levels of standing diversity. Frontiers in Microbiology, 2015, 6, 996.	1.5	42
2074	RNA-seq de novo Assembly Reveals Differential Gene Expression in Glossina palpalis gambiensis Infected with Trypanosoma brucei gambiense vs. Non-Infected and Self-Cured Flies. Frontiers in Microbiology, 2015, 6, 1259.	1.5	26
2075	Expression of ionotropic receptors in terrestrial hermit crab's olfactory sensory neurons. Frontiers in Cellular Neuroscience, 2014, 8, 448.	1.8	34
2076	Transcriptomic identification of chemoreceptor genes in the red palm weevil Rhynchophorus ferrugineus. Genetics and Molecular Research, 2015, 14, 7469-7480.	0.3	12
2077	Transcriptomic Response to Nitric Oxide Treatment in Larix olgensis Henry. International Journal of Molecular Sciences, 2015, 16, 28582-28597.	1.8	23
2078	Pan-Genome Analysis of Brazilian Lineage A Amoebal Mimiviruses. Viruses, 2015, 7, 3483-3499.	1.5	26
2079	A Computational Strategy to Select Optimized Protein Targets for Drug Development toward the Control of Cancer Diseases. PLoS ONE, 2015, 10, e0115054.	1.1	40
2080	De Novo Assembly of Transcriptome Sequencing in Caragana korshinskii Kom. and Characterization of EST-SSR Markers. PLoS ONE, 2015, 10, e0115805.	1.1	20
2081	Antennal Transcriptome Analysis and Comparison of Chemosensory Gene Families in Two Closely Related Noctuidae Moths, Helicoverpa armigera and H. assulta. PLoS ONE, 2015, 10, e0117054.	1.1	109
2082	An Assessment of Heavy Ion Irradiation Mutagenesis for Reverse Genetics in Wheat (Triticum aestivum) Tj ETQq1 1 0.784314 rgBT /Ove	1.1	23
2083	Physiological and Proteomic Adaptation of the Alpine Grass Stipa purpurea to a Drought Gradient. PLoS ONE, 2015, 10, e0117475.	1.1	17
2084	Sugarcane Giant Borer Transcriptome Analysis and Identification of Genes Related to Digestion. PLoS ONE, 2015, 10, e0118231.	1.1	13
2085	Transcriptomic Responses of Atlantic Salmon (Salmo salar) to Environmental Enrichment during Juvenile Rearing. PLoS ONE, 2015, 10, e0118378.	1.1	17
2086	De Novo Transcriptome Assembly of Pummelo and Molecular Marker Development. PLoS ONE, 2015, 10, e0120615.	1.1	26
2087	A New Set of ESTs from Chickpea (Cicer arietinum L.) Embryo Reveals Two Novel F-Box Genes, CarF-box_PP2 and CarF-box_LysM, with Potential Roles in Seed Development. PLoS ONE, 2015, 10, e0121100.	1.1	8
2088	Plasmodium knowlesi Genome Sequences from Clinical Isolates Reveal Extensive Genomic Dimorphism. PLoS ONE, 2015, 10, e0121303.	1.1	54

#	Article	IF	Citations
2089	Transcriptome Analysis and Gene Expression Profiling of Abortive and Developing Ovules during Fruit Development in Hazelnut. PLoS ONE, 2015, 10, e0122072.	1.1	25
2090	Analysis of Genomic Regions of Trichoderma harzianum IOC-3844 Related to Biomass Degradation. PLoS ONE, 2015, 10, e0122122.	1.1	17
2091	Binary Gene Expression Patterning of the Molt Cycle: The Case of Chitin Metabolism. PLoS ONE, 2015, 10, e0122602.	1.1	25
2092	De novo Assembly and Transcriptomic Profiling of the Grazing Response in Stipa grandis. PLoS ONE, 2015, 10, e0122641.	1.1	15
2093	Transcriptome Analysis and Its Application in Identifying Genes Associated with Fruiting Body Development in Basidiomycete Hypsizygus marmoreus. PLoS ONE, 2015, 10, e0123025.	1.1	54
2094	Genome-Wide Transcriptome and Expression Profile Analysis of Phalaenopsis during Explant Browning. PLoS ONE, 2015, 10, e0123356.	1.1	16
2095	Genome-Wide SNP Identification and Characterization in Two Soybean Cultivars with Contrasting Mungbean Yellow Mosaic India Virus Disease Resistance Traits. PLoS ONE, 2015, 10, e0123897.	1.1	34
2096	De Novo Transcriptome Assembly and Identification of Gene Candidates for Rapid Evolution of Soil Al Tolerance in Anthoxanthum odoratum at the Long-Term Park Grass Experiment. PLoS ONE, 2015, 10, e0124424.	1.1	11
2097	Effect of Embryo Vitrification on Rabbit Foetal Placenta Proteome during Pregnancy. PLoS ONE, 2015, 10, e0125157.	1.1	9
2098	Sequence Analysis of Insecticide Action and Detoxification-Related Genes in the Insect Pest Natural Enemy Pardosa pseudoannulata. PLoS ONE, 2015, 10, e0125242.	1.1	29
2099	Transcriptome-Wide Identification of miRNAs and Their Targets from Typha angustifolia by RNA-Seq and Their Response to Cadmium Stress. PLoS ONE, 2015, 10, e0125462.	1.1	20
2100	Novel Detection of Insecticide Resistance Related P450 Genes and Transcriptome Analysis of the Hemimetabolous Pest Erthesina fullo (Thunberg) (Hemiptera: Heteroptera). PLoS ONE, 2015, 10, e0125970.	1.1	3
2101	Comparative Transcriptome and iTRAQ Proteome Analyses of Citrus Root Responses to Candidatus Liberibacter asiaticus Infection. PLoS ONE, 2015, 10, e0126973.	1.1	70
2102	Whole Transcriptome Analysis Using Next-Generation Sequencing of Sterile-Cultured Eisenia andrei for Immune System Research. PLoS ONE, 2015, 10, e0118587.	1.1	6
2103	Transcriptome Sequencing of Codonopsis pilosula and Identification of Candidate Genes Involved in Polysaccharide Biosynthesis. PLoS ONE, 2015, 10, e0117342.	1.1	35
2104	Functional Marker Detection and Analysis on a Comprehensive Transcriptome of Large Yellow Croaker by Next Generation Sequencing. PLoS ONE, 2015, 10, e0124432.	1.1	38
2105	Genome Sequence and Transcriptome Analyses of Chrysochromulina tobin: Metabolic Tools for Enhanced Algal Fitness in the Prominent Order Prymnesiales (Haptophyceae). PLoS Genetics, 2015, 11, e1005469.	1.5	58
2106	Protein Composition of Infectious Spores Reveals Novel Sexual Development and Germination Factors in Cryptococcus. PLoS Genetics, 2015, 11, e1005490.	1.5	25

#	ARTICLE	IF	CITATIONS
2107	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	1.5	57
2108	Fungal Infection Induces Sex-Specific Transcriptional Changes and Alters Sexual Dimorphism in the Dioecious Plant Silene latifolia. PLoS Genetics, 2015, 11, e1005536.	1.5	24
2109	Pathways of Amino Acid Degradation in Nilaparvata lugens (StÃ¥l) with Special Reference to Lysine-Ketoglutarate Reductase/Saccharopine Dehydrogenase (LKR/SDH). PLoS ONE, 2015, 10, e0127789.	1.1	18
2110	A Novel Chitin Binding Crayfish Molar Tooth Protein with Elasticity Properties. PLoS ONE, 2015, 10, e0127871.	1.1	9
2111	Transcriptome Characterization of Cymbidium sinense 'Dharma' Using 454 Pyrosequencing and Its Application in the Identification of Genes Associated with Leaf Color Variation. PLoS ONE, 2015, 10, e0128592.	1.1	34
2112	De novo Assembly, Characterization of Immature Seed Transcriptome and Development of Genic-SSR Markers in Black Gram [Vigna mungo (L.) Hepper]. PLoS ONE, 2015, 10, e0128748.	1.1	41
2113	Discovery of Chemosensory Genes in the Oriental Fruit Fly, Bactrocera dorsalis. PLoS ONE, 2015, 10, e0129794.	1.1	42
2114	The Differential Expression of Immune Genes between Water Buffalo and Yellow Cattle Determines Species-Specific Susceptibility to Schistosoma japonicum Infection. PLoS ONE, 2015, 10, e0130344.	1.1	10
2115	In-Depth Transcriptome Sequencing of Mexican Lime Trees Infected with Candidatus Phytoplasma aurantifolia. PLoS ONE, 2015, 10, e0130425.	1.1	39
2116	Global Transcriptome Profiles of 'Meyer' Zoysiagrass in Response to Cold Stress. PLoS ONE, 2015, 10, e0131153.	1.1	30
2117	Transcriptional Responses Associated with Virulence and Defence in the Interaction between Heterobasidion annosum s.s. and Norway Spruce. PLoS ONE, 2015, 10, e0131182.	1.1	24
2118	Transcriptome and Molecular Pathway Analysis of the Hepatopancreas in the Pacific White Shrimp Litopenaeus vannamei under Chronic Low-Salinity Stress. PLoS ONE, 2015, 10, e0131503.	1.1	85
2119	Genome Wide Distributions and Functional Characterization of Copy Number Variations between Chinese and Western Pigs. PLoS ONE, 2015, 10, e0131522.	1.1	47
2120	Transcriptome Analysis of Beta macrocarpa and Identification of Differentially Expressed Transcripts in Response to Beet Necrotic Yellow Vein Virus Infection. PLoS ONE, 2015, 10, e0132277.	1.1	11
2121	De Novo Characterization of the Mung Bean Transcriptome and Transcriptomic Analysis of Adventitious Rooting in Seedlings Using RNA-Seq. PLoS ONE, 2015, 10, e0132969.	1.1	31
2122	De Novo Assembly and Annotation of the Chinese Chive (Allium tuberosum Rottler ex Spr.) Transcriptome Using the Illumina Platform. PLoS ONE, 2015, 10, e0133312.	1.1	23
2123	Transcriptomic Profiling Reveals Complex Molecular Regulation in Cotton Genic Male Sterile Mutant Yu98-8A. PLoS ONE, 2015, 10, e0133425.	1.1	8
2124	Transcriptomics Analysis of Crassostrea hongkongensis for the Discovery of Reproduction-Related Genes. PLoS ONE, 2015, 10, e0134280.	1.1	69

#	ARTICLE	IF	CITATIONS
2125	Comparative Transcriptome Analysis of Differentially Expressed Genes and Signaling Pathways between XY and YY Testis in Yellow Catfish. PLoS ONE, 2015, 10, e0134626.	1.1	23
2126	Transcriptome Analysis of the Emerald Ash Borer (EAB), Agrilus planipennis: De Novo Assembly, Functional Annotation and Comparative Analysis. PLoS ONE, 2015, 10, e0134824.	1.1	9
2127	Assembly and Analysis of Differential Transcriptome Responses of Hevea brasiliensis on Interaction with Microcyclus ulei. PLoS ONE, 2015, 10, e0134837.	1.1	18
2128	De Novo Transcriptome Assembly and Comparative Analysis Elucidate Complicated Mechanism Regulating Astragalus chrysochlorus Response to Selenium Stimuli. PLoS ONE, 2015, 10, e0135677.	1.1	16
2129	Virus-Induced Gene Silencing Using Tobacco Rattle Virus as a Tool to Study the Interaction between Nicotiana attenuata and Rhizophagus irregularis. PLoS ONE, 2015, 10, e0136234.	1.1	6
2130	Genomic and Phenomic Study of Mammary Pathogenic Escherichia coli. PLoS ONE, 2015, 10, e0136387.	1.1	46
2131	Characterization of the Transcriptome of the Xerophyte Ammopiptanthus mongolicus Leaves under Drought Stress by 454 Pyrosequencing. PLoS ONE, 2015, 10, e0136495.	1.1	8
2132	Time-Course RNA-Seq Analysis Reveals Transcriptional Changes in Rice Plants Triggered by Rice stripe virus Infection. PLoS ONE, 2015, 10, e0136736.	1.1	26
2133	Transcriptome Analysis Reveals the Mechanism Underlying the Production of a High Quantity of Chlorogenic Acid in Young Leaves of Lonicera macranthoides Hand.-Mazz. PLoS ONE, 2015, 10, e0137212.	1.1	26
2134	Transcriptome Sequencing, De Novo Assembly and Differential Gene Expression Analysis of the Early Development of Acipenser baeri. PLoS ONE, 2015, 10, e0137450.	1.1	15
2135	Transcriptome Analysis of Poplar during Leaf Spot Infection with Sphaerulina spp.. PLoS ONE, 2015, 10, e0138162.	1.1	29
2136	Differential microRNA Analysis of Glandular Trichomes and Young Leaves in Xanthium strumarium L. Reveals Their Putative Roles in Regulating Terpenoid Biosynthesis. PLoS ONE, 2015, 10, e0139002.	1.1	59
2137	The Effects of Synthetic Estrogen Exposure on the Sexually Dimorphic Liver Transcriptome of the Sex-Role-Reversed Gulf Pipefish. PLoS ONE, 2015, 10, e0139401.	1.1	15
2138	Comparative Transcriptome Analysis of the Less-Dormant Taiwanese Pear and the Dormant Japanese Pear during Winter Season. PLoS ONE, 2015, 10, e0139595.	1.1	20
2139	Phylogeny of Morella rubra and Its Relatives (Myricaceae) and Genetic Resources of Chinese Bayberry Using RAD Sequencing. PLoS ONE, 2015, 10, e0139840.	1.1	18
2140	Identification and Expression Profiles of Sex Pheromone Biosynthesis and Transport Related Genes in Spodoptera litura. PLoS ONE, 2015, 10, e0140019.	1.1	46
2141	A Transcriptomic Analysis of Cave, Surface, and Hybrid Isopod Crustaceans of the Species Asellus aquaticus. PLoS ONE, 2015, 10, e0140484.	1.1	24
2142	RNA-Seq Based Identification of Candidate Parasitism Genes of Cereal Cyst Nematode (Heterodera) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	20

#	ARTICLE	IF	CITATIONS
2143	Whole-Genome Sequencing and Comparative Genome Analysis of Bacillus subtilis Strains Isolated from Non-Salted Fermented Soybean Foods. PLoS ONE, 2015, 10, e0141369.	1.1	32
2144	Digital Gene Expression Analysis Based on De Novo Transcriptome Assembly Reveals New Genes Associated with Floral Organ Differentiation of the Orchid Plant Cymbidium ensifolium. PLoS ONE, 2015, 10, e0142434.	1.1	12
2145	Identification of Putative Nuclear Receptors and Steroidogenic Enzymes in Murray-Darling Rainbowfish (Melanotaenia fluviatilis) Using RNA-Seq and De Novo Transcriptome Assembly. PLoS ONE, 2015, 10, e0142636.	1.1	2
2146	Analysis of Pigeon (Columba) Ovary Transcriptomes to Identify Genes Involved in Blue Light Regulation. PLoS ONE, 2015, 10, e0143568.	1.1	6
2147	Transcript Quantification by RNA-Seq Reveals Differentially Expressed Genes in the Red and Yellow Fruits of Fragaria vesca. PLoS ONE, 2015, 10, e0144356.	1.1	46
2148	Comparison between the Amount of Environmental Change and the Amount of Transcriptome Change. PLoS ONE, 2015, 10, e0144822.	1.1	15
2149	Comparative Transcriptome Analysis in the Hepatopancreas Tissue of Pacific White Shrimp Litopenaeus vannamei Fed Different Lipid Sources at Low Salinity. PLoS ONE, 2015, 10, e0144889.	1.1	23
2150	Novel Essential Role of Ethanol Oxidation Genes at Low Temperature Revealed by Transcriptome Analysis in the Antarctic Bacterium Pseudomonas extremaustralis. PLoS ONE, 2015, 10, e0145353.	1.1	45
2151	De Novo Assembly of Coding Sequences of the Mangrove Palm (Nypa fruticans) Using RNA-Seq and Discovery of Whole-Genome Duplications in the Ancestor of Palms. PLoS ONE, 2015, 10, e0145385.	1.1	27
2152	In Silico Comparative Transcriptome Analysis of Two Color Morphs of the Common Coral Trout (Plectropomus Leopardus). PLoS ONE, 2015, 10, e0145868.	1.1	20
2153	Development and Validation of EST-SSR Markers from the Transcriptome of Adzuki Bean (Vigna) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.1	61
2154	Sequencing, de novo assembly and comparative analysis of Raphanus sativus transcriptome. Frontiers in Plant Science, 2015, 6, 198.	1.7	25
2155	De novo assembly of a genome-wide transcriptome map of Vicia faba (L.) for transfer cell research. Frontiers in Plant Science, 2015, 6, 217.	1.7	25
2156	Genome-wide association mapping unravels the genetic control of seed germination and vigor in Brassica napus. Frontiers in Plant Science, 2015, 6, 221.	1.7	150
2157	Structure, expression profile and phylogenetic inference of chalcone isomerase-like genes from the narrow-leafed lupin (Lupinus angustifolius L.) genome. Frontiers in Plant Science, 2015, 6, 268.	1.7	32
2158	Garlic (Allium sativum L.) fertility: transcriptome and proteome analyses provide insight into flower and pollen development. Frontiers in Plant Science, 2015, 6, 271.	1.7	47
2159	An improved fruit transcriptome and the identification of the candidate genes involved in fruit abscission induced by carbohydrate stress in litchi. Frontiers in Plant Science, 2015, 6, 439.	1.7	42
2160	Digital gene expression analysis of male and female bud transition in Metasequoia reveals high activity of MADS-box transcription factors and hormone-mediated sugar pathways. Frontiers in Plant Science, 2015, 6, 467.	1.7	8

#	Article	IF	Citations
2161	The role of proteomics in progressing insights into plant secondary metabolism. Frontiers in Plant Science, 2015, 6, 504.	1.7	30
2162	Identification of novel drought-tolerant-associated SNPs in common bean (Phaseolus vulgaris). Frontiers in Plant Science, 2015, 6, 546.	1.7	51
2163	Proteomic analysis and candidate allergenic proteins in Populus deltoides CL. â€œ2KEN8â€•mature pollen. Frontiers in Plant Science, 2015, 6, 548.	1.7	14
2164	New insights into plant glycoside hydrolase family 32 in Agave species. Frontiers in Plant Science, 2015, 6, 594.	1.7	20
2165	Multiplex staining of 2-DE gels for an initial phosphoproteome analysis of germinating seeds and early grown seedlings from a non-orthodox specie: Quercus ilex L. subsp. ballota [Desf.] Samp.. Frontiers in Plant Science, 2015, 6, 620.	1.7	33
2166	RNA-Seq analysis identifies key genes associated with haustorial development in the root hemiparasite Santalum album. Frontiers in Plant Science, 2015, 6, 661.	1.7	49
2167	De novo assembly and transcriptome analysis of two contrary tillering mutants to learn the mechanisms of tillers outgrowth in switchgrass (Panicum virgatum L.). Frontiers in Plant Science, 2015, 6, 749.	1.7	9
2168	Transcriptomic analysis of fruit stored under cold conditions using controlled atmosphere in Prunus persica cv. â€œRed Pearlâ€• Frontiers in Plant Science, 2015, 6, 788.	1.7	50
2169	Transcriptome profiling reveals differential gene expression in proanthocyanidin biosynthesis associated with red/green skin color mutant of pear (Pyrus communis L.). Frontiers in Plant Science, 2015, 6, 795.	1.7	53
2170	Dynamic transcription profiles of â€œQinguanâ€•apple (Malus Ã— domestica) leaves in response to Marssonina coronaria inoculation. Frontiers in Plant Science, 2015, 6, 842.	1.7	16
2171	Global analysis of WRKY transcription factor superfamily in Setaria identifies potential candidates involved in abiotic stress signaling. Frontiers in Plant Science, 2015, 6, 910.	1.7	96
2172	Population Structure, Genetic Variation, and Linkage Disequilibrium in Perennial Ryegrass Populations Divergently Selected for Freezing Tolerance. Frontiers in Plant Science, 2015, 6, 929.	1.7	14
2173	A genome-wide identification of the miRNAome in response to salinity stress in date palm (Phoenix) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	54
2174	Transcriptome sequencing of purple petal spot region in tree peony reveals differentially expressed anthocyanin structural genes. Frontiers in Plant Science, 2015, 6, 964.	1.7	58
2175	Gene Expression Reaction Norms Unravel the Molecular and Cellular Processes Underpinning the Plastic Phenotypes of Alternanthera Philoxeroides in Contrasting Hydrological Conditions. Frontiers in Plant Science, 2015, 6, 991.	1.7	9
2176	Identification of Putative Candidate Genes for Water Stress Tolerance in Canola (Brassica napus). Frontiers in Plant Science, 2015, 6, 1058.	1.7	73
2177	Genome-Wide Transcriptional Profiling and Metabolic Analysis Uncover Multiple Molecular Responses of the Grass Species Lolium perenne Under Low-Intensity Xenobiotic Stress. Frontiers in Plant Science, 2015, 6, 1124.	1.7	18
2178	Cystoisospora suisâ€‰â€“â€‰A Model of Mammalian Cystoisosporosis. Frontiers in Veterinary Science, 2015, 2, 68.	0.9	25

#	Article	IF	Citations
2179	Screening potential SSR markers of the anadromous fish Coilia nasus by de novo transcriptome analysis using Illumina sequencing. Genetics and Molecular Research, 2015, 14, 14181-14188.	0.3	9
2180	Bioinformatics-Aided Venomics. Toxins, 2015, 7, 2159-2187.	1.5	38
2181	De Novo Assembly and Transcriptome Characterization of Canine Retina Using High-Throughput Sequencing. Genetics Research International, 2015, 2015, 1-11.	2.0	3
2182	<i>De Novo</i>Transcriptome Sequencing of the Orange-Fleshed Sweet Potato and Analysis of Differentially Expressed Genes Related to Carotenoid Biosynthesis. International Journal of Genomics, 2015, 2015, 1-10.	0.8	27
2183	Genes associated with ant social behavior show distinct transcriptional and evolutionary patterns. ELife, 2015, 4, e04775.	2.8	78
2184	Development of Microsatellite Markers Derived from Expressed Sequence Tags of Polyporales for Genetic Diversity Analysis of Endangered<i>Polyporus umbellatus</i>. BioMed Research International, 2015, 2015, 1-11.	0.9	3
2185	Informative Established Sequence Traits in Tepary Bean (Phaseolus Acutifolius A. Gray) for Drought Stress. Journal of Agricultural Studies, 2015, 4, 55.	0.2	0
2186	Large number of putative chemoreception and pheromone biosynthesis genes revealed by analyzing transcriptome from ovipositor-pheromone glands of Chilo suppressalis. Scientific Reports, 2015, 5, 7888.	1.6	69
2187	De novo assembly, transcriptome characterization, lignin accumulation and anatomic characteristics: novel insights into lignin biosynthesis during celery leaf development. Scientific Reports, 2015, 5, 8259.	1.6	78
2188	Differentially expressed genes match bill morphology and plumage despite largely undifferentiated genomes in a <scp>H</scp>olarctic songbird. Molecular Ecology, 2015, 24, 3009-3025.	2.0	82
2189	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 1820-1826.	1.2	17
2190	Molecular Evolution of Freshwater Snails with Contrasting Mating Systems. Molecular Biology and Evolution, 2015, 32, 2403-2416.	3.5	54
2191	Proteomic and metabolomic analyses provide insight into production of volatile and non-volatile flavor components in mandarin hybrid fruit. BMC Plant Biology, 2015, 15, 76.	1.6	22
2192	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. Fish and Shellfish Immunology, 2015, 45, 619-629.	1.6	33
2193	Modulation of insulin-like receptor gene (MdIR) in response to feeding in the surf clam Mesodesma donacium (Lamarck, 1818). Journal of Molluscan Studies, 2015, 81, 37-43.	0.4	9
2194	Horsetails Are Ancient Polyploids: Evidence from <i>Equisetum giganteum</i>. Plant Cell, 2015, 27, 1567-1578.	3.1	78
2195	Genome-wide changes in histone H3 lysine 27 trimethylation associated with bud dormancy release in peach. Tree Genetics and Genomes, 2015, 11, 1.	0.6	59
2196	RNA-seq based whole transcriptome analysis of the cyclopoid copepod Paracyclopina nana focusing on xenobiotics metabolism. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 15, 12-19.	0.4	21

#	Article	IF	Citations
2197	A Comprehensive Analysis of Codon Usage Patterns in Blunt Snout Bream (Megalobrama amblycephala) Based on RNA-Seq Data. International Journal of Molecular Sciences, 2015, 16, 11996-12013.	1.8	15
2198	Single cell subtractive transcriptomics for identification of cell-specifically expressed candidate genes of pyrrolizidine alkaloid biosynthesis. Phytochemistry, 2015, 117, 17-24.	1.4	7
2199	An alternative method for serum protein depletion/enrichment by precipitation at mildly acidic pH values and low ionic strength. Proteomics, 2015, 15, 1935-1940.	1.3	13
2201	Small RNA and degradome sequencing reveals microRNAs and their targets involved in tomato pedicel abscission. Planta, 2015, 242, 963-984.	1.6	22
2202	FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. Journal of Microbiological Methods, 2015, 115, 121-128.	0.7	2
2203	Transcriptome sequencing of three Ranunculus species (Ranunculaceae) reveals candidate genes in adaptation from terrestrial to aquatic habitats. Scientific Reports, 2015, 5, 10098.	1.6	24
2204	Genome-Wide Identification of microRNAs and Their Targets in Cold-Stored Potato Tubers by Deep Sequencing and Degradome Analysis. Plant Molecular Biology Reporter, 2015, 33, 584-597.	1.0	17
2205	Construction of a Spinach Bacterial Artificial Chromosome (BAC) Library as a Resource for Gene Identification and Marker Development. Plant Molecular Biology Reporter, 2015, 33, 1996-2005.	1.0	15
2206	Transcriptome sequencing and differential gene expression analysis in Viola yedoensis Makino (Fam.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Communications, 2015, 459, 60-65.	1.0	26
2207	Identification of xenobiotic biodegradation and metabolism-related genes in the copepod Tigriopus japonicus whole transcriptome analysis. Marine Genomics, 2015, 24, 207-208.	0.4	73
2208	Transcriptomics of mRNA and egg quality in farmed fish: Some recent developments and future directions. General and Comparative Endocrinology, 2015, 221, 23-30.	0.8	58
2209	Uniconazole-induced starch accumulation in the bioenergy crop duckweed (Landoltia punctata) I: transcriptome analysis of the effects of uniconazole on chlorophyll and endogenous hormone biosynthesis. Biotechnology for Biofuels, 2015, 8, 57.	6.2	38
2210	The proteome of Hypobaric Induced Hypoxic Lung: Insights from Temporal Proteomic Profiling for Biomarker Discovery. Scientific Reports, 2015, 5, 10681.	1.6	34
2211	Comparative Transcriptome Analysis between the Cytoplasmic Male Sterile Line NJCMS1A and Its Maintainer NJCMS1B in Soybean (Glycine max (L.) Merr.). PLoS ONE, 2015, 10, e0126771.	1.1	53
2212	Codon usage and codon context bias in Xanthophyllomyces dendrorhous. BMC Genomics, 2015, 16, 293.	1.2	40
2213	Draft Genome Sequence of Lactobacillus plantarum Lp90 Isolated from Wine. Genome Announcements, 2015, 3, .	0.8	17
2214	Identification of sialylated glycoproteins from metabolically oligosaccharide engineered pancreatic cells. Clinical Proteomics, 2015, 12, 11.	1.1	33
2215	Inferring bona fide transfrags in RNA-Seq derived-transcriptome assemblies of non-model organisms. BMC Bioinformatics, 2015, 16, 58.	1.2	7

#	ARTICLE	IF	CITATIONS
2216	Identification and characterisation of putative seminal fluid proteins from male reproductive tissue EST libraries in tiger beetles. BMC Genomics, 2015, 16, 391.	1.2	7
2217	Abiotic and Biotic Stressors Causing Equivalent Mortality Induce Highly Variable Transcriptional Responses in the Soybean Aphid. G3: Genes, Genomes, Genetics, 2015, 5, 261-270.	0.8	34
2218	Network of GRAS Transcription Factors Involved in the Control of Arbuscule Development in<i>Lotus japonicus</i>Â Â. Plant Physiology, 2015, 167, 854-871.	2.3	151
2219	Transcriptomic profiling of linolenic acid-responsive genes in ROS signaling from RNA-seq data in Arabidopsis. Frontiers in Plant Science, 2015, 6, 122.	1.7	51
2220	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. Genetics, 2015, 200, 91-104.	1.2	37
2221	Local adaptation of Gymnocypris przewalskii (Cyprinidae) on the Tibetan Plateau. Scientific Reports, 2015, 5, 9780.	1.6	48
2222	De novo assembly and characterization of the skeletal muscle transcriptome of sheep using Illumina paired-end sequencing. Biotechnology Letters, 2015, 37, 1747-1756.	1.1	6
2223	Genome-Wide Analysis Reveals Diverged Patterns of Codon Bias, Gene Expression, and Rates of Sequence Evolution in Picea Gene Families. Genome Biology and Evolution, 2015, 7, 1002-1015.	1.1	63
2224	Homologs to Cry toxin receptor genes in a de novo transcriptome and their altered expression in resistant Spodoptera litura larvae. Journal of Invertebrate Pathology, 2015, 129, 1-6.	1.5	11
2225	De novo RNA-Seq Analysis of the Venus Clam, Cyclina sinensis, and the Identification of Immune-Related Genes. PLoS ONE, 2015, 10, e0123296.	1.1	15
2226	Detoxification strategies and regulation of oxygen production and flowering of Platanus acerifolia under lead (Pb) stress by transcriptome analysis. Environmental Science and Pollution Research, 2015, 22, 12747-12758.	2.7	19
2227	Genome-Wide Characterization of miRNAs Involved in N Gene-Mediated Immunity in Response to Tobacco Mosaic Virus in Nicotiana benthamiana. Evolutionary Bioinformatics, 2015, 11s1, EBO.S20744.	0.6	20
2228	Early transcriptional events linked to induction of diapause revealed by RNAseq in larvae of drosophilid fly, Chymomyza costata. BMC Genomics, 2015, 16, 720.	1.2	87
2229	Transcriptome profiling of a spirodiclofen susceptible and resistant strain of the European red mite Panonychus ulmi using strand-specific RNA-seq. BMC Genomics, 2015, 16, 974.	1.2	54
2230	Removal of redundant contigs from de novo RNA-Seq assemblies via homology search improves accurate detection of differentially expressed genes. BMC Genomics, 2015, 16, 1031.	1.2	30
2231	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. New Phytologist, 2015, 208, 1227-1240.	3.5	165
2232	The Genome of the â€œGreat Speciatorâ€•Provides Insights into Bird Diversification. Genome Biology and Evolution, 2015, 7, 2680-2691.	1.1	55
2233	Comparative Genomics of Sibling Fungal Pathogenic Taxa Identifies Adaptive Evolution without Divergence in Pathogenicity Genes or Genomic Structure. Genome Biology and Evolution, 2015, 7, 3190-3206.	1.1	32

#	ARTICLE	IF	CITATIONS
2234	Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall synthesis, represses lignification, and prolongs elongation. BMC Genomics, 2015, 16, 477.	1.2	72
2235	Eukaryotic translation elongation factor-1 alpha is associated with a specific subset of mRNAs in Trypanosoma cruzi. BMC Microbiology, 2015, 15, 104.	1.3	20
2236	RNA-seq analysis of Macrobrachium rosenbergii hepatopancreas in response to Vibrio parahaemolyticus infection. Gut Pathogens, 2015, 7, 6.	1.6	66
2237	Unraveling dual feeding associated molecular complexity of salivary glands in the mosquito Anopheles culicifacies. Biology Open, 2015, 4, 1002-1015.	0.6	32
2238	Transcriptomic Analysis of <i>Musca domestica</i> to Reveal Key Genes of the Prophenoloxidase-Activating System. G3: Genes, Genomes, Genetics, 2015, 5, 1827-1841.	0.8	15
2239	Transcriptional Response to Acute Thermal Exposure in Juvenile Chinook Salmon Determined by RNAseq. G3: Genes, Genomes, Genetics, 2015, 5, 1335-1349.	0.8	61
2240	The genome sequence of Acinetobacter baumannii isolated from a septicemic patient in a local hospital in Malaysia. Genomics Data, 2015, 6, 128-129.	1.3	4
2241	Transcriptome changes associated with cold acclimation in leaves of olive tree (Olea europaea L.). Tree Genetics and Genomes, 2015, 11, 1.	0.6	31
2242	Transcriptome Differences between Alternative Sex Determining Genotypes in the House Fly,<i>Musca domestica</i>. Genome Biology and Evolution, 2015, 7, 2051-2061.	1.1	30
2243	Interspecific Differential Expression Analysis of RNA-Seq Data Yields Insight into Life Cycle Variation in Hydractiniid Hydrozoans. Genome Biology and Evolution, 2015, 7, 2417-2431.	1.1	22
2244	NCBI-compliant genome submissions: tips and tricks to save time and money: Table 1. Briefings in Bioinformatics, 2015, 18, bbv104.	3.2	14
2245	De novo assembly and functional annotation of Myrciaria dubia fruit transcriptome reveals multiple metabolic pathways for L-ascorbic acid biosynthesis. BMC Genomics, 2015, 16, 997.	1.2	25
2246	The genetic architecture of sexually selected traits in two natural populations of Drosophila montana. Heredity, 2015, 115, 565-572.	1.2	7
2247	Insights from the genome of Ophiocordyceps polyrhachis-furcata to pathogenicity and host specificity in insect fungi. BMC Genomics, 2015, 16, 881.	1.2	34
2248	De novo transcriptome sequencing and comparative analysis of differentially expressed genes in kiwifruit under waterlogging stress. Molecular Breeding, 2015, 35, 1.	1.0	36
2249	RNA-Seq Transcriptome Analysis in Date Palm Suggests Multi-Dimensional Responses to Salinity Stress. Tropical Plant Biology, 2015, 8, 74-86.	1.0	25
2250	Delineating the glycoproteome of elongating cotton fiber cells. Data in Brief, 2015, 5, 717-725.	0.5	4
2252	High-Throughput Transcriptome Analysis of Plant Stress Responses. , 2015, , 195-209.		0

#	ARTICLE	IF	CITATIONS
2253	Identification of novel and differentially expressed microRNAs in ovine ovary and testis tissues using Solexa sequencing and bioinformatics. Journal of Integrative Agriculture, 2015, 14, 1604-1616.	1.7	2
2254	High CO₂ alters the hypoxia response of the Pacific whiteleg shrimp (<i>Litopenaeus) Tj ETQq1 1 0.784314 rgBT /Overlock Genomics, 2015, 47, 548-558.	1.0	23
2255	Candidate chemosensory genes identified in Colaphellus bowringi by antennal transcriptome analysis. BMC Genomics, 2015, 16, 1028.	1.2	90
2256	Ameliorated de novo transcriptome assembly using Illumina paired end sequence data with Trinity Assembler. Genomics Data, 2015, 5, 352-359.	1.3	40
2257	In silico analysis, annotation and characterisation of putative ESTs from Sorghum bicolor associated with heat stress. International Journal of Bioinformatics Research and Applications, 2015, 11, 547.	0.1	0
2258	Genomic characterization of Sinorhizobium meliloti AK21, a wild isolate from the Aral Sea Region. SpringerPlus, 2015, 4, 259.	1.2	5
2259	Differential proteomic profiling of primary and recurrent chordomas. Oncology Reports, 2015, 33, 2207-2218.	1.2	8
2260	The transcriptome recipe for the venom cocktail of Tityus bahiensis scorpion. Toxicon, 2015, 95, 52-61.	0.8	61
2261	RNA-seq-mediated transcriptome analysis of actively growing and winter dormant shoots identifies non-deciduous habit of evergreen tree tea during winters. Scientific Reports, 2014, 4, 5932.	1.6	52
2262	An immune-enriched oligo-microarray analysis of gene expression in Manila clam (Venerupis) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 275-286.	1.6	30
2263	High-throughput transcriptome analysis of barley (Hordeum vulgare) exposed to excessive boron. Gene, 2015, 557, 71-81.	1.0	50
2264	Characterization of the global transcriptome using Illumina sequencing and novel microsatellite marker information in seashore paspalum. Genes and Genomics, 2015, 37, 77-86.	0.5	16
2265	Different Gene Expressions of Resistant and Susceptible Hop Cultivars in Response to Infection with a Highly Aggressive Strain of Verticillium albo-atrum. Plant Molecular Biology Reporter, 2015, 33, 689-704.	1.0	28
2266	Proteome response of wild wheat relative Kengyilia thoroldiana to drought stress. Canadian Journal of Plant Science, 2015, 95, 237-249.	0.3	6
2267	Complete mitogenome of the edible sea urchin Loxechinus albus: genetic structure and comparative genomics within Echinozoa. Molecular Biology Reports, 2015, 42, 1081-1089.	1.0	6
2268	Gene transcription patterns and energy reserves in Daphnia magna show no nanoparticle specific toxicity when exposed to ZnO and CuO nanoparticles.. Environmental Research, 2015, 138, 82-92.	3.7	41
2269	Comparative proteomic analysis of hyphae and germinating cysts of Phytophthora pisi and Phytophthora sojae. Journal of Proteomics, 2015, 117, 24-40.	1.2	16
2270	A selective sweep in a Varroa destructor resistant honeybee (Apis mellifera) population. Infection, Genetics and Evolution, 2015, 31, 169-176.	1.0	21

#	ARTICLE	IF	CITATIONS
2271	Behavioral and genomic characterization of molt-sleep in the tobacco hornworm, Manduca sexta. Insect Biochemistry and Molecular Biology, 2015, 62, 154-167.	1.2	12
2272	In silico mining, characterization and cross-species transferability of EST-SSR markers for European hazelnut (Corylus avellana L.). Molecular Breeding, 2015, 35, 1.	1.0	29
2273	Distribution and analysis of SSR in mung bean (Vigna radiata L.) genome based on an SSR-enriched library. Molecular Breeding, 2015, 35, 1.	1.0	18
2274	Genomic patterns of species diversity and divergence in <i>Eucalyptus</i>. New Phytologist, 2015, 206, 1378-1390.	3.5	20
2275	Tomato Whole Genome Transcriptional Response to <i>Tetranychus urticae</i> Identifies Divergence of Spider Mite-Induced Responses Between Tomato and <i>Arabidopsis</i>. Molecular Plant-Microbe Interactions, 2015, 28, 343-361.	1.4	90
2276	Temperature and light interactively modulate gene expression in <i>Saccharina latissima</i> (Phaeophyceae). Journal of Phycology, 2015, 51, 93-108.	1.0	37
2277	iTRAQ-based comparative proteomic analysis of embryogenic and non-embryogenic tissues of Prince Rupprechtâ€™s larch (Larix principis-rupprechtii Mayr). Plant Cell, Tissue and Organ Culture, 2015, 120, 655-669.	1.2	54
2278	FungiFun2: a comprehensive online resource for systematic analysis of gene lists from fungal species. Bioinformatics, 2015, 31, 445-446.	1.8	228
2279	Acetylome Analysis Reveals the Involvement of Lysine Acetylation in Photosynthesis and Carbon Metabolism in the Model Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. Journal of Proteome Research, 2015, 14, 1275-1286.	1.8	119
2280	Text as data: Using text-based features for proteins representation and for computational prediction of their characteristics. Methods, 2015, 74, 54-64.	1.9	21
2281	Draft genome sequence of the intestinal parasite Blastocystis subtype 4-isolate WR1. Genomics Data, 2015, 4, 22-23.	1.3	27
2282	The draft genome, transcriptome, and microbiome of Dermatophagoides farinae reveal a broad spectrum of dust mite allergens. Journal of Allergy and Clinical Immunology, 2015, 135, 539-548.	1.5	172
2283	Targeting Enterococcus faecalis Biofilms with Phage Therapy. Applied and Environmental Microbiology, 2015, 81, 2696-2705.	1.4	164
2284	Genetic architecture of carbon isotope composition and growth in <i><scp>E</scp>ucalyptus</i> across multiple environments. New Phytologist, 2015, 206, 1437-1449.	3.5	20
2285	De novo transcriptome assembly for a non-model species, the blood-sucking bug Triatoma brasiliensis, a vector of Chagas disease. Genetica, 2015, 143, 225-239.	0.5	31
2286	Genome-Wide Patterns of Genetic Polymorphism and Signatures of Selection in Plasmodium vivax. Genome Biology and Evolution, 2015, 7, 106-119.	1.1	44
2287	Gd-metallofullerenol nanomaterial as non-toxic breast cancer stem cell-specific inhibitor. Nature Communications, 2015, 6, 5988.	5.8	164
2288	Draft Genome Sequence and Gene Annotation of the Entomopathogenic Fungus <i>Verticillium hemipterigenum</i>. Genome Announcements, 2015, 3, .	0.8	1

#	Article	IF	Citations
2289	Transcriptome sequencing and comparative analysis of diploid and autotetraploid Paulownia australis. Tree Genetics and Genomes, 2015, 11, 1.	0.6	3
2290	Transcriptomics of two evolutionary novelties: how to make a spermâ€transfer organ out of an anal fin and a sexually selected â€œswordâ€• out of a caudal fin. Ecology and Evolution, 2015, 5, 848-864.	0.8	11
2291	Genome-Wide Analysis of Adaptive Molecular Evolution in the Carnivorous Plant Utricularia gibba. Genome Biology and Evolution, 2015, 7, 444-456.	1.1	33
2292	The MYB182 Protein Down-Regulates Proanthocyanidin and Anthocyanin Biosynthesis in Poplar by Repressing Both Structural and Regulatory Flavonoid Genes Â. Plant Physiology, 2015, 167, 693-710.	2.3	177
2293	Transcriptome-wide identification of the genes responding to replanting disease in Rehmannia glutinosa L. roots. Molecular Biology Reports, 2015, 42, 881-892.	1.0	23
2294	Modulation of the spleen transcriptome in domestic turkey (Meleagris gallopavo) in response to aflatoxin B1 and probiotics. Immunogenetics, 2015, 67, 163-178.	1.2	24
2295	Identification and characterization of mRNA-like noncoding RNAs in Salvia miltiorrhiza. Planta, 2015, 241, 1131-1143.	1.6	21
2296	Data for iTRAQ-based quantitative proteomics analysis of Brassica napus leaves in response to chlorophyll deficiency. Data in Brief, 2015, 2, 6-11.	0.5	3
2297	Spaceflight Induces Specific Alterations in the Proteomes of Arabidopsis. Astrobiology, 2015, 15, 32-56.	1.5	63
2298	Line differences in Cor/Lea and fructan biosynthesis-related gene transcript accumulation are related to distinct freezing tolerance levels in synthetic wheat hexaploids. Journal of Plant Physiology, 2015, 176, 78-88.	1.6	19
2299	Transcriptome characterization of the ascidian Pyura chilensis using 454-pyrosequencing data from two distant localities on the southeast Pacific. Marine Genomics, 2015, 20, 19-22.	0.4	0
2300	Discovering candidate genes that regulate resin canal number in <i><scp>P</scp>inus taeda</i> stems by integrating genetic analysis across environments, ages, and populations. New Phytologist, 2015, 205, 627-641.	3.5	45
2301	Comparative transcriptomic analysis provides insights into the molecular basis of brachyurization and adaptation to benthic lifestyle in Eriocheir sinensis. Gene, 2015, 558, 88-98.	1.0	19
2302	Large-scale detection and analysis of adenosine-to-inosine RNA editing during development in Plutella xylostella. Molecular Genetics and Genomics, 2015, 290, 929-937.	1.0	5
2303	Hybrid Dysfunction and Physiological Compensation in Gene Expression. Molecular Biology and Evolution, 2015, 32, 613-622.	3.5	67
2304	First insights into the giant panda (<i><scp>A</scp>iluropoda melanoleuca</i>) blood transcriptome: a resource for novel gene loci and immunogenetics. Molecular Ecology Resources, 2015, 15, 1001-1013.	2.2	25
2305	Shifting habitats, morphology, and selective pressures: Developmental polyphenism in an adaptive radiation of Hawaiian spiders. Evolution; International Journal of Organic Evolution, 2015, 69, 162-178.	1.1	17
2306	Comparison of two FFPE preparation methods using label-free shotgun proteomics: Application to tissues of diverticulitis patients. Journal of Proteomics, 2015, 112, 250-261.	1.2	19

#	ARTICLE	IF	CITATIONS
2307	Expression and characterization of digestive enzyme genes from hepatopancreatic transcripts from redclaw crayfish (<i>Cherax quadricarinatus</i>). Aquaculture Nutrition, 2015, 21, 868-880.	1.1	14
2308	Genotyping-by-sequencing based intra-specific genetic map refines a â€˜â€˜QTL-hotspotâ€•region for drought tolerance in chickpea. Molecular Genetics and Genomics, 2015, 290, 559-571.	1.0	180
2309	Defining the transcriptomic landscape of <i>Candida glabrata</i> by RNA-Seq. Nucleic Acids Research, 2015, 43, 1392-1406.	6.5	74
2310	Comparative Proteomic Analysis of Developing Rhizomes of the Ancient Vascular Plant <i>Equisetum hyemale</i> and Different Monocot Species. Journal of Proteome Research, 2015, 14, 1779-1791.	1.8	8
2311	Dual analysis of host and pathogen transcriptomes in ostreid herpesvirus 1â€•positive <scp><i>C</i></scp><i>rassostrea gigas</i>. Environmental Microbiology, 2015, 17, 4200-4212.	1.8	75
2312	Genome-wide patterns of genetic variation among silkworms. Molecular Genetics and Genomics, 2015, 290, 1575-1587.	1.0	5
2313	Transcriptome exploration for further understanding of the tropane alkaloids biosynthesis in Anisodus acutangulus. Molecular Genetics and Genomics, 2015, 290, 1367-1377.	1.0	18
2314	ocsESTdb: a database of oil crop seed EST sequences for comparative analysis and investigation of a global metabolic network and oil accumulation metabolism. BMC Plant Biology, 2015, 15, 19.	1.6	15
2315	SSAP analysis reveals candidate genes associated with deastringency in persimmon (Diospyros kaki) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	14
2316	Transcriptome analysis reveals the role of BpGH3.5 in root elongation of Betula platyphyllaÂÃ—ÂB. pendula. Plant Cell, Tissue and Organ Culture, 2015, 121, 605-617.	1.2	5
2317	A Eukaryotic Translation Initiation Factor 4E (eIF4E) is Responsible for the â€œvaâ€•Tobacco Recessive Resistance to Potyviruses. Plant Molecular Biology Reporter, 2015, 33, 609-623.	1.0	40
2318	Double-stranded RNA in the biological control of grain aphid (Sitobion avenae F.). Functional and Integrative Genomics, 2015, 15, 211-223.	1.4	32
2319	De novo transcriptome analysis of the gametophyte of Undaria pinnatifida (Phaeophyceae). Journal of Applied Phycology, 2015, 27, 1011-1019.	1.5	31
2320	Identification of proteins associated with pyrethroid resistance by iTRAQ-based quantitative proteomic analysis in Culex pipiens pallens. Parasites and Vectors, 2015, 8, 95.	1.0	34
2321	Pathways associated with lignin biosynthesis in lignomaniac jute fibres. Molecular Genetics and Genomics, 2015, 290, 1523-1542.	1.0	39
2322	De novo sequencing analysis of the Rosa roxburghii fruit transcriptome reveals putative ascorbate biosynthetic genes and EST-SSR markers. Gene, 2015, 561, 54-62.	1.0	41
2323	SNARE-RNAi Results in Higher Terpene Emission from Ectopically Expressed Caryophyllene Synthase in Nicotiana benthamiana. Molecular Plant, 2015, 8, 454-466.	3.9	12
2324	Gene expression profile affected by volatiles of new plant growth promoting rhizobacteria, Bacillus subtilis strain JS, in tobacco. Genes and Genomics, 2015, 37, 387-397.	0.5	25

#	ARTICLE	IF	CITATIONS
2325	Annocript: a flexible pipeline for the annotation of transcriptomes able to identify putative long noncoding RNAs. Bioinformatics, 2015, 31, 2199-2201.	1.8	94
2326	High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant Utricularia gibba. Molecular Biology and Evolution, 2015, 32, 1284-1295.	3.5	53
2327	Involvement of a citrus meiotic recombination TTC-repeat motif in the formation of gross deletions generated by ionizing radiation and MULE activation. BMC Genomics, 2015, 16, 69.	1.2	15
2328	The transcriptomic profile of Pseudozyma aphidis during production of mannosylerythritol lipids. Applied Microbiology and Biotechnology, 2015, 99, 1375-1388.	1.7	30
2329	Gene loss in the fungal canola pathogen Leptosphaeria maculans. Functional and Integrative Genomics, 2015, 15, 189-196.	1.4	50
2330	Proteomic Analysis of Mature Lagenaria siceraria Seed. Applied Biochemistry and Biotechnology, 2015, 175, 3643-3656.	1.4	4
2331	Identification, validation and cross-species transferability of novel Lavandula EST-SSRs. Planta, 2015, 241, 987-1004.	1.6	28
2332	RNA Sequencing to Study Gene Expression and SNP Variations Associated with Growth in Zebrafish Fed a Plant Protein-Based Diet. Marine Biotechnology, 2015, 17, 353-363.	1.1	32
2333	Characterisation of the Manduca sexta sperm proteome: Genetic novelty underlying sperm composition in Lepidoptera. Insect Biochemistry and Molecular Biology, 2015, 62, 183-193.	1.2	27
2334	Effector discovery in the fungal wheat pathogen <i><scp>Z</scp>ymoseptoria tritici</i>. Molecular Plant Pathology, 2015, 16, 931-945.	2.0	76
2335	Ovary transcriptome profiling of Coilia nasus during spawning migration stages by Illumina sequencing. Marine Genomics, 2015, 21, 17-19.	0.4	18
2336	Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. BMC Genomics, 2015, 16, 60.	1.2	84
2337	Venomics of the Australian eastern brown snake (Pseudonaja textilis): Detection of new venom proteins and splicing variants. Toxicon, 2015, 107, 252-265.	0.8	28
2338	The elucidation of stress memory inheritance in Brassica rapa plants. Frontiers in Plant Science, 2015, 6, 5.	1.7	102
2339	Comparison of gene expression profiles and responses to zinc chloride among inter- and intraspecific hybrids with growth abnormalities in wheat and its relatives. Plant Molecular Biology, 2015, 88, 487-502.	2.0	10
2340	Phenotype and transcriptome analysis reveals chloroplast development and pigment biosynthesis together influenced the leaf color formation in mutants of Anthurium andraeanum â€˜Sonataâ€™. Frontiers in Plant Science, 2015, 6, 139.	1.7	99
2341	Transcriptome-based gene profiling provides novel insights into the characteristics of radish root response to Cr stress with next-generation sequencing. Frontiers in Plant Science, 2015, 6, 202.	1.7	65
2342	Physiological and Proteomics Analyses Reveal the Mechanism of Eichhornia crassipes Tolerance to High-Concentration Cadmium Stress Compared with Pistia stratiotes. PLoS ONE, 2015, 10, e0124304.	1.1	29

#	Article	IF	Citations
2343	RNA-Seq Transcriptome Analysis of Maize Inbred Carrying Nicosulfuron-Tolerant and Nicosulfuron-Susceptible Alleles. International Journal of Molecular Sciences, 2015, 16, 5975-5989.	1.8	28
2345	Characterisation of Dermanyssus gallinae glutathione S-transferases and their potential as acaricide detoxification proteins. Parasites and Vectors, 2015, 8, 350.	1.0	22
2346	Enhanced biological processes associated with alopecia in polar bears (Ursus maritimus). Science of the Total Environment, 2015, 529, 114-120.	3.9	16
2347	Transcriptome Analysis of Invasive Plants in Response to Mineral Toxicity of Reclaimed Coal-Mine Soil in the Appalachian Region. Environmental Science & Technology, 2015, 49, 10320-10329.	4.6	16
2348	De novo assembly and analysis of tissue-specific transcriptomes revealed the tissue-specific genes and profile of immunity from Strongylocentrotus intermedius. Fish and Shellfish Immunology, 2015, 46, 723-736.	1.6	21
2349	Comparative transcriptome analyses of drought-resistant and - susceptible Brassica napus L. and development of EST-SSR markers by RNA-Seq. Journal of Plant Biology, 2015, 58, 259-269.	0.9	48
2350	Characterization of six small HSP genes from Chironomus riparius (Diptera, Chironomidae): Differential expression under conditions of normal growth and heat-induced stress. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2015, 188, 76-86.	0.8	40
2351	iTRAQ-Based Quantitative Proteomic Analysis of the Antimicrobial Mechanism of Peptide F1 against <i>Escherichia coli</i>. Journal of Agricultural and Food Chemistry, 2015, 63, 7190-7197.	2.4	32
2352	Transcriptomic response to low salinity stress in gills of the Pacific white shrimp, Litopenaeus vannamei. Marine Genomics, 2015, 24, 297-304.	0.4	40
2353	De novo transcriptome characterization of the ghost moth, Thitarodes pui, and elevation-based differences in the gene expression of its larvae. Gene, 2015, 574, 95-105.	1.0	10
2354	Dynamic transcriptome analysis and volatile profiling of Gossypium hirsutum in response to the cotton bollworm Helicoverpa armigera. Scientific Reports, 2015, 5, 11867.	1.6	41
2355	Transcriptional profiling of canola developing embryo and identification of the important roles of<i>BnDof5.6</i>in embryo development and fatty acids synthesis. Plant and Cell Physiology, 2015, 56, 1624-1640.	1.5	24
2356	Gene Transcription, Metabolite and Lipid Profiling in Eco-Indicator <i>Daphnia magna</i> Indicate Diverse Mechanisms of Toxicity by Legacy and Emerging Flame-Retardants. Environmental Science & Technology, 2015, 49, 7400-7410.	4.6	54
2357	Complete Dosage Compensation in<i>Anopheles stephensi</i>and the Evolution of Sex-Biased Genes in Mosquitoes. Genome Biology and Evolution, 2015, 7, 1914-1924.	1.1	40
2358	Genetic and epigenetic architecture of sex-biased expression in the jewel wasps <i>Nasonia vitripennis</i> and <i>giraulti</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3545-54.	3.3	53
2359	A transcriptomic analysis of the response of the arctic pteropod Limacina helicina to carbon dioxide-driven seawater acidification. Polar Biology, 2015, 38, 1727-1740.	0.5	33
2360	Morphology and Proteome Characterization of the Salivary Glands of the Western Chinch Bug (Hemiptera: Blissidae). Journal of Economic Entomology, 2015, 108, 2055-2064.	0.8	7
2361	Transcriptome analyses to investigate symbiotic relationships between marine protists. Frontiers in Microbiology, 2015, 6, 98.	1.5	40

#	Article	IF	Citations
2362	Floral Transcriptome Analyses of Four Paphiopedilum Orchids with Distinct Flowering Behaviors and Development of Simple Sequence Repeat Markers. Plant Molecular Biology Reporter, 2015, 33, 1928-1952.	1.0	8
2363	Key metabolic pathways involved in xenobiotic biotransformation and stress responses revealed by transcriptomics of the mangrove oyster Crassostrea brasiliana. Aquatic Toxicology, 2015, 166, 10-20.	1.9	53
2364	Elucidation of the growth delimitation of Dunaliella tertiolecta under nitrogen stress by integrating transcriptome and peptidome analysis. Bioresource Technology, 2015, 194, 57-66.	4.8	51
2365	The global transcriptional landscape of Bacillus amyloliquefaciens XH7 and high-throughput screening of strong promoters based on RNA-seq data. Gene, 2015, 571, 252-262.	1.0	34
2366	A genomic and transcriptomic approach to investigate the blue pigment phenotype in Pseudomonas fluorescens. International Journal of Food Microbiology, 2015, 213, 88-98.	2.1	61
2367	Transcriptome analysis of the biofilm formed by methicillin-susceptible Staphylococcus aureus. Scientific Reports, 2015, 5, 11997.	1.6	75
2368	Novel insights into the molecular mechanisms underlying the resistance of Camellia sinensis to Ectropis oblique provided by strategic transcriptomic comparisons. Scientia Horticulturae, 2015, 192, 429-440.	1.7	24
2369	The Secreted Proteins of Achlya hypogyna and Thraustotheca clavata Identify the Ancestral Oomycete Secretome and Reveal Gene Acquisitions by Horizontal Gene Transfer. Genome Biology and Evolution, 2015, 7, 120-135.	1.1	34
2370	A Novel Pathogenic Mammalian Orthoreovirus from Diarrheic Pigs and Swine Blood Meal in the United States. MBio, 2015, 6, e00593-15.	1.8	56
2371	Transcriptome analysis of the Japanese pine sawyer beetle, Monochamus alternatus (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overloc 439-445.	0.4	22
2372	Analysis of antennal transcriptome and odorant binding protein expression profiles of the recently identified parasitoid wasp, Sclerodermus sp.. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 10-19.	0.4	37
2373	Low-molecular-mass secretome profiling identifies HMGA2 and MIF as prognostic biomarkers for oral cavity squamous cell carcinoma. Scientific Reports, 2015, 5, 11689.	1.6	37
2374	Effects of low temperature on mRNA and small RNA transcriptomes in Solanum lycopersicoides leaf revealed by RNA-Seq. Biochemical and Biophysical Research Communications, 2015, 464, 768-773.	1.0	22
2375	An integrated transcriptomic and proteomic analysis of sea star epidermal secretions identifies proteins involved in defense and adhesion. Journal of Proteomics, 2015, 128, 83-91.	1.2	66
2376	Transcriptomic and proteomic analysis of pre-diapause and non-diapause eggs of migratory locust, Locusta migratoria L. (Orthoptera: Acridoidea). Scientific Reports, 2015, 5, 11402.	1.6	79
2377	Transcriptome sequencing and development of EST-SSR markers in Pinus dabeshanensis, an endangered conifer endemic to China. Molecular Breeding, 2015, 35, 1.	1.0	46
2378	Transcriptome profiling of the eyestalk of precocious juvenile Chinese mitten crab reveals putative neuropeptides and differentially expressed genes. Gene, 2015, 569, 280-286.	1.0	21
2379	Transcriptomes analysis of Aeromonas molluscorum Av27 cells exposed to tributyltin (TBT): Unravelling the effects from the molecular level to the organism. Marine Environmental Research, 2015, 109, 132-139.	1.1	8

#	Article	IF	Citations
2380	Diversity of freshwater<i>Epsilonproteobacteria</i>and dark inorganic carbon fixation in the sulphidic redoxcline of a meromictic karstic lake. FEMS Microbiology Ecology, 2015, 91, fiv086.	1.3	22
2381	Whole transcriptome analysis reveals changes in expression of immune-related genes during and after bleaching in a reef-building coral. Royal Society Open Science, 2015, 2, 140214.	1.1	189
2382	Inbreeding Affects Gene Expression Differently in Two Self-Incompatible<i>Arabidopsis lyrata</i>Populations with Similar Levels of Inbreeding Depression. Molecular Biology and Evolution, 2015, 32, 2036-2047.	3.5	15
2383	Assembling of Holotrichia parallela (dark black chafer) midgut tissue transcriptome and identification of midgut proteins that bind to Cry8Ea toxin from Bacillus thuringiensis. Applied Microbiology and Biotechnology, 2015, 99, 7209-7218.	1.7	19
2384	Secretomic Analysis Reveals Multi-Enzymatic Complexes in Trichoderma reesei Grown in Media Containing Lactose or Galactose. Bioenergy Research, 2015, 8, 1906-1911.	2.2	6
2385	Testes transcriptome profiles of the anadromous fish Coilia nasus during the onset of spermatogenesis. Marine Genomics, 2015, 24, 241-243.	0.4	12
2386	Characterization of the bay scallop (Argopecten irradians concentricus Say) transcriptome and identification of growth-related genes. Marine Genomics, 2015, 24, 225-227.	0.4	5
2387	Proteomic profile of Bithynia siamensis goniomphalos snails upon infection with the carcinogenic liver fluke Opisthorchis viverrini. Journal of Proteomics, 2015, 113, 281-291.	1.2	17
2388	Next-generation transcriptome analysis in transgenic birch overexpressing and suppressing APETALA1 sheds lights in reproduction development and diterpenoid biosynthesis. Plant Cell Reports, 2015, 34, 1663-1680.	2.8	6
2389	Transcriptome analysis of the adult rumen fluke Paramphistomum cervi following next generation sequencing. Gene, 2015, 570, 64-70.	1.0	16
2390	RNA-Seq analysis of resistant and susceptible potato varieties during the early stages of potato virus Y infection. BMC Genomics, 2015, 16, 472.	1.2	74
2391	Comparative proteomics of Bt-transgenic and non-transgenic cotton leaves. Proteome Science, 2015, 13, 15.	0.7	41
2392	Transcriptome Sequencing of Mung Bean (Vigna radiate L.) Genes and the Identification of EST-SSR Markers. PLoS ONE, 2015, 10, e0120273.	1.1	84
2393	Analysis of plant gene expression during passion fruitâ€"<i>Xanthomonas axonopodis</i> interaction implicates lipoxygenase 2 in host defence. Annals of Applied Biology, 2015, 167, 135-155.	1.3	33
2394	Multiple mutations and increased RNA expression in tetracycline-resistant <i>Streptococcus pneumoniae</i> as determined by genome-wide DNA and mRNA sequencing. Journal of Antimicrobial Chemotherapy, 2015, 70, 1946-1959.	1.3	22
2395	Transcriptional Profiling of Resistant and Susceptible Buffalograsses in Response to Blissus occiduus (Hemiptera: Blissidae) Feeding. Journal of Economic Entomology, 2015, 108, 1354-1362.	0.8	12
2396	Transcriptome-wide analysis of the response of the thecosome pteropod Clio pyramidata to short-term CO2 exposure. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 1-9.	0.4	37
2397	Transcriptome Analysis of Methyl Jasmonate-Elicited Panax ginseng Adventitious Roots to Discover Putative Ginsenoside Biosynthesis and Transport Genes. International Journal of Molecular Sciences, 2015, 16, 3035-3057.	1.8	54

#	ARTICLE	IF	CITATIONS
2398	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. Plant Molecular Biology, 2015, 88, 531-543.	2.0	46
2399	Identification and expression pattern of candidate olfactory genes in Chrysoperla sinica by antennal transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 15, 28-38.	0.4	25
2400	Morphological and Molecular Descriptors of the Developmental Cycle of Babesia divergens Parasites in Human Erythrocytes. PLoS Neglected Tropical Diseases, 2015, 9, e0003711.	1.3	23
2401	De Novo Transcriptome Sequencing of Low Temperature-Treated Phlox subulata and Analysis of the Genes Involved in Cold Stress. International Journal of Molecular Sciences, 2015, 16, 9732-9748.	1.8	17
2402	Transcriptome profiling analysis of naked carp (Gymnocypris przewalskii) provides insights into the immune-related genes in highland fish. Fish and Shellfish Immunology, 2015, 46, 366-377.	1.6	36
2403	Firing the Sting: Chemically Induced Discharge of Cnidae Reveals Novel Proteins and Peptides from Box Jellyfish (Chironex fleckeri) Venom. Toxins, 2015, 7, 936-950.	1.5	47
2404	Transcriptional Responses of a Bicarbonate-Tolerant Monocot, Puccinellia tenuiflora, and a Related Bicarbonate-Sensitive Species, Poa annua, to NaHCO3 Stress. International Journal of Molecular Sciences, 2015, 16, 496-509.	1.8	17
2405	Genomic sequencing and microsatellite marker development for Boswellia papyrifera, an economically important but threatened tree native to dry tropical forests. AoB PLANTS, 2015, 7, .	1.2	20
2406	Comparative genomics of Australian isolates of the wheat stem rust pathogen Puccinia graminis f. sp. tritici reveals extensive polymorphism in candidate effector genes. Frontiers in Plant Science, 2014, 5, 759.	1.7	98
2407	De Novo Assembly and Characterization of the Transcriptome and Molecular Discovery in Capsicum Annuum L. R597. International Journal of Control and Automation, 2015, 8, 105-116.	0.3	0
2408	Comparative proteomic analysis of melon phloem exudates in response to viral infection. Journal of Proteomics, 2015, 124, 11-24.	1.2	26
2409	Early transcriptional changes in Beta vulgaris in response to low temperature. Planta, 2015, 242, 187-201.	1.6	31
2410	Comparative analysis of chrysanthemum transcriptome in response to three RNA viruses: Cucumber mosaic virus, Tomato spotted wilt virus and Potato virus X. Plant Molecular Biology, 2015, 88, 233-248.	2.0	29
2411	Characterization of Lipids and Proteins Associated to the Cell Wall of the Acapsular Mutant <i>Cryptococcus neoformans</i> Cap 67. Journal of Eukaryotic Microbiology, 2015, 62, 591-604.	0.8	5
2412	Structural and Functional Diversity of Peptide Toxins from Tarantula Haplopelma hainanum (Ornithoctonus hainana) Venom Revealed by Transcriptomic, Peptidomic, and Patch Clamp Approaches. Journal of Biological Chemistry, 2015, 290, 14192-14207.	1.6	18
2413	Genomeâ€wide patterns of differentiation and spatially varying selection between postglacial recolonization lineages of <i>Populus alba</i> (Salicaceae), a widespread forest tree. New Phytologist, 2015, 207, 723-734.	3.5	40
2414	Mutualistic root endophytism is not associated with the reduction of saprotrophic traits and requires a noncompromised plant innate immunity. New Phytologist, 2015, 207, 841-857.	3.5	139
2415	A quantitative proteomic analysis of the tegumental proteins from Schistosoma mansoni schistosomula reveals novel potential therapeutic targets. International Journal for Parasitology, 2015, 45, 505-516.	1.3	103

#	ARTICLE	IF	CITATIONS
2416	Histological and transcript analyses of intact somatic embryos in an elite maize (Zea mays L.) inbred line Y423. Plant Physiology and Biochemistry, 2015, 92, 81-91.	2.8	8
2417	Light-dependent transcriptional events during resting egg hatching of the rotifer Brachionus manjavacas. Marine Genomics, 2015, 20, 25-31.	0.4	13
2418	Identification and characterization of androgenic gland specific insulin-like peptide-encoding transcripts in two spiny lobster species: Sagmariasus verreauxi and Jasus edwardsii. General and Comparative Endocrinology, 2015, 214, 126-133.	0.8	36
2419	Global analysis of transcriptional response of Chinese cabbage to methyl jasmonate reveals JA signaling on enhancement of secondary metabolism pathways. Scientia Horticulturae, 2015, 189, 159-167.	1.7	17
2420	Metabolic and transcriptional transitions in barley glumes reveal a role as transitory resource buffers during endosperm filling. Journal of Experimental Botany, 2015, 66, 1397-1411.	2.4	35
2421	RNA-Seq-based transcriptome analysis of stem development and dwarfing regulation in Agapanthus praecox ssp. orientalis (Leighton) Leighton. Gene, 2015, 565, 252-267.	1.0	33
2422	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. Journal of Proteome Research, 2015, 14, 2207-2218.	1.8	7
2423	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	9.4	1,560
2424	Transcriptional profile of the human pathogenic fungus Paracoccidioides lutzii in response to sulfamethoxazole. Medical Mycology, 2015, 53, 477-492.	0.3	9
2425	Localization of quantitative trait loci for diapause and other photoperiodically regulated life history traits important in adaptation to seasonally varying environments. Molecular Ecology, 2015, 24, 2809-2819.	2.0	28
2426	Analyzing serial cDNA libraries revealed reactive oxygen species and gibberellins signaling pathways in the salt response of Upland cotton (Gossypium hirsutum L.). Plant Cell Reports, 2015, 34, 1005-1023.	2.8	26
2427	Comparative transcriptome of rhizome and leaf in Ligusticum Chuanxiong. Plant Systematics and Evolution, 2015, 301, 2073-2085.	0.3	9
2428	An Ixodes scapularis cell line with a predominantly neuron-like phenotype. Experimental and Applied Acarology, 2015, 66, 427-442.	0.7	31
2429	Hex1-related transcriptome of Trichoderma atroviride reveals expression patterns of ABC transporters associated with tolerance to dichlorvos. Biotechnology Letters, 2015, 37, 1421-1429.	1.1	22
2430	Anther proteomic characterization in temperature sensitive Bainong male sterile wheat. Biologia Plantarum, 2015, 59, 273-282.	1.9	3
2431	De novo assembly, gene annotation, and marker development of mulberry (Morus atropurpurea) transcriptome. Tree Genetics and Genomes, 2015, 11, 1.	0.6	19
2432	RNA-Seq analysis for transcriptome assembly, gene identification, and SSR mining in ginkgo (Ginkgo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.6	23
2433	Comparative proteomics exploring the molecular mechanism of eutrophic water purification using water hyacinth (Eichhornia crassipes). Environmental Science and Pollution Research, 2015, 22, 8643-8658.	2.7	16

#	Article	IF	Citations
2434	Chronic exposures to low and high concentrations of ibuprofen elicit different gene response patterns in a euryhaline fish. Environmental Science and Pollution Research, 2015, 22, 17397-17413.	2.7	47
2435	Identification and characterization of presence/absence variation in maize genotype Mo17. Genes and Genomics, 2015, 37, 503-515.	0.5	7
2436	Assessment of genetic diversity and population structure of mung bean (Vigna radiata) germplasm using EST-based and genomic SSR markers. Gene, 2015, 566, 175-183.	1.0	42
2437	Next-generation sequencing (NGS) transcriptomes reveal association of multiple genes and pathways contributing to secondary metabolites accumulation in tuberous roots of Aconitum heterophyllum Wall.. Planta, 2015, 242, 239-258.	1.6	34
2438	Identification of horizontally transferred genes in the genus Colletotrichum reveals a steady tempo of bacterial to fungal gene transfer. BMC Genomics, 2015, 16, 2.	1.2	49
2439	Abiotic stress and genome dynamics: specific genes and transposable elements response to iron excess in rice. Rice, 2015, 8, 13.	1.7	87
2440	MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. BMC Bioinformatics, 2015, 16, 45.	1.2	40
2441	Transcriptome analysis between invasive Pomacea canaliculata and indigenous Cipangopaludina cahayensis reveals genomic divergence and diagnostic microsatellite/SSR markers. BMC Genetics, 2015, 16, 12.	2.7	15
2442	RNA-Seq analysis and transcriptome assembly for blackberry (Rubus sp. Var. Lochness) fruit. BMC Genomics, 2015, 16, 5.	1.2	62
2443	Integrated transcriptome catalogue and organ-specific profiling of gene expression in fertile garlic (Allium sativum L.). BMC Genomics, 2015, 16, 12.	1.2	85
2444	Transcriptome analysis reveals in vitro cultured Withania somnifera leaf and root tissues as a promising source for targeted withanolide biosynthesis. BMC Genomics, 2015, 16, 14.	1.2	34
2445	Re-annotation of the woodland strawberry (Fragaria vesca) genome. BMC Genomics, 2015, 16, 29.	1.2	60
2446	Transcriptome changes in rice (Oryza sativa L.) in response to high night temperature stress at the early milky stage. BMC Genomics, 2015, 16, 18.	1.2	54
2447	RNA-seq analysis reveals the role of red light in resistance against Pseudomonas syringae pv. tomato DC3000 in tomato plants. BMC Genomics, 2015, 16, 120.	1.2	82
2448	Transcriptomic response to heat stress among ecologically divergent populations of redband trout. BMC Genomics, 2015, 16, 103.	1.2	106
2449	Genome-wide survey and expression analysis of F-box genes in chickpea. BMC Genomics, 2015, 16, 67.	1.2	68
2450	Comprehensive analysis of CCCH-type zinc finger family genes facilitates functional gene discovery and reflects recent allopolyploidization event in tetraploid switchgrass. BMC Genomics, 2015, 16, 129.	1.2	38
2451	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	1.2	49

#	Article	IF	Citations
2452	Transcriptome analysis of Panax vietnamensis var. fuscidicus discovers putative ocotillol-type ginsenosides biosynthesis genes and genetic markers. BMC Genomics, 2015, 16, 159.	1.2	42
2453	Retained duplicate genes in green alga Chlamydomonas reinhardtii tend to be stress responsive and experience frequent response gains. BMC Genomics, 2015, 16, 149.	1.2	12
2454	The genome of the basal agaricomycete Xanthophyllomyces dendrorhous provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. BMC Genomics, 2015, 16, 233.	1.2	47
2455	Nourishment level affects caste-related gene expression in Polistes wasps. BMC Genomics, 2015, 16, 235.	1.2	50
2456	A RNA-seq approach to identify putative toxins from acrorhagi in aggressive and non-aggressive Anthopleura elegantissima polyps. BMC Genomics, 2015, 16, 221.	1.2	60
2457	Chemosensory genes identified in the antennal transcriptome of the blowfly Calliphora stygia. BMC Genomics, 2015, 16, 255.	1.2	58
2458	Identification and characterization of rye genes not expressed in allohexaploid triticale. BMC Genomics, 2015, 16, 281.	1.2	43
2459	Columnar apple primary roots share some features of the columnar-specific gene expression profile of aerial plant parts as evidenced by RNA-Seq analysis. BMC Plant Biology, 2015, 15, 34.	1.6	17
2460	Digital gene expression analysis of gene expression differences within Brassica diploids and allopolyploids. BMC Plant Biology, 2015, 15, 22.	1.6	26
2461	The transcriptome of Utricularia vulgaris, a rootless plant with minimalist genome, reveals extreme alternative splicing and only moderate sequence similarity with Utricularia gibba. BMC Plant Biology, 2015, 15, 78.	1.6	14
2462	Using the canary genome to decipher the evolution of hormone-sensitive gene regulation in seasonal singing birds. Genome Biology, 2015, 16, 19.	3.8	60
2463	Uniconazole-induced starch accumulation in the bioenergy crop duckweed (Landoltia punctata) II: transcriptome alterations of pathways involved in carbohydrate metabolism and endogenous hormone crosstalk. Biotechnology for Biofuels, 2015, 8, 64.	6.2	72
2464	Functional analysis of Girardia tigrina transcriptome seeds pipeline for anthelmintic target discovery. Parasites and Vectors, 2015, 8, 34.	1.0	12
2465	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. GigaScience, 2015, 4, 5.	3.3	138
2466	Transcriptomic screening for cyclotides and other cysteine-rich proteins in the metallophyte Viola baoshanensis. Journal of Plant Physiology, 2015, 178, 17-26.	1.6	30
2467	Comparative Analysis of Testis Transcriptomes from Triploid and Fertile Diploid Cyprinid Fish1. Biology of Reproduction, 2015, 92, 95.	1.2	32
2468	Transcriptome of an entomophthoralean fungus (Pandora formicae) shows molecular machinery adjusted for successful host exploitation and transmission. Journal of Invertebrate Pathology, 2015, 128, 47-56.	1.5	42
2469	Gene discovery in the developing xylem tissue of a tropical timber tree species: Neolamarckia cadamba (Roxb.) Bosser (kelampayan). Tree Genetics and Genomes, 2015, 11, 1.	0.6	6

#	ARTICLE	IF	CITATIONS
2470	De novo sequencing of root transcriptome reveals complex cadmium-responsive regulatory networks in radish (Raphanus sativus L.). Plant Science, 2015, 236, 313-323.	1.7	75
2471	Dissection of the styleâ€™s response to pollination using transcriptome profiling in self-compatible (Solanum pimpinellifolium) and self-incompatible (Solanum chilense) tomato species. BMC Plant Biology, 2015, 15, 119.	1.6	20
2472	Comparative transcriptome profiling approach to glean virulence and immunomodulation-related genes of Fasciola hepatica. BMC Genomics, 2015, 16, 366.	1.2	15
2473	Transcriptome differences between Cry1Ab resistant and susceptible strains of Asian corn borer. BMC Genomics, 2015, 16, 173.	1.2	42
2474	Deep sequencing of the scallop Chlamys farreri transcriptome response to tetrabromobisphenol A (TBBPA) stress. Marine Genomics, 2015, 19, 31-38.	0.4	28
2475	CHAPTER 1. Seeing the Woods for the Trees: Understanding Venom Evolution as a Guide for Biodiscovery. RSC Drug Discovery Series, 2015, , 1-36.	0.2	13
2476	RNA Sequencing of Laser-Capture Microdissected Compartments of the Maize Kernel Identifies Regulatory Modules Associated with Endosperm Cell Differentiation. Plant Cell, 2015, 27, 513-531.	3.1	206
2477	Transcriptional responses to fluctuating thermal regimes underpinning differences in survival in the solitary bee <i>Megachile rotundata</i>. Journal of Experimental Biology, 2015, 218, 1060-1068.	0.8	66
2478	Microarray Analysis of Immunity Against WSSV in Response to Injection of Non-specific Long dsRNA in Kuruma Shrimp, Marsupenaeus japonicus. Marine Biotechnology, 2015, 17, 493-501.	1.1	15
2479	Phosphoproteome Analysis Links Protein Phosphorylation to Cellular Remodeling and Metabolic Adaptation during <i>Magnaporthe oryzae</i> Appressorium Development. Journal of Proteome Research, 2015, 14, 2408-2424.	1.8	42
2480	RNA-seq analysis evidences multiple gene responses in Caligus rogercresseyi exposed to the anti-salmon lice drug azamethiphos. Aquaculture, 2015, 446, 156-166.	1.7	18
2481	Screening and transcriptome analysis of water deficiency tolerant germplasms in peanut (Arachis) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	8
2482	De-novo transcriptome analysis of the banana shrimp (Fenneropenaeus merguiensis) and identification of genes associated with reproduction and development. Marine Genomics, 2015, 22, 71-78.	0.4	66
2483	FurA contributes to the oxidative stress response regulation of Mycobacterium avium ssp. paratuberculosis. Frontiers in Microbiology, 2015, 6, 16.	1.5	15
2484	Transcriptomic profiles of the smoke tree wilt fungus Verticillium dahliae under nutrient starvation stresses. Molecular Genetics and Genomics, 2015, 290, 1963-1977.	1.0	13
2485	Whole transcriptome analysis of the monogonont rotifer Brachionus koreanus provides molecular resources for developing biomarkers of carbohydrate metabolism. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 14, 33-41.	0.4	11
2486	Prohibitin-2 gene reveals sex-related differences in the salmon louse Caligus rogercresseyi. Gene, 2015, 564, 73-80.	1.0	9
2487	Proteomics profiling of ethylene-induced tomato flower pedicel abscission. Journal of Proteomics, 2015, 121, 67-87.	1.2	27

#	Article	IF	Citations
2488	Transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber (Cucumis sativus L.). Scientific Reports, 2015, 5, 8031.	1.6	89
2489	Development of DArT-based PCR markers for selecting drought-tolerant spring barley. Journal of Applied Genetics, 2015, 56, 299-309.	1.0	19
2490	De novo assembly and characterization of the spleen transcriptome ofÂcommon carp (Cyprinus carpio) using Illumina paired-end sequencing. Fish and Shellfish Immunology, 2015, 44, 420-429.	1.6	57
2491	<i>De novo</i>transcriptome sequencing to identify the sex-determination genes in<i>Hyriopsis schlegelii</i>. Bioscience, Biotechnology and Biochemistry, 2015, 79, 1257-1265.	0.6	30
2492	Discovery of germline-related genes in Cephalochordate amphioxus: A genome wide survey using genome annotation and transcriptome data. Marine Genomics, 2015, 24, 147-157.	0.4	7
2493	Early and delayed long-term transcriptional changes and short-term transient responses during cold acclimation in olive leaves. DNA Research, 2015, 22, 1-11.	1.5	67
2494	Regulatory Divergence between Parental Alleles Determines Gene Expression Patterns in Hybrids. Genome Biology and Evolution, 2015, 7, 1110-1121.	1.1	94
2495	In-depth proteomic analysis of nacre, prism, and myostracum of Mytilus shell. Journal of Proteomics, 2015, 122, 26-40.	1.2	93
2496	Functional diversification of the dehydrin gene family in apple and its contribution to cold acclimation during dormancy. Physiologia Plantarum, 2015, 155, 315-329.	2.6	18
2497	Transcriptional analysis of susceptible and resistant European corn borer strains and their response to Cry1F protoxin. BMC Genomics, 2015, 16, 558.	1.2	27
2498	Transcripts involved in hemostasis: Exploring salivary complexes from Haementeria vizottoi leeches through transcriptomics, phylogenetic studies and structural features. Toxicon, 2015, 106, 20-29.	0.8	12
2499	Development of SSR markers and assessment of genetic diversity of adzuki bean in the Chinese germplasm collection. Molecular Breeding, 2015, 35, 1.	1.0	16
2500	Prediction of Leymus arenarius (L.) antimicrobial peptides based on de novo transcriptome assembly. Plant Molecular Biology, 2015, 89, 203-214.	2.0	20
2501	Genomic sequence of the aflatoxigenic filamentous fungus Aspergillus nomius. BMC Genomics, 2015, 16, 551.	1.2	33
2502	Transcriptomic and phytochemical analysis of the biosynthesis of characteristic constituents in tea (Camellia sinensis) compared with oil tea (Camellia oleifera). BMC Plant Biology, 2015, 15, 190.	1.6	128
2503	Adaptation to Low Salinity Promotes Genomic Divergence in Atlantic Cod (Gadus morhua L.). Genome Biology and Evolution, 2015, 7, 1644-1663.	1.1	167
2504	Expression profiling of potato cultivars with contrasting tuberization at elevated temperature using microarray analysis. Plant Physiology and Biochemistry, 2015, 97, 108-116.	2.8	27
2505	An efficient transcriptome analysis pipeline to accelerate venom peptide discovery and characterisation. Toxicon, 2015, 107, 282-289.	0.8	17

#	Article	IF	Citations
2506	The Plant Ovule Secretome: A Different View toward Pollenâ€“Pistil Interactions. Journal of Proteome Research, 2015, 14, 4763-4775.	1.8	13
2507	Transciptome analysis reveals flavonoid biosynthesis regulation and simple sequence repeats in yam (Dioscorea alata L.) tubers. BMC Genomics, 2015, 16, 346.	1.2	45
2508	Bacterial clade with the ribosomal RNA operon on a small plasmid rather than the chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14343-14347.	3.3	47
2509	Comparative transcriptomic analysis revealed adaptation mechanism of Phrynocephalus erythrurus, the highest altitude Lizard living in the Qinghai-Tibet Plateau. BMC Evolutionary Biology, 2015, 15, 101.	3.2	50
2510	Use of the de novo transcriptome analysis of silver-leaf nightshade (Solanum elaeagnifolium) to identify gene expression changes associated with wounding and terpene biosynthesis. BMC Genomics, 2015, 16, 504.	1.2	24
2511	Transcriptome and expression profiling analysis link patterns of gene expression to antennal responses in Spodoptera litura. BMC Genomics, 2015, 16, 269.	1.2	34
2512	De novo transcriptome characterization and gene expression profiling of the desiccation tolerant moss Bryum argenteum following rehydration. BMC Genomics, 2015, 16, 416.	1.2	73
2513	GO2TR: a gene ontology-based workflow to generate target regions for target enrichment experiments. Conservation Genetics Resources, 2015, 7, 851-857.	0.4	5
2514	Phenylpropanoid metabolism, hormone biosynthesis and signal transduction-related genes play crucial roles in the resistance of Paulownia fortunei to paulownia witchesâ€™ broom phytoplasma infection. Genes and Genomics, 2015, 37, 913-929.	0.5	28
2515	The venomous cocktail of the vampire snail Colubraria reticulata (Mollusca, Gastropoda). BMC Genomics, 2015, 16, 441.	1.2	41
2516	Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	1.2	58
2517	No evidence for Fabaceae Gametophytic self-incompatibility being determined by Rosaceae, Solanaceae, and Plantaginaceae S-RNase lineage genes. BMC Plant Biology, 2015, 15, 129.	1.6	15
2518	Identification, sequencing and comparative analysis of pBp15.S plasmid from the newly described entomopathogen Bacillus pumilus 15.1. Plasmid, 2015, 82, 17-27.	0.4	4
2519	De novo assembly of the Carcinus maenas transcriptome and characterization of innate immune system pathways. BMC Genomics, 2015, 16, 458.	1.2	48
2520	Positive selection in development and growth rate regulation genes involved in species divergence of the genus Radix. BMC Evolutionary Biology, 2015, 15, 164.	3.2	13
2521	Transcriptome sequencing and annotation of the polychaete Hermodice carunculata (Annelida,) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	23
2522	Deep sequencing-based characterization of transcriptome of trifoliate orange (Poncirus trifoliata (L.)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.2	57
2523	Identification and characterization of long non-coding RNAs involved in osmotic and salt stress in Medicago truncatula using genome-wide high-throughput sequencing. BMC Plant Biology, 2015, 15, 131.	1.6	181

#	Article	IF	Citations
2524	Analysis of global gene expression profiles in tobacco roots under drought stress. Open Life Sciences, 2014, 10, .	0.6	2
2525	Genes related to antioxidant metabolism are involved in Methylobacterium mesophilicum-soybean interaction. Antonie Van Leeuwenhoek, 2015, 108, 951-963.	0.7	11
2526	Comprehensive transcriptome and improved genome annotation of <i>Bacillus licheniformis</i> WXâ€02. FEBS Letters, 2015, 589, 2372-2381.	1.3	19
2527	Carboxyl-modified single-walled carbon nanotubes negatively affect bacterial growth and denitrification activity. Scientific Reports, 2014, 4, 5653.	1.6	38
2528	Identification of genetic variations associated with epsilon-poly-lysine biosynthesis in Streptomyces albulus ZPM by genome sequencing. Scientific Reports, 2015, 5, 9201.	1.6	28
2529	Transcriptome comparison of the sex pheromone glands from two sibling Helicoverpa species with opposite sex pheromone components. Scientific Reports, 2015, 5, 9324.	1.6	32
2530	Individual intestinal symbionts induce a distinct population of RORÎ³ ⁺ regulatory T cells. Science, 2015, 349, 993-997.	6.0	707
2531	Genome and physiology of the ascomycete filamentous fungus <scp><i>X</i></scp><i>eromyces bisporus</i>, the most xerophilic organism isolated to date. Environmental Microbiology, 2015, 17, 496-513.	1.8	34
2532	Comparative transcriptome resources of eleven <i>Primulina</i> species, a group of â€˜stone plantsâ€™ from a biodiversity hot spot. Molecular Ecology Resources, 2015, 15, 619-632.	2.2	45
2533	Transcriptome of a specialized extraâ€embryonic cell, teratocyte, and its host immunosuppressive role revealed by <i>ex vivo</i>â€…<scp>RNA</scp> interference. Insect Molecular Biology, 2015, 24, 13-28.	1.0	19
2534	Key molecular processes of the diapause to postâ€diapause quiescence transition in the alfalfa leafcutting bee <i><scp>M</scp>egachile rotundata</i> identified by comparative transcriptome analysis. Physiological Entomology, 2015, 40, 103-112.	0.6	54
2535	Identification of the Gene Cluster for the Anaerobic Degradation of 3,5-Dihydroxybenzoate (Î±-Resorcylate) in Thauera aromatica Strain AR-1. Applied and Environmental Microbiology, 2015, 81, 7201-7214.	1.4	21
2536	Deciphering the Venomic Transcriptome of Killer-Wasp Vespa velutina. Scientific Reports, 2015, 5, 9454.	1.6	49
2537	De novo assembly of kenaf (Hibiscus cannabinus) transcriptome using Illumina sequencing for gene discovery and marker identification. Molecular Breeding, 2015, 35, 1.	1.0	23
2538	Target-site resistance mutations (kdr and RDL), but not metabolic resistance, negatively impact male mating competiveness in the malaria vector Anopheles gambiae. Heredity, 2015, 115, 243-252.	1.2	76
2539	Transcriptome sequencing and characterization for<i>Kappaphycus alvarezii</i>. European Journal of Phycology, 2015, 50, 400-407.	0.9	9
2540	Basidioascus undulatus: genome, origins, and sexuality. IMA Fungus, 2015, 6, 215-231.	1.7	9
2541	Microarray: a global analysis of biomineralization-related gene expression profiles during larval development in the pearl oyster, Pinctada fucata. BMC Genomics, 2015, 16, 325.	1.2	58

#	Article	IF	Citations
2542	Proteomics analysis reveals differentially activated pathways that operate in peanut gynophores at different developmental stages. BMC Plant Biology, 2015, 15, 188.	1.6	26
2543	Transcriptome analysis for identification of indigo biosynthesis pathway genes in Polygonum tinctorium. Biologia (Poland), 2015, 70, 1026-1032.	0.8	12
2544	Top Down Proteomics Reveals Mature Proteoforms Expressed in Subcellular Fractions of the <i>Echinococcus granulosus</i> Preadult Stage. Journal of Proteome Research, 2015, 14, 4805-4814.	1.8	19
2545	Differential gene expression between hygienic and non-hygienic honeybee (Apis mellifera L.) hives. BMC Genomics, 2015, 16, 500.	1.2	38
2546	De novo transcriptome assembly and analysis to identify potential gene targets for RNAi-mediated control of the tomato leafminer (Tuta absoluta). BMC Genomics, 2015, 16, 635.	1.2	31
2547	Co-occurence of filamentation defects and impaired biofilms in<i>Candida albicans</i>protein kinase mutants. FEMS Yeast Research, 2015, 15, fov092.	1.1	14
2548	Harnessing cross-species alignment to discover SNPs and generate a draft genome sequence of a bighorn sheep (Ovis canadensis). BMC Genomics, 2015, 16, 397.	1.2	19
2549	Distinctive expansion of gene families associated with plant cell wall degradation, secondary metabolism, and nutrient uptake in the genomes of grapevine trunk pathogens. BMC Genomics, 2015, 16, 469.	1.2	168
2550	Temporal patterns of gene expression associated with tuberous root formation and development in sweetpotato (Ipomoea batatas). BMC Plant Biology, 2015, 15, 180.	1.6	31
2551	Global Transcriptome Profiling of Developing Leaf and Shoot Apices Reveals Distinct Genetic and Environmental Control of Floral Transition and Inflorescence Development in Barley. Plant Cell, 2015, 27, 2318-2334.	3.1	93
2552	Transcriptomic changes in the plant pathogenic fungus Rhizoctonia solani AG-3 in response to the antagonistic bacteria Serratia proteamaculans and Serratia plymuthica. BMC Genomics, 2015, 16, 630.	1.2	97
2553	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
2554	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
2555	Tissue-specific transcriptome analysis within the maturing sugarcane stalk reveals spatial regulation in the expression of cellulose synthase and sucrose transporter gene families. Plant Molecular Biology, 2015, 89, 607-628.	2.0	55
2556	RNA-Seq analysis for indigo biosynthesis pathway genes in Indigofera tinctoria and Polygonum tinctorium. Genomics Data, 2015, 6, 212-213.	1.3	14
2557	Contrasting hostâ€"pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. Nature Communications, 2015, 6, 7121.	5.8	90
2558	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
2559	Whole transcriptome profiling of the vernalization process in Lilium longiflorum (cultivar White) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	45

#	ARTICLE	IF	CITATIONS
2560	Comprehensive analysis of Panax ginseng root transcriptomes. BMC Plant Biology, 2015, 15, 138.	1.6	55
2561	Identification of promising host-induced silencing targets among genes preferentially transcribed in haustoria of Puccinia. BMC Genomics, 2015, 16, 579.	1.2	47
2562	Characterization of the cork oak transcriptome dynamics during acorn development. BMC Plant Biology, 2015, 15, 158.	1.6	22
2563	Deciphering common and specific transcriptional immune responses in pea towards the oomycete pathogens Aphanomyces euteiches and Phytophthora pisi. BMC Genomics, 2015, 16, 627.	1.2	22
2564	Developmental and metabolic plasticity of white-skinned grape berries in response to Botrytis cinerea during noble rot. Plant Physiology, 2015, 169, pp.00852.2015.	2.3	84
2565	Identification and transcriptomic profiling of genes involved in increasing sugar content during salt stress in sweet sorghum leaves. BMC Genomics, 2015, 16, 534.	1.2	144
2566	Development of EST-SSR markers for Taxus cuspidata from publicly available transcriptome sequences. Biochemical Systematics and Ecology, 2015, 63, 20-26.	0.6	17
2567	Comparative Genomics Including the Early-Diverging Smut Fungus<i>Ceraceosorus bombacis</i>Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. Genome Biology and Evolution, 2015, 7, 2781-2798.	1.1	16
2568	Identification of Theobroma cacao genes differentially expressed during Phytophthora megakarya infection. Physiological and Molecular Plant Pathology, 2015, 92, 1-13.	1.3	22
2569	Transcriptional analysis of adult cutting and juvenile seedling olive roots. Tree Genetics and Genomes, 2015, 11, 1.	0.6	7
2570	Neuropeptide Y family receptors Y1 and Y2 from sea lamprey, Petromyzon marinus. General and Comparative Endocrinology, 2015, 222, 106-115.	0.8	3
2571	SNP discovery in large yellow croaker (Larimichthys crocea) using Roche 454 pyrosequencing sequencing platform. Conservation Genetics Resources, 2015, 7, 777-779.	0.4	2
2572	Dissecting the fungal biology of Bipolaris papendorfii: from phylogenetic to comparative genomic analysis. DNA Research, 2015, 22, 219-232.	1.5	29
2573	Comparison of the sensitivity of four native Canadian fish species to 17-Î± ethinylestradiol, using an in vitro liver explant assay. Environmental Science and Pollution Research, 2015, 22, 20186-20197.	2.7	9
2574	MicroRNAs and targets in senescent litchi fruit during ambient storage and post-cold storage shelf life. BMC Plant Biology, 2015, 15, 181.	1.6	37
2575	Differential expression of the chemosensory transcriptome in two populations of the stemborer Sesamia nonagrioides. Insect Biochemistry and Molecular Biology, 2015, 65, 28-34.	1.2	16
2576	Museum samples reveal rapid evolution by wild honey bees exposed to a novel parasite. Nature Communications, 2015, 6, 7991.	5.8	81
2577	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian) Tj ETQq1 1 0.784314 rgBT /Overl esterases and an arabinopyranosidase. Applied Microbiology and Biotechnology, 2015, 99, 10031-10046.	1.7	36

#	Article	IF	Citations
2578	Comparative proteomic analysis of silkworm fat body after knocking out fibroin heavy chain gene: a novel insight into cross-talk between tissues. Functional and Integrative Genomics, 2015, 15, 611-637.	1.4	15
2579	Transcriptome profiling of larvae of the marine medaka Oryzias melastigma by Illumina RNA-seq. Marine Genomics, 2015, 24, 255-258.	0.4	11
2580	Transcriptomic Analyses Reveal Novel Genes with Sexually Dimorphic Expression in Yellow Catfish (Pelteobagrus fulvidraco) Brain. Marine Biotechnology, 2015, 17, 613-623.	1.1	27
2581	Proteome Analysis Unravels Mechanism Underling the Embryogenesis of the Honeybee Drone and Its Divergence with the Worker (<i>Apis mellifera lingustica</i>). Journal of Proteome Research, 2015, 14, 4059-4071.	1.8	22
2582	The Brassica rapa Genome. Compendium of Plant Genomes, 2015, , .	0.3	8
2583	A global transcriptional analysis of Megalobrama amblycephala revealing the molecular determinants of diet-induced hepatic steatosis. Gene, 2015, 570, 255-263.	1.0	11
2584	Complete Genome Sequence of a Western Siberian Lymantria dispar Multiple Nucleopolyhedrovirus Isolate. Genome Announcements, 2015, 3, .	0.8	6
2585	Spatio-temporal transcriptome analysis in the marine snail Tegula atra along central-northern Chile (28â€“31Â°S). Marine Genomics, 2015, 23, 61-65.	0.4	2
2586	Generation of expressed sequence tags from a cDNA library of Coleus forskohlii for identification of genes involved in terpene biosynthesis. Biologia Plantarum, 2015, 59, 463-468.	1.9	5
2587	Effects of Phosphorylation of Î² Subunits of Phycocyanins on State Transition in the Model Cyanobacterium<i>Synechocystis</i>sp. PCC 6803. Plant and Cell Physiology, 2015, 56, 1997-2013.	1.5	37
2588	In-depth study of <i>Mollivirus sibericum</i> , a new 30,000-y-old giant virus infecting <i>Acanthamoeba</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5327-35.	3.3	284
2589	Genetic architecture of cyst nematode resistance revealed by genome-wide association study in soybean. BMC Genomics, 2015, 16, 593.	1.2	111
2590	Comparative RNA-seq analysis of the Tritrichomonas foetus PIG30/1 isolate from pigs reveals close association with Tritrichomonas foetus BP-4 isolate â€˜bovine genotypeâ€™. Veterinary Parasitology, 2015, 212, 111-117.	0.7	17
2591	Embryonic gene expression of Coregonus palaea (whitefish) under pathogen stress as analyzed by high-throughput RNA-sequencing. Fish and Shellfish Immunology, 2015, 47, 130-140.	1.6	7
2592	Nitrate sensing by the maize root apex transition zone: a merged transcriptomic and proteomic survey. Journal of Experimental Botany, 2015, 66, 3699-3715.	2.4	61
2593	Genomics of Adaptation to Multiple Concurrent Stresses: Insights from Comparative Transcriptomics of a Cichlid Fish from One of Earthâ€™s Most Extreme Environments, the Hypersaline Soda Lake Magadi in Kenya, East Africa. Journal of Molecular Evolution, 2015, 81, 90-109.	0.8	42
2594	Transcriptome comparative analysis revealed poly(I:C) activated RIG-I/MDA5-mediated signaling pathway in miiuy croaker. Fish and Shellfish Immunology, 2015, 47, 168-174.	1.6	41
2595	Genome Evolution and Innovation across the Four Major Lineages of Cryptococcus gattii. MBio, 2015, 6, e00868-15.	1.8	101

#	Article	IF	Citations
2596	Identification of soybean herbivory-regulated genes and a transgenic investigation of their potential in insect resistance. Plant Cell, Tissue and Organ Culture, 2015, 123, 321-340.	1.2	13
2597	Expressed sequence tag analyses of three leukocyte subpopulations in ayu Plecoglossus altivelis altivelis, separated by monoclonal antibodies. Marine Genomics, 2015, 23, 123-132.	0.4	5
2598	Transcriptome analysis of vertebral bone in the flounder, Paralichthys olivaceus (Teleostei,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662 Td	0.4	9
2599	De novo assembly and characterization of transcriptome using Illumina sequencing and development of twenty five microsatellite markers for an endemic tree Juglans hopeiensis Hu in China. Biochemical Systematics and Ecology, 2015, 63, 201-211.	0.6	41
2600	Draft genome sequence of Citrobacter freundii strain ST2, a Î³-proteobacterium that produces N-acylhomoserine lactones. Genomics Data, 2015, 6, 234-236.	1.3	6
2601	Isobaric tags for relative and absolute quantitation (iTRAQ)-based proteomic analysis of Cryptococcus humicola response to aluminum stress. Journal of Bioscience and Bioengineering, 2015, 120, 359-363.	1.1	13
2602	Combined Transcriptomics Analysis for Classification of Adverse Effects As a Potential End Point in Effect Based Screening. Environmental Science & Technology, 2015, 49, 14274-14281.	4.6	9
2603	Identification of genes related to learning and memory in the brain transcriptome of the mollusc, <i>Hermissenda crassicornis</i>. Learning and Memory, 2015, 22, 617-621.	0.5	13
2604	De novo sequencing of the Hypericum perforatum L. flower transcriptome to identify potential genes that are related to plant reproduction sensu lato. BMC Genomics, 2015, 16, 254.	1.2	37
2605	Genetic signatures of adaptation revealed from transcriptome sequencing of Arctic and red foxes. BMC Genomics, 2015, 16, 585.	1.2	22
2606	The cell envelope proteome of <i>Aggregatibacter actinomycetemcomitans</i>. Molecular Oral Microbiology, 2015, 30, 97-110.	1.3	9
2607	PdbrlA, PdabaA and PdwetA control distinct stages of conidiogenesis in Penicillium digitatum. Research in Microbiology, 2015, 166, 56-65.	1.0	56
2608	Novel transcriptome assembly and improved annotation of the whiteleg shrimp (Litopenaeus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.6	89
2609	VennBLASTâ€"Whole transcriptome comparison and visualization tool. Genomics, 2015, 105, 131-136.	1.3	3
2610	Two Blast-independent tools, CyPerl and CyExcel, for harvesting hundreds of novel cyclotides and analogues from plant genomes and protein databases. Planta, 2015, 241, 929-940.	1.6	18
2611	Venom-Related Transcripts from Bothrops jararaca Tissues Provide Novel Molecular Insights into the Production and Evolution of Snake Venom. Molecular Biology and Evolution, 2015, 32, 754-766.	3.5	76
2612	New insights into the wheat chromosome 4D structure and virtual gene order, revealed by survey pyrosequencing. Plant Science, 2015, 233, 200-212.	1.7	20
2613	De novo assembly of the transcriptome of <i>Acanthaster planci</i> testes. Molecular Ecology Resources, 2015, 15, 953-966.	2.2	17

#	ARTICLE	IF	CITATIONS
2614	The Dynamically Evolving Nematocyst Content of an Anthozoan, a Scyphozoan, and a Hydrozoan. Molecular Biology and Evolution, 2015, 32, 740-753.	3.5	90
2615	Characterizing the proteome and oxi-proteome of apple in response to a host (Penicillium expansum) and a non-host (Penicillium digitatum) pathogen. Journal of Proteomics, 2015, 114, 136-151.	1.2	26
2616	Transcriptome analysis reveals diversified adaptation of Stipa purpurea along a drought gradient on the Tibetan Plateau. Functional and Integrative Genomics, 2015, 15, 295-307.	1.4	36
2617	RNA-Seq-based transcriptome analysis of dormant flower buds of Chinese cherry (Prunus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	83
2618	A mutation in the aroE gene affects pigment production, virulence, and chemotaxis in Xanthomonas oryzae pv. oryzae. Microbiological Research, 2015, 170, 124-130.	2.5	4
2619	Diofenolan induces male offspring production through binding to the juvenile hormone receptor in Daphnia magna. Aquatic Toxicology, 2015, 159, 44-51.	1.9	32
2620	De novo characterization of the Lycium chinense Mill. leaf transcriptome and analysis of candidate genes involved in carotenoid biosynthesis. Gene, 2015, 555, 458-463.	1.0	21
2621	Transcriptional Reprogramming of the Mycoparasitic Fungus <i>Ampelomyces quisqualis</i> During the Powdery Mildew Host-Induced Germination. Phytopathology, 2015, 105, 199-209.	1.1	22
2622	Molecular Landscape of Helopeltis theivora Induced Transcriptome and Defense Gene Expression in Tea. Plant Molecular Biology Reporter, 2015, 33, 1042-1057.	1.0	9
2623	De novo transcriptome assembly, gene annotation, marker development, and miRNA potential target genes validation under abiotic stresses in Oenanthe javanica. Molecular Genetics and Genomics, 2015, 290, 671-683.	1.0	48
2624	The Tribolium castaneum cell line TcA: a new tool kit for cell biology. Scientific Reports, 2014, 4, 6840.	1.6	18
2625	Comparative Transcriptomics of Convergent Evolution: Different Genes but Conserved Pathways Underlie Caste Phenotypes across Lineages of Eusocial Insects. Molecular Biology and Evolution, 2015, 32, 690-703.	3.5	161
2626	Characterization of Coffee Genes Involved in Isoprenoid and Diterpene Metabolic Pathways. , 2015, , 45-51.		4
2627	Genome-wide development of transposable elements-based markers in foxtail millet and construction of an integrated database. DNA Research, 2015, 22, 79-90.	1.5	71
2628	Stage-specific reprogramming of gene expression characterizes Lr48-mediated adult plant leaf rust resistance in wheat. Functional and Integrative Genomics, 2015, 15, 233-245.	1.4	11
2629	Transcriptome profiling of the testis reveals genes involved in spermatogenesis and marker discovery in the oriental fruit fly, <i><scp>B</scp>actrocera dorsalis</i>. Insect Molecular Biology, 2015, 24, 41-57.	1.0	62
2630	Mapping active promoters by Ch<scp>IP</scp>â€seq profiling of H3K4me3 in cichlid fish â€" a first step to uncover cisâ€regulatory elements in ecological model teleosts. Molecular Ecology Resources, 2015, 15, 761-771.	2.2	22
2631	The Draft Genome of Hop (Humulus lupulus), an Essence for Brewing. Plant and Cell Physiology, 2015, 56, 428-441.	1.5	111

#	Article	IF	Citations
2632	TRANSCRIPTOME ANALYSIS OF AN ENDOPARASITOID WASP <i>Cotesia chilonis</i> (HYMENOPTERA:) Tj ETQq0 0 0 rgBT /Overlock 10 T and Physiology, 2015, 88, 203-221.	0.6	17
2633	Female transcriptomic response to male genetic and nongenetic ejaculate variation. Behavioral Ecology, 2015, 26, 681-688.	1.0	7
2634	SNP discovery and gene annotation in the surf clam<i>Mesodesma donacium</i>. Aquaculture Research, 2015, 46, 1175-1187.	0.9	4
2635	<i>De novo</i> assembly and comparative analysis of the <i><scp>C</scp>eratodon purpureus</i> transcriptome. Molecular Ecology Resources, 2015, 15, 203-215.	2.2	43
2636	Genome, Transcriptome, and Functional Analyses of <i>Penicillium expansum</i> Provide New Insights Into Secondary Metabolism and Pathogenicity. Molecular Plant-Microbe Interactions, 2015, 28, 232-248.	1.4	183
2637	Characterization of novel insect associated peptidases for hydrolysis of food proteins. European Food Research and Technology, 2015, 240, 431-439.	1.6	14
2638	Liver immune responses to inflammatory stimuli in a diet-induced obesity model of zebrafish. Journal of Endocrinology, 2015, 224, 159-170.	1.2	37
2639	Development of chemical and EST-SSR markers for Ocimum genus. Industrial Crops and Products, 2015, 63, 65-70.	2.5	14
2640	A family of variable immunoglobulin and lectin domain containing molecules in the snail Biomphalaria glabrata. Developmental and Comparative Immunology, 2015, 48, 234-243.	1.0	85
2642	Transcriptome Analysis of a Subtropical Deciduous Tree: Autumn Leaf Senescence Gene Expression Profile of Formosan Gum. Plant and Cell Physiology, 2015, 56, 163-174.	1.5	34
2643	Identification of Genes Involved in the Biosynthesis of Tripterygium wilfordii Hook.f. Secondary Metabolites by Suppression Subtractive Hybridization. Plant Molecular Biology Reporter, 2015, 33, 756-769.	1.0	9
2644	De novo transcriptome characterization of Lilium â€˜Sorbonneâ€™ and key enzymes related to the flavonoid biosynthesis. Molecular Genetics and Genomics, 2015, 290, 399-412.	1.0	39
2645	Comparative transcriptomic analysis provides insights into the molecular basis of the metamorphosis and nutrition metabolism change from zoeae to megalopae in Eriocheir sinensis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 13, 1-9.	0.4	27
2646	Proteomic profile in Perna viridis after exposed to Prorocentrum lima, a dinoflagellate producing DSP toxins. Environmental Pollution, 2015, 196, 350-357.	3.7	48
2647	Genome-wide identification and structure-function studies of proteases and protease inhibitors in Cicer arietinum (chickpea). Computers in Biology and Medicine, 2015, 56, 67-81.	3.9	7
2648	<i>Petunia</i>â€‰Ã—â€‰<i>hybrida</i> floral scent production is negatively affected by highâ€temperature growth conditions. Plant, Cell and Environment, 2015, 38, 1333-1346.	2.8	49
2649	New Insights into Fruit Firmness and Weight Control in Sweet Cherry. Plant Molecular Biology Reporter, 2015, 33, 783-796.	1.0	39
2650	iTRAQ-based quantitative proteomics analysis of Brassica napus leaves reveals pathways associated with chlorophyll deficiency. Journal of Proteomics, 2015, 113, 244-259.	1.2	111

#	ARTICLE	IF	CITATIONS
2651	Characterization of the <scp>A</scp>ntarctic sea urchin (<i><scp>S</scp>terechinus neumayeri</i>) transcriptome and mitogenome: a molecular resource for phylogenetics, ecophysiology and global change biology. Molecular Ecology Resources, 2015, 15, 425-436.	2.2	21
2652	Comparative subproteome analysis of three representative Leptospira interrogans vaccine strains reveals cross-reactive antigens and novel virulence determinants. Journal of Proteomics, 2015, 112, 27-37.	1.2	7
2653	Transcriptomic and proteomic analyses of embryogenic tissues in <i>Picea balfouriana</i> treated with 6â€benzylaminopurine. Physiologia Plantarum, 2015, 154, 95-113.	2.6	36
2654	Genome of the halotolerant green alga <scp><i>P</i></scp><i>icochlorum</i> sp. reveals strategies for thriving under fluctuating environmental conditions. Environmental Microbiology, 2015, 17, 412-426.	1.8	85
2655	Whole genome and transcriptome analyses of environmental antibiotic sensitive and multiâ€resistant <scp><i>P</i></scp><i>seudomonas aeruginosa</i> isolates exposed to waste water and tap water. Microbial Biotechnology, 2015, 8, 116-130.	2.0	21
2656	Population transcriptomics reveals a potentially positive role of expression diversity in adaptation. Journal of Integrative Plant Biology, 2015, 57, 284-299.	4.1	26
2657	Normal operating range (NOR) in Enchytraeus albidus â€" Transcriptional responses to control conditions. Applied Soil Ecology, 2015, 85, 1-10.	2.1	4
2658	Design of a 9K illumina BeadChip for polar bears (<i><scp>U</scp>rsus maritimus</i>) from <scp>RAD</scp> and transcriptome sequencing. Molecular Ecology Resources, 2015, 15, 587-600.	2.2	45
2659	Comparative transcriptome analysis of early somatic embryo formation and seed development in Brazilian pine, Araucaria angustifolia (Bertol.) Kuntze. Plant Cell, Tissue and Organ Culture, 2015, 120, 903-915.	1.2	59
2660	Gene expression changes in tomato during symptom development in response to leaf curl virus infection. Journal of Plant Biochemistry and Biotechnology, 2015, 24, 347-354.	0.9	11
2661	Analysis of the Drought Stress-Responsive Transcriptome of Black Cottonwood (Populus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (	1.0	40
2662	Gene expression plasticity resulting from parental leaf damage in M imulus guttatus. New Phytologist, 2015, 205, 894-906.	3.5	22
2663	Next-Generation Sequencing: A Review of Technologies and Tools for Wound Microbiome Research. Advances in Wound Care, 2015, 4, 50-58.	2.6	109
2664	Transcriptome resources for the whiteâ€footed mouse (<i>Peromyscus leucopus</i>): new genomic tools for investigating ecologically divergent urban and rural populations. Molecular Ecology Resources, 2015, 15, 382-394.	2.2	52
2665	The Genome of the Saprophytic Fungus <i>Verticillium tricorpus</i> Reveals a Complex Effector Repertoire Resembling That of Its Pathogenic Relatives. Molecular Plant-Microbe Interactions, 2015, 28, 362-373.	1.4	61
2666	Genomic exploration and molecular marker development in a large and complex conifer genome using RADseq and mRNAseq. Molecular Ecology Resources, 2015, 15, 601-612.	2.2	25
2667	Characterization of the â€˜Xiangshuiâ€™ lemon transcriptome by de novo assembly to discover genes associated with self-incompatibility. Molecular Genetics and Genomics, 2015, 290, 365-375.	1.0	39
2668	De Novo Assembled Transcriptome Analysis and SSR Marker Development of a Mixture of Six Tissues from Lilium Oriental Hybrid â€˜Sorbonneâ€™. Plant Molecular Biology Reporter, 2015, 33, 281-293.	1.0	54

#	Article	IF	Citations
2669	Differences in Physiological Characteristics and Gene Expression Levels in Fruits between Japanese Persimmon (<i>Diospyros kaki</i> Thunb.) â€˜Hiratanenashiâ€™ and Its Small Fruit Mutant â€˜Totsutanenashiâ€™. Horticulture Journal, 2016, 85, 306-314.	0.3	8
2670	Bioinformatics Tools and Genomic Resources Available in Understanding the Structure and Function of Gossypium. , 2016, , .		4
2671	De novo assembly and characterization of Gleditsia sinensis transcriptome and subsequent gene identification and SSR mining. Genetics and Molecular Research, 2016, 15, .	0.3	4
2672	Whole-transcriptome sequencing of Pinellia ternata using the Illumina platform. Genetics and Molecular Research, 2016, 15, .	0.3	3
2673	In silico identification of putative expressed sequence tag (EST)-simple sequence repeats (SSRs) markers of resistance to Meloidogyne spp. in common bean. African Journal of Agricultural Research Vol Pp, 2016, 11, 2007-2012.	0.2	0
2674	Draft Genome Sequence of <i>Capniomyces stellatus</i> , the Obligate Gut Fungal Symbiont of Stonefly. Genome Announcements, 2016, 4, .	0.8	5
2675	Transcriptome Analysis of Ramie (Boehmeria niveaL. Gaud.) in Response to Ramie Moth (Cocytodes) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	9
2676	Sixteen kiwi (Apteryx spp) transcriptomes provide a wealth of genetic markers and insight into sex chromosome evolution in birds. BMC Genomics, 2016, 17, 410.	1.2	16
2677	RNA-sequencing of the sturgeon Acipenser baeri provides insights into expression dynamics of morphogenic differentiation and developmental regulatory genes in early versus late developmental stages. BMC Genomics, 2016, 17, 564.	1.2	13
2678	Tsetse fly tolerance to T. brucei infection: transcriptome analysis of trypanosome-associated changes in the tsetse fly salivary gland. BMC Genomics, 2016, 17, 971.	1.2	38
2679	De novo Transcriptome Generation and Annotation for Two Korean Endemic Land Snails, Aegista chejuensis and Aegista quelpartensis, Using Illumina Paired-End Sequencing Technology. International Journal of Molecular Sciences, 2016, 17, 379.	1.8	7
2680	Sexually Dimorphic Gene Expression Associated with Growth and Reproduction of Tongue Sole (Cynoglossus semilaevis) Revealed by Brain Transcriptome Analysis. International Journal of Molecular Sciences, 2016, 17, 1402.	1.8	15
2681	Generation and Characterisation of a Reference Transcriptome for Lentil (Lens culinaris Medik.). International Journal of Molecular Sciences, 2016, 17, 1887.	1.8	49
2682	Hierarchical Map of Orthologous Genomic Regions Reconstructed from Two Closely Related Genomes: Cucumber Case Study. Plant Genome, 2016, 9, plantgenome2015.10.0099.	1.6	1
2683	RNA Sequencing and Transcriptome Analyses for Cercis Gigantean. Current Bioinformatics, 2016, 11, 32-39.	0.7	0
2684	The early events underlying genome evolution in a localized Sinorhizobium meliloti population. BMC Genomics, 2016, 17, 556.	1.2	5
2685	Development, characterization, and annotation of potential simple sequence repeats by transcriptome sequencing in pears (Pyrus pyrifolia Nakai). Genetics and Molecular Research, 2016, 15, .	0.3	4
2686	Toward a First High-quality Genome Draft for Marker-assisted Breeding in Leaf Chicory, Radicchio (Cichorium intybus L.). , 0, , .		11

#	Article	IF	Citations
2687	OGS2: genome re-annotation of the jewel wasp Nasonia vitripennis. BMC Genomics, 2016, 17, 678.	1.2	35
2688	The genome of the emerging barley pathogen Ramularia collo-cygni. BMC Genomics, 2016, 17, 584.	1.2	36
2689	De novo assembly and analysis of changes in the protein-coding transcriptome of the freshwater shrimp Paratya australiensis (Decapoda: Atyidae) in response to acid sulfate drainage water. BMC Genomics, 2016, 17, 890.	1.2	12
2690	In-Silico Prediction and Functional Analysis of Salt Stress Responsive Genes in Rice (Oryza sativa). Rice Research Open Access, 2016, 4, .	0.4	7
2691	Transcriptome analysis of potential simple sequence repeat markers in Ammopiptanthus mongolicus. Genetics and Molecular Research, 2016, 15, .	0.3	3
2692	Transcriptomic Analysis ofEucryptorrhynchus chinensis(Coleoptera: Curculionidae) Using 454 Pyrosequencing Technology. Journal of Insect Science, 2016, 16, 82.	0.6	6
2693	Extracellular Matrix Proteome and Phosphoproteome of Potato Reveals Functionally Distinct and Diverse Canonical and Non-Canonical Proteoforms. Proteomes, 2016, 4, 20.	1.7	9
2694	RareDDB: An Integrated Catalog of Rare Disease Database. Clinical & Medical Biochemistry Open Access, 2016, , .	0.1	1
2695	Spider phylogenomics: untangling the Spider Tree of Life. PeerJ, 2016, 4, e1719.	0.9	253
2696	Proteomic profiling change during the early development of silicosis disease. Journal of Thoracic Disease, 2016, 8, 329-341.	0.6	12
2697	Proteomic profiling differences in serum from silicosis and chronic bronchitis patients: a comparative analysis. Journal of Thoracic Disease, 2016, 8, 439-450.	0.6	5
2698	De novo Assembly and Analysis of the Chilean Pencil Catfish Trichomycterus areolatus Transcriptome. Journal of Genomics, 2016, 4, 29-41.	0.6	7
2699	RNA-seq profiling of mRNA associated with hypertrophic cardiomyopathy. Molecular Medicine Reports, 2016, 14, 5573-5586.	1.1	18
2700	Analysis of Gene Expression in an Inbred Line of Soft-Shell Clams (Mya arenaria) Displaying Growth Heterosis: Regulation of Structural Genes and the NOD2 Pathway. International Journal of Genomics, 2016, 2016, 1-10.	0.8	2
2701	<i>De Novo</i>Transcriptome Sequencing of<i>Olea europaea</i>L. to Identify Genes Involved in the Development of the Pollen Tube. Scientific World Journal, The, 2016, 2016, 1-7.	0.8	13
2702	Differential Gene Expression during Larval Metamorphic Development in the Pearl Oyster,<i>Pinctada fucata</i>, Based on Transcriptome Analysis. International Journal of Genomics, 2016, 2016, 1-15.	0.8	9
2703	Transcriptome Profile of the Asian Giant Hornet (<i>Vespa mandarinia</i>) Using Illumina HiSeq 4000 Sequencing:<i>De Novo</i>Assembly, Functional Annotation, and Discovery of SSR Markers. International Journal of Genomics, 2016, 2016, 1-15.	0.8	24
2704	Analyses of Physcomitrella patens Ankyrin Repeat Proteins by Computational Approach. Molecular Biology International, 2016, 2016, 1-8.	1.7	1

#	Article	IF	Citations
2705	Whole Blood Transcriptome Sequencing Reveals Gene Expression Differences between Dapulian and Landrace Piglets. BioMed Research International, 2016, 2016, 1-10.	0.9	3
2706	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). G3: Genes, Genomes, Genetics, 2016, 6, 3787-3802.	0.8	51
2707	RNA-Seq analysis of seasonal and individual variation in blood transcriptomes of healthy managed bottlenose dolphins. BMC Genomics, 2016, 17, 720.	1.2	33
2708	Transcriptomics of Intralocus Sexual Conflict: Gene Expression Patterns in Females Change in Response to Selection on a Male Secondary Sexual Trait in the Bulb Mite. Genome Biology and Evolution, 2016, 8, 2351-2357.	1.1	20
2709	Transcriptome Sequencing and Development of Genic SSR Markers of an Endangered Chinese Endemic Genus Dipteronia Oliver (Aceraceae). Molecules, 2016, 21, 166.	1.7	24
2710	Transcriptome analysis and de novo annotation of the critically endangered Amur sturgeon (Acipenser schrenckii). Genetics and Molecular Research, 2016, 15, .	0.3	9
2711	Identification of Mild Freezing Shock Response Pathways in Barley Based on Transcriptome Profiling. Frontiers in Plant Science, 2016, 7, 106.	1.7	22
2712	Insight into the Exoproteome of the Tissue-Derived Trypomastigote form of Trypanosoma cruzi. Frontiers in Chemistry, 2016, 4, 42.	1.8	22
2713	From Mollusks to Medicine: A Venomics Approach for the Discovery and Characterization of Therapeutics from Terebridae Peptide Toxins. Toxins, 2016, 8, 117.	1.5	40
2714	Colubrid Venom Composition: An -Omics Perspective. Toxins, 2016, 8, 230.	1.5	61
2715	Transcriptome Analysis to Understand the Toxicity of Latrodectus tredecimguttatus Eggs. Toxins, 2016, 8, 378.	1.5	13
2716	A Brazilian Marseillevirus Is the Founding Member of a Lineage in Family Marseilleviridae. Viruses, 2016, 8, 76.	1.5	74
2717	De Novo Transcriptome Analysis Shows That SAV-3 Infection Upregulates Pattern Recognition Receptors of the Endosomal Toll-Like and RIG-I-Like Receptor Signaling Pathways in Macrophage/Dendritic Like TO-Cells. Viruses, 2016, 8, 114.	1.5	38
2718	Aphis Glycines Virus 2, a Novel Insect Virus with a Unique Genome Structure. Viruses, 2016, 8, 315.	1.5	17
2719	P- and N-Depletion Trigger Similar Cellular Responses to Promote Senescence in Eukaryotic Phytoplankton. Frontiers in Marine Science, 2016, 3, .	1.2	28
2720	Ontogenetic Changes in the Bacterial Symbiont Community of the Tropical Demosponge Amphimedon queenslandica: Metamorphosis Is a New Beginning. Frontiers in Marine Science, 2016, 3, .	1.2	49
2721	Comparative Analysis of Salivary Gland Proteomes of Two Glossina Species that Exhibit Differential Hytrosavirus Pathologies. Frontiers in Microbiology, 2016, 7, 89.	1.5	8
2722	Understanding the Role of the Master Regulator XYR1 in Trichoderma reesei by Global Transcriptional Analysis. Frontiers in Microbiology, 2016, 7, 175.	1.5	91

#	ARTICLE	IF	CITATIONS
2723	Tricking Arthrinium malaysianum into Producing Industrially Important Enzymes Under 2-Deoxy D-Glucose Treatment. Frontiers in Microbiology, 2016, 7, 596.	1.5	10
2724	Fungal and Prokaryotic Activities in the Marine Subsurface Biosphere at Peru Margin and Canterbury Basin Inferred from RNA-Based Analyses and Microscopy. Frontiers in Microbiology, 2016, 7, 846.	1.5	52
2725	From DNA to FBA: How to Build Your Own Genome-Scale Metabolic Model. Frontiers in Microbiology, 2016, 7, 907.	1.5	40
2726	Transcriptome Analysis Reveals the Genetic Basis of the Resveratrol Biosynthesis Pathway in an Endophytic Fungus (Alternaria sp. MG1) Isolated from Vitis vinifera. Frontiers in Microbiology, 2016, 7, 1257.	1.5	18
2727	Quantitative Proteomic Analysis of Germination of Nosema bombycis Spores under Extremely Alkaline Conditions. Frontiers in Microbiology, 2016, 7, 1459.	1.5	29
2728	Rhamnolipid Biosurfactant against Fusarium verticillioides to Control Stalk and Ear Rot Disease of Maize. Frontiers in Microbiology, 2016, 7, 1505.	1.5	64
2729	RNAseq Analysis of Endornavirus-Infected vs. Endornavirus-Free Common Bean (Phaseolus vulgaris) Cultivar Black Turtle Soup. Frontiers in Microbiology, 2016, 7, 1905.	1.5	12
2730	CpG Oligodeoxynucleotides Induce Differential Cytokine and Chemokine Gene Expression Profiles in Dapulian and Landrace Pigs. Frontiers in Microbiology, 2016, 7, 1992.	1.5	14
2731	The Different Roles of Penicillium oxalicum LaeA in the Production of Extracellular Cellulase and Î²-xylosidase. Frontiers in Microbiology, 2016, 7, 2091.	1.5	50
2732	De Novo Assembly and Characterization of Bud, Leaf and Flowers Transcriptome from Juglans Regia L. for the Identification and Characterization of New EST-SSRs. Forests, 2016, 7, 247.	0.9	52
2733	Transcriptomic Analysis of the Endangered Neritid Species Clithon retropictus: De Novo Assembly, Functional Annotation, and Marker Discovery. Genes, 2016, 7, 35.	1.0	13
2734	Transcriptome Analysis of the Tadpole Shrimp (Triops longicaudatus) by Illumina Paired-End Sequencing: Assembly, Annotation, and Marker Discovery. Genes, 2016, 7, 114.	1.0	15
2735	Identification of Differentially Expressed Genes between â€œHoneycrispâ€•and â€œGolden Deliciousâ€•Apple Fruit Tissues Reveal Candidates for Crop Improvement. Horticulturae, 2016, 2, 11.	1.2	3
2736	Transcriptome-Based Identification of Differently Expressed Genes from Xanthomonas oryzae pv. oryzae Strains Exhibiting Different Virulence in Rice Varieties. International Journal of Molecular Sciences, 2016, 17, 259.	1.8	6
2737	De Novo Transcriptome Assembly in Shiraia bambusicola to Investigate Putative Genes Involved in the Biosynthesis of Hypocrellin A. International Journal of Molecular Sciences, 2016, 17, 311.	1.8	45
2738	Transcriptome and Gene Ontology (GO) Enrichment Analysis Reveals Genes Involved in Biotin Metabolism That Affect l-Lysine Production in Corynebacterium glutamicum. International Journal of Molecular Sciences, 2016, 17, 353.	1.8	16
2739	Transcriptome Sequencing Analyses between the Cytoplasmic Male Sterile Line and Its Maintainer Line in Welsh Onion (Allium fistulosum L.). International Journal of Molecular Sciences, 2016, 17, 1058.	1.8	26
2740	De Novo Assembly and Characterization of the Transcriptome of Grasshopper Shirakiacris shirakii. International Journal of Molecular Sciences, 2016, 17, 1110.	1.8	10

#	Article	IF	Citations
2741	De Novo Analysis of the Transcriptome of Meloidogyne enterolobii to Uncover Potential Target Genes for Biological Control. International Journal of Molecular Sciences, 2016, 17, 1442.	1.8	17
2742	Identification and Functional Analysis of microRNAs Involved in the Anther Development in Cotton Genic Male Sterile Line Yu98-8A. International Journal of Molecular Sciences, 2016, 17, 1677.	1.8	14
2743	Transcriptome Sequencing and De Novo Assembly of Golden Cuttlefish Sepia esculenta Hoyle. International Journal of Molecular Sciences, 2016, 17, 1749.	1.8	15
2744	Comparative Transcriptional Analysis of Loquat Fruit Identifies Major Signal Networks Involved in Fruit Development and Ripening Process. International Journal of Molecular Sciences, 2016, 17, 1837.	1.8	11
2745	Functional Annotations of Paralogs: A Blessing and a Curse. Life, 2016, 6, 39.	1.1	45
2746	Antifungal Activity of Eucalyptus Oil against Rice Blast Fungi and the Possible Mechanism of Gene Expression Pattern. Molecules, 2016, 21, 621.	1.7	24
2747	Comparative Transcriptomic Analysis of Grape Berry in Response to Root Restriction during Developmental Stages. Molecules, 2016, 21, 1431.	1.7	21
2748	Pinpointing genes underlying annual/perennial transitions with comparative genomics. BMC Genomics, 2016, 17, 921.	1.2	16
2749	Transcriptome comparison reveals key candidate genes in response to vernalization of Oriental lily. BMC Genomics, 2016, 17, 664.	1.2	22
2750	Genetic mapping of Pinus flexilis major gene (Cr4) for resistance to white pine blister rust using transcriptome-based SNP genotyping. BMC Genomics, 2016, 17, 753.	1.2	33
2751	Transcriptome profiling analysis for two Tibetan wild barley genotypes in responses to low nitrogen. BMC Plant Biology, 2016, 16, 30.	1.6	104
2752	A proteomics approach reveals molecular manipulators of distinct cellular processes in the salivary glands of Glossina m. morsitans in response to Trypanosoma b. brucei infections. Parasites and Vectors, 2016, 9, 424.	1.0	11
2753	An MYB transcription factor regulating specialized metabolisms in <i>Ophiorrhiza pumila</i>. Plant Biotechnology, 2016, 33, 1-9.	0.5	35
2754	iTRAQ-Based Quantitative Proteomics Analysis of Black Rice Grain Development Reveals Metabolic Pathways Associated with Anthocyanin Biosynthesis. PLoS ONE, 2016, 11, e0159238.	1.1	21
2755	Biosynthesis of Antibiotic Leucinostatins in Bio-control Fungus Purpureocillium lilacinum and Their Inhibition on Phytophthora Revealed by Genome Mining. PLoS Pathogens, 2016, 12, e1005685.	2.1	122
2756	Genome Anatomy of Pyrenochaeta unguis-hominis UM 256, a Multidrug Resistant Strain Isolated from Skin Scraping. PLoS ONE, 2016, 11, e0162095.	1.1	9
2757	Proteinaceous Pheromone Homologs Identified from the Cloacal Gland Transcriptome of a Male Axolotl, Ambystoma mexicanum. PLoS ONE, 2016, 11, e0146851.	1.1	6
2758	iTRAQ-Based Quantitative Proteomic Analysis of Cotton Roots and Leaves Reveals Pathways Associated with Salt Stress. PLoS ONE, 2016, 11, e0148487.	1.1	71

#	ARTICLE	IF	CITATIONS
2759	Sex-Biased Transcriptome of Schistosoma mansoni: Host-Parasite Interaction, Genetic Determinants and Epigenetic Regulators Are Associated with Sexual Differentiation. PLoS Neglected Tropical Diseases, 2016, 10, e0004930.	1.3	57
2760	Mevalonate-Farnesal Biosynthesis in Ticks: Comparative Synganglion Transcriptomics and a New Perspective. PLoS ONE, 2016, 11, e0141084.	1.1	19
2761	RNA-Seq Reveals OTA-Related Gene Transcriptional Changes in Aspergillus carbonarius. PLoS ONE, 2016, 11, e0147089.	1.1	23
2762	Characterizing Molecular Mechanisms of Imidacloprid Resistance in Select Populations of Leptinotarsa decemlineata in the Central Sands Region of Wisconsin. PLoS ONE, 2016, 11, e0147844.	1.1	57
2763	De Novo Assembled Wheat Transcriptomes Delineate Differentially Expressed Host Genes in Response to Leaf Rust Infection. PLoS ONE, 2016, 11, e0148453.	1.1	36
2764	Transcriptome Analysis of an Anthracnose-Resistant Tea Plant Cultivar Reveals Genes Associated with Resistance to Colletotrichum camelliae. PLoS ONE, 2016, 11, e0148535.	1.1	55
2765	Multiple I-Type Lysozymes in the Hydrothermal Vent Mussel Bathymodiolus azoricus and Their Role in Symbiotic Plasticity. PLoS ONE, 2016, 11, e0148988.	1.1	14
2766	Effects of Weaning on Intestinal Upper Villus Epithelial Cells of Piglets. PLoS ONE, 2016, 11, e0150216.	1.1	44
2767	Transcriptomic and Proteomic Analysis of Arion vulgarisâ€"Proteins for Probably Successful Survival Strategies?. PLoS ONE, 2016, 11, e0150614.	1.1	12
2768	Pyrosequencing the Midgut Transcriptome of the Banana Weevil Cosmopolites sordidus (Germar) (Coleoptera: Curculionidae) Reveals Multiple Protease-Like Transcripts. PLoS ONE, 2016, 11, e0151001.	1.1	11
2769	Development of Gene-Based SSR Markers in Rice Bean (Vigna umbellata L.) Based on Transcriptome Data. PLoS ONE, 2016, 11, e0151040.	1.1	29
2770	De Novo Transcriptome Analysis Provides Insights into Immune Related Genes and the RIG-I-Like Receptor Signaling Pathway in the Freshwater Planarian (Dugesia japonica). PLoS ONE, 2016, 11, e0151597.	1.1	34
2771	De Novo Adult Transcriptomes of Two European Brittle Stars: Spotlight on Opsin-Based Photoreception. PLoS ONE, 2016, 11, e0152988.	1.1	23
2772	Metabolic Context of the Competence-Induced Checkpoint for Cell Replication in Streptococcus suis. PLoS ONE, 2016, 11, e0153571.	1.1	17
2773	De Novo Transcriptome Analysis of Two Seahorse Species (Hippocampus erectus and H. mohnikei) and the Development of Molecular Markers for Population Genetics. PLoS ONE, 2016, 11, e0154096.	1.1	5
2774	VennPainter: A Tool for the Comparison and Identification of Candidate Genes Based on Venn Diagrams. PLoS ONE, 2016, 11, e0154315.	1.1	67
2775	Molecular Characterization and Sex Distribution of Chemosensory Receptor Gene Family Based on Transcriptome Analysis of Scaeva pyrastri. PLoS ONE, 2016, 11, e0155323.	1.1	14
2776	A Single Transcriptome of a Green Toad (Bufo viridis) Yields Candidate Genes for Sex Determination and -Differentiation and Non-Anonymous Population Genetic Markers. PLoS ONE, 2016, 11, e0156419.	1.1	18

#	Article	IF	Citations
2777	Insights into Sexual Precocity of Female Oriental River Prawn Macrobrachium nipponense through Transcriptome Analysis. PLoS ONE, 2016, 11, e0157173.	1.1	13
2778	Whole Genome Re-Sequencing and Characterization of Powdery Mildew Disease-Associated Allelic Variation in Melon. PLoS ONE, 2016, 11, e0157524.	1.1	32
2779	De Novo Transcriptome Analysis of the Common New Zealand Stick Insect Clitarchus hookeri (Phasmatodea) Reveals Genes Involved in Olfaction, Digestion and Sexual Reproduction. PLoS ONE, 2016, 11, e0157783.	1.1	18
2780	The De Novo Transcriptome and Its Functional Annotation in the Seed Beetle Callosobruchus maculatus. PLoS ONE, 2016, 11, e0158565.	1.1	52
2781	De Novo Assembly and Developmental Transcriptome Analysis of the Small White Butterfly Pieris rapae. PLoS ONE, 2016, 11, e0159258.	1.1	24
2782	Transcriptomic and Expression Analysis of the Salivary Glands in White-Backed Planthoppers, Sogatella furcifera. PLoS ONE, 2016, 11, e0159393.	1.1	18
2783	Transcriptomic Analysis of Multipurpose Timber Yielding Tree Neolamarckia cadamba during Xylogenesis Using RNA-Seq. PLoS ONE, 2016, 11, e0159407.	1.1	26
2784	De Novo Transcriptome Assembly and Annotation of the Leaves and Callus of Cyclocarya Paliurus (Bata1) Iljinskaja. PLoS ONE, 2016, 11, e0160279.	1.1	3
2785	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
2786	Genomic Analyses of Cladophialophora bantiana, a Major Cause of Cerebral Phaeohyphomycosis Provides Insight into Its Lifestyle, Virulence and Adaption in Host. PLoS ONE, 2016, 11, e0161008.	1.1	17
2787	Transcriptomic Profiling Analysis of Arabidopsis thaliana Treated with Exogenous Myo-Inositol. PLoS ONE, 2016, 11, e0161949.	1.1	12
2788	De Novo Assembly and Transcriptome Analysis of Bulb Onion (Allium cepa L.) during Cold Acclimation Using Contrasting Genotypes. PLoS ONE, 2016, 11, e0161987.	1.1	28
2789	De novo Analysis of the Epiphytic Transcriptome of the Cucurbit Powdery Mildew Fungus Podosphaera xanthii and Identification of Candidate Secreted Effector Proteins. PLoS ONE, 2016, 11, e0163379.	1.1	29
2790	De Novo Transcriptomes of Forsythia koreana Using a Novel Assembly Method: Insight into Tissue- and Species-Specific Expression of Lignan Biosynthesis-Related Gene. PLoS ONE, 2016, 11, e0164805.	1.1	26
2791	Deciphering Transcriptional Programming during Pod and Seed Development Using RNA-Seq in Pigeonpea (Cajanus cajan). PLoS ONE, 2016, 11, e0164959.	1.1	11
2792	Gene Expression Dynamics Accompanying the Sponge Thermal Stress Response. PLoS ONE, 2016, 11, e0165368.	1.1	57
2793	Transcriptional Responses and Gentiopicroside Biosynthesis in Methyl Jasmonate-Treated Gentiana macrophylla Seedlings. PLoS ONE, 2016, 11, e0166493.	1.1	14
2794	Transcriptome Analysis of Ceriops tagal in Saline Environments Using RNA-Sequencing. PLoS ONE, 2016, 11, e0167551.	1.1	8

#	ARTICLE	IF	CITATIONS
2795	Insecticidal Activity of Melaleuca alternifolia Essential Oil and RNA-Seq Analysis of Sitophilus zeamais Transcriptome in Response to Oil Fumigation. PLoS ONE, 2016, 11, e0167748.	1.1	85
2796	Integrative Transcriptome, Genome and Quantitative Trait Loci Resources Identify Single Nucleotide Polymorphisms in Candidate Genes for Growth Traits in Turbot. International Journal of Molecular Sciences, 2016, 17, 243.	1.8	45
2797	Gene Expression Profiling Reveals Functional Specialization along the Intestinal Tract of a Carnivorous Teleostean Fish (Dicentrarchus labrax). Frontiers in Physiology, 2016, 7, 359.	1.3	42
2798	Transcriptome Analysis of Brassica rapa Near-Isogenic Lines Carrying Clubroot-Resistant and â€“Susceptible Alleles in Response to Plasmodiophora brassicae during Early Infection. Frontiers in Plant Science, 2015, 6, 1183.	1.7	118
2799	RNA-Seq and Gene Network Analysis Uncover Activation of an ABA-Dependent Signalosome During the Cork Oak Root Response to Drought. Frontiers in Plant Science, 2015, 6, 1195.	1.7	30
2800	Extensive Transcriptome Changes Underlying the Flower Color Intensity Variation in Paeonia ostii. Frontiers in Plant Science, 2015, 6, 1205.	1.7	44
2801	Transcriptomic Analysis for Different Sex Types of Ricinus communis L. during Development from Apical Buds to Inflorescences by Digital Gene Expression Profiling. Frontiers in Plant Science, 2015, 6, 1208.	1.7	21
2802	Heat Shock Factor Genes of Tall Fescue and Perennial Ryegrass in Response to Temperature Stress by RNA-Seq Analysis. Frontiers in Plant Science, 2015, 6, 1226.	1.7	39
2803	A De novo Transcriptomic Approach to Identify Flavonoids and Anthocyanins â€œSwitch-Offâ€•in Olive (Olea europaea L.) Drupes at Different Stages of Maturation. Frontiers in Plant Science, 2015, 6, 1246.	1.7	40
2804	Transcriptome Analysis of Dendrobium officinale and its Application to the Identification of Genes Associated with Polysaccharide Synthesis. Frontiers in Plant Science, 2016, 7, 5.	1.7	72
2805	RNA-SEQ Reveals Transcriptional Level Changes of Poplar Roots in Different Forms of Nitrogen Treatments. Frontiers in Plant Science, 2016, 7, 51.	1.7	27
2806	Transcriptome Analysis Identifies Candidate Genes Related to Triacylglycerol and Pigment Biosynthesis and Photoperiodic Flowering in the Ornamental and Oil-Producing Plant, Camellia reticulata (Theaceae). Frontiers in Plant Science, 2016, 7, 163.	1.7	29
2807	Transcriptome Characterization of Gnetum parvifolium Reveals Candidate Genes Involved in Important Secondary Metabolic Pathways of Flavonoids and Stilbenoids. Frontiers in Plant Science, 2016, 7, 174.	1.7	42
2808	De novo Transcriptome Assembly of Floral Buds of Pineapple and Identification of Differentially Expressed Genes in Response to Ethephon Induction. Frontiers in Plant Science, 2016, 7, 203.	1.7	17
2809	Transcriptomic Analysis Using Olive Varieties and Breeding Progenies Identifies Candidate Genes Involved in Plant Architecture. Frontiers in Plant Science, 2016, 7, 240.	1.7	25
2810	Transcriptome Analysis of Gerbera hybrida Including in silico Confirmation of Defense Genes Found. Frontiers in Plant Science, 2016, 7, 247.	1.7	23
2811	The Pokeweed Leaf mRNA Transcriptome and Its Regulation by Jasmonic Acid. Frontiers in Plant Science, 2016, 7, 283.	1.7	30
2812	Transcriptome Response Mediated by Cold Stress in Lotus japonicus. Frontiers in Plant Science, 2016, 7, 374.	1.7	61

#	Article	IF	Citations
2813	Changes in Transcript Related to Osmosis and Intracellular Ion Homeostasis in Paulownia tomentosa under Salt Stress. Frontiers in Plant Science, 2016, 7, 384.	1.7	18
2814	Transcriptome Analysis of Differentially Expressed Genes Provides Insight into Stolon Formation in Tulipa edulis. Frontiers in Plant Science, 2016, 7, 409.	1.7	27
2815	Comparative Proteomic Analysis Reveals Differential Root Proteins in Medicago sativa and Medicago truncatula in Response to Salt Stress. Frontiers in Plant Science, 2016, 7, 424.	1.7	41
2816	Learning from Co-expression Networks: Possibilities and Challenges. Frontiers in Plant Science, 2016, 7, 444.	1.7	268
2817	Global Transcriptome Profiling Analysis of Inhibitory Effects of Paclobutrazol on Leaf Growth in Lily (Lilium Longiflorum-Asiatic Hybrid). Frontiers in Plant Science, 2016, 7, 491.	1.7	15
2818	MYB Transcription Factors in Chinese Pear (Pyrus bretschneideri Rehd.): Genome-Wide Identification, Classification, and Expression Profiling during Fruit Development. Frontiers in Plant Science, 2016, 7, 577.	1.7	143
2819	De novo Taproot Transcriptome Sequencing and Analysis of Major Genes Involved in Sucrose Metabolism in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 585.	1.7	36
2820	Different Gene Expression Patterns between Leaves and Flowers in Lonicera japonica Revealed by Transcriptome Analysis. Frontiers in Plant Science, 2016, 7, 637.	1.7	9
2821	Candidate Genes Involved in the Biosynthesis of Triterpenoid Saponins in Platycodon grandiflorum Identified by Transcriptome Analysis. Frontiers in Plant Science, 2016, 7, 673.	1.7	33
2822	Transcriptomic Analysis Identifies Differentially Expressed Genes (DEGs) Associated with Bolting and Flowering in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 682.	1.7	26
2823	Transcriptome Profiling of Buffalograss Challenged with the Leaf Spot Pathogen Curvularia inaequalis. Frontiers in Plant Science, 2016, 7, 715.	1.7	10
2824	Identification of Genes in a Partially Resistant Genotype of Avena sativa Expressed in Response to Puccinia coronata Infection. Frontiers in Plant Science, 2016, 7, 731.	1.7	14
2825	Comparative Physiological and Transcriptomic Analyses Reveal the Actions of Melatonin in the Delay of Postharvest Physiological Deterioration of Cassava. Frontiers in Plant Science, 2016, 7, 736.	1.7	72
2826	Transcriptome- Assisted Label-Free Quantitative Proteomics Analysis Reveals Novel Insights into Piper nigrumâ€"Phytophthora capsici Phytopathosystem. Frontiers in Plant Science, 2016, 7, 785.	1.7	29
2827	Floral Nectary Morphology and Proteomic Analysis of Nectar of Liriodendron tulipifera Linn.. Frontiers in Plant Science, 2016, 7, 826.	1.7	34
2828	De novo Transcriptome Sequencing to Dissect Candidate Genes Associated with Pearl Millet-Downy Mildew (Sclerospora graminicola Sacc.) Interaction. Frontiers in Plant Science, 2016, 7, 847.	1.7	39
2829	Transcriptome Profiling Revealed Stress-Induced and Disease Resistance Genes Up-Regulated in PRSV Resistant Transgenic Papaya. Frontiers in Plant Science, 2016, 7, 855.	1.7	28
2830	Transcriptome Profile Analysis from Different Sex Types of Ginkgo biloba L.. Frontiers in Plant Science, 2016, 7, 871.	1.7	21

#	ARTICLE	IF	CITATIONS
2831	Shotgun Label-free Proteomic Analysis of Clubroot (Plasmodiophora brassicae) Resistance Conferred by the Gene Rcr1 in Brassica rapa. Frontiers in Plant Science, 2016, 7, 1013.	1.7	32
2832	Proteometabolomic Study of Compatible Interaction in Tomato Fruit Challenged with Sclerotinia rolfsii Illustrates Novel Protein Network during Disease Progression. Frontiers in Plant Science, 2016, 7, 1034.	1.7	7
2833	Genome-Wide Association Study Identifies Candidate Genes for Starch Content Regulation in Maize Kernels. Frontiers in Plant Science, 2016, 7, 1046.	1.7	85
2834	De novo Assembly and Characterization of the Transcriptome of Broomcorn Millet (Panicum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.7	29
2835	Comparative Proteomics of Oxalate Downregulated Tomatoes Points toward Cross Talk of Signal Components and Metabolic Consequences during Post-harvest Storage. Frontiers in Plant Science, 2016, 7, 1147.	1.7	7
2836	Temporal-Spatial Transcriptome Analyses Provide Insights into the Development of Petaloid Androecium in Canna indica. Frontiers in Plant Science, 2016, 7, 1194.	1.7	12
2837	Comparative Transcriptome Analysis of Latex Reveals Molecular Mechanisms Underlying Increased Rubber Yield in Hevea brasiliensis Self-Rooting Juvenile Clones. Frontiers in Plant Science, 2016, 7, 1204.	1.7	21
2838	De novo Sequencing and Transcriptome Analysis of Pinellia ternata Identify the Candidate Genes Involved in the Biosynthesis of Benzoic Acid and Ephedrine. Frontiers in Plant Science, 2016, 7, 1209.	1.7	26
2839	Genome-Wide Association Study of Resistance to Soybean Cyst Nematode (Heterodera glycines) HG Type 2.5.7 in Wild Soybean (Glycine soja). Frontiers in Plant Science, 2016, 7, 1214.	1.7	68
2840	Morphological Structure and Transcriptome Comparison of the Cytoplasmic Male Sterility Line in Brassica napus (SaNa-1A) Derived from Somatic Hybridization and Its Maintainer Line SaNa-1B. Frontiers in Plant Science, 2016, 7, 1313.	1.7	38
2841	Proteomic Studies on the Effects of Lipo-Chitooligosaccharide and Thuricin 17 under Unstressed and Salt Stressed Conditions in Arabidopsis thaliana. Frontiers in Plant Science, 2016, 7, 1314.	1.7	50
2842	Comparative Transcriptome Analysis Identifies Putative Genes Involved in the Biosynthesis of Xanthanolides in Xanthium strumarium L.. Frontiers in Plant Science, 2016, 7, 1317.	1.7	9
2843	Identification of Candidate Anthocyanin-Related Genes by Transcriptomic Analysis of â€˜Furongliâ€™ Plum (Prunus salicina Lindl.) during Fruit Ripening Using RNA-Seq. Frontiers in Plant Science, 2016, 7, 1338.	1.7	67
2844	Transcriptome Analysis of Stem and Globally Comparison with Other Tissues in Brassica napus. Frontiers in Plant Science, 2016, 7, 1403.	1.7	49
2845	Transcriptome Analysis of Sucrose Metabolism during Bulb Swelling and Development in Onion (Allium cepa L.). Frontiers in Plant Science, 2016, 7, 1425.	1.7	49
2846	Quantitative Resistance to Verticillium Wilt in Medicago truncatula Involves Eradication of the Fungus from Roots and Is Associated with Transcriptional Responses Related to Innate Immunity. Frontiers in Plant Science, 2016, 7, 1431.	1.7	13
2847	A Genome-Wide Association Study Reveals New Loci for Resistance to Clubroot Disease in Brassica napus. Frontiers in Plant Science, 2016, 7, 1483.	1.7	74
2848	Comparative Transcriptome and Chloroplast Genome Analyses of Two Related Dipteronia Species. Frontiers in Plant Science, 2016, 7, 1512.	1.7	46

#	Article	IF	Citations
2849	Transcriptome Analysis of Green Peach Aphid (Myzus persicae): Insight into Developmental Regulation and Inter-Species Divergence. Frontiers in Plant Science, 2016, 7, 1562.	1.7	16
2850	Transcriptome Sequencing and Expression Analysis of Cadmium (Cd) Transport and Detoxification Related Genes in Cd-Accumulating Salix integra. Frontiers in Plant Science, 2016, 7, 1577.	1.7	54
2851	Transcriptome Dynamics in Mango Fruit Peel Reveals Mechanisms of Chilling Stress. Frontiers in Plant Science, 2016, 7, 1579.	1.7	69
2852	Differential Gene Expression in Rhododendron fortunei Roots Colonized by an Ericoid Mycorrhizal Fungus and Increased Nitrogen Absorption and Plant Growth. Frontiers in Plant Science, 2016, 7, 1594.	1.7	21
2853	DArT Markers Effectively Target Gene Space in the Rye Genome. Frontiers in Plant Science, 2016, 07, 1600.	1.7	33
2854	Insights into the Sesquiterpenoid Pathway by Metabolic Profiling and De novo Transcriptome Assembly of Stem-Chicory (Cichorium intybus Cultigroup â€œCatalognaâ€). Frontiers in Plant Science, 2016, 7, 1676.	1.7	20
2855	Tissue-Specific Transcriptome and Hormonal Regulation of Pollinated and Parthenocarpic Fig (Ficus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Frontiers in Plant Science, 2016, 7, 1696.	1.7	27
2856	Tomato FK506 Binding Protein 12KD (FKBP12) Mediates the Interaction between Rapamycin and Target of Rapamycin (TOR). Frontiers in Plant Science, 2016, 7, 1746.	1.7	40
2857	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (Pyrus bretschneideri Rehd), Poplar (Populous), Grape (Vitis vinifera), Arabidopsis and Rice (Oryza sativa). Frontiers in Plant Science, 2016, 7, 1750.	1.7	97
2858	RNA-seq Transcriptome Response of Flax (Linum usitatissimum L.) to the Pathogenic Fungus Fusarium oxysporum f. sp. lini. Frontiers in Plant Science, 2016, 7, 1766.	1.7	67
2859	Revisiting Vitis vinifera Subtilase Gene Family: A Possible Role in Grapevine Resistance against Plasmopara viticola. Frontiers in Plant Science, 2016, 7, 1783.	1.7	31
2860	Insights into the Role of the Berry-Specific Ethylene Responsive Factor VviERF045. Frontiers in Plant Science, 2016, 7, 1793.	1.7	38
2861	Transcriptome Analysis to Identify the Putative Biosynthesis and Transport Genes Associated with the Medicinal Components of Achyranthes bidentata Bl.. Frontiers in Plant Science, 2016, 7, 1860.	1.7	16
2862	Functional and Integrative Analysis of the Proteomic Profile of Radish Root under Pb Exposure. Frontiers in Plant Science, 2016, 7, 1871.	1.7	28
2863	Comparative Characterization of the Leaf Tissue of Physalis alkekengi and Physalis peruviana Using RNA-seq and Metabolite Profiling. Frontiers in Plant Science, 2016, 7, 1883.	1.7	27
2864	Comparative Transcriptome Analysis between Broccoli (Brassica oleracea var. italica) and Wild Cabbage (Brassica macrocarpa Guss.) in Response to Plasmodiophora brassicae during Different Infection Stages. Frontiers in Plant Science, 2016, 7, 1929.	1.7	69
2865	De novo Sequencing and Comparative Transcriptomics of Floral Development of the Distylous Species Lithospermum multiflorum. Frontiers in Plant Science, 2016, 7, 1934.	1.7	15
2866	Comparative Transcriptomics Atlases Reveals Different Gene Expression Pattern Related to Fusarium Wilt Disease Resistance and Susceptibility in Two Vernicia Species. Frontiers in Plant Science, 2016, 7, 1974.	1.7	18

#	ARTICLE	IF	CITATIONS
2867	Identification of novel and useful EST-SSR markers from de novo transcriptome sequence of wheat (Triticum aestivum L.). Genetics and Molecular Research, 2016, 15, .	0.3	10
2868	Preliminary analysis on the transcripts involved in resistance responses to eumusae leaf spot disease of banana caused by Mycosphaerella eumusae, a recent add-on of the sigatoka disease complex. Turkish Journal of Botany, 2016, 40, 461-471.	0.5	7
2869	Nearâ€future pH conditions severely impact calcification, metabolism and the nervous system in the pteropod <i>Heliconoides inflatus</i>. Global Change Biology, 2016, 22, 3888-3900.	4.2	68
2870	Global transcriptome analysis of Sabina chinensis (Cupressaceae), a valuable reforestation conifer. Molecular Breeding, 2016, 36, 1.	1.0	6
2871	Genomic analysis of snub-nosed monkeys (Rhinopithecus) identifies genes and processes related to high-altitude adaptation. Nature Genetics, 2016, 48, 947-952.	9.4	109
2872	Genetic variability, local selection and demographic history: genomic evidence of evolving towards allopatric speciation in Asian seabass. Molecular Ecology, 2016, 25, 3605-3621.	2.0	32
2873	Comparative transcriptomic analyses of <scp><i>Z</i></scp><i>ymoseptoria tritici</i> strains show complex lifestyle transitions and intraspecific variability in transcription profiles. Molecular Plant Pathology, 2016, 17, 845-859.	2.0	82
2874	Putative methyltransferase LaeA and transcription factor CreA are necessary for proper asexual development and controlling secondary metabolic gene cluster expression. Fungal Genetics and Biology, 2016, 94, 32-46.	0.9	35
2875	Transcriptome analysis of beer-spoiling Lactobacillus brevis BSO 464 during growth in degassed and gassed beer. International Journal of Food Microbiology, 2016, 235, 28-35.	2.1	25
2876	Long Non-Coding RNAs (lncRNAs) of Sea Cucumber: Large-Scale Prediction, Expression Profiling, Non-Coding Network Construction, and lncRNA-microRNA-Gene Interaction Analysis of lncRNAs in Apostichopus japonicus and Holothuria glaberrima During LPS Challenge and Radial Organ Complex Regeneration. Marine Biotechnology, 2016, 18, 485-499.	1.1	30
2877	Systems genetics reveals key genetic elements of drought induced gene regulation in diploid potato. Plant, Cell and Environment, 2016, 39, 1895-1908.	2.8	14
2878	High-throughput sequencing and de novo transcriptome assembly of Swertia japonica to identify genes involved in the biosynthesis of therapeutic metabolites. Plant Cell Reports, 2016, 35, 2091-2111.	2.8	38
2879	DemaDb: an integrated dematiaceous fungal genomes database. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw008.	1.4	4
2880	Identification and phylogeny of putative PEPC genes in three toxinâ€producing Karenia (Dinophyta) species. Journal of Phycology, 2016, 52, 618-625.	1.0	5
2881	Gene expression patterns underlying parasiteâ€induced alterations in host behaviour and life history. Molecular Ecology, 2016, 25, 648-660.	2.0	24
2882	Gene expression under thermal stress varies across a geographical range expansion front. Molecular Ecology, 2016, 25, 1141-1156.	2.0	73
2883	Frequency and mitotic heritability of epimutations in <i>Schistosoma mansoni</i>. Molecular Ecology, 2016, 25, 1741-1758.	2.0	19
2884	The gut microbiota of the pine weevil is similar across Europe and resembles that of other coniferâ€feeding beetles. Molecular Ecology, 2016, 25, 4014-4031.	2.0	75

#	ARTICLE	IF	CITATIONS
2885	Chronic toxicological effects of Î²â€diketone antibiotics on <scp>Z</scp>ebrafish (<scp><i>D</i></scp><i>anio rerio</i>) using transcriptome profiling of deep sequencing. Environmental Toxicology, 2016, 31, 1357-1371.	2.1	15
2886	Identification of miRNAs and their targets involved in the secondary metabolic pathways of Mentha spp.. Computational Biology and Chemistry, 2016, 64, 154-162.	1.1	58
2887	Lifeâ€history evolution in response to changes in metapopulation structure in an arthropod herbivore. Functional Ecology, 2016, 30, 1408-1417.	1.7	20
2888	Transcriptome profile of Chinese bush cricket, <i>Gampsocleis gratiosa</i>: A resource for microsatellite marker development. Entomological Research, 2016, 46, 197-205.	0.6	4
2889	Comparative proteomics analysis of silkworm hemolymph during the stages of metamorphosis via liquid chromatography and mass spectrometry. Proteomics, 2016, 16, 1421-1431.	1.3	23
2890	Proteomics of the red blood cell carbonylome during blood banking of erythrocyte concentrates. Proteomics - Clinical Applications, 2016, 10, 257-266.	0.8	44
2891	Influence of preâ€harvest calcium, potassium and triazole application on the proteome of apple at harvest. Journal of the Science of Food and Agriculture, 2016, 96, 4984-4993.	1.7	8
2892	Evidence of divergent selection for drought and cold tolerance at landscape and local scales in <i>Abies alba</i> Mill. in the French Mediterranean Alps. Molecular Ecology, 2016, 25, 776-794.	2.0	64
2893	Disruption of <i>Os<scp>SULTR</scp>3;3</i> reduces phytate and phosphorus concentrations and alters the metabolite profile in rice grains. New Phytologist, 2016, 211, 926-939.	3.5	72
2894	Narrowing down the single homoeologous <i>Fa<scp>PFRU</scp></i> locus controlling flowering in cultivated octoploid strawberry using a selective mapping strategy. Plant Biotechnology Journal, 2016, 14, 2176-2189.	4.1	48
2895	Draft Genome Sequences of Fungus Aspergillus calidoustus. Genome Announcements, 2016, 4, .	0.8	13
2896	Impact of Environmental Chemicals on the Transcriptome of Primary Human Hepatocytes: Potential for Health Effects. Journal of Biochemical and Molecular Toxicology, 2016, 30, 375-395.	1.4	9
2897	De novo annotation of the immune-enriched transcriptome provides insights into immune system genes of Chinese sturgeon (Acipenser sinensis). Fish and Shellfish Immunology, 2016, 55, 699-716.	1.6	40
2898	Discovery and identification of candidate sex-related genes based on transcriptome sequencing of Russian sturgeon (<i>Acipenser gueldenstaedtii</i>) gonads. Physiological Genomics, 2016, 48, 464-476.	1.0	23
2899	Comparative transcriptome analysis of differentially expressed genes between the curly and normal leaves of Cymbidium goeringii var. longibracteatum. Genes and Genomics, 2016, 38, 985-998.	0.5	7
2900	Proteomic profiling of cellular steatosis with concomitant oxidative stress in vitro. Lipids in Health and Disease, 2016, 15, 114.	1.2	10
2901	Proteomic analysis of the venom and venom sac of the woodwasp, Sirex noctilio - Towards understanding its biological impact. Journal of Proteomics, 2016, 146, 195-206.	1.2	23
2902	The population genomic basis of geographic differentiation in <scp>N</scp>orth <scp>A</scp>merican common ragweed (<i><scp>A</scp>mbrosia artemisiifolia </i><scp>L</scp>.). Ecology and Evolution, 2016, 6, 3760-3771.	0.8	35

#	Article	IF	Citations
2903	Postmating transcriptional changes in the female reproductive tract of the European corn borer moth. Insect Molecular Biology, 2016, 25, 629-645.	1.0	15
2904	Small <scp>RNA</scp> and degradome profiling reveals important roles for <scp>microRNAs</scp> and their targets in tea plant response to drought stress. Physiologia Plantarum, 2016, 158, 435-451.	2.6	51
2905	Construction and Characterization of Two Novel Transcriptome Assemblies in the Congeneric Porcelain Crabs Petrolisthes cinctipes and P. manimaculis. Integrative and Comparative Biology, 2016, 56, 1092-1102.	0.9	6
2906	Mechanisms of phenanthrene toxicity in the soil invertebrate, <i>Enchytraeus crypticus</i>. Environmental Toxicology and Chemistry, 2016, 35, 2713-2720.	2.2	16
2907	De novo assembly and characterization of leaf and floral transcriptomes of the hybridizing bromeliad species (<i>Pitcairnia</i> spp.) adapted to Neotropical Inselbergs. Molecular Ecology Resources, 2016, 16, 1012-1022.	2.2	37
2908	A genes eye view of ontogeny: <i>de novo</i> assembly and profiling of the <i>Gryllus rubens</i> transcriptome. Molecular Ecology Resources, 2016, 16, 1478-1490.	2.2	37
2909	Symbiosis induces widespread changes in the proteome of the model cnidarian<i>Aiptasia</i>. Cellular Microbiology, 2016, 18, 1009-1023.	1.1	79
2910	Identification and expression profile of odorantâ€binding proteins in <i>Halyomorpha halys</i> (Hemiptera: Pentatomidae). Insect Molecular Biology, 2016, 25, 580-594.	1.0	87
2911	Rapid evolution and gene expression: a rapidly evolving Mendelian trait that silences field crickets has widespread effects on m<scp>RNA</scp> and protein expression. Journal of Evolutionary Biology, 2016, 29, 1234-1246.	0.8	23
2912	Gene expression and variation in social aggression by queens of the harvester ant Pogonomyrmex californicus. Molecular Ecology, 2016, 25, 3716-3730.	2.0	18
2913	Transcriptional reprogramming underpins enhanced plant growth promotion by the biocontrol fungus <i>Trichoderma hamatum</i> GD12 during antagonistic interactions with <i>Sclerotinia sclerotiorum</i> in soil. Molecular Plant Pathology, 2016, 17, 1425-1441.	2.0	32
2914	Elucidation of the first committed step in betalain biosynthesis enables the heterologous engineering of betalain pigments in plants. New Phytologist, 2016, 210, 269-283.	3.5	147
2915	Drought and flooding have distinct effects on herbivoreâ€induced responses and resistance in <i>Solanum dulcamara</i>. Plant, Cell and Environment, 2016, 39, 1485-1499.	2.8	59
2916	Nitrogen starvationâ€induced accumulation of triacylglycerol in the green algae: evidence for a role for <scp>ROC</scp>40, a transcription factor involved in circadian rhythm. Plant Journal, 2016, 85, 743-757.	2.8	49
2917	Using Genotyping by Sequencing to Map Two Novel Anthracnose Resistance Loci in<i>Sorghum bicolor</i>. G3: Genes, Genomes, Genetics, 2016, 6, 1935-1946.	0.8	29
2918	Transcriptomic analysis of differentially expressed genes in the floral transition of the summer flowering chrysanthemum. BMC Genomics, 2016, 17, 673.	1.2	27
2919	Transcriptome profiles of metamorphosis in the ornamented pygmy frog Microhyla fissipes clarify the functions of thyroid hormone receptors in metamorphosis. Scientific Reports, 2016, 6, 27310.	1.6	39
2920	Integrative analysis of transcriptomics and proteomics of skeletal muscles of the Chinese indigenous Shaziling pig compared with the Yorkshire breed. BMC Genetics, 2016, 17, 80.	2.7	58

#	Article	IF	Citations
2921	Genome wide transcriptome profiling reveals differential gene expression in secondary metabolite pathway of Cymbopogon winterianus. Scientific Reports, 2016, 6, 21026.	1.6	27
2922	The Spatial and Temporal Transcriptomic Landscapes of Ginseng, Panax ginseng C. A. Meyer. Scientific Reports, 2016, 5, 18283.	1.6	63
2923	De novo Transcriptome Assembly and Dynamic Spatial Gene Expression Analysis in Red Clover. Plant Genome, 2016, 9, plantgenome2015.06.0048.	1.6	20
2924	NGS-Based Expression Profiling of HSP Genes During Cold and Freeze Stress in Seabuckthorn (Hippophae rhamnoides L.). Heat Shock Proteins, 2016, , 309-327.	0.2	2
2925	Identification of candidate thermotolerance genes during early seedling stage in upland cotton (Gossypium hirsutum L.) revealed by comparative transcriptome analysis. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	1
2926	Deep sequencing of transcriptomes from the nervous systems of two decapod crustaceans to characterize genes important for neural circuit function and modulation. BMC Genomics, 2016, 17, 868.	1.2	62
2927	Development, evaluation, and validation of new EST-SSR markers in olive (Olea europaea L.). Tree Genetics and Genomes, 2016, 12, 1.	0.6	56
2928	Identification and expression analysis of an olfactory receptor gene family in green plant bug Apolygus lucorum (Meyer-DÃ¼r). Scientific Reports, 2016, 6, 37870.	1.6	41
2929	Conserved Noncoding Elements in the Most Distant Genera of Cephalochordates: The Goldilocks Principle. Genome Biology and Evolution, 2016, 8, 2387-2405.	1.1	23
2930	Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: Phaffia rhodozyma. BMC Genomics, 2016, 17, 901.	1.2	35
2931	In-depth comparative transcriptome analysis of intestines of red swamp crayfish, Procambarus clarkii, infected with WSSV. Scientific Reports, 2016, 6, 26780.	1.6	30
2932	Mass spectrometry analysis and transcriptome sequencing reveal glowing squid crystal proteins are in the same superfamily as firefly luciferase. Scientific Reports, 2016, 6, 27638.	1.6	18
2933	Sublethal salinity stress contributes to habitat limitation in an endangered estuarine fish. Evolutionary Applications, 2016, 9, 963-981.	1.5	47
2934	Gene expression changes triggered by end-of-day far-red light treatment on early developmental stages of Eustoma grandiflorum (Raf.) Shinn.. Scientific Reports, 2016, 5, 17864.	1.6	8
2935	High throughput sequencing of small RNAs transcriptomes in two Crassostrea oysters identifies microRNAs involved in osmotic stress response. Scientific Reports, 2016, 6, 22687.	1.6	44
2936	Transcriptome analyses reveal molecular mechanism underlying tapping panel dryness of rubber tree (Hevea brasiliensis). Scientific Reports, 2016, 6, 23540.	1.6	35
2937	Transcriptome Analysis of the Signalling Networks in Coronatine-Induced Secondary Laticifer Differentiation from Vascular Cambia in Rubber Trees. Scientific Reports, 2016, 6, 36384.	1.6	25
2938	Identification of vernalization responsive genes in the winter wheat cultivar Jing841 by transcriptome sequencing. Journal of Genetics, 2016, 95, 957-964.	0.4	7

#	ARTICLE	IF	CITATIONS
2939	Analysis of transcriptional response to heat stress in Rhazya stricta. BMC Plant Biology, 2016, 16, 252.	1.6	39
2940	MicroRNAs in Honey Bee Caste Determination. Scientific Reports, 2016, 6, 18794.	1.6	99
2941	Deciphering the transcriptomic response of Fusarium verticillioides in relation to nitrogen availability and the development of sugarcane pokkah boeng disease. Scientific Reports, 2016, 6, 29692.	1.6	23
2942	Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat. Scientific Reports, 2016, 6, 23805.	1.6	29
2943	Comparative transcriptome analyses of seven anurans reveal functions and adaptations of amphibian skin. Scientific Reports, 2016, 6, 24069.	1.6	36
2944	Transcriptome profiling of Diachasmimorpha longicaudata towards useful molecular tools for population management. BMC Genomics, 2016, 17, 793.	1.2	3
2945	The SEB-1 Transcription Factor Binds to the STRE Motif in <i>Neurospora crassa</i> and Regulates a Variety of Cellular Processes Including the Stress Response and Reserve Carbohydrate Metabolism. G3: Genes, Genomes, Genetics, 2016, 6, 1327-1343.	0.8	16
2946	Comparative transcriptomics enlarges the toolkit of known developmental genes in mollusks. BMC Genomics, 2016, 17, 905.	1.2	41
2947	Transcriptome analysis revealed the dynamic oil accumulation in Symplocos paniculata fruit. BMC Genomics, 2016, 17, 929.	1.2	15
2948	Bifunctional CYP81AA proteins catalyse identical hydroxylations but alternative regioselective phenol couplings in plant xanthone biosynthesis. Nature Communications, 2016, 7, 11472.	5.8	46
2949	De novo transcriptome assembly, development of EST-SSR markers and population genetic analyses for the desert biomass willow, Salix psammophila. Scientific Reports, 2016, 6, 39591.	1.6	36
2950	A new method for decontamination of <i>de novo</i> transcriptomes using a hierarchical clustering algorithm. Bioinformatics, 2017, 33, 1293-1300.	1.8	26
2951	Evolution of chemosensory gene families in arthropods: Insight from the first inclusive comparative transcriptome analysis across spider appendages. Genome Biology and Evolution, 2017, 9, evw296.	1.1	43
2952	Draft Genome Sequence of Two Monosporidial Lines of the Karnal Bunt Fungus <i>Tilletia indica</i> Mitra (PSWKBGH-1 and PSWKBGH-2). Genome Announcements, 2016, 4, .	0.8	11
2953	The testes transcriptome of the New World Screwworm, Cochliomyia hominivorax. Data in Brief, 2016, 9, 1141-1146.	0.5	1
2954	Analysis of Annotation and Differential Expression Methods used in RNA-seq Studies in Crustacean Systems. Integrative and Comparative Biology, 2016, 56, 1067-1079.	0.9	20
2955	Host Transcriptional Profiling at Early and Later Stages of the Compatible Interaction Between <i>Phaseolus vulgaris</i> and <i>Meloidogyne incognita</i>. Phytopathology, 2016, 106, 282-294.	1.1	16
2956	Genetic linkage of distinct adaptive traits in sympatrically speciating crater lake cichlid fish. Nature Communications, 2016, 7, 12736.	5.8	61

#	ARTICLE	IF	CITATIONS
2957	Transcriptome responses in alfalfa associated with tolerance to intensive animal grazing. Scientific Reports, 2016, 6, 19438.	1.6	15
2958	Transcriptome analysis of root development in bottle gourd (Lagenaria siceraria). Acta Horticulturae, 2016, , 41-48.	0.1	2
2959	A hormone-related female anti-aphrodisiac signals temporary infertility and causes sexual abstinence to synchronize parental care. Nature Communications, 2016, 7, 11035.	5.8	48
2960	Maize Cytolines Unmask Key Nuclear Genes That Are under the Control of Retrograde Signaling Pathways in Plants. Genome Biology and Evolution, 2016, 8, 3256-3270.	1.1	14
2961	A genome-wide BAC-end sequence survey provides first insights into sweetpotato (Ipomoea batatas (L.)) Tj ETQq0 0 0 rgBT /Overlock 1	1.2	10
2962	Sequencing, de novo assembly and annotation of a pink bollworm larval midgut transcriptome. GigaScience, 2016, 5, 28.	3.3	12
2963	Bursaphelenchus xylophilus and B. mucronatus secretomes: a comparative proteomic analysis. Scientific Reports, 2016, 6, 39007.	1.6	25
2964	Tolerance and responsive gene expression of Sogatella furcifera under extreme temperature stresses are altered by its vectored plant virus. Scientific Reports, 2016, 6, 31521.	1.6	28
2965	Genome-wide transcriptional response of the Arctic bacterium Pseudoalteromonas sp. A2 to oxidative stress induced by hydrogen peroxide. Acta Oceanologica Sinica, 2016, 35, 73-80.	0.4	9
2966	The miRNAome of durum wheat: isolation and characterisation of conserved and novel microRNAs and their target genes. BMC Genomics, 2016, 17, 505.	1.2	44
2967	Validated methodology for quantifying infestation levels of dreissenid mussels in environmental DNA (eDNA) samples. Scientific Reports, 2016, 6, 39067.	1.6	12
2968	The draft genome of whitefly Bemisia tabaci MEAM1, a global crop pest, provides novel insights into virus transmission, host adaptation, and insecticide resistance. BMC Biology, 2016, 14, 110.	1.7	265
2969	Genetics and Genomics of Cucurbita spp.. Plant Genetics and Genomics: Crops and Models, 2016, , 211-227.	0.3	4
2970	Survey of the genome of Pogostemon cablin provides insights into its evolutionary history and sesquiterpenoid biosynthesis. Scientific Reports, 2016, 6, 26405.	1.6	21
2971	Molecular characterization of firefly nuptial gifts: a multi-omics approach sheds light on postcopulatory sexual selection. Scientific Reports, 2016, 6, 38556.	1.6	11
2972	Proteomic and oxi-proteomic response of apple to a compatible (<i>P. expansum</i>) and a non-host (<i>P. digitatum</i>) pathogen. Acta Horticulturae, 2016, , 17-28.	0.1	0
2973	Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus Acrostichum. Scientific Reports, 2016, 6, 35634.	1.6	25
2974	Construction of an Ostrea edulis database from genomic and expressed sequence tags (ESTs) obtained from Bonamia ostreae infected haemocytes: Development of an immune-enriched oligo-microarray. Fish and Shellfish Immunology, 2016, 59, 331-344.	1.6	20

#	ARTICLE	IF	CITATIONS
2975	The Spermatophore in Glossina morsitans morsitans: Insights into Male Contributions to Reproduction. Scientific Reports, 2016, 6, 20334.	1.6	40
2976	Genomics of <i>Cynara cardunculus</i> through the exploitation of NGS technologies. Acta Horticulturae, 2016, , 1-8.	0.1	0
2977	Transcriptome sequencing and marker development in winged bean (Psophocarpus tetragonolobus;) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	67
2978	Global transcriptional analysis suggests Lasiodiplodia theobromae pathogenicity factors involved in modulation of grapevine defensive response. BMC Genomics, 2016, 17, 615.	1.2	51
2979	Draft genome sequencing and secretome analysis of fungal phytopathogen Ascochyta rabiei provides insight into the necrotrophic effector repertoire. Scientific Reports, 2016, 6, 24638.	1.6	57
2980	The Fusarium crown rot pathogen<i>Fusarium pseudograminearum</i>triggers a suite of transcriptional and metabolic changes in bread wheat (<i>Triticum aestivum</i>L.). Annals of Botany, 2017, 119, mcw207.	1.4	52
2981	The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. Scientific Reports, 2016, 6, 28594.	1.6	118
2982	Transcriptome and Gene Expression Analysis of Cylas formicarius (Coleoptera: Brentidae) During Different Development Stages. Journal of Insect Science, 2016, 16, .	0.6	14
2983	Whole genome sequencing and comparative genomics of closely related Fusarium Head Blight fungi: Fusarium graminearum, F. meridionale and F. asiaticum. BMC Genomics, 2016, 17, 1014.	1.2	58
2984	Pangenome and immuno-proteomics analysis of Acinetobacter baumannii strains revealed the core peptide vaccine targets. BMC Genomics, 2016, 17, 732.	1.2	100
2985	Medicinal plant transcriptomes: the new gateways for accelerated understanding of plant secondary metabolism. Plant Genetic Resources: Characterisation and Utilisation, 2016, 14, 256-269.	0.4	21
2986	High-throughput sequencing and degradome analysis reveal altered expression of miRNAs and their targets in a male-sterile cybrid pummelo (Citrus grandis). BMC Genomics, 2016, 17, 591.	1.2	36
2987	Localisation and origin of the bacteriochlorophyll-derived photosensitizer in the retina of the deep-sea dragon fish Malacosteus niger. Scientific Reports, 2016, 6, 39395.	1.6	10
2988	Role and mechanism of the AMPK pathway in waterborne Zn exposure influencing the hepatic energy metabolism of Synechogobius hasta. Scientific Reports, 2016, 6, 38716.	1.6	34
2989	Role of Genomics in Enhancing Nutrition Content of Cereals. , 2016, , 77-96.		1
2990	Comparative transcriptomics across populations offers new insights into the evolution of thermal resistance in marine snails. Marine Biology, 2016, 163, 1.	0.7	7
2991	RNA-Seq analysis of immune-relevant genes in Lateolabrax japonicus during Vibrio anguillarum infection. Fish and Shellfish Immunology, 2016, 52, 57-64.	1.6	33
2992	Draft genome sequence of Psychrobacter sp. ENNN9_III, a strain isolated from water in a polluted temperate estuarine system (Ria de Aveiro , Portugal). Genomics Data, 2016, 8, 21-24.	1.3	0

#	ARTICLE	IF	CITATIONS
2993	Shared and nonshared genomic divergence in parallel ecotypes of <i><scp>L</scp>ittorina saxatilis</i> at a local scale. Molecular Ecology, 2016, 25, 287-305.	2.0	142
2994	Genomeâ€wide transcriptomic and proteomic analyses of bollwormâ€infested developing cotton bolls revealed the genes and pathways involved in the insect pest defence mechanism. Plant Biotechnology Journal, 2016, 14, 1438-1455.	4.1	18
2995	Hydroxyproline <i>O</i>â€arabinosyltransferase mutants oppositely alter tip growth in <i>Arabidopsis thaliana</i> and <i>Physcomitrella patens</i>. Plant Journal, 2016, 85, 193-208.	2.8	40
2996	Transcriptome Sequencing of the Sweet Potato Progenitor (Ipomoea Trifida (H.B.K.) G. Don.) and Discovery of Drought Tolerance Genes. Tropical Plant Biology, 2016, 9, 63-72.	1.0	21
2997	Insights from the pollination drop proteome and the ovule transcriptome of<i>Cephalotaxus</i>at the time of pollination drop production. Annals of Botany, 2016, 117, 973-984.	1.4	14
2998	Transcriptome analysis reveals a comprehensive insect resistance response mechanism in cotton to infestation by the phloem feeding insect Bemisia tabaci (whitefly). Plant Biotechnology Journal, 2016, 14, 1956-1975.	4.1	109
2999	Comparative transcriptome analyses indicate enhanced cellular protection against FMDV in PK15 cells pretreated with IFN-Î³. Gene, 2016, 586, 206-215.	1.0	8
3000	Genetic architecture of wood properties based on association analysis and coâ€expression networks in white spruce. New Phytologist, 2016, 210, 240-255.	3.5	43
3001	Postmatingâ€“prezygotic isolation between two allopatric populations of <i>Drosophila montana</i>: fertilisation success differs under sperm competition. Ecology and Evolution, 2016, 6, 1679-1691.	0.8	5
3002	Differential transcriptomic responses to Fusarium graminearum infection in two barley quantitative trait loci associated with Fusarium head blight resistance. BMC Genomics, 2016, 17, 387.	1.2	64
3003	Genome-wide analysis of shoot growth-associated alternative splicing in moso bamboo. Molecular Genetics and Genomics, 2016, 291, 1695-1714.	1.0	33
3004	Cytochrome P450 CYP71AT96 catalyses the final step of herbivore-induced phenylacetonitrile biosynthesis in the giant knotweed, Fallopia sachalinensis. Plant Molecular Biology, 2016, 91, 229-239.	2.0	30
3005	Genetic basis of adult migration timing in anadromous steelhead discovered through multivariate association testing. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20153064.	1.2	107
3006	A Metabolic Gene Cluster in the Wheat <i>W1</i> and the Barley <i>Cer-cqu</i> Loci Determines Î²-Diketone Biosynthesis and Glaucousness. Plant Cell, 2016, 28, 1440-1460.	3.1	123
3007	Differential expression of photosynthesis-related genes and quantification of gas exchange in rice plants under abiotic stress. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	22
3008	The genome and genetics of a high oxidative stress tolerant Serratia sp. LCN16 isolated from the plant parasitic nematode Bursaphelenchus xylophilus. BMC Genomics, 2016, 17, 301.	1.2	18
3009	Quantitative proteomics and phosphoproteomics of sugar beet monosomic addition line M14 in response to salt stress. Journal of Proteomics, 2016, 143, 286-297.	1.2	37
3010	Comparative Transcriptome Analysis between Low- and High-Cadmium-Accumulating Genotypes of Pakchoi (<i>Brassica chinensis</i> L.) in Response to Cadmium Stress. Environmental Science & Technology, 2016, 50, 6485-6494.	4.6	167

#	Article	IF	Citations
3011	De novo transcriptome analysis in radish (Raphanus sativus L.) and identification of critical genes involved in bolting and flowering. BMC Genomics, 2016, 17, 389.	1.2	53
3012	Transcriptomic effects of the non-steroidal anti-inflammatory drug Ibuprofen in the marine bivalve Mytilus galloprovincialis Lam.. Marine Environmental Research, 2016, 119, 31-39.	1.1	18
3013	Identification of differentially expressed genes and signalling pathways in bark of Hevea brasiliensis seedlings associated with secondary laticifer differentiation using gene expression microarray. Plant Physiology and Biochemistry, 2016, 107, 45-55.	2.8	14
3014	Gene expression profiling during seed-filling process in peanut with emphasis on oil biosynthesis networks. Plant Science, 2016, 248, 116-127.	1.7	21
3015	The unexpected extremophile: Tolerance to fluctuating salinity in the green alga Picochlorum. Algal Research, 2016, 16, 465-472.	2.4	67
3016	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. Marine Genomics, 2016, 30, 3-13.	0.4	164
3017	De novo assembly and annotation of the marine mysid (Neomysis awatschensis) transcriptome. Marine Genomics, 2016, 28, 41-43.	0.4	8
3018	Integration of Hormonal and Nutritional Cues Orchestrates Progressive Corolla Opening Â. Plant Physiology, 2016, 171, 1209-1229.	2.3	24
3019	De novo assembly and comparative transcriptome analysis of Euglena gracilis in response to anaerobic conditions. BMC Genomics, 2016, 17, 182.	1.2	78
3020	Identification of myogenic regulatory genes in the muscle transcriptome of beltfish (Trichiurus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 8, 81-84.	1.3	9
3021	Identification of chemosensory gene families in Rhyzopertha dominica (Coleoptera: Bostrichidae). Canadian Entomologist, 2016, 148, 8-21.	0.4	26
3022	Transcriptome based identification and tissue expression profiles of chemosensory genes in Blattella germanica (Blattaria: Blattidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 18, 30-43.	0.4	19
3023	Transcriptomic Responses of the Interactions between Clostridium cellulovorans 743B and Rhodopseudomonas palustris CGA009 in a Cellulose-Grown Coculture for Enhanced Hydrogen Production. Applied and Environmental Microbiology, 2016, 82, 4546-4559.	1.4	22
3024	Genetic variation between Schistosoma japonicum lineages from lake and mountainous regions in China revealed by resequencing whole genomes. Acta Tropica, 2016, 161, 79-85.	0.9	7
3025	Bifidobacterium thermophilum RBL67 impacts on growth and virulence gene expression of Salmonella enterica subsp. enterica serovar Typhimurium. BMC Microbiology, 2016, 16, 46.	1.3	33
3026	Transcriptomic changes underlie altered egg protein production and reduced fecundity in an estuarine model fish exposed to bifenthrin. Aquatic Toxicology, 2016, 174, 247-260.	1.9	80
3027	A <i>myo</i>â€inositolâ€1â€phosphate synthase gene, <i>Ib<scp>MIPS</scp>1</i>, enhances salt and drought tolerance and stem nematode resistance in transgenic sweet potato. Plant Biotechnology Journal, 2016, 14, 592-602.	4.1	175
3028	Nextâ€generation sequencing for identification of candidate genes for <i>Fusarium</i> wilt and sterility mosaic disease in pigeonpea (<i><scp>C</scp>ajanus cajan</i>). Plant Biotechnology Journal, 2016, 14, 1183-1194.	4.1	108

#	Article	IF	Citations
3029	<i>Fusarium oxysporum</i> mediates systems metabolic reprogramming of chickpea roots as revealed by a combination of proteomics and metabolomics. Plant Biotechnology Journal, 2016, 14, 1589-1603.	4.1	63
3030	Two-dimensional gel electrophoresis-based analysis provides global insights into the cotton ovule and fiber proteomes. Science China Life Sciences, 2016, 59, 154-163.	2.3	16
3031	Transcriptional response of yellow perch to changes in ambient metal concentrationsâ€”A reciprocal field transplantation experiment. Aquatic Toxicology, 2016, 173, 132-142.	1.9	13
3032	An <scp>RNA</scp>â€•Seqâ€•based reference transcriptome for Citrus. Plant Biotechnology Journal, 2016, 14, 938-950.	4.1	21
3033	Coordinated Regulation of Species-Specific Hydroxycinnamic Acid Degradation and Siderophore Biosynthesis Pathways in Agrobacterium fabrum. Applied and Environmental Microbiology, 2016, 82, 3515-3524.	1.4	12
3034	Effects of drought and salt-stresses on gene expression in Caragana korshinskii seedlings revealed by RNA-seq. BMC Genomics, 2016, 17, 200.	1.2	47
3035	Two Oyster Species That Show Differential Susceptibility to Virus Infection Also Show Differential Proteomic Responses to Generic dsRNA. Journal of Proteome Research, 2016, 15, 1735-1746.	1.8	16
3036	Characterization of the orthodox Pinus occidentalis seed and pollen proteomes by using complementary gel-based and gel-free approaches. Journal of Proteomics, 2016, 143, 382-389.	1.2	10
3037	Comparison of transcriptomes of wild-type and isothiazolone-resistant Pseudomonas aeruginosa by using RNA-seq. Molecular Biology Reports, 2016, 43, 527-540.	1.0	5
3038	The Genome and Methylome of a Subsocial Small Carpenter Bee,<i>Ceratina calcarata</i>. Genome Biology and Evolution, 2016, 8, 1401-1410.	1.1	71
3039	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	13.7	1,021
3040	Anthocyanin Biosynthesis Regulation in the Fruit of Citrus sinensis cv. Tarocco. Plant Molecular Biology Reporter, 2016, 34, 1043-1055.	1.0	10
3041	RNA-seq analysis in forest tree species: bioinformatic problems and solutions. Tree Genetics and Genomes, 2016, 12, 1.	0.6	25
3042	Potato tuber expression of Arabidopsis WRINKLED1 increase triacylglycerol and membrane lipids while affecting central carbohydrate metabolism. Plant Biotechnology Journal, 2016, 14, 1883-1898.	4.1	74
3043	Transcriptome reveals senescing callus tissue of Aquilaria malaccensis, an endangered tropical tree, triggers similar response as wounding with respect to terpenoid biosynthesis. Tree Genetics and Genomes, 2016, 12, 1.	0.6	15
3044	Differential transcriptome analysis of leaves of tea plant (Camellia sinensis) provides comprehensive insights into the defense responses to Ectropis oblique attack using RNA-Seq. Functional and Integrative Genomics, 2016, 16, 383-398.	1.4	98
3045	Global comparative analysis of expressed genes in ovules and leaves of Ginkgo biloba L.. Tree Genetics and Genomes, 2016, 12, 1.	0.6	12
3046	Discovery of Organophosphate Resistance-Related Genes Associated With Well-known Resistance Mechanisms of<i>Plutella xylostella</i>(L.) (Lepidoptera: Plutellidae) by RNA-Seq. Journal of Economic Entomology, 2016, 109, 1378-1386.	0.8	18

#	Article	IF	Citations
3047	Vibrio elicits targeted transcriptional responses from copepod hosts. FEMS Microbiology Ecology, 2016, 92, fiw072.	1.3	21
3048	RNA-seq analysis of early enteromyxosis in turbot (Scophthalmus maximus): new insights into parasite invasion and immune evasion strategies. International Journal for Parasitology, 2016, 46, 507-517.	1.3	50
3049	Complete Genome Sequence of the Larvicidal Bacterium Lysinibacillus sphaericus Strain OT4b.25. Genome Announcements, 2016, 4, .	0.8	9
3050	Transcriptome analysis of genes responding to NNV infection in Asian seabass epithelial cells. Fish and Shellfish Immunology, 2016, 54, 342-352.	1.6	62
3051	Transcriptome datasets supply basic gene information for RNAi pest management and gene functional studies in Nephotettix cincticeps (Uhler). Journal of Integrative Agriculture, 2016, 15, 840-847.	1.7	0
3052	Transcriptome analysis of the copepod Eurytemora affinis upon exposure to endocrine disruptor pesticides: Focus on reproduction and development. Aquatic Toxicology, 2016, 176, 64-75.	1.9	32
3053	Effects of condensed tannin fractions of different molecular weights on population and diversity of bovine rumen methanogenic archaea in vitro , as determined by high-throughput sequencing. Animal Feed Science and Technology, 2016, 216, 146-160.	1.1	41
3054	The application of GBS markers for extending the dense genetic map of rye (Secale cereale L.) and the localization of the Rfc1 gene restoring male fertility in plants with the C source of sterility-inducing cytoplasm. Journal of Applied Genetics, 2016, 57, 439-451.	1.0	22
3055	Complete genome sequences and analysis of the Fusobacterium nucleatum subspecies animalis 7-1 bacteriophage É,Funu1 and É,Funu2. Anaerobe, 2016, 38, 125-129.	1.0	11
3056	Identification of membrane proteins of the midgut of Zabrotes subfasciatus larvae associated with the insecticidal mechanism of PF2 lectin. Journal of Asia-Pacific Entomology, 2016, 19, 677-682.	0.4	8
3057	Molecular mechanism of ethylene stimulation of latex yield in rubber tree (Hevea brasiliensis) revealed by de novo sequencing and transcriptome analysis. BMC Genomics, 2016, 17, 257.	1.2	33
3058	Evidence of recent signatures of selection during domestication in an Atlantic salmon population. Marine Genomics, 2016, 26, 41-50.	0.4	62
3059	The chemical toxicity of cesium in Indian mustard (Brassica juncea L.) seedlings. Journal of Environmental Radioactivity, 2016, 160, 93-101.	0.9	13
3060	De novo assembly and annotation of the Antarctic copepod (Tigriopus kingsejongensis) transcriptome. Marine Genomics, 2016, 28, 37-39.	0.4	22
3061	Fusarium mycotoxin enniatin B: Cytotoxic effects and changes in gene expression profile. Toxicology in Vitro, 2016, 34, 309-320.	1.1	20
3062	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. Genome Research, 2016, 26, 812-825.	2.4	88
3063	Comparative transcriptome analysis of female and hermaphrodite flower buds in bitter gourd (Momordica charantia L.) by RNA sequencing. Journal of Horticultural Science and Biotechnology, 2016, 91, 250-257.	0.9	6
3064	De novo assembly and characterization of the floral transcriptome of an economically important tree species, Lindera glauca (Lauraceae), including the development of EST-SSR markers for population genetics. Molecular Biology Reports, 2016, 43, 1243-1250.	1.0	13

#	Article	IF	Citations
3065	Draft genome sequence and annotation ofLactobacillus acetotoleransBM-LA14527, a beer-spoilage bacteria. FEMS Microbiology Letters, 2016, 363, fnw201.	0.7	45
3066	Genome microsatellite diversity within the Apicomplexa phylum. Molecular Genetics and Genomics, 2016, 291, 2117-2129.	1.0	1
3067	Stronger sink demand for metabolites supports dominance of the apical bud in etiolated growth. Journal of Experimental Botany, 2016, 67, 5495-5508.	2.4	13
3068	Transcriptome sequencing reveals genome-wide variation in molecular evolutionary rate among ferns. BMC Genomics, 2016, 17, 692.	1.2	16
3069	Time-scale dynamics of proteome and transcriptome of the white-rot fungus Phlebia radiata: growth on spruce wood and decay effect on lignocellulose. Biotechnology for Biofuels, 2016, 9, 192.	6.2	95
3070	Microalgae Isolation and Selection for Prospective Biodiesel Production. , 2016, , 285-304.		1
3071	Developmental Changes in Scots Pine Transcriptome during Heartwood Formation. Plant Physiology, 2016, 172, 1403-1417.	2.3	46
3072	Behavioral Genetic Toolkits. Current Topics in Developmental Biology, 2016, 119, 157-204.	1.0	46
3073	A yeast library-hybrid assay to screen maize- Rhizoctonia transcription factors and protein-protein interactions in one experimental pipeline. Agri Gene, 2016, 1, 15-22.	1.9	1
3074	Transcriptome analysis of grey mullet (Mugil cephalus) after challenge with Lactococcus garvieae. Fish and Shellfish Immunology, 2016, 58, 593-603.	1.6	33
3075	De novo assembly of Zea nicaraguensis root transcriptome identified 5 261 full-length transcripts. Journal of Integrative Agriculture, 2016, 15, 1207-1217.	1.7	1
3076	Transcriptome response of wheat Norin 10 to long-term elevated CO2 under high yield field condition. Journal of Integrative Agriculture, 2016, 15, 2142-2152.	1.7	3
3077	De novo transcriptome assembly and development of SSR markers of oaks Quercus austrocochinchinensis and Q. kerrii (Fagaceae). Tree Genetics and Genomes, 2016, 12, 1.	0.6	20
3078	Complete genome sequencing and comparative genomic analysis of functionally diverse Lysinibacillus sphaericus III(3)7. Genomics Data, 2016, 9, 78-86.	1.3	12
3079	The Onion Genomic Resource: A genomics and bioinformatics driven resource for onion breeding. Plant Gene, 2016, 8, 9-15.	1.4	7
3080	Genome scan reveals selection acting on genes linked to stress response in wild pearl millet. Molecular Ecology, 2016, 25, 5500-5512.	2.0	30
3081	De-novo transcriptome assembly for gene identification, analysis, annotation, and molecular marker discovery in Onobrychis viciifolia. BMC Genomics, 2016, 17, 756.	1.2	32
3082	De novo transcriptome sequencing of pakchoi (Brassica rapa L. chinensis) reveals the key genes related to the response of heat stress. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	8

#	ARTICLE	IF	CITATIONS
3083	Transcriptome sequencing of Mycosphaerella fijiensis during association with Musa acuminata reveals candidate pathogenicity genes. BMC Genomics, 2016, 17, 690.	1.2	20
3084	Comparative study of host response to chytridiomycosis in a susceptible and a resistant toad species. Molecular Ecology, 2016, 25, 5663-5679.	2.0	31
3085	Physical mapping of NBS-coding resistance genes to the Me-gene cluster on chromosome P9 reveals markers tightly linked to the N gene for root-knot nematode resistance in pepper. Molecular Breeding, 2016, 36, 1.	1.0	16
3086	Dry and wet approaches for genome-wide functional annotation of conventional and unconventional transcriptional activators. Computational and Structural Biotechnology Journal, 2016, 14, 262-270.	1.9	6
3087	A larval transcriptome of the limnephilid caddisfly<i>Micropterna lateralis</i>(Stephens, 1837) (Trichoptera: Limnephilidae). Aquatic Insects, 2016, 37, 253-257.	0.6	3
3088	A deep sequencing analysis of transcriptomes and the development of EST-SSR markers in mungbean (Vigna radiata). Journal of Genetics, 2016, 95, 527-535.	0.4	28
3089	Genome-wide identification of microRNAs and their target genes in Cynoglossus semilaevis using computational approach. Gene Reports, 2016, 4, 235-243.	0.4	1
3090	Genetic basis of priority effects: insights from nectar yeast. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161455.	1.2	44
3091	De novo assembly and characterization of antennal transcriptome reveal chemosensory system in Nysius ericae. Journal of Asia-Pacific Entomology, 2016, 19, 1077-1087.	0.4	19
3092	The build-up of osmotic stress responses within the growing root apex using kinematics and RNA-sequencing. Journal of Experimental Botany, 2016, 67, 5961-5973.	2.4	12
3093	Elodea nuttallii exposure to mercury exposure under enhanced ultraviolet radiation: Effects on bioaccumulation, transcriptome, pigment content and oxidative stress. Aquatic Toxicology, 2016, 180, 218-226.	1.9	15
3094	Convergent local adaptation to climate in distantly related conifers. Science, 2016, 353, 1431-1433.	6.0	303
3095	Sarcoptes scabiei: genomics to proteomics to biology. Parasites and Vectors, 2016, 9, 380.	1.0	28
3096	Metabolic profiles of planktonic and biofilm cells of <i>Candida orthopsilosis</i>. Future Microbiology, 2016, 11, 1299-1313.	1.0	7
3097	Substitutions in the Glycogenin-1 Gene Are Associated with the Evolution of Endothermy in Sharks and Tunas. Genome Biology and Evolution, 2016, 8, 3011-3021.	1.1	11
3098	Agroinfiltration contributes to VP1 recombinant protein degradation. Bioengineered, 2016, 7, 459-477.	1.4	10
3099	Comprehensive transcriptome-based characterization of differentially expressed genes involved in microsporogenesis of radish CMS line and its maintainer. Functional and Integrative Genomics, 2016, 16, 529-543.	1.4	12
3100	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	13.7	160

#	Article	IF	Citations
3101	Transcriptome modulation during host shift is driven by secondary metabolites in desert <i><scp>D</scp>rosophila</i>. Molecular Ecology, 2016, 25, 4534-4550.	2.0	40
3102	Genomics-Based Discovery of Plant Genes for Synthetic Biology of Terpenoid Fragrances. Methods in Enzymology, 2016, 576, 47-67.	0.4	10
3103	De novo transcriptome assembly of the marine gastropod Reishia clavigera for supporting toxic mechanism studies. Aquatic Toxicology, 2016, 178, 39-48.	1.9	15
3104	Differential gene expression according to race and host plant in the pea aphid. Molecular Ecology, 2016, 25, 4197-4215.	2.0	59
3105	In Depth Proteome Analysis of Ripening Muscadine Grape Berry cv. Carlos Reveals Proteins Associated with Flavor and Aroma Compounds. Journal of Proteome Research, 2016, 15, 2910-2923.	1.8	14
3106	Transcriptome comparison of resistant and susceptible sesame (<i>Sesamum indicum</i> L.) varieties inoculated with <i>Fusarium oxysporum</i> f.Âsp<i>.Âsesami</i>. Plant Breeding, 2016, 135, 627-635.	1.0	11
3107	Cysteine redox proteomics of the hemoglobinâ€depleted cytosolic fraction of stored red blood cells. Proteomics - Clinical Applications, 2016, 10, 883-893.	0.8	15
3108	The citrus postharvest pathogen Penicillium digitatum depends on the PdMpkB kinase for developmental and virulence functions. International Journal of Food Microbiology, 2016, 236, 167-176.	2.1	29
3109	Characterization of the Poplar Pan-Genome by Genome-Wide Identification of Structural Variation. Molecular Biology and Evolution, 2016, 33, 2706-2719.	3.5	95
3110	Pangolin genomes and the evolution of mammalian scales and immunity. Genome Research, 2016, 26, 1312-1322.	2.4	95
3111	Transcriptome sequencing and de novo characterization of Korean endemic land snail, Koreanohadra kurodana for functional transcripts and SSR markers. Molecular Genetics and Genomics, 2016, 291, 1999-2014.	1.0	14
3112	Genome-wide identification and domain organization of lectin domains in cucumber. Plant Physiology and Biochemistry, 2016, 108, 165-176.	2.8	23
3113	Functional Genomic Analysis of the Impact of Camelina (Camelina sativa) Meal on Atlantic Salmon (Salmo salar) Distal Intestine Gene Expression and Physiology. Marine Biotechnology, 2016, 18, 418-435.	1.1	20
3114	Comparative genomeâ€wide analysis reveals that <i>Burkholderia contaminans </i><scp>MS</scp>14 possesses multiple antimicrobial biosynthesis genes but not major genetic loci required for pathogenesis. MicrobiologyOpen, 2016, 5, 353-369.	1.2	44
3115	Comparative transcriptome resources of two <i>Dysosma</i> species (Berberidaceae) and molecular evolution of the <i><scp>CYP</scp>719A</i> gene in Podophylloideae. Molecular Ecology Resources, 2016, 16, 228-241.	2.2	13
3116	Comparison of synganglion neuropeptides, neuropeptide receptors and neurotransmitter receptors and their gene expression in response to feeding in <scp><i>I</i></scp><i>xodes scapularis</i> (<scp>I</scp>xodidae) vs. <scp><i>O</i></scp><i>rnithodoros turicata</i> (<scp>A</scp>rgasidae). Insect Molecular Biology, 2016, 25, 72-92.	1.0	20
3117	Cry1Ab-expressing rice did not influence expression of fecundity-related genes in the wolf spider Pardosa pseudoannulata. Gene, 2016, 592, 1-7.	1.0	12
3118	Genomeâ€wide gene expression dynamics of the fungal pathogen <i><scp>D</scp>othistroma septosporum</i> throughout its infection cycle of the gymnosperm host <i><scp>P</scp>inus radiata</i>. Molecular Plant Pathology, 2016, 17, 210-224.	2.0	48

#	ARTICLE	IF	CITATIONS
3119	Transcriptional responses in Ecklonia cava to short-term exposure to hyperthermal stress. Toxicology and Environmental Health Sciences, 2016, 8, 181-188.	1.1	1
3120	Evidence for an Opportunistic and Endophytic Lifestyle of the Bursaphelenchus xylophilus-Associated Bacteria Serratia marcescens PWN146 Isolated from Wilting Pinus pinaster. Microbial Ecology, 2016, 72, 669-681.	1.4	22
3121	Comparative transcriptomics of rice plants under cold, iron, and salt stresses. Functional and Integrative Genomics, 2016, 16, 567-579.	1.4	37
3122	Genome-Wide Discovery of Tissue-Specific Genes in Maize. Plant Molecular Biology Reporter, 2016, 34, 1204-1214.	1.0	3
3123	Analyses of Drought-Tolerance Mechanism of Rice Based on the Transcriptome and Gene Ontology Data. , 2016, , 415-432.		2
3124	Genome-wide identification of salinity responsive HSP70s in common bean. Molecular Biology Reports, 2016, 43, 1251-1266.	1.0	31
3125	Characterisation and expression analysis of UBC9 and UBS27 genes in developing gonads of cicindelids (Coleoptera: Cicindelidae). Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2016, 202, 75-82.	0.7	1
3126	The transcriptome response of <i>Heliconius melpomene</i> larvae to a novel host plant. Molecular Ecology, 2016, 25, 4850-4865.	2.0	39
3127	Riverscape genomics of a threatened fish across a hydroclimatically heterogeneous river basin. Molecular Ecology, 2016, 25, 5093-5113.	2.0	91
3128	Employing artificial neural networks for constructing metadata-based model to automatically select an appropriate data visualization technique. Applied Soft Computing Journal, 2016, 49, 365-384.	4.1	34
3129	Local Auxin Biosynthesis Mediated by a YUCCA Flavin Monooxygenase Regulates Haustorium Development in the Parasitic Plant <i>Phtheirospermum japonicum</i>. Plant Cell, 2016, 28, 1795-1814.	3.1	102
3130	Subtractive transcriptome analysis of leaf and rhizome reveals differentially expressed transcripts in Panax sokpayensis. Functional and Integrative Genomics, 2016, 16, 619-639.	1.4	22
3131	Dynamic Rearrangement in Snake Venom Gland Proteome: Insights into <i>Bothrops jararaca</i> Intraspecific Venom Variation. Journal of Proteome Research, 2016, 15, 3752-3762.	1.8	30
3132	The transcriptome of metamorphosing flatfish. BMC Genomics, 2016, 17, 413.	1.2	17
3133	Draft genome sequence of Staphylococcus aureus KT/312045, an ST1-MSSA PVL positive isolated from pus sample in East Coast Malaysia. Genomics Data, 2016, 9, 111-112.	1.3	5
3134	Transcriptome sequencing and de novo analysis of a recessive genic male sterile line in cabbage (Brassica oleracea L. var. capitata). Molecular Breeding, 2016, 36, 1.	1.0	10
3135	miRNA Profiling in Plants: Current Identification and Expression Approaches. , 2016, , 189-215.		0
3136	Comparative epigenomic and transcriptomic analysis of Populus roots under excess Zn. Environmental and Experimental Botany, 2016, 132, 16-27.	2.0	8

#	Article	IF	Citations
3137	A Comparison of Resources for the Annotation of a<i>De Novo</i>Assembled Transcriptome in the Molting Gland (Y-Organ) of the Blackback Land Crab,<i>Gecarcinus lateralis</i>. Integrative and Comparative Biology, 2016, 56, 1103-1112.	0.9	17
3138	Selecting Hypomethylated Genomic Regions Using MRE-Seq. Methods in Molecular Biology, 2016, 1482, 83-102.	0.4	5
3139	Comparative analysis of transcriptomes in aerial stems and roots of Ephedra sinica based on high-throughput mRNA sequencing. Genomics Data, 2016, 10, 4-11.	1.3	6
3140	Gene Duplication and Gene Expression Changes Play a Role in the Evolution of Candidate Pollen Feeding Genes in<i>Heliconius</i>Butterflies. Genome Biology and Evolution, 2016, 8, 2581-2596.	1.1	21
3141	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. Journal of Heredity, 2016, 107, 481-495.	1.0	50
3142	Comparative RNA-sequencing profiling reveals novel Delta-class glutathione S-transferases relative genes expression patterns in Tribolium castaneum. Gene, 2016, 593, 13-20.	1.0	24
3143	Genomic Analysis of Genes Involved in the Biosynthesis of Very Long Chain Polyunsaturated Fatty Acids in <i>Thraustochytrium</i> sp. 26185. Lipids, 2016, 51, 1065-1075.	0.7	20
3144	Proteomic analysis of the response of Î±-ketoglutarate-producer Yarrowia lipolytica WSH-Z06 to environmental pH stimuli. Applied Microbiology and Biotechnology, 2016, 100, 8829-8841.	1.7	8
3145	Rice Plasma Membrane Proteomics Reveals <i>Magnaporthe oryzae</i> Promotes Susceptibility by Sequential Activation of Host Hormone Signaling Pathways. Molecular Plant-Microbe Interactions, 2016, 29, 902-913.	1.4	29
3147	The genetic map of goldfish (Carassius auratus) provided insights to the divergent genome evolutions in the Cyprinidae family. Scientific Reports, 2016, 6, 34849.	1.6	25
3148	mRNA changes in nucleus accumbens related to methamphetamine addiction in mice. Scientific Reports, 2016, 6, 36993.	1.6	41
3149	De novo transcriptome sequencing in Monsonia burkeana revealed putative genes for key metabolic pathways involved in tea quality and medicinal value. 3 Biotech, 2016, 6, 250.	1.1	3
3150	Crosstalk between sugarcane and a plant-growth promoting Burkholderia species. Scientific Reports, 2016, 6, 37389.	1.6	92
3151	A Genome-Wide Association Study for Partial Resistance to Maize Common Rust. Phytopathology, 2016, 106, 745-751.	1.1	51
3152	Transcriptomic and proteomic insights into innate immunity and adaptations to a symbiotic lifestyle in the gutless marine worm Olavius algarvensis. BMC Genomics, 2016, 17, 942.	1.2	41
3153	Transcriptomic responses of the calanoid copepod Calanus finmarchicus to the saxitoxin producing dinoflagellate Alexandrium fundyense. Scientific Reports, 2016, 6, 25708.	1.6	29
3154	Comparative transcriptomic analysis uncovers the complex genetic network for resistance to Sclerotinia sclerotiorum in Brassica napus. Scientific Reports, 2016, 6, 19007.	1.6	126
3155	Reference Transcriptomes and Detection of Duplicated Copies in Hexaploid and Allododecaploid<i>Spartina</i>Species (Poaceae). Genome Biology and Evolution, 2016, 8, 3030-3044.	1.1	18

#	Article	IF	Citations
3156	Transcriptome analysis deciphers evolutionary mechanisms underlying genetic differentiation between coastal and offshore anchovy populations in the Bay of Biscay. Marine Biology, 2016, 163, 1.	0.7	14
3157	ChIP-Seq-Annotated Heliconius erato Genome Highlights Patterns of cis -Regulatory Evolution in Lepidoptera. Cell Reports, 2016, 16, 2855-2863.	2.9	43
3158	Microarrayâ€based annotation of the gut transcriptome of the migratory locust, <i>Locusta migratoria</i>. Insect Molecular Biology, 2016, 25, 745-756.	1.0	8
3159	Genome-scale mRNA and small RNA transcriptomic insights into initiation of citrus apomixis. Journal of Experimental Botany, 2016, 67, 5743-5756.	2.4	36
3160	Comparative transcriptomic analyses of two bighead carp (Hypophthalmichthys nobilis) groups with different growth rates. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 20, 111-117.	0.4	10
3161	Sunflower HaGPAT9-1 is the predominant GPAT during seed development. Plant Science, 2016, 252, 42-52.	1.7	30
3162	De novo transcriptomic analysis and development of EST-SSR markers in the Siberian tiger (Panthera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	5
3163	De Novo Transcriptome Assembly and Sex-Biased Gene Expression in the Cyclical ParthenogeneticDaphnia galeata. Genome Biology and Evolution, 2016, 8, 3120-3139.	1.1	38
3164	Comparative transcriptomics of anal fin pigmentation patterns in cichlid fishes. BMC Genomics, 2016, 17, 712.	1.2	35
3165	Extensive transcriptomic studies on the roles played by abscisic acid and auxins in the development and ripening of strawberry fruits. Functional and Integrative Genomics, 2016, 16, 671-692.	1.4	67
3166	Transcriptome-wide identification and characterization of CAD isoforms specific for podophyllotoxin biosynthesis from Podophyllum hexandrum. Plant Molecular Biology, 2016, 92, 1-23.	2.0	18
3167	De novo sequencing of Eucommia ulmoides flower bud transcriptomes for identification of genes related to floral development. Genomics Data, 2016, 9, 105-110.	1.3	12
3168	Effector profiles distinguish <i>formae speciales</i> of <i>Fusarium oxysporum</i>. Environmental Microbiology, 2016, 18, 4087-4102.	1.8	179
3169	Transcriptome profiling of Camelina sativa to identify genes involved in triacylglycerol biosynthesis and accumulation in the developing seeds. Biotechnology for Biofuels, 2016, 9, 136.	6.2	53
3170	De novo assembly and characterization of leaf transcriptome for the development of EST-SSR markers of the non-model species Indigofera szechuensis. Biochemical Systematics and Ecology, 2016, 68, 36-43.	0.6	9
3171	The genomewide transcriptional response underlying the pea aphid wing polyphenism. Molecular Ecology, 2016, 25, 4146-4160.	2.0	60
3172	Transcriptome analysis of woodland strawberry (Fragaria vesca) response to the infection by Strawberry vein banding virus (SVBV). Virology Journal, 2016, 13, 128.	1.4	24
3173	De novo transcriptome sequencing of a non-model polychaete species. Marine Genomics, 2016, 29, 31-34.	0.4	2

#	ARTICLE	IF	CITATIONS
3174	The Identification of the Closest Living Relative(s) of Tetrapods: Phylogenomic Lessons for Resolving Short Ancient Internodes. Systematic Biology, 2016, 65, 1057-1075.	2.7	45
3175	De Novo Deep Transcriptome Analysis of Medicinal Plants for Gene Discovery in Biosynthesis of Plant Natural Products. Methods in Enzymology, 2016, 576, 19-45.	0.4	31
3176	Dataset for transcriptional response of barley (Hordeum vulgare) exposed to drought and subsequent re-watering. Data in Brief, 2016, 8, 334-341.	0.5	5
3177	Comparison of microsatellite distribution in genomes of Centruroides exilicauda and Mesobuthus martensii. Gene, 2016, 594, 41-46.	1.0	6
3178	Transcriptome analysis reveals that insulin is an immunomodulatory hormone in common carp. Fish and Shellfish Immunology, 2016, 59, 213-219.	1.6	6
3179	Analysis of proteome dynamics inside the silk gland lumen of Bombyx mori. Scientific Reports, 2016, 6, 21158.	1.6	36
3180	The pangenome of an agronomically important crop plant Brassica oleracea. Nature Communications, 2016, 7, 13390.	5.8	375
3181	Critical Role of COI1-Dependent Jasmonate Pathway in AAL toxin induced PCD in Tomato Revealed by Comparative Proteomics. Scientific Reports, 2016, 6, 28451.	1.6	14
3182	Soil metaproteomics reveals an inter-kingdom stress response to the presence of black truffles. Scientific Reports, 2016, 6, 25773.	1.6	56
3183	Transcriptome profiling of the salt-stress response in Triticum aestivum cv. Kharchia Local. Scientific Reports, 2016, 6, 27752.	1.6	82
3184	Genome wide transcriptome profiling of Fusarium oxysporum f sp. ciceris conidial germination reveals new insights into infection-related genes. Scientific Reports, 2016, 6, 37353.	1.6	45
3185	Rapid identification of fruit length loci in cucumber (Cucumis sativus L.) using next-generation sequencing (NGS)-based QTL analysis. Scientific Reports, 2016, 6, 27496.	1.6	63
3186	De novo transcriptome sequencing and gene expression profiling of Elymus nutans under cold stress. BMC Genomics, 2016, 17, 870.	1.2	49
3187	Identification and characterization of microRNAs in Humulus lupulus using high-throughput sequencing and their response to Citrus bark cracking viroid (CBCVd) infection. BMC Genomics, 2016, 17, 919.	1.2	26
3188	Chromosome-specific sequencing reveals an extensive dispensable genome component in wheat. Scientific Reports, 2016, 6, 36398.	1.6	24
3189	Comparative transcriptome analysis of chemosensory genes in two sister leaf beetles provides insights into chemosensory speciation. Insect Biochemistry and Molecular Biology, 2016, 79, 108-118.	1.2	36
3190	First genetic linkage map of Taraxacum koksaghyz Rodin based on AFLP, SSR, COS and EST-SSR markers. Scientific Reports, 2016, 6, 31031.	1.6	23
3191	Genome Sequence of <i>Vaccinia virus</i> Strain Lister-Butantan, a Lister Vaccine Variant Used during a Smallpox Eradication Campaign in Brazil. Genome Announcements, 2016, 4, .	0.8	0

#	ARTICLE	IF	CITATIONS
3192	Whole-genome de novo sequencing, combined with RNA-Seq analysis, reveals unique genome and physiological features of the amylolytic yeast Saccharomycopsis fibuligera and its interspecies hybrid. Biotechnology for Biofuels, 2016, 9, 246.	6.2	43
3193	Identification and developmental expression profiling of putative alkaloid biosynthetic genes in Corydalis yanhusuo bulbs. Scientific Reports, 2016, 6, 19460.	1.6	18
3194	Leaf transcriptome of two highly divergent genotypes of Urochloa humidicola (Poaceae), a tropical polyploid forage grass adapted to acidic soils and temporary flooding areas. BMC Genomics, 2016, 17, 910.	1.2	15
3195	Effects of weaning on intestinal crypt epithelial cells in piglets. Scientific Reports, 2016, 6, 36939.	1.6	44
3196	Population genomic analysis uncovers environmental stress-driven selection and adaptation of Lentinula edodes population in China. Scientific Reports, 2016, 6, 36789.	1.6	23
3197	The genome of the miiuy croaker reveals well-developed innate immune and sensory systems. Scientific Reports, 2016, 6, 21902.	1.6	67
3198	Overexpression of the Eggplant (Solanum melongena) NAC Family Transcription Factor SmNAC Suppresses Resistance to Bacterial Wilt. Scientific Reports, 2016, 6, 31568.	1.6	31
3199	De novo transcriptome sequencing of black pepper (Piper nigrum L.) and an analysis of genes involved in phenylpropanoid metabolism in response to Phytophthora capsici. BMC Genomics, 2016, 17, 822.	1.2	36
3200	Expression and chromatin structures of cellulolytic enzyme gene regulated by heterochromatin protein 1. Biotechnology for Biofuels, 2016, 9, 206.	6.2	29
3201	Big Data Analytics in Genomics. , 2016, , .		7
3202	Construction of a draft reference transcripts of onion (Allium cepa) using long-read sequencing. Plant Biotechnology Reports, 2016, 10, 383-390.	0.9	18
3203	Development of novel simple sequence repeat markers from ramie (Boehmeria nivea L. Gaudich) and analysis of genetic diversity in its genetic resources. Horticulture Environment and Biotechnology, 2016, 57, 519-528.	0.7	2
3204	Isolation of two insecticidal toxins from venom of the Australian theraphosid spider Coremiocnemis tropix. Toxicon, 2016, 123, 62-70.	0.8	14
3205	Genome-scale DNA variant analysis and functional validation of a SNP underlying yellow fruit color in wild strawberry. Scientific Reports, 2016, 6, 29017.	1.6	70
3206	Transcriptomic analysis of heteromorphic stamens in Cassia biscapsularis L.. Scientific Reports, 2016, 6, 31600.	1.6	3
3207	Transcriptomic analysis of the highly efficient oil-degrading bacterium<i>Acinetobacter venetianus</i>RAG-1 reveals genes important in dodecane uptake and utilization. FEMS Microbiology Letters, 2016, 363, fnw224.	0.7	14
3208	Global Phosphoproteomic Analysis Reveals the Involvement of Phosphorylation in Aflatoxins Biosynthesis in the Pathogenic Fungus Aspergillus flavus. Scientific Reports, 2016, 6, 34078.	1.6	38
3209	Characterization of microRNAs by deep sequencing in red claw crayfish Cherax quadricarinatus haematopoietic tissue cells after white spot syndrome virus infection. Fish and Shellfish Immunology, 2016, 59, 469-483.	1.6	29

#	Article	IF	Citations
3210	Transcriptome assembly and expression profiling of molecular responses to cadmium toxicity in hepatopancreas of the freshwater crab Sinopotamon henanense. Scientific Reports, 2016, 6, 19405.	1.6	63
3211	Transcriptomic comparison of invasive bigheaded carps (<i>Hypophthalmichthys nobilis</i> and) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.8	6
3212	Widespread adaptive evolution during repeated evolutionary radiations in New World lupins. Nature Communications, 2016, 7, 12384.	5.8	80
3213	Functional insights into the testis transcriptome of the edible sea urchin Loxechinus albus. Scientific Reports, 2016, 6, 36516.	1.6	17
3214	Transcriptome differences between fiber-type and seed-type Cannabis sativa variety exposed to salinity. Physiology and Molecular Biology of Plants, 2016, 22, 429-443.	1.4	33
3215	Genome of Leptomonas pyrrhocoris: a high-quality reference for monoxenous trypanosomatids and new insights into evolution of Leishmania. Scientific Reports, 2016, 6, 23704.	1.6	74
3216	Tissue-Specific Venom Composition and Differential Gene Expression in Sea Anemones. Genome Biology and Evolution, 2016, 8, 2358-2375.	1.1	72
3217	Genomic, Transcriptomic, and Proteomic Analysis Provide Insights Into the Cold Adaptation Mechanism of the Obligate Psychrophilic Fungus <i>Mrakia psychrophila</i>. G3: Genes, Genomes, Genetics, 2016, 6, 3603-3613.	0.8	41
3218	Analysis of liver and gill miRNAs of Larimichthys crocea against Cryptocryon irritans challenge. Fish and Shellfish Immunology, 2016, 59, 484-491.	1.6	25
3219	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. Nature Communications, 2016, 7, 11362.	5.8	214
3220	Proteome-wide analysis of lysine acetylation in the plant pathogen Botrytis cinerea. Scientific Reports, 2016, 6, 29313.	1.6	77
3221	Rapid Evolutionary Rates and Unique Genomic Signatures Discovered in the First Reference Genome for the Southern Ocean Salp,<i>Salpa thompsoni</i>(Urochordata, Thaliacea). Genome Biology and Evolution, 2016, 8, 3171-3186.	1.1	25
3222	Insecticide resistance mediated by an exon skipping event. Molecular Ecology, 2016, 25, 5692-5704.	2.0	44
3223	Dynamics of genome change among Legionella species. Scientific Reports, 2016, 6, 33442.	1.6	18
3224	Genomic survey of a hyperparasitic microsporidianAmphiamblyssp. (Metchnikovellidae). Genome Biology and Evolution, 2016, 9, evw235.	1.1	41
3225	Gene expression profile indicates involvement of NO in Camellia sinensis pollen tube growth at low temperature. BMC Genomics, 2016, 17, 809.	1.2	24
3226	Hypoxic stress -responsive genes in air breathing catfish, Clarias magur (Hamilton 1822) and their possible physiological adaptive function. Fish and Shellfish Immunology, 2016, 59, 46-56.	1.6	8
3227	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. Scientific Reports, 2016, 6, 28199.	1.6	16

#	Article	IF	Citations
3228	Transcriptome Comparison Analysis of Ostrinia furnacalis in Four Developmental Stages. Scientific Reports, 2016, 6, 35008.	1.6	21
3229	Jute : Emerging Resources and Tools for. Sustainable Development and Biodiversity, 2016, , 155-200.	1.4	11
3230	Transcriptome response of cassava leaves under natural shade. Scientific Reports, 2016, 6, 31673.	1.6	43
3231	Transcriptional Analysis of The Adaptive Digestive System of The Migratory Locust in Response to Plant Defensive Protease Inhibitors. Scientific Reports, 2016, 6, 32460.	1.6	19
3232	Reproductive switching analysis of Daphnia similoides between sexual female and parthenogenetic female by transcriptome comparison. Scientific Reports, 2016, 6, 34241.	1.6	31
3233	A specialized flavone biosynthetic pathway has evolved in the medicinal plant, <i>Scutellaria baicalensis</i>. Science Advances, 2016, 2, e1501780.	4.7	165
3234	Transcriptome analysis of dormant tomonts of the marine fish ectoparasitic ciliate Cryptocaryon irritansÂunder lowÂtemperature. Parasites and Vectors, 2016, 9, 280.	1.0	19
3235	Improving Re-annotation of Annotated Eukaryotic Genomes. , 2016, , 171-195.		2
3236	Fiber Plants. Sustainable Development and Biodiversity, 2016, , .	1.4	6
3237	Comparative transcriptome analysis reveals insights into the streamlined genomes of haplosclerid demosponges. Scientific Reports, 2016, 6, 18774.	1.6	28
3238	Characterization of the transcriptomes and cuticular protein gene expression of alate adult, brachypterous neotenic and adultoid reproductives of Reticulitermes labralis. Scientific Reports, 2016, 6, 34183.	1.6	11
3239	Genomic Evolution of Two Acinetobacter baumannii Clinical Strains from ST-2 Clones Isolated in 2000 and 2010 (ST-2_clon_2000 and ST-2_clon_2010). Genome Announcements, 2016, 4, .	0.8	6
3240	Whole-transcriptome analysis of differentially expressed genes in the ray florets and disc florets of Chrysanthemum morifolium. BMC Genomics, 2016, 17, 398.	1.2	39
3241	Differential Expression of Hyperhydricity Responsive Peach MicroRNAs. Journal of Integrative Bioinformatics, 2016, 13, .	1.0	3
3242	Transcriptome analysis of root response to citrus blight based on the newly assembled Swingle citrumelo draft genome. BMC Genomics, 2016, 17, 485.	1.2	15
3243	Preparing for Winter: The Transcriptomic Response Associated with Different Day Lengths in <i>Drosophila montana</i>. G3: Genes, Genomes, Genetics, 2016, 6, 1373-1381.	0.8	36
3244	Draft Genome Sequence of Micromonospora sp . Strain HK10, Isolated from Kaziranga National Park, India. Genome Announcements, 2016, 4, .	0.8	1
3245	Transcriptome characterisation and simple sequence repeat marker discovery in the seagrass Posidonia oceanica. Scientific Data, 2016, 3, 160115.	2.4	13

#	Article	IF	Citations
3246	Three chromosomal rearrangements promote genomic divergence between migratory and stationary ecotypes of Atlantic cod. Scientific Reports, 2016, 6, 23246.	1.6	128
3247	Gene set of chemosensory receptors in the polyembryonic endoparasitoid Macrocentrus cingulum. Scientific Reports, 2016, 6, 24078.	1.6	20
3248	Exploring lateral genetic transfer among microbial genomes using TF-IDF. Scientific Reports, 2016, 6, 29319.	1.6	12
3249	A proteinaceous organic matrix regulates carbonate mineral production in the marine teleost intestine. Scientific Reports, 2016, 6, 34494.	1.6	11
3250	De novo sequencing and analysis of the transcriptome of Panax ginseng in the leaf-expansion period. Molecular Medicine Reports, 2016, 14, 1404-1412.	1.1	13
3251	Development of a toolbox to dissect host-endosymbiont interactions and protein trafficking in the trypanosomatid Angomonas deanei. BMC Evolutionary Biology, 2016, 16, 247.	3.2	26
3252	PARRoT- a homology-based strategy to quantify and compare RNA-sequencing from non-model organisms. BMC Bioinformatics, 2016, 17, 513.	1.2	6
3253	Genome-wide analysis of gene expression reveals gene regulatory networks that regulate chasmogamous and cleistogamous flowering in Pseudostellaria heterophylla (Caryophyllaceae). BMC Genomics, 2016, 17, 382.	1.2	17
3254	Refining borders of genome-rearrangements including repetitions. BMC Genomics, 2016, 17, 804.	1.2	0
3255	Transcriptome analysis reveals the genetic basis underlying the seasonal development of keratinized nuptial spines in Leptobrachium boringii. BMC Genomics, 2016, 17, 978.	1.2	11
3256	Transcriptome profiling in the damselfly Ischnura elegans identifies genes with sex-biased expression. BMC Genomics, 2016, 17, 985.	1.2	25
3257	Comparative genomics of Beauveria bassiana: uncovering signatures of virulence against mosquitoes. BMC Genomics, 2016, 17, 986.	1.2	38
3258	Deep, multi-stage transcriptome of the schistosomiasis vector Biomphalaria glabrata provides platform for understanding molluscan disease-related pathways. BMC Infectious Diseases, 2016, 16, 618.	1.3	22
3259	Identification and preliminary characterization of chemosensory perception-associated proteins in the melon fly Bactrocera cucurbitae using RNA-seq. Scientific Reports, 2016, 6, 19112.	1.6	29
3260	Molecular analysis of the Sydney rock oyster (Saccostrea glomerata) CO2 stress response. Climate Change Responses, 2016, 3, .	2.6	9
3261	PGD: a pangolin genome hub for the research community. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw063.	1.4	5
3262	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw081.	1.4	22
3263	PvTFDB: a<i>Phaseolus vulgaris</i>transcription factors database for expediting functional genomics in legumes. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw114.	1.4	12

#	ARTICLE	IF	CITATIONS
3264	Preliminary analysis of Psoroptes ovis transcriptome in different developmental stages. Parasites and Vectors, 2016, 9, 570.	1.0	16
3265	Use of Metatranscriptomics in Microbiome Research. Bioinformatics and Biology Insights, 2016, 10, BBI.S34610.	1.0	328
3266	Transcriptomeâ€wide patterns of divergence during allopatric evolution. Molecular Ecology, 2016, 25, 1478-1493.	2.0	52
3267	Resistance to <i>Streptomyces turgidiscabies</i> in potato involves an early and sustained transcriptional reprogramming at initial stages of tuber formation. Molecular Plant Pathology, 2016, 17, 703-713.	2.0	10
3268	Transcriptome sequencing and de novo analysis of Rosa multiflora under cold stress. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	19
3269	Paralog analyses reveal gene duplication events and genes under positive selection in Ixodes scapularis and other ixodid ticks. BMC Genomics, 2016, 17, 241.	1.2	18
3270	Fungal and host transcriptome analysis of pH-regulated genes during colonization of apple fruits by Penicillium expansum. BMC Genomics, 2016, 17, 330.	1.2	41
3271	Shared and divergent pathways for flower abscission are triggered by gibberellic acid and carbon starvation in seedless Vitis vinifera L. BMC Plant Biology, 2016, 16, 38.	1.6	27
3272	Identification of candidate genes for drought tolerance in coffee by high-throughput sequencing in the shoot apex of different Coffea arabica cultivars. BMC Plant Biology, 2016, 16, 94.	1.6	48
3273	Analysis of wheat microspore embryogenesis induction by transcriptome and small RNA sequencing using the highly responsive cultivar â€œSvilenaâ€. BMC Plant Biology, 2016, 16, 97.	1.6	38
3274	Transcriptomic analysis of developing embryos of apricot (Prunus armeniaca L.). Horticulture Environment and Biotechnology, 2016, 57, 197-206.	0.7	1
3275	Identification and Characterization of Pathogen-Response Genes (<I>repat</I>) in <I>Spodoptera frugiperda</I> (Lepidoptera: Noctuidae). Folia Biologica, 2016, 64, 23-29.	0.1	6
3276	Expression of a Nicotiana tabacum pathogen-induced gene is involved in the susceptibility to black shank. Functional Plant Biology, 2016, 43, 534.	1.1	3
3277	Comparative Transcriptome Analysis of Two <i>Ipomoea aquatica</i> Forsk. Cultivars Targeted To Explore Possible Mechanism of Genotype-Dependent Accumulation of Cadmium. Journal of Agricultural and Food Chemistry, 2016, 64, 5241-5250.	2.4	46
3278	Transcriptional analysis of porcine intestinal mucosa infected with Salmonella Typhimurium revealed a massive inflammatory response and disruption of bile acid absorption in ileum. Veterinary Research, 2016, 47, 11.	1.1	29
3279	De novo sequencing and characterization of seed transcriptome of the tree legume Millettia pinnata for gene discovery and SSR marker development. Molecular Breeding, 2016, 36, 1.	1.0	17
3280	Transcription, Signaling Receptor Activity, Oxidative Phosphorylation, and Fatty Acid Metabolism Mediate the Presence of Closely Related Species in Distinct Intertidal and Cold-Seep Habitats. Genome Biology and Evolution, 2016, 8, 51-69.	1.1	13
3281	Regulation, overexpression, and target gene identification of<i>Potato Homeobox 15</i>(<i>POTH15</i>) â€“ a class-I<i>KNOX</i>gene in potato. Journal of Experimental Botany, 2016, 67, 4255-4272.	2.4	20

#	ARTICLE	IF	CITATIONS
3282	Molecular identification and sex distribution of two chemosensory receptor families in Athetis lepigone by antennal transcriptome analysis. Journal of Asia-Pacific Entomology, 2016, 19, 571-580.	0.4	18
3283	Viable But Not Culturable (VBNC) state of Brettanomyces bruxellensis in wine: New insights on molecular basis of VBNC behaviour using a transcriptomic approach. Food Microbiology, 2016, 59, 196-204.	2.1	76
3284	In-depth proteomic analysis of the byssus from marine mussel Mytilus coruscus. Journal of Proteomics, 2016, 144, 87-98.	1.2	45
3285	Thermal stress induces a distinct transcriptome profile in the Pacific oyster Crassostrea gigas. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 19, 62-70.	0.4	35
3286	Differentially expressed transcripts in stomach of Penaeus monodon in response to AHPND infection. Developmental and Comparative Immunology, 2016, 65, 53-63.	1.0	54
3287	Vaccine-induced modulation of gene expression in turbot peritoneal cells. A microarray approach. Molecular Immunology, 2016, 75, 188-199.	1.0	8
3288	Genetic structure based on ESTâ€“SSR: a putative tool for fruit color selection in Japanese plum (Prunus salicina L.) breeding programs. Molecular Breeding, 2016, 36, 1.	1.0	18
3289	Mechanisms and metabolic regulation of PPARÎ± activation in Nile tilapia (Oreochromis niloticus). Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2016, 1861, 1036-1048.	1.2	80
3290	Light Remodels Lipid Biosynthesis in <i>Nannochloropsis gaditana</i> by Modulating Carbon Partitioning between Organelles. Plant Physiology, 2016, 171, 2468-2482.	2.3	106
3291	Identification of conserved miRNAs and their putative target genes in Podophyllum hexandrum (Himalayan Mayapple). Plant Gene, 2016, 6, 82-89.	1.4	61
3292	A sunflower WRKY transcription factor stimulates the mobilization of seed-stored reserves during germination and post-germination growth. Plant Cell Reports, 2016, 35, 1875-1890.	2.8	27
3293	Transcriptional profiling of overwintering gene expression in the small carpenter bee, Ceratina calcarata. Apidologie, 2016, 47, 572-582.	0.9	33
3294	Cell mediated immune response of the Mediterranean sea urchin Paracentrotus lividus after PAMPs stimulation. Developmental and Comparative Immunology, 2016, 62, 29-38.	1.0	19
3295	Transcriptome profiling of the antiviral immune response in Atlantic cod macrophages. Developmental and Comparative Immunology, 2016, 63, 187-205.	1.0	57
3296	Effects of high temperatures on threatened estuarine fishes during periods of extreme drought. Journal of Experimental Biology, 2016, 219, 1705-1716.	0.8	86
3297	Aquaporin family genes exhibit developmentally-regulated and host-dependent transcription patterns in the sea louse Caligus rogercresseyi. Gene, 2016, 585, 119-127.	1.0	7
3298	De novo assembly and transcriptome analysis of sclerotial development in Wolfiporia cocos. Gene, 2016, 588, 149-155.	1.0	16
3299	The role of melanin pathways in extremotolerance and virulence of<i>Fonsecaea</i>revealed by<i>de novo</i>assembly transcriptomics using illumina paired-end sequencing. Studies in Mycology, 2016, 83, 1-18.	4.5	35

#	Article	IF	Citations
3300	Predicting chemical bioavailability using microarray gene expression data and regression modeling: A tale of three explosive compounds. BMC Genomics, 2016, 17, 205.	1.2	1
3301	Analysis of simple sequence repeats in rice bean (Vigna umbellata) using an SSR-enriched library. Crop Journal, 2016, 4, 40-47.	2.3	10
3302	Proteomic dataset of the sea urchin Paracentrotus lividus adhesive organs and secreted adhesive. Data in Brief, 2016, 7, 1497-1505.	0.5	3
3303	Data set for diet specific differential gene expression analysis in three Spodoptera moths. Data in Brief, 2016, 8, 448-455.	0.5	1
3304	UV filters induce transcriptional changes of different hormonal receptors in Chironomus riparius embryos and larvae. Environmental Pollution, 2016, 214, 239-247.	3.7	39
3305	Complete genome sequence of a giant Vibrio phage ValKK3 infecting Vibrio alginolyticus. Genomics Data, 2016, 8, 37-38.	1.3	16
3306	Transcriptome profiling of the microalga Chlorella pyrenoidosa in response to different carbon dioxide concentrations. Marine Genomics, 2016, 29, 81-87.	0.4	10
3307	Molecular evolution of candidate male reproductive genes in the brown algal model Ectocarpus. BMC Evolutionary Biology, 2016, 16, 5.	3.2	9
3308	Transcriptomic profiles reveal the genome-wide responses of the harmful dinoflagellate Cochlodinium polykrikoides when exposed to the algicide copper sulfate. BMC Genomics, 2016, 17, 29.	1.2	57
3309	Identification of the genes involved in odorant reception and detection in the palm weevil Rhynchophorus ferrugineus, an important quarantine pest, by antennal transcriptome analysis. BMC Genomics, 2016, 17, 69.	1.2	102
3310	Transcriptomic analysis reveals the gene expression profile that specifically responds to IBA during adventitious rooting in mung bean seedlings. BMC Genomics, 2016, 17, 43.	1.2	31
3311	RNA-seq analysis of the gonadal transcriptome during Alligator mississippiensis temperature-dependent sex determination and differentiation. BMC Genomics, 2016, 17, 77.	1.2	86
3312	The genome of newly classified Ochroconis mirabilis: Insights into fungal adaptation to different living conditions. BMC Genomics, 2016, 17, 91.	1.2	26
3313	Transcriptome wide analyses reveal a sustained cellular stress response in the gill tissue of Trematomus bernacchii after acclimation to multiple stressors. BMC Genomics, 2016, 17, 127.	1.2	91
3314	Multi-omics analysis reveals regulators of the response to nitrogen limitation in Yarrowia lipolytica. BMC Genomics, 2016, 17, 138.	1.2	62
3315	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. BMC Genomics, 2016, 17, 172.	1.2	92
3316	Identification and functional analyses of sex determination genes in the sexually dimorphic stag beetle Cyclommatus metallifer. BMC Genomics, 2016, 17, 250.	1.2	27
3317	An iNTT system for the large-scale screening of differentially expressed, nuclear-targeted proteins: cold-treatment-induced nucleoproteins in Rye (Secale cereale L.). BMC Genomics, 2016, 17, 189.	1.2	3

#	Article	IF	Citations
3318	Transcription profile of Trichophyton rubrum conidia grown on keratin reveals the induction of an adhesin-like protein gene with a tandem repeat pattern. BMC Genomics, 2016, 17, 249.	1.2	36
3319	Deciphering the transcriptional regulation and spatiotemporal distribution of immunity response in barley to Pyrenophora graminea fungal invasion. BMC Genomics, 2016, 17, 256.	1.2	11
3320	The compact genome of the plant pathogen Plasmodiophora brassicae is adapted to intracellular interactions with host Brassica spp. BMC Genomics, 2016, 17, 272.	1.2	107
3321	Transcriptome dynamics in the asexual cycle of the chordate Botryllus schlosseri. BMC Genomics, 2016, 17, 275.	1.2	20
3322	Gene expression comparison of resistant and susceptible Atlantic salmon fry challenged with Infectious Pancreatic Necrosis virus reveals a marked contrast in immune response. BMC Genomics, 2016, 17, 279.	1.2	78
3323	A subtracted cDNA library identifies genes up-regulated during PHOT1-mediated early step of de-etiolation in tomato (Solanum lycopersicum L.). BMC Genomics, 2016, 17, 291.	1.2	6
3324	The Trichoderma atroviride putative transcription factor Blu7 controls light responsiveness and tolerance. BMC Genomics, 2016, 17, 327.	1.2	25
3325	Gene and transposable element methylation in great tit (Parus major) brain and blood. BMC Genomics, 2016, 17, 332.	1.2	66
3326	The amyR-deletion strain of Aspergillus niger CICC2462 is a suitable host strain to express secreted protein with a low background. Microbial Cell Factories, 2016, 15, 68.	1.9	28
3327	De novo transcriptomic analysis of the female and male adults of the blood fluke Schistosoma turkestanicum. Parasites and Vectors, 2016, 9, 143.	1.0	12
3328	Transcriptome analysis reveals self-incompatibility in the tea plant (Camellia sinensis) might be under gametophytic control. BMC Genomics, 2016, 17, 359.	1.2	50
3329	A newly isolated and identified vitamin B12 producing strain: Sinorhizobium meliloti 320. Bioprocess and Biosystems Engineering, 2016, 39, 1527-1537.	1.7	17
3330	Salinity stress induces the production of 2-(2-phenylethyl)chromones and regulates novel classes of responsive genes involved in signal transduction in Aquilaria sinensis calli. BMC Plant Biology, 2016, 16, 119.	1.6	39
3331	A New Species of<i>Oobius</i>Trjapitzin (Hymenoptera: Encyrtidae) From the Russian Far East That Parasitizes Eggs of Emerald Ash Borer (Coleoptera: Buprestidae). Annals of the Entomological Society of America, 2016, 109, 629-638.	1.3	17
3332	Genomic Profiles of Diversification and Genotypeâ€“Phenotype Association in Island Nematode Lineages. Molecular Biology and Evolution, 2016, 33, 2257-2272.	3.5	31
3333	The genome of the yellow potato cyst nematode, Globodera rostochiensis, reveals insights into the basis of parasitism and virulence. Genome Biology, 2016, 17, 124.	3.8	156
3334	BLAST-based structural annotation of protein residues using Protein Data Bank. Biology Direct, 2016, 11, 4.	1.9	14
3335	Definitive host influences the proteomic profile of excretory/secretory products of the trematode Echinostoma caproni. Parasites and Vectors, 2016, 9, 185.	1.0	10

#	ARTICLE	IF	CITATIONS
3336	Combined exposure to pyrene and fluoranthene and their molecular effects on the Sydney rock oyster, Saccostrea glomerata. Aquatic Toxicology, 2016, 177, 136-145.	1.9	14
3337	Deep-sequencing transcriptome analysis of field-grown Medicago sativa L. crown buds acclimated to freezing stress. Functional and Integrative Genomics, 2016, 16, 495-511.	1.4	28
3338	Using digital gene expression profile to detect representational difference of Chlamys farreri genes after laboratory exposure to persistent organic pollutants. Genes and Genomics, 2016, 38, 263-274.	0.5	2
3339	Genome-wide analysis of transcription and photosynthesis inhibition in the harmful dinoflagellate Prorocentrum minimum in response to the biocide copper sulfate. Harmful Algae, 2016, 57, 27-38.	2.2	26
3340	Biological Activity of Polynesian Calophyllum inophyllum Oil Extract on Human Skin Cells. Planta Medica, 2016, 82, 961-966.	0.7	28
3341	Comparative genomics reveals genes significantly associated with woody hosts in the plant pathogen <i>Pseudomonas syringae</i>. Molecular Plant Pathology, 2016, 17, 1409-1424.	2.0	56
3342	Transcriptome asymmetry in synthetic and natural allotetraploid wheats, revealed by <scp>RNA</scp>â€sequencing. New Phytologist, 2016, 209, 1264-1277.	3.5	63
3343	Transcriptome and metabolome of synthetic <i>Solanum</i> autotetraploids reveal key genomic stress events following polyploidization. New Phytologist, 2016, 210, 1382-1394.	3.5	67
3344	Analyses of transcriptome sequences reveal multiple ancient largeâ€scale duplication events in the ancestor of Sphagnopsida (Bryophyta). New Phytologist, 2016, 211, 300-318.	3.5	56
3345	Salivary proteins of spider mites suppress defenses in <i>Nicotiana benthamiana</i> and promote mite reproduction. Plant Journal, 2016, 86, 119-131.	2.8	149
3346	Mechanistic underpinnings of dehydration stress in the American dog tick revealed through RNA-Seq and metabolomics. Journal of Experimental Biology, 2016, 219, 1808-1819.	0.8	41
3347	Genome-wide identification of SNPs and copy number variation in common bean (Phaseolus vulgaris L.) using genotyping-by-sequencing (GBS). Molecular Breeding, 2016, 36, 1.	1.0	87
3348	Genome-Wide Survey of Gut Fungi (Harpellales) Reveals the First Horizontally Transferred Ubiquitin Gene from a Mosquito Host. Molecular Biology and Evolution, 2016, 33, 2544-2554.	3.5	28
3349	Host specialization of the blast fungus Magnaporthe oryzae is associated with dynamic gain and loss of genes linked to transposable elements. BMC Genomics, 2016, 17, 370.	1.2	157
3350	Genome-wide transcriptome analysis of female-sterile rice ovule shed light on its abortive mechanism. Planta, 2016, 244, 1011-1028.	1.6	18
3351	Comparative proteomic analysis of Phalaenopsis leaves in the vegetative and flowering phase. Acta Physiologiae Plantarum, 2016, 38, 1.	1.0	4
3352	Characterization of the transcriptome and gene expression of four different tissues in the ecologically relevant sea urchin <i>Arbacia lixula</i> using <scp>RNA</scp>â€seq. Molecular Ecology Resources, 2016, 16, 794-808.	2.2	21
3353	A <i>de novo</i> transcriptomic analysis to reveal functional genes in <i>Apolygus lucorum</i>. Insect Science, 2016, 23, 2-14.	1.5	15

#	ARTICLE	IF	CITATIONS
3354	De novo transcriptome analyses of host-fungal interactions in oil palm (Elaeis guineensis Jacq.). BMC Genomics, 2016, 17, 66.	1.2	67
3355	Orphan Crops Browser: a bridge between model and orphan crops. Molecular Breeding, 2016, 36, 9.	1.0	18
3356	Molecular candidates for early-stage flower-to-fruit transition in stenospermocarpic table grape (Vitis vinifera L.) inflorescences ascribed by differential transcriptome and metabolome profiles. Plant Science, 2016, 244, 40-56.	1.7	18
3357	Draft genome sequence and chemical profiling of Fusarium langsethiae, an emerging producer of type A trichothecenes. International Journal of Food Microbiology, 2016, 221, 29-36.	2.1	27
3358	Quantitative metabolome, proteome and transcriptome analysis of midgut and fat body tissues in the mountain pine beetle, Dendroctonus ponderosae Hopkins, and insights into pheromone biosynthesis. Insect Biochemistry and Molecular Biology, 2016, 70, 170-183.	1.2	37
3359	Integrative Proteomics and Metabolomics Analysis of Insect Larva Brain: Novel Insights into the Molecular Mechanism of Insect Wandering Behavior. Journal of Proteome Research, 2016, 15, 193-204.	1.8	23
3360	Global transcriptome profiling analysis reveals insight into saliva-responsive genes in alfalfa. Plant Cell Reports, 2016, 35, 561-571.	2.8	29
3361	De novo assembly and analysis of midgut transcriptome of Haemaphysalis flava and identification of genes involved in blood digestion, feeding and defending from pathogens. Infection, Genetics and Evolution, 2016, 38, 62-72.	1.0	29
3362	Analysis of the Protein Kinase A-Regulated Proteome of Cryptococcus neoformans Identifies a Role for the Ubiquitin-Proteasome Pathway in Capsule Formation. MBio, 2016, 7, e01862-15.	1.8	62
3363	De novo characterization of the liver transcriptome of javelin goby Synechogobius hasta and analysis of its transcriptomic profile following waterborne copper exposure. Fish Physiology and Biochemistry, 2016, 42, 979-994.	0.9	21
3364	Adjustments of molecular key components of branchial ion and pH regulation in Atlantic cod (Gadus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Biochemistry and Molecular Biology, 2016, 193, 33-46.	0.7	26
3365	Development and validation of novel fiber relevant dbESTâ€“SSR markers and their utility in revealing genetic diversity in diploid cotton (Gossypium herbaceum and G. arboreum). Industrial Crops and Products, 2016, 83, 620-629.	2.5	18
3366	Deep Sequencing of the Fruit Transcriptome and Lipid Accumulation in a Non-Seed Tissue of Chinese Tallow, a Potential Biofuel Crop. Plant and Cell Physiology, 2016, 57, 125-137.	1.5	17
3367	Proteomic analysis of Puccina striiformis f. sp. tritici (Pst) during uredospore germination. European Journal of Plant Pathology, 2016, 144, 121-132.	0.8	7
3368	Identification and profiling of microRNAs in the ovaries of polytocous and monotocous goats during estrus. Theriogenology, 2016, 85, 769-780.	0.9	21
3369	Microarray analysis of gene expression in olive flounder liver infected with viral haemorrhagic septicaemia virus (VHSV). Fish and Shellfish Immunology, 2016, 49, 66-78.	1.6	15
3370	Combined effects of n-TiO2 and 2,3,7,8-TCDD in Mytilus galloprovincialis digestive gland: A transcriptomic and immunohistochemical study. Environmental Research, 2016, 145, 135-144.	3.7	57
3371	Proteomic analysis of Magnolia sieboldii K. Koch seed germination. Journal of Proteomics, 2016, 133, 76-85.	1.2	12

#	Article	IF	Citations
3372	Phloem transcriptome signatures underpin the physiological differentiation of the pedicel, stalk and fruit of cucumber (<i>Cucumis sativus</i>L.). Plant and Cell Physiology, 2016, 57, 19-34.	1.5	27
3373	Evaluation of potential candidate genes involved in salinity tolerance in striped catfish () Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.4	44
3374	Identification and localization of xylose-binding proteins as potential biomarkers for liver fibrosis/cirrhosis. Molecular BioSystems, 2016, 12, 598-605.	2.9	10
3375	iTRAQ protein profile analysis provides integrated insight into mechanisms of tolerance to TMV in tobacco (Nicotiana tabacum). Journal of Proteomics, 2016, 132, 21-30.	1.2	35
3376	Comparative Transcriptome Analysis between the Fungal Plant PathogensSclerotinia sclerotiorumandS. trifoliorumUsing RNA Sequencing. Journal of Heredity, 2016, 107, 163-172.	1.0	9
3377	Expression of mitochondria-related genes is elevated in overfeeding-induced goose fatty liver. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2016, 192, 30-37.	0.7	22
3378	Transcriptome profiling and digital gene expression by deep sequencing in early somatic embryogenesis of endangered medicinal Eleutherococcus senticosus Maxim.. Gene, 2016, 578, 17-24.	1.0	13
3379	De novo analysis of transcriptome reveals genes associated with leaf abscission in sugarcane (Saccharum officinarum L.). BMC Genomics, 2016, 17, 195.	1.2	51
3380	GeneAnalytics: An Integrative Gene Set Analysis Tool for Next Generation Sequencing, RNAseq and Microarray Data. OMICS A Journal of Integrative Biology, 2016, 20, 139-151.	1.0	187
3381	Diet dependent metabolic responses in three generalist insect herbivores Spodoptera spp. Insect Biochemistry and Molecular Biology, 2016, 71, 91-105.	1.2	81
3382	De Novo assembly and annotation of the freshwater crayfish Astacus astacus transcriptome. Marine Genomics, 2016, 28, 7-10.	0.4	59
3383	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. Genome Biology and Evolution, 2016, 8, 681-704.	1.1	125
3384	Genome-Scale Screening and Validation of Targets for Identification of Salmonella enterica and Serovar Prediction. Journal of Food Protection, 2016, 79, 376-383.	0.8	3
3385	RNA-seq reveals a diminished acclimation response to the combined effects of ocean acidification and elevated seawater temperature in Pagothenia borchgrevinki. Marine Genomics, 2016, 28, 87-97.	0.4	34
3386	De novo transcriptomic assembly and profiling of Rigidoporus microporus during saprotrophic growth on rubber wood. BMC Genomics, 2016, 17, 234.	1.2	12
3387	Genome-Wide Analysis Indicates Lineage-Specific Gene Loss during Papilionoideae Evolution. Genome Biology and Evolution, 2016, 8, 635-648.	1.1	11
3388	A comprehensive transcriptome of early development in yellowtail kingfish (<i><scp>S</scp>eriola) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.2	17
3389	The transcriptomic basis of tissueâ€•and nutritionâ€dependent sexual dimorphism in the beetle Onthophagus taurus. Ecology and Evolution, 2016, 6, 1601-1613.	0.8	18

#	ARTICLE	IF	CITATIONS
3390	Two small secreted proteins fromPuccinia triticinainduce reduction of ÃŸ-glucoronidase transient expression in wheat isolines containingLr9, Lr24andLr26. Canadian Journal of Plant Pathology, 2016, 38, 91-102.	0.8	11
3391	A single generation of domestication heritably alters the expression of hundreds of genes. Nature Communications, 2016, 7, 10676.	5.8	191
3392	Analysis of differentially expressed proteins in Yersinia enterocolitica-infected HeLa cells. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 562-569.	1.1	8
3393	Complex patterns of differential expression in candidate master regulatory genes for social behavior in honey bees. Behavioral Ecology and Sociobiology, 2016, 70, 1033-1043.	0.6	23
3394	De novo assembly and annotation of the salivary gland transcriptome of Rhipicephalus appendiculatus male and female ticks during blood feeding. Ticks and Tick-borne Diseases, 2016, 7, 536-548.	1.1	55
3395	RNA sequencing of an nsdC mutant reveals global regulation of secondary metabolic gene clusters in Aspergillus flavus. Microbiological Research, 2016, 182, 150-161.	2.5	43
3396	A transcriptome study on Macrobrachium rosenbergii hepatopancreas experimentally challenged with white spot syndrome virus (WSSV). Journal of Invertebrate Pathology, 2016, 136, 10-22.	1.5	62
3397	Whole transcriptome analysis of transgenic barley with altered cytokinin homeostasis and increased tolerance to drought stress. New Biotechnology, 2016, 33, 676-691.	2.4	51
3398	Transcriptome analysis reveals that up-regulation of the fatty acid synthase gene promotes the accumulation of docosahexaenoic acid in Schizochytrium sp. S056 when glycerol is used. Algal Research, 2016, 15, 83-92.	2.4	58
3399	A Tale of Transmission: Aeromonas veronii Activity within Leech-Exuded Mucus. Applied and Environmental Microbiology, 2016, 82, 2644-2655.	1.4	9
3400	Quantitative and qualitative transcriptome analysis of four industrial strains of Claviceps purpurea with respect to ergot alkaloid production. New Biotechnology, 2016, 33, 743-754.	2.4	6
3401	Comparative proteomics analysis of apoptotic Spodoptera frugiperda cells during p35 knockout Autographa californica multiple nucleopolyhedrovirus infection. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 18, 21-29.	0.4	4
3402	Transcriptional response to heat shock in liver of snow trout (Schizothorax richardsonii)â€"a vulnerable Himalayan Cyprinid fish. Functional and Integrative Genomics, 2016, 16, 203-213.	1.4	34
3403	Oyster reproduction is affected by exposure to polystyrene microplastics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2430-2435.	3.3	1,253
3404	Proteome profiling reveals tissue-specific protein expression in male and female accessory glands of the silkworm, Bombyx mori. Amino Acids, 2016, 48, 1173-1183.	1.2	9
3405	Overexpression of Rosa rugosa anthocyanidin reductase enhances tobacco tolerance to abiotic stress through increased ROS scavenging and modulation of ABA signaling. Plant Science, 2016, 245, 35-49.	1.7	59
3406	Venomous extract protein profile of Brazilian tarantula Grammostola iheringi: searching for potential biotechnological applications. Journal of Proteomics, 2016, 136, 35-47.	1.2	41
3407	Nitro-Fatty Acids in Plant Signaling: Nitro-Linolenic Acid Induces the Molecular Chaperone Network in Arabidopsis. Plant Physiology, 2016, 170, 686-701.	2.3	116

#	ARTICLE	IF	CITATIONS
3408	Transcriptome of High-Sucrose Sugarcane Variety GT35. Sugar Tech, 2016, 18, 520-528.	0.9	29
3409	Transcriptomic analysis of the succulent xerophyte Zygophyllum xanthoxylum in response to salt treatment and osmotic stress. Plant and Soil, 2016, 402, 343-361.	1.8	46
3410	The mitogen-activated protein kinase gene, VdHog1, regulates osmotic stress response, microsclerotia formation and virulence in Verticillium dahliae. Fungal Genetics and Biology, 2016, 88, 13-23.	0.9	71
3411	The testis and ovary transcriptomes of the rock bream (Oplegnathus fasciatus): A bony fish with a unique neo Y chromosome. Genomics Data, 2016, 7, 210-213.	1.3	16
3412	De novo transcriptome assembly of Perkinsus olseni trophozoite stimulated in vitro with Manila clam (Ruditapes philippinarum) plasma. Journal of Invertebrate Pathology, 2016, 135, 22-33.	1.5	14
3413	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	3.8	1,898
3414	Transcriptome dynamics of a susceptible wheat upon Fusarium head blight reveals that molecular responses to Fusarium graminearum infection fit over the grain development processes. Functional and Integrative Genomics, 2016, 16, 183-201.	1.4	49
3415	IsoSeq analysis and functional annotation of the infratentorial ependymoma tumor tissue on PacBio RSII platform. Meta Gene, 2016, 7, 70-75.	0.3	15
3416	Transcriptic analysis of Huanghai No. 1 strain of Chinese shrimp Fenneropenaeus chinensis using 454 pyrosequencing. Fisheries Science, 2016, 82, 327-336.	0.7	1
3417	Genome-wide transcriptomic profiles reveal multiple regulatory responses of poplar to Lonsdalea quercina infection. Trees - Structure and Function, 2016, 30, 1389-1402.	0.9	7
3418	4Pipe4 â€“ A 454 data analysis pipeline for SNP detection in datasets with no reference sequence or strain information. BMC Bioinformatics, 2016, 17, 41.	1.2	2
3419	Protease encoding microbial communities and protease activity of the rhizosphere and bulk soils of two maize lines with different N uptake efficiency. Soil Biology and Biochemistry, 2016, 96, 176-179.	4.2	49
3420	Genome-Wide Identification, Evolution and Functional Divergence of MYB Transcription Factors in Chinese White Pear (<i>Pyrus bretschneideri</i>). Plant and Cell Physiology, 2016, 57, 824-847.	1.5	89
3421	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. ISME Journal, 2016, 10, 2092-2105.	4.4	63
3422	De novo transcriptome profiling and characterization of voltage-sensitive sodium channel gene of Tropilaelaps mercedesae parasitizing honey bees. Journal of Asia-Pacific Entomology, 2016, 19, 89-93.	0.4	1
3423	Hemocytome: deep sequencing analysis of mosquito blood cells in Indian malarial vector Anopheles stephensi. Gene, 2016, 585, 177-190.	1.0	34
3424	Overexpression of mitochondrial uncoupling protein 1 (UCP1) induces a hypoxic response in<i>Nicotiana tabacum</i>leaves. Journal of Experimental Botany, 2016, 67, 301-313.	2.4	19
3425	Proteomic characterization of mucosal secretions in the eastern oyster, Crassostrea virginica. Journal of Proteomics, 2016, 132, 63-76.	1.2	62

#	Article	IF	Citations
3426	SNP discovery in common bean by restriction-associated DNA (RAD) sequencing for genetic diversity and population structure analysis. Molecular Genetics and Genomics, 2016, 291, 1277-1291.	1.0	18
3427	Complete Genome Sequence of Lactobacillus acidophilus MN-BM-F01. Genome Announcements, 2016, 4, .	0.8	2
3428	Deciphering the molecular mechanisms underlying sea urchin reversible adhesion: A quantitative proteomics approach. Journal of Proteomics, 2016, 138, 61-71.	1.2	35
3429	Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants. Genome Biology, 2016, 17, 43.	3.8	70
3430	Transcriptome sequencing and characterization of ungerminated and germinated spores of &lt;italic&gt;Nosema bombycis&lt;/italic&gt;. Acta Biochimica Et Biophysica Sinica, 2016, 48, 246-256.	0.9	20
3431	Transcriptional changes in Crassostrea gigas oyster spat following a parental exposure to the herbicide diuron. Aquatic Toxicology, 2016, 175, 47-55.	1.9	17
3432	Transcriptomic responses of the basidiomycete yeast Sporobolomyces sp. to the mycotoxin patulin. BMC Genomics, 2016, 17, 210.	1.2	42
3433	Transcriptome analysis of stress tolerance in entomopathogenic nematodes of the genus Steinernema. International Journal for Parasitology, 2016, 46, 83-95.	1.3	14
3434	De novo assembly and characterization of the Welsh onion (Allium fistulosum L.) transcriptome using Illumina technology. Molecular Genetics and Genomics, 2016, 291, 647-659.	1.0	22
3435	Transcriptome mining: Multigene panel to test delousing drug response in the sea louse Caligus rogercresseyi. Marine Genomics, 2016, 25, 103-113.	0.4	5
3436	Transcriptome profiling of the Pacific oyster Crassostrea gigas by Illumina RNA-seq. Genes and Genomics, 2016, 38, 359-365.	0.5	9
3437	Retene causes multifunctional transcriptomic changes in the heart of rainbow trout (Oncorhynchus) Tj ETQq1 1 0.784314 rgBT /Overlo	2.0	18
3438	Genome-wide identification and comparative analysis of grafting-responsive mRNA in watermelon grafted onto bottle gourd and squash rootstocks by high-throughput sequencing. Molecular Genetics and Genomics, 2016, 291, 621-633.	1.0	55
3439	Transcriptome analysis of the molting gland (Y-organ) from the blackback land crab, Gecarcinus lateralis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 17, 26-40.	0.4	21
3440	Penicillium oxalicum PoFlbC regulates fungal asexual development and is important for cellulase gene expression. Fungal Genetics and Biology, 2016, 86, 91-102.	0.9	34
3441	Characterization of gonadal transcriptomes from the turbot (<i>Scophthalmus maximus</i>). Genome, 2016, 59, 1-10.	0.9	19
3442	Effects of DNA Methylation and Chromatin State on Rates of Molecular Evolution in Insects. G3: Genes, Genomes, Genetics, 2016, 6, 357-363.	0.8	37
3443	Transgenic barley overexpressing a cytokinin dehydrogenase gene shows greater tolerance to drought stress. New Biotechnology, 2016, 33, 692-705.	2.4	117

#	ARTICLE	IF	CITATIONS
3444	Proteomics of survival structures of fungal pathogens. New Biotechnology, 2016, 33, 655-665.	2.4	13
3445	Repetitive sequences in Eragrostis curvula cDNA EST libraries obtained from genotypes with different ploidy. Biologia Plantarum, 2016, 60, 55-67.	1.9	7
3446	Generating Sample-Specific Databases for Mass Spectrometry-Based Proteomic Analysis by Using RNA Sequencing. Methods in Molecular Biology, 2016, 1394, 219-232.	0.4	4
3447	Physiological and Molecular Alterations Promoted by <i>Schizotetranychus oryzae</i> Mite Infestation in Rice Leaves. Journal of Proteome Research, 2016, 15, 431-446.	1.8	22
3449	Origin matters â€" Comparative transcriptomics in Saccharina latissima (Phaeophyceae). Journal of Experimental Marine Biology and Ecology, 2016, 476, 22-30.	0.7	12
3450	Transcriptome profiling of two Iberian freshwater fish exposed to thermal stress. Journal of Thermal Biology, 2016, 55, 54-61.	1.1	42
3451	Comparison of Illumina de novo assembled and Sanger sequenced viral genomes: A case study for RNA viruses recovered from the plant pathogenic fungus Sclerotinia sclerotiorum. Virus Research, 2016, 219, 51-57.	1.1	28
3452	Interactive Effects of Seawater Acidification and Elevated Temperature on the Transcriptome and Biomineralization in the Pearl Oyster <i>Pinctada fucata</i>. Environmental Science & Technology, 2016, 50, 1157-1165.	4.6	71
3453	Dynamic transcriptome analysis reveals AP2/ERF transcription factors responsible for cold stress in rapeseed (Brassica napusÂL.). Molecular Genetics and Genomics, 2016, 291, 1053-1067.	1.0	58
3454	Establishing a herbicide-metabolizing enzyme library in<i>Beckmannia syzigachne</i>to identify genes associated with metabolic resistance. Journal of Experimental Botany, 2016, 67, 1745-1757.	2.4	77
3455	Applying genotoxicology tools to identify environmental stressors in support of river management. Chemosphere, 2016, 144, 319-329.	4.2	11
3456	Gene-expression profile of developing pollen tube of Pyrus bretschneideri. Gene Expression Patterns, 2016, 20, 11-21.	0.3	40
3457	Transcriptome analysis of the endangered Chinese giant salamander (Andrias davidianus): Immune modulation in response to Aeromonas hydrophila infection. Veterinary Immunology and Immunopathology, 2016, 169, 85-95.	0.5	41
3458	De novo transcriptome sequencing and discovery of genes related to copper tolerance in Paeonia ostii. Gene, 2016, 576, 126-135.	1.0	40
3459	De novo assembly and characterization of the leaf, bud, and fruit transcriptome from the vulnerable tree Juglans mandshurica for the development of 20 new microsatellite markers using Illumina sequencing. Molecular Genetics and Genomics, 2016, 291, 849-862.	1.0	65
3460	De novo assembly and characterization of foot transcriptome and microsatellite marker development for Paphia textile. Gene, 2016, 576, 537-543.	1.0	26
3461	Data set for transcriptome analysis of the Chinese giant salamander (Andrias davidianus). Data in Brief, 2016, 6, 12-14.	0.5	5
3462	Transcriptome profiling of the cysticercus stage of the laboratory model Taenia crassiceps, strain ORF. Acta Tropica, 2016, 154, 50-62.	0.9	13

#	ARTICLE	IF	CITATIONS
3463	Immune response and survival of Circulifer haematoceps to Spiroplasma citri infection requires expression of the gene hexamerin. Developmental and Comparative Immunology, 2016, 54, 7-19.	1.0	38
3464	Transcriptome analysis of the Larimichthys crocea liver in response to Cryptocaryon irritans. Fish and Shellfish Immunology, 2016, 48, 1-11.	1.6	88
3465	GoFDR: A sequence alignment based method for predicting protein functions. Methods, 2016, 93, 3-14.	1.9	57
3466	Multi-tissue transcriptome profiles for coho salmon (Oncorhynchus kisutch), a species undergoing rediploidization following whole-genome duplication. Marine Genomics, 2016, 25, 33-37.	0.4	19
3467	Comprehensive transcriptomic analysis of the process of gonadal sex differentiation in the turbot () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	47
3468	De-novo assembly and characterization of Chlorella minutissima UTEX2341 transcriptome by paired-end sequencing and the identification of genes related to the biosynthesis of lipids for biodiesel. Marine Genomics, 2016, 25, 69-74.	0.4	11
3469	Drought-Responsive Hsp70 Gene Analysis in Populus at Genome-Wide Level. Plant Molecular Biology Reporter, 2016, 34, 483-500.	1.0	24
3470	Genome-wide functional analysis of SSR for an edible mushroom Pleurotus ostreatus. Gene, 2016, 575, 524-530.	1.0	27
3471	De novo transcriptome sequencing of Cryptotermes domesticus and comparative analysis of gene expression in response to different wood species. Gene, 2016, 575, 655-666.	1.0	9
3472	Characterisation of transcriptional responses to dioxins and dioxin-like contaminants in roach () Tj ETQq1 1 0.784314 rgBT /Overlock 412-423.	3.9	29
3473	Deep sequencing reveals transcriptome re-programming of Polygonum multiflorum thunb. roots to the elicitation with methyl jasmonate. Molecular Genetics and Genomics, 2016, 291, 337-348.	1.0	7
3474	Gene transcript profiles in the desert plant Nitraria tangutorum during fruit development and ripening. Molecular Genetics and Genomics, 2016, 291, 383-398.	1.0	4
3475	Molecular marker development from transcript sequences and germplasm evaluation for cultivated peanut (Arachis hypogaea L.). Molecular Genetics and Genomics, 2016, 291, 363-381.	1.0	21
3476	Immunity comes first: The effect of parasite genotypes on adaptive immunity and immunization in three-spined sticklebacks. Developmental and Comparative Immunology, 2016, 54, 137-144.	1.0	12
3477	Proteomic characterization of pleural effusion, a specific host niche of Mycoplasma mycoides subsp. mycoides from cattle with contagious bovine pleuropneumonia (CBPP). Journal of Proteomics, 2016, 131, 93-103.	1.2	12
3478	De novo transcriptome analysis of Inonotus baumii by RNA-seq. Journal of Bioscience and Bioengineering, 2016, 121, 380-384.	1.1	20
3479	De novo transcriptome analysis of carotenoid and polyunsaturated fatty acid metabolism in Rhodomonas sp.. Journal of Applied Phycology, 2016, 28, 1649-1656.	1.5	10
3480	Transcriptome Sequencing and Analysis of Wild Pear (Pyrus hopeiensis) Using the Illumina Platform. Arabian Journal for Science and Engineering, 2016, 41, 45-53.	1.1	4

#	Article	IF	Citations
3481	Development and validation of EST-derived SSR markers and diversity analysis in cluster bean (Cyamopsis tetragonoloba). Journal of Plant Biochemistry and Biotechnology, 2016, 25, 263-269.	0.9	28
3482	Different gene expression profiles between normal and thermally selected strains of rainbow trout, Oncorhynchus mykiss, as revealed by comprehensive transcriptome analysis. Gene, 2016, 576, 637-643.	1.0	20
3483	De novo assembly and characterization of the transcriptome of the pancreatic fluke Eurytrema pancreaticum (trematoda: Dicrocoeliidae) using Illumina paired-end sequencing. Gene, 2016, 576, 333-338.	1.0	14
3484	High-throughput sequencing and degradome analysis reveal neutral evolution of Cercis gigantea microRNAs and their targets. Planta, 2016, 243, 83-95.	1.6	10
3485	Faecal proteomics: A tool to investigate dysbiosis and inflammation in patients with cystic fibrosis. Journal of Cystic Fibrosis, 2016, 15, 242-250.	0.3	72
3486	Transcriptome analysis to identify genes for peptides and proteins involved in immunity and reproduction from male accessory glands and ejaculatory duct of Bactrocera dorsalis. Peptides, 2016, 80, 48-60.	1.2	23
3487	De novo sequencing transcriptome of endemic Gentiana straminea (Gentianaceae) to identify genes involved in the biosynthesis of active ingredients. Gene, 2016, 575, 160-170.	1.0	16
3488	Transcriptome analysis in Coffea eugenioides, an Arabica coffee ancestor, reveals differentially expressed genes in leaves and fruits. Molecular Genetics and Genomics, 2016, 291, 323-336.	1.0	26
3489	Development of genic SSR marker resource from RNA-Seq data in Dendrocalamus latiflorus. Journal of Plant Biochemistry and Biotechnology, 2016, 25, 179-190.	0.9	27
3490	Complementary transcriptomic and proteomic analyses of a chlorophyll-deficient tea plant cultivar reveal multiple metabolic pathway changes. Journal of Proteomics, 2016, 130, 160-169.	1.2	61
3491	Functional analysis of NtMPK2 uncovers its positive role in response to Pseudomonas syringae pv. tomato DC3000 in tobacco. Plant Molecular Biology, 2016, 90, 19-31.	2.0	6
3492	Quantitative proteomic analysis of Araucaria angustifolia (Bertol.) Kuntze cell lines with contrasting embryogenic potential. Journal of Proteomics, 2016, 130, 180-189.	1.2	40
3493	Putrescine induces somatic embryo development and proteomic changes in embryogenic callus of sugarcane. Journal of Proteomics, 2016, 130, 170-179.	1.2	77
3494	Increased chitin biosynthesis contributes to the resistance of Penicillium polonicum against the antifungal protein PgAFP. Applied Microbiology and Biotechnology, 2016, 100, 371-383.	1.7	16
3495	Quantitative proteomics reveals the central changes of wheat in response to powdery mildew. Journal of Proteomics, 2016, 130, 108-119.	1.2	45
3496	Transcriptome Sequencing Determined Flowering Pathway Genes in Aechmea fasciata Treated with Ethylene. Journal of Plant Growth Regulation, 2016, 35, 316-329.	2.8	22
3497	In silico transcriptome analysis of cuticle-related genes associated with delousing drug responses in the sea louse Caligus rogercresseyi. Aquaculture, 2016, 450, 123-135.	1.7	14
3498	De novo assembly and characterization of global transcriptome of coconut palm (Cocos nucifera L.) embryogenic calli using Illumina paired-end sequencing. Protoplasma, 2016, 253, 913-928.	1.0	50

#	Article	IF	Citations
3499	Combined venomics, venom gland transcriptomics, bioactivities, and antivenomics of two Bothrops jararaca populations from geographic isolated regions within the Brazilian Atlantic rainforest. Journal of Proteomics, 2016, 135, 73-89.	1.2	110
3500	De novo characterization of Larimichthys crocea transcriptome for growth-/immune-related gene identification and massive microsatellite (SSR) marker development. Chinese Journal of Oceanology and Limnology, 2017, 35, 225-234.	0.7	2
3501	Faba bean drought responsive gene identification and validation. Saudi Journal of Biological Sciences, 2017, 24, 80-89.	1.8	16
3502	Transcriptome of larvae representing the Rhipicephalus sanguineus complex. Molecular and Cellular Probes, 2017, 31, 85-90.	0.9	10
3503	Proteomic characterization of the internalization of Opisthorchis viverrini excretory/secretory products in human cells. Parasitology International, 2017, 66, 494-502.	0.6	18
3504	Odorant-binding and chemosensory proteins identified in the antennal transcriptome of Adelphocoris suturalis Jakovlev. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 24, 139-145.	0.4	33
3505	Prediction of the <i>in planta Phakopsora pachyrhizi</i> secretome and potential effector families. Molecular Plant Pathology, 2017, 18, 363-377.	2.0	30
3506	The novel fungalâ€specific gene FUG1 has a role in pathogenicity and fumonisin biosynthesis in Fusarium verticillioides. Molecular Plant Pathology, 2017, 18, 513-528.	2.0	24
3507	Physiological adjustments and transcriptome reprogramming are involved in the acclimation to salinity gradients in diatoms. Environmental Microbiology, 2017, 19, 909-925.	1.8	29
3508	Glucoseâ€mediated regulation of glycerol uptake in <i>Rhodosporidium toruloides</i>: Insights through transcriptomic analysis on dual substrate fermentation. Engineering in Life Sciences, 2017, 17, 282-291.	2.0	32
3509	Characterization and analysis of a <i>de novo</i> transcriptome from the pygmy grasshopper <i>Tetrix japonica</i>. Molecular Ecology Resources, 2017, 17, 381-392.	2.2	33
3510	Testisâ€specific <scp>RNA</scp>â€Seq of <i>Calligrapha</i> (Chrysomelidae) as a transcriptomic resource for maleâ€biased gene inquiry in Coleoptera. Molecular Ecology Resources, 2017, 17, 533-545.	2.2	1
3511	Global transcriptomic profiling in barramundi (<i>Lates calcarifer</i>) from rivers impacted by differing agricultural land uses. Environmental Toxicology and Chemistry, 2017, 36, 103-112.	2.2	23
3512	Towards understanding the genetic basis of mouth asymmetry in the scaleâ€eating cichlid <i>Perissodus microlepis</i>. Molecular Ecology, 2017, 26, 77-91.	2.0	25
3513	Comparative proteomic analysis of two pathogenic Tritrichomonas foetus genotypes: there is more to the proteome than meets the eye. International Journal for Parasitology, 2017, 47, 203-213.	1.3	16
3514	Development and Evaluation of a High Density Genotyping â€˜Axiom_Arachisâ€™ Array with 58â€‰K SNPs for Accelerating Genetics and Breeding in Groundnut. Scientific Reports, 2017, 7, 40577.	1.6	144
3515	The population genomic signature of environmental association and gene flow in an ecologically divergent tree species <i>Metrosideros polymorpha</i> (Myrtaceae). Molecular Ecology, 2017, 26, 1515-1532.	2.0	22
3516	Translating Omics to Food Microbiology. Annual Review of Food Science and Technology, 2017, 8, 113-134.	5.1	82

#	ARTICLE	IF	CITATIONS
3517	Comparative RNA-seq based transcriptomic analysis of bud dormancy in grape. BMC Plant Biology, 2017, 17, 18.	1.6	87
3518	Daylily protein constituents of the pollen and stigma a proteomics approach. Journal of Plant Physiology, 2017, 212, 1-12.	1.6	4
3519	De novo assembly and characterization of the transcriptome of the newly described dinoflagellate Ansanella granifera : Spotlight on flagellum-associated genes. Marine Genomics, 2017, 33, 47-55.	0.4	8
3520	An insight into differentially regulated genes in resistant and susceptible genotypes of potato in response to tomato leaf curl New Delhi virus-[potato] infection. Virus Research, 2017, 232, 22-33.	1.1	25
3521	Expression profile analysis of Isoetes sinensis in response to light-dark shift under terrestrial and submerged conditions. Plant Gene, 2017, 9, 26-33.	1.4	1
3522	PanViz: interactive visualization of the structure of functionally annotated pangenomes. Bioinformatics, 2017, 33, 1081-1082.	1.8	21
3523	Co-option and <i>de novo</i> gene evolution underlie molluscan shell diversity. Molecular Biology and Evolution, 2017, 34, msw294.	3.5	67
3524	The molecular sensory machinery of a Chagas disease vector: expression changes through imaginal moult and sexually dimorphic features. Scientific Reports, 2017, 7, 40049.	1.6	44
3525	Integrating genomic resources of flatfish (Pleuronectiformes) to boost aquaculture production. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 41-55.	0.4	21
3526	Transcriptomic analysis of spleen infected with infectious salmon anemia virus reveals distinct pattern of viral replication on resistant and susceptible Atlantic salmon (Salmo salar). Fish and Shellfish Immunology, 2017, 61, 187-193.	1.6	40
3527	Genome-wide analysis of long non-coding RNAs at the mature stage of sea buckthorn (Hippophae) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	41
3528	Depletion of juvenile hormone esterase extends larval growth in Bombyx mori. Insect Biochemistry and Molecular Biology, 2017, 81, 72-79.	1.2	48
3529	Comparative genome-wide phylogenetic and expression analysis of SBP genes from potato (Solanum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	14
3530	Transcriptome profiles reveal gene regulation of peanut (Arachis hypogaea L.) nodulation. Scientific Reports, 2017, 7, 40066.	1.6	42
3531	Identification of initial responsive genes to systemic dsRNA ingestion in the two-spotted spider mite, Tetranychus urticae Koch. Journal of Asia-Pacific Entomology, 2017, 20, 229-235.	0.4	3
3532	Molecular response of <i>Sargassum vulgare</i> to acidification at volcanic <scp>CO</scp>₂ vents: insights from de novo transcriptomic analysis. Molecular Ecology, 2017, 26, 2276-2290.	2.0	21
3533	Comparative transcriptomics of elasmobranchs and teleosts highlight important processes in adaptive immunity and regional endothermy. BMC Genomics, 2017, 18, 87.	1.2	31
3534	What killed Karl Patterson Schmidt? Combined venom gland transcriptomic, venomic and antivenomic analysis of the South African green tree snake (the boomslang), Dispholidus typus. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 814-823.	1.1	56

#	Article	IF	Citations
3535	Gene expression patterns regulating embryogenesis based on the integrated de novo transcriptome assembly of the Japanese flounder. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 58-66.	0.4	3
3536	Range expansion underlies historical introgressive hybridization in the Iberian hare. Scientific Reports, 2017, 7, 40788.	1.6	35
3537	Multiple horizontal transfers of nuclear ribosomal genes between phylogenetically distinct grass lineages. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1726-1731.	3.3	34
3538	Comparative transcriptional survey between self-incompatibility and self-compatibility in Citrus reticulata Blanco. Gene, 2017, 609, 52-61.	1.0	12
3539	Transcriptome dynamics over a lunar month in a broadcast spawning acroporid coral. Molecular Ecology, 2017, 26, 2514-2526.	2.0	32
3540	Impact of an arbuscular mycorrhizal fungus versus a mixed microbial inoculum on the transcriptome reprogramming of grapevine roots. Mycorrhiza, 2017, 27, 417-430.	1.3	44
3541	The Role of Microsatellites in Streptophyta Gene Evolution. Journal of Molecular Evolution, 2017, 84, 144-148.	0.8	0
3542	Development and validation of EST derived SSR markers with relevance to downy mildew (Sclerospora) Tj ETQq1 1 0.784314 rgBT /Ov Biochemistry and Biotechnology, 2017, 26, 356-365.	0.9	6
3543	Proteolysis of chloroplast proteins is responsible for accumulation of free amino acids in dark-treated tea (Camellia sinensis) leaves. Journal of Proteomics, 2017, 157, 10-17.	1.2	105
3544	Candidate chemosensory genes identified in the endoparasitoid Meteorus pulchricornis (Hymenoptera: Braconidae) by antennal transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 20-31.	0.4	48
3545	Diversity, distribution, and significance of transposable elements in the genome of the only selfing hermaphroditic vertebrate Kryptolebias marmoratus. Scientific Reports, 2017, 7, 40121.	1.6	28
3546	Genomeâ€wide selection components analysis in a fish with male pregnancy. Evolution; International Journal of Organic Evolution, 2017, 71, 1096-1105.	1.1	32
3547	Identification of differentially expressed genes from Trichoderma atroviride strain SS003 in the presence of cell wall of Cronartium ribicola. Genes and Genomics, 2017, 39, 473-484.	0.5	4
3548	Potentially adaptive mitochondrial haplotypes as a tool to identify divergent nuclear loci. Methods in Ecology and Evolution, 2017, 8, 821-834.	2.2	10
3549	Comparative proteomics analysis of the effect of combined red and blue lights on sugarcane somatic embryogenesis. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	34
3550	Characterization of transcriptome and identification of biomineralization genes in winged pearl oyster (Pteria penguin) mantle tissue. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 67-76.	0.4	13
3551	The major constituents of the venom gland of a braconid endoparasitoid, Meteorus pulchricornis (Hymenoptera: Braconidae). Applied Entomology and Zoology, 2017, 52, 271-285.	0.6	7
3552	Transcriptome-wide identification and functional investigation of circular RNA in the teleost large yellow croaker (Larimichthys crocea). Marine Genomics, 2017, 32, 71-78.	0.4	38

#	Article	IF	Citations
3553	Large-scale transcriptome comparison of sunflower genes responsive to Verticillium dahliae. BMC Genomics, 2017, 18, 42.	1.2	39
3554	Transcriptome profiling of spleen provides insights into the antiviral mechanism in Schizothorax prenanti after poly (I: C) challenge. Fish and Shellfish Immunology, 2017, 62, 13-23.	1.6	30
3555	Positive selection on sperm ion channels in a brooding brittle star: consequence of lifeâ€history traits evolution. Molecular Ecology, 2017, 26, 3744-3759.	2.0	20
3556	A metaproteomic approach dissecting major bacterial functions in the rhizosphere of plants living in serpentine soil. Analytical and Bioanalytical Chemistry, 2017, 409, 2327-2339.	1.9	46
3557	Immune transcriptome reveals the mincle C-type lectin receptor acts as a partial replacement for TLR4 in lipopolysaccharide-mediated inflammatory response in barramundi (Lates calcarifer). Molecular Immunology, 2017, 83, 33-45.	1.0	22
3558	De novo transcriptome assembly of heavy metal tolerant Silene dioica. Genomics Data, 2017, 11, 118-119.	1.3	3
3559	Two vitellogenins in the loliginid squid Uroteuthis edulis : Identification and specific expression in ovarian follicles. Molecular Reproduction and Development, 2017, 84, 363-375.	1.0	8
3560	Characterisation of the transcriptome of male and female wild-type guppy brains with RNA-Seq and consequences of exposure to the pharmaceutical pollutant, 17Î±-ethinyl estradiol. Aquatic Toxicology, 2017, 186, 28-39.	1.9	15
3561	Plasticity in gene transcription explains the differential performance of two invasive fish species. Evolutionary Applications, 2017, 10, 563-576.	1.5	51
3562	Regulation of Nitrogen Metabolism by GATA Zinc Finger Transcription Factors in Yarrowia lipolytica. MSphere, 2017, 2, .	1.3	29
3563	Transcriptomic profiling provides molecular insights into hydrogen peroxide-induced adventitious rooting in mung bean seedlings. BMC Genomics, 2017, 18, 188.	1.2	31
3564	Adaptation of acaricide stress facilitates <i>Tetranychus urticae</i> expanding against <i>Tetranychus cinnabarinus</i> in China. Ecology and Evolution, 2017, 7, 1233-1249.	0.8	24
3565	The genome of the protozoan parasite Cystoisospora suis and a reverse vaccinology approach to identify vaccine candidates. International Journal for Parasitology, 2017, 47, 189-202.	1.3	28
3566	Histopathology combined with transcriptome analyses reveals the mechanism of resistance to Meloidogyne incognita in Cucumis metuliferus. Journal of Plant Physiology, 2017, 212, 115-124.	1.6	27
3567	Transcriptomic responses of the olive fruit fly Bactrocera oleae and its symbiont Candidatus Erwinia dacicola to olive feeding. Scientific Reports, 2017, 7, 42633.	1.6	58
3568	Genetic and genomic evidence of niche partitioning and adaptive radiation in mountain pine beetle fungal symbionts. Molecular Ecology, 2017, 26, 2077-2091.	2.0	52
3569	Immune system stimulation by the gut symbiont <i>Frischella perrara</i> in the honey bee (<i>Apis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	141
3570	Changes in protein expression after treatment with Ancylostoma caninum excretory/secretory products in a mouse model of colitis. Scientific Reports, 2017, 7, 41883.	1.6	8

#	Article	IF	Citations
3571	High flavonoid accompanied with high starch accumulation triggered by nutrient starvation in bioenergy crop duckweed (Landoltia punctata). BMC Genomics, 2017, 18, 166.	1.2	29
3572	Transcriptome assembly and identification of genes and SNPs associated with growth traits in largemouth bass (Micropterus salmoides). Genetica, 2017, 145, 175-187.	0.5	37
3573	De novo sequencing and comparative transcriptome analysis of adventitious root development induced by exogenous indole-3-butyric acid in cuttings of tetraploid black locust. BMC Genomics, 2017, 18, 179.	1.2	27
3574	Identification of differentially expressed placental transcripts during multiple gestations in the Eurasian beaver (Castor fiber L.). Reproduction, Fertility and Development, 2017, 29, 2073.	0.1	5
3575	Identification of effector-like proteins in Trichoderma spp. and role of a hydrophobin in the plant-fungus interaction and mycoparasitism. BMC Genetics, 2017, 18, 16.	2.7	122
3576	Effect of light and prey availability on gene expression of the mixotrophic chrysophyte, Ochromonas sp.. BMC Genomics, 2017, 18, 163.	1.2	28
3577	Evolutionary constraints shape caste-specific gene expression across 15 ant species. Evolution; International Journal of Organic Evolution, 2017, 71, 1273-1284.	1.1	11
3578	Elucidation of terpenoid metabolism in Scoparia dulcis by RNA-seq analysis. Scientific Reports, 2017, 7, 43311.	1.6	9
3579	Improved drought tolerance in wheat plants overexpressing a synthetic bacterial cold shock protein gene SeCspA. Scientific Reports, 2017, 7, 44050.	1.6	73
3580	Diversity in sequences, post-translational modifications and expected pharmacological activities of toxins from four Conus species revealed by the combination of cutting-edge proteomics, transcriptomics and bioinformatics. Toxicon, 2017, 130, 116-125.	0.8	14
3581	First <i>in Vivo Batrachochytrium dendrobatidis</i> Transcriptomes Reveal Mechanisms of Host Exploitation, Host-Specific Gene Expression, and Expressed Genotype Shifts. G3: Genes, Genomes, Genetics, 2017, 7, 269-278.	0.8	25
3582	Asymmetric interactions between doublesex and tissue- and sex-specific target genes mediate sexual dimorphism in beetles. Nature Communications, 2017, 8, 14593.	5.8	71
3583	Recently differentiated epimastigotes from <i>Trypanosoma cruzi</i> are infective to the mammalian host. Molecular Microbiology, 2017, 104, 712-736.	1.2	43
3584	Molecular analysis of the early interaction between the grapevine flower and <scp><i>Botrytis cinerea</i></scp> reveals that prompt activation of specific host pathways leads to fungus quiescence. Plant, Cell and Environment, 2017, 40, 1409-1428.	2.8	44
3585	Anatomical and transcriptional dynamics of early floral development of mulberry (Morus alba). Tree Genetics and Genomes, 2017, 13, 1.	0.6	9
3586	Next-generation sequencing of representational difference analysis products for identification of genes involved in diosgenin biosynthesis in fenugreek (Trigonella foenum-graecum). Planta, 2017, 245, 977-991.	1.6	46
3589	Candidate genes for adaptation to an aquatic habitat recovered from Ranunculus bungei and Ranunculus sceleratus. Biochemical Systematics and Ecology, 2017, 71, 16-25.	0.6	0
3590	Comparative transcriptome analysis of two contrasting watermelon genotypes during fruit development and ripening. BMC Genomics, 2017, 18, 3.	1.2	72

#	ARTICLE	IF	CITATIONS
3591	De Novo Transcriptome Characterization and Growth-Related Gene Expression Profiling of Diploid and Triploid Bighead Catfish (Clarias macrocephalus GÃ¼nther, 1864). Marine Biotechnology, 2017, 19, 36-48.	1.1	37
3592	Genome content analysis yields new insights into the relationship between the human malaria parasite Plasmodium falciparum and its anopheline vectors. BMC Genomics, 2017, 18, 205.	1.2	2
3593	Unity in defence: honeybee workers exhibit conserved molecular responses to diverse pathogens. BMC Genomics, 2017, 18, 207.	1.2	100
3594	Gene discovery and marker resource development by transcriptome sequencing from a shortâ€rotation coppice willow, <i><scp>S</scp>alix suchowensis</i>. Plant Breeding, 2017, 136, 279-286.	1.0	2
3595	ATGC transcriptomics: a web-based application to integrate, explore and analyze de novo transcriptomic data. BMC Bioinformatics, 2017, 18, 121.	1.2	6
3596	Influence of agricultural activities in the structure and metabolic functionality of paramo soil samples in Colombia studied using a metagenomics analysis in dynamic state. Ecological Modelling, 2017, 351, 63-76.	1.2	11
3597	Transcriptome analysis of Dioscorea zingiberensis identifies genes involved in diosgenin biosynthesis. Genes and Genomics, 2017, 39, 509-520.	0.5	12
3598	Transcriptome analysis of Ruditapes philippinarum hepatopancreas provides insights into immune signaling pathways under Vibrio anguillarum infection. Fish and Shellfish Immunology, 2017, 64, 14-23.	1.6	35
3599	Transcriptome analysis reveals a complex interplay between resistance and effector genes during the compatible lentil-Colletotrichum lentis interaction. Scientific Reports, 2017, 7, 42338.	1.6	21
3600	Transcriptome analysis reveals the complexity of alternative splicing regulation in the fungus Verticillium dahliae. BMC Genomics, 2017, 18, 130.	1.2	71
3601	Transcriptional comparison of the photogenic and non-photogenic tissues of Phrixothrix hirtus (Coleoptera: Phengodidae) and non-luminescent Chauliognathus flavipes (Coleoptera: Cantharidae) give insights on the origin of lanterns in railroad worms. Gene Reports, 2017, 7, 78-86.	0.4	16
3602	Comparative transcriptome analysis provides insight into differentially expressed genes related to cytoplasmic male sterility in broccoli (Brassica oleracea var. italica). Scientia Horticulturae, 2017, 217, 234-242.	1.7	18
3603	Transcriptome analysis around the onset of strawberry fruit ripening uncovers an important role of oxidative phosphorylation in ripening. Scientific Reports, 2017, 7, 41477.	1.6	58
3604	Holotrichia oblita Midgut Proteins That Bind to Bacillus thuringiensis Cry8-Like Toxin and Assembly of the H. oblita Midgut Tissue Transcriptome. Applied and Environmental Microbiology, 2017, 83, .	1.4	10
3605	Genome-wide identification and characterization of NB-ARC resistant genes in wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18	2.8	30
3606	An integrative overview of the molecular and physiological responses of sugarcane under drought conditions. Plant Molecular Biology, 2017, 94, 577-594.	2.0	37
3607	Proteomic analysis of sockeye salmon serum as a tool for biomarker discovery and new insight into the sublethal toxicity of diluted bitumen. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 157-166.	0.4	23
3608	Mapping of powdery mildew resistance genes in melon (Cucumis melo L.) by bulked segregant analysis. Scientia Horticulturae, 2017, 220, 160-167.	1.7	59

#	Article	IF	Citations
3609	The transcription factor bZIP14 regulates the TCA cycle in the diatom <i>Phaeodactylum tricornutum</i>. EMBO Journal, 2017, 36, 1559-1576.	3.5	64
3610	Effect of methyl-Î²-cyclodextrin on gene expression in microbial conversion of phytosterol. Applied Microbiology and Biotechnology, 2017, 101, 4659-4667.	1.7	23
3611	Identification of genes that potentially affect social dominance hierarchy in adult male giant freshwater prawns (Macrobrachium rosenbergii). Aquaculture, 2017, 476, 168-184.	1.7	18
3612	Genomic evidence for populationâ€specific responses to coâ€evolving parasites in a New Zealand freshwater snail. Molecular Ecology, 2017, 26, 3663-3675.	2.0	32
3613	Molecular adaptation in the world's deepestâ€living animal: Insights from transcriptome sequencing of the hadal amphipod <i>Hirondellea gigas</i>. Molecular Ecology, 2017, 26, 3732-3743.	2.0	69
3614	Genome-Wide Transcription and Functional Analyses Reveal Heterogeneous Molecular Mechanisms Driving Pyrethroids Resistance in the Major Malaria Vector <i>Anopheles funestus</i> Across Africa. G3: Genes, Genomes, Genetics, 2017, 7, 1819-1832.	0.8	49
3615	Comparative proteomics of hydatid fluids from two Echinococcus multilocularis isolates. Journal of Proteomics, 2017, 162, 40-51.	1.2	19
3616	Factors involved in early polarization of the anteriorâ€posterior axis in the milkweed bug <i>Oncopeltus fasciatus</i>. Genesis, 2017, 55, e23027.	0.8	23
3617	Generation and characterization of the blood transcriptome of Macaca thibetana and comparative analysis with M. mulatta. Molecular BioSystems, 2017, 13, 1121-1130.	2.9	4
3618	Genomic data for 78 chickens from 14 populations. GigaScience, 2017, 6, 1-5.	3.3	28
3619	Comparative Transcriptome Analysis of Three<i>Bactrocera dorsalis</i>(Diptera: Tephritidae) Organs to Identify Functional Genes in the Male Accessory Glands and Ejaculatory Duct. Florida Entomologist, 2017, 100, 42-51.	0.2	11
3620	Characterization of transcriptome in the Indian meal moth Plodia interpunctella (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	22
3621	Signals of selection in conditionally expressed genes in the diversification of three horned beetle species. Journal of Evolutionary Biology, 2017, 30, 1644-1657.	0.8	10
3622	Contrasting evolutionary genome dynamics between domesticated and wild yeasts. Nature Genetics, 2017, 49, 913-924.	9.4	340
3623	Identification and expression of cuticular protein genes based on Locusta migratoria transcriptome. Scientific Reports, 2017, 7, 45462.	1.6	48
3624	Increased taxon sampling reveals thousands of hidden orthologs in flatworms. Genome Research, 2017, 27, 1263-1272.	2.4	39
3625	Transcriptome profile of the human placenta. Functional and Integrative Genomics, 2017, 17, 551-563.	1.4	29
3626	Transcriptomic analyses reveal biosynthetic genes related to rosmarinic acid in Dracocephalum tanguticum. Scientific Reports, 2017, 7, 74.	1.6	27

#	Article	IF	Citations
3627	Genome sequence of Plasmopara viticola and insight into the pathogenic mechanism. Scientific Reports, 2017, 7, 46553.	1.6	81
3628	Comprehensive transcriptomic analysis of Tibetan Schizothoracinae fish Gymnocypris przewalskii reveals how it adapts to a high altitude aquatic life. BMC Evolutionary Biology, 2017, 17, 74.	3.2	47
3629	Unraveling the complexity of transcriptomic, metabolomic and quality environmental response of tomato fruit. BMC Plant Biology, 2017, 17, 66.	1.6	48
3630	agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. Nucleic Acids Research, 2017, 45, W122-W129.	6.5	1,872
3631	Substrates and oxygen dependent citric acid production by Yarrowia lipolytica: insights through transcriptome and fluxome analyses. Microbial Cell Factories, 2017, 16, 78.	1.9	80
3632	Identification of putative flavonoid-biosynthetic genes through transcriptome analysis of Taihe Toona sinensis bud. Acta Physiologiae Plantarum, 2017, 39, 1.	1.0	14
3633	Transcriptomic and macroevolutionary evidence for phenotypic uncoupling between frog life history phases. Nature Communications, 2017, 8, 15213.	5.8	40
3634	Comprehensive profiling of rhizomeâ€associated alternative splicing and alternative polyadenylation in moso bamboo (<i>Phyllostachys edulis</i>). Plant Journal, 2017, 91, 684-699.	2.8	170
3635	Identification and Differential Expression of Biomineralization Genes in the Mantle of Pearl Oyster Pinctada fucata. Marine Biotechnology, 2017, 19, 266-276.	1.1	13
3636	Development of a set of SSR markers for genetic polymorphism detection and interspecific hybrid jute breeding. Crop Journal, 2017, 5, 416-429.	2.3	35
3637	Genome-Wide Function Analysis of lincRNAs as miRNA Targets or Decoys in Plant. RNA Technologies, 2017, , 149-162.	0.2	3
3638	Gene co-expression network analysis identifies porcine genes associated with variation in metabolizing fenbendazole and flunixin meglumine in the liver. Scientific Reports, 2017, 7, 1357.	1.6	10
3639	Transcriptional analysis of the adaptation ofUstilago maydisduring growth under nitrogen fixation conditions. Journal of Basic Microbiology, 2017, 57, 597-604.	1.8	4
3640	Identification of 28 cytochrome P450 genes from the transcriptome of the marine rotifer Brachionus plicatilis and analysis of their expression. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 23, 1-7.	0.4	6
3641	Dynamics of the Interaction between Cotton Bollworm Helicoverpa armigera and Nucleopolyhedrovirus as Revealed by Integrated Transcriptomic and Proteomic Analyses. Molecular and Cellular Proteomics, 2017, 16, 1009-1028.	2.5	40
3642	Candidate genes mediating magnetoreception in rainbow trout (<i>Oncorhynchus mykiss</i>). Biology Letters, 2017, 13, 20170142.	1.0	21
3643	Transcriptomic Analysis of Male Black Tiger Shrimp (Penaeus monodon) After Polychaete Feeding to Enhance Testicular Maturation. Marine Biotechnology, 2017, 19, 125-135.	1.1	6
3644	Sporobolus stapfianus: Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. BMC Plant Biology, 2017, 17, 67.	1.6	61

#	ARTICLE	IF	CITATIONS
3645	Transcriptome profiling of sulfate deprivation responses in two agarophytes Gracilaria changii and Gracilaria salicornia (Rhodophyta). Scientific Reports, 2017, 7, 46563.	1.6	15
3646	De novo transcriptomic analysis to reveal insecticide action and detoxification-related genes of the predatory bug, Cyrtorhinus lividipennis. Journal of Asia-Pacific Entomology, 2017, 20, 720-727.	0.4	5
3647	Computational prediction of drug-drug interactions based on drugs functional similarities. Journal of Biomedical Informatics, 2017, 70, 54-64.	2.5	127
3648	Cadmium inÂvivo exposure alters stress response and endocrine-related genes in the freshwater snail Physa acuta. New biomarker genes in a new model organism. Environmental Pollution, 2017, 220, 1488-1497.	3.7	14
3649	Global transcriptome analysis of Halolamina sp. to decipher the salt tolerance in extremely halophilic archaea. Gene, 2017, 601, 56-64.	1.0	21
3650	Transcriptome analysis reveals potential mechanisms for inhibition of intumescence development by UV radiation in tomato. Environmental and Experimental Botany, 2017, 134, 130-140.	2.0	6
3651	Drought-Tolerant Brassica rapa Shows Rapid Expression of Gene Networks for General Stress Responses and Programmed Cell Death Under Simulated Drought Stress. Plant Molecular Biology Reporter, 2017, 35, 416-430.	1.0	30
3652	Transcriptomic response of the insect vector, Peregrinus maidis, to Maize mosaic rhabdovirus and identification of conserved responses to propagative viruses in hopper vectors. Virology, 2017, 509, 71-81.	1.1	24
3653	Cognitive specialization for learning faces is associated with shifts in the brain transcriptome of a social wasp. Journal of Experimental Biology, 2017, 220, 2149-2153.	0.8	10
3654	Insights from the complete genome sequence of <i>Clostridium tyrobutyricum</i> provide a platform for biotechnological and industrial applications. Journal of Industrial Microbiology and Biotechnology, 2017, 44, 1245-1260.	1.4	16
3655	Transcriptome analysis on the exoskeleton formation in early developmetal stages and reconstruction scenario in growth-moulting in Litopenaeus vannamei. Scientific Reports, 2017, 7, 1098.	1.6	33
3656	LdtR is a master regulator of gene expression in <i><scp>L</scp>iberibacter asiaticus</i>. Microbial Biotechnology, 2017, 10, 896-909.	2.0	21
3657	Transcriptomic approach for assessment of the impact on microalga and macrophyte of in-situ exposure in river sites contaminated by chlor-alkali plant effluents. Water Research, 2017, 121, 86-94.	5.3	20
3658	Genetics of mycorrhizal symbiosis in winter wheat (<i>Triticum aestivum</i>). New Phytologist, 2017, 215, 779-791.	3.5	76
3659	Sma3s: A universal tool for easy functional annotation of proteomes and transcriptomes. Proteomics, 2017, 17, 1700071.	1.3	71
3660	Transcriptomic variation of locally-infected skin of Epinephelus coioides reveals the mucosal immune mechanism against Cryptocaryon irritans. Fish and Shellfish Immunology, 2017, 66, 398-410.	1.6	65
3661	Comparison of Microbiomes between Red Poultry Mite Populations (Dermanyssus gallinae): Predominance of Bartonella-like Bacteria. Microbial Ecology, 2017, 74, 947-960.	1.4	51
3662	Novel reductive dehalogenases from the marine sponge associated bacterium <i>Desulfoluna spongiiphila</i>. Environmental Microbiology Reports, 2017, 9, 537-549.	1.0	18

#	ARTICLE	IF	CITATIONS
3663	Grain subproteome responses to nitrogen and sulfur supply in diploid wheat <i>Triticum monococcum</i> ssp. <i>monococcum</i>. Plant Journal, 2017, 91, 894-910.	2.8	54
3664	Lineage-specific rediploidization is a mechanism to explain time-lags between genome duplication and evolutionary diversification. Genome Biology, 2017, 18, 111.	3.8	136
3665	Putrescine promotes changes in the endogenous polyamine levels and proteomic profiles to regulate organogenesis in Cedrela fissilis Vellozo (Meliaceae). Plant Cell, Tissue and Organ Culture, 2017, 130, 495-505.	1.2	20
3666	Comparative transcriptome analysis of Sinonovacula constricta in gills and hepatopancreas in response to Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2017, 67, 523-535.	1.6	36
3667	Distinct Biological Potential of Streptococcus gordonii and Streptococcus sanguinis Revealed by Comparative Genome Analysis. Scientific Reports, 2017, 7, 2949.	1.6	28
3668	Contrasting gene expression programs correspond with predatorâ€induced phenotypic plasticity within and across generations in <i>Daphnia</i>. Molecular Ecology, 2017, 26, 5003-5015.	2.0	39
3669	The gene expression landscape of pine seedling tissues. Plant Journal, 2017, 91, 1064-1087.	2.8	41
3670	<i>De Novo</i>Transcriptome Characterization of a Sterilizing Trematode Parasite (<i>Microphallus</i>sp.) from Two Species of New Zealand Snails. G3: Genes, Genomes, Genetics, 2017, 7, 871-880.	0.8	6
3671	Hepatic transcriptomic profiles from barramundi, Lates calcarifer, as a means of assessing organism health and identifying stressors in rivers in northern Queensland. Marine Environmental Research, 2017, 129, 166-179.	1.1	10
3672	Overexpression of Lsi1 in cold-sensitive rice mediates transcriptional regulatory networks and enhances resistance to chilling stress. Plant Science, 2017, 262, 115-126.	1.7	41
3673	Comparative de novo transcriptome profiles in Asparagus officinalis and A. kiusianus during the early stage of Phomopsis asparagi infection. Scientific Reports, 2017, 7, 2608.	1.6	28
3674	Analysis of survival and hatching transcriptomes from potato cyst nematodes, Globodera rostochiensis and G. pallida. Scientific Reports, 2017, 7, 3882.	1.6	21
3675	Effects of 1â€methylcyclopropene on postharvest storage performance and the transcriptome of cactus pear fruit. International Journal of Food Science and Technology, 2017, 52, 1801-1809.	1.3	6
3676	A comprehensive proteogenomic study of the human Brucella vaccine strain 104ÂM. BMC Genomics, 2017, 18, 402.	1.2	12
3677	Comparative transcriptome analysis of lipid biosynthesis in seeds and non-seed tissues of sea buckthorn. Genes and Genomics, 2017, 39, 1021-1033.	0.5	10
3678	Transcriptome analysis of Cinnamomum longepaniculatum by high-throughput sequencing. Electronic Journal of Biotechnology, 2017, 28, 58-66.	1.2	28
3679	A Three-Way Transcriptomic Interaction Study of a Biocontrol Agent (<i>Clonostachys rosea</i>), a Fungal Pathogen (<i>Helminthosporium solani</i>), and a Potato Host (<i>Solanum tuberosum</i>). Molecular Plant-Microbe Interactions, 2017, 30, 646-655.	1.4	41
3680	<i>Tetranychus urticae</i> mites do not mount an induced immune response against bacteria. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170401.	1.2	21

#	ARTICLE	IF	CITATIONS
3681	Draft Genome Sequence of a Lipolytic Yeast, Candida aaseri SH-14. Genome Announcements, 2017, 5, .	0.8	2
3682	Biphasic Metabolism and Host Interaction of a Chlamydial Symbiont. MSystems, 2017, 2, .	1.7	32
3683	Genome-wide expression profiling in leaves and roots of date palm (Phoenix dactylifera L.) exposed to salinity. BMC Genomics, 2017, 18, 246.	1.2	80
3684	Complexities of gene expression patterns in natural populations of an extremophile fish (<i>Poecilia) Tj ETQq1 1 0.784314 rgBT /Overloc	2.0	21
3685	Identification of conserved genes triggering puberty in European sea bass males (Dicentrarchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	1.2	12
3686	De novo transcriptome sequencing and comparative analysis to discover genes involved in ovarian maturity in Strongylocentrotus nudus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 23, 27-38.	0.4	17
3687	Proteomic profiling of German Dornfelder grape berries using data-independent acquisition. Plant Physiology and Biochemistry, 2017, 118, 64-70.	2.8	9
3688	Excretory/secretory products from the gastrointestinal nematode Trichuris muris. Experimental Parasitology, 2017, 178, 30-36.	0.5	49
3689	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. BMC Genomics, 2017, 18, 72.	1.2	91
3690	Draft genome of spinach and transcriptome diversity of 120 Spinacia accessions. Nature Communications, 2017, 8, 15275.	5.8	156
3691	Rapid radiations of both kiwifruit hybrid lineages and their parents shed light on a twoâ€layer mode of species diversification. New Phytologist, 2017, 215, 877-890.	3.5	52
3692	Transcriptional regulation of hormoneâ€synthesis and signaling pathways by overexpressing cytokininâ€synthesis contributes to improved drought tolerance in creeping bentgrass. Physiologia Plantarum, 2017, 161, 235-256.	2.6	22
3693	De novo assembly and analysis of the Pugionium cornutum (L.) Gaertn. transcriptome and identification of genes involved in the drought response. Gene, 2017, 626, 290-297.	1.0	16
3694	Transcriptome profiling of the Macrobrachium rosenbergii lymphoid organ under the white spot syndrome virus challenge. Fish and Shellfish Immunology, 2017, 67, 27-39.	1.6	38
3695	Comparative Transcriptomic Analysis of Race 1 and Race 4 of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Induced with Different Carbon Sources. G3: Genes, Genomes, Genetics, 2017, 7, 2125-2138.	0.8	22
3696	Lysine Acetylome Analysis Reveals Photosystem II Manganese-stabilizing Protein Acetylation is Involved in Negative Regulation of Oxygen Evolution in Model Cyanobacterium Synechococcus sp. PCC 7002. Molecular and Cellular Proteomics, 2017, 16, 1297-1311.	2.5	26
3697	Tissue-specific transcriptomic profiling provides new insights into the reproductive ecology and biology of the iconic seagrass species Posidonia oceanica. Marine Genomics, 2017, 35, 51-61.	0.4	10
3698	Additive QTLs on three chromosomes control flowering time in woodland strawberry (Fragaria vesca) Tj ETQq1 1 0.784314 rgBT /Overlo	2.9	29

#	ARTICLE	IF	CITATIONS
3699	Identification of Genes for Synthesis of the Blue Pigment, Biliverdin IX<i>Î±</i>, in the Blue Coral <i>Heliopora coerulea</i>. Biological Bulletin, 2017, 232, 71-81.	0.7	11
3700	Identification and expression profiling of novel plant cell wall degrading enzymes from a destructive pest of palm trees, <i>Rhynchophorus ferrugineus</i>. Insect Molecular Biology, 2017, 26, 469-484.	1.0	21
3701	Identification of Expressed Sequence Tag-simple Sequence Repeat Markers from the De Novo Transcriptome Sequence of Red Raspberry (Rubus idaeus L.). Hortscience: A Publication of the American Society for Hortcultural Science, 2017, 52, 554-559.	0.5	0
3702	Comparative transcriptomic analysis of Listeria monocytogenes reveals upregulation of stress genes and downregulation of virulence genes in response to essential oil extracted from Baccharis psiadioides. Annals of Microbiology, 2017, 67, 479-490.	1.1	10
3703	Comparative Proteomic Analysis of Posterior Silk Glands of Wild and Domesticated Silkworms Reveals Functional Evolution during Domestication. Journal of Proteome Research, 2017, 16, 2495-2507.	1.8	28
3704	De novo assembly, functional annotation, and analysis of the giant reed (Arundo donax L.) leaf transcriptome provide tools for the development of a biofuel feedstock. Biotechnology for Biofuels, 2017, 10, 138.	6.2	37
3705	Triterpenoid biosynthesis and the transcriptional response elicited by nitric oxide in submerged fermenting Ganoderma lucidum. Process Biochemistry, 2017, 60, 19-26.	1.8	21
3706	Oral immune priming with Bacillus thuringiensis induces a shift in the gene expression of Tribolium castaneum larvae. BMC Genomics, 2017, 18, 329.	1.2	61
3707	Determination of the protein expression profiles of Propsilocerus akamusi (Tokunaga) Malpighian tubules response to cadmium stress by iTRAQ coupled LCâ€“MS/MS. Journal of Proteomics, 2017, 164, 85-93.	1.2	11
3708	A New Sugarcane Cystatin Strongly Binds to Dental Enamel and Reduces Erosion. Journal of Dental Research, 2017, 96, 1051-1057.	2.5	48
3709	Transcriptome comparative analysis between the cytoplasmic male sterile line and fertile line in soybean (Glycine max (L.) Merr.). Genes and Genomics, 2017, 39, 1117-1127.	0.5	7
3710	Fine mapping and candidate gene analysis of qFL-chr1, a fiber length QTL in cotton. Theoretical and Applied Genetics, 2017, 130, 1309-1319.	1.8	33
3711	De novo assembly, gene annotation, and molecular marker development using Illumina paired-end transcriptome sequencing in the clam Saxidomus purpuratus. Genes and Genomics, 2017, 39, 675-685.	0.5	7
3712	Novel insights into cardiac remodelling revealed by proteomic analysis of the trout heart during exercise training. Journal of Proteomics, 2017, 161, 38-46.	1.2	12
3713	RNA-seq reveals mechanisms of SlMX1 for enhanced carotenoids and terpenoids accumulation along with stress resistance in tomato. Science Bulletin, 2017, 62, 476-485.	4.3	20
3714	Deciphering genes associated with root wilt disease of coconut and development of its transcriptomic database (CnTDB). Physiological and Molecular Plant Pathology, 2017, 100, 255-263.	1.3	12
3715	Genomic patterns of diversity and divergence of two introduced salmonid species in Patagonia, South America. Evolutionary Applications, 2017, 10, 402-416.	1.5	17
3716	A microRNA regulates the response of corals to thermal stress. Molecular Ecology, 2017, 26, 3472-3483.	2.0	31

#	ARTICLE	IF	CITATIONS
3717	Comparative analysis of the liver transcriptome of Pelteobagrus vachellii with an alternative feeding time. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 131-138.	0.4	12
3718	The heterochronic gene Lin28 regulates amphibian metamorphosis through disturbance of thyroid hormone function. Developmental Biology, 2017, 425, 142-151.	0.9	21
3719	Protein-coding genes in B chromosomes of the grasshopper Eyprepocnemis plorans. Scientific Reports, 2017, 7, 45200.	1.6	53
3720	Poplar MYB115 and MYB134 Transcription Factors Regulate Proanthocyanidin Synthesis and Structure. Plant Physiology, 2017, 174, 154-171.	2.3	122
3721	Gene expression profiling during the embryoâ€toâ€larva transition in the giant red sea urchin <i>Mesocentrotus franciscanus</i>. Ecology and Evolution, 2017, 7, 2798-2811.	0.8	11
3722	Fractionation of the Gulf toadfish intestinal precipitate organic matrix reveals potential functions of individual proteins. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2017, 208, 35-45.	0.8	7
3723	Draft genome sequence of Cercospora sojina isolate S9, a fungus causing frogeye leaf spot (FLS) disease of soybean. Genomics Data, 2017, 12, 79-80.	1.3	10
3724	Comparative study the expression of calcium cycling genes in Bombay duck (Harpadon nehereus) and beltfish (Trichiurus lepturus) with different swimming activities. Genomics Data, 2017, 12, 58-61.	1.3	16
3725	Characterization of Leaf Transcriptome in Banksia hookeriana. Genomics, Proteomics and Bioinformatics, 2017, 15, 49-56.	3.0	14
3726	Comparative transcriptome analysis of berry-sizing effects of gibberellin (GA3) on seedless Vitis vinifera L.. Genes and Genomics, 2017, 39, 493-507.	0.5	14
3727	De novo analysis of the oriental armyworm Mythimna separata antennal transcriptome and expression patterns of odorant-binding proteins. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 120-130.	0.4	32
3728	Comparative immunogenomics of molluscs. Developmental and Comparative Immunology, 2017, 75, 3-15.	1.0	46
3729	Decay of the glycolytic pathway and adaptation to intranuclear parasitism within Enterocytozoonidae microsporidia. Environmental Microbiology, 2017, 19, 2077-2089.	1.8	74
3730	A shift in the virulence potential of Corynebacterium pseudotuberculosis biovar ovis after passage in a murine host demonstrated through comparative proteomics. BMC Microbiology, 2017, 17, 55.	1.3	16
3732	Transcriptome-based analysis of the saprophytic fungus Abortiporus biennis â€" response to oxalic acid. Microbiological Research, 2017, 199, 79-88.	2.5	9
3733	Transcriptomics and Lipidomics of the Environmental Strain <i>Rhodococcus ruber</i> Point out Consumption Pathways and Potential Metabolic Bottlenecks for Polyethylene Degradation. Environmental Science & Technology, 2017, 51, 5172-5181.	4.6	94
3734	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. Nature Communications, 2017, 8, 14742.	5.8	96
3735	A footprint of desiccation tolerance in the genome of Xerophyta viscosa. Nature Plants, 2017, 3, 17038.	4.7	123

#	Article	IF	Citations
3736	Populus trichocarpa encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports, 2017, 7, 382.	1.6	36
3737	Malonylome Analysis Reveals the Involvement of Lysine Malonylation in Metabolism and Photosynthesis in Cyanobacteria. Journal of Proteome Research, 2017, 16, 2030-2043.	1.8	28
3738	Light influences cytokinin biosynthesis and sensing in <i>Nostoc</i> (cyanobacteria). Journal of Phycology, 2017, 53, 703-714.	1.0	19
3739	EXPath toolâ€"a system for comprehensively analyzing regulatory pathways and coexpression networks from high-throughput transcriptome data. DNA Research, 2017, 24, 371-375.	1.5	12
3740	Developmental, chemical and transcriptional characteristics of artificially pollinated and hormone-induced parthenocarpic fruits of Siraitia grosvenorii. RSC Advances, 2017, 7, 12419-12428.	1.7	11
3741	Copy number increases of transposable elements and proteinâ€coding genes in an invasive fish of hybrid origin. Molecular Ecology, 2017, 26, 4712-4724.	2.0	28
3742	Molecular identification of differential expression genes associated with sex pheromone biosynthesis in Spodoptera exigua. Molecular Genetics and Genomics, 2017, 292, 795-809.	1.0	21
3743	Transcriptome analysis of molecular mechanisms responsible for light-stress response in Mythimna separata (Walker). Scientific Reports, 2017, 7, 45188.	1.6	28
3744	Comparative transcriptome analyses of flower development in four species of Achimenes (Gesneriaceae). BMC Genomics, 2017, 18, 240.	1.2	41
3745	Uncovering SNP and indel variations of tetraploid cottons by SLAF-seq. BMC Genomics, 2017, 18, 247.	1.2	29
3746	Intestinal transcriptome modulation by functional diets in rainbow trout: A high-throughput sequencing appraisal to highlight GALT immunomodulation. Fish and Shellfish Immunology, 2017, 64, 325-338.	1.6	22
3747	De novo transcriptome sequencing and analysis of the juvenile and adult stages of Fasciola gigantica. Infection, Genetics and Evolution, 2017, 51, 33-40.	1.0	18
3748	A potential regulatory network underlying distinct fate commitment of myogenic and adipogenic cells in skeletal muscle. Scientific Reports, 2017, 7, 44133.	1.6	22
3749	De novo transcriptome sequencing of Vaccinium dunalianum Wight to investigate arbutin and 6'-O-caffeoylarbutin synthesis. Russian Journal of Plant Physiology, 2017, 64, 260-282.	0.5	1
3750	Development of SNP markers based on transcriptome sequences and their application in germplasm identification in radish (Raphanus sativus L.). Molecular Breeding, 2017, 37, 1.	1.0	17
3751	New EST-SSR markers reveal strong genetic differentiation in native and introduced populations of the mealybug destroyer Cryptolaemus montrouzieri. Biological Control, 2017, 109, 21-26.	1.4	4
3752	Transcriptomic characterization of gall tissue of Japanese elm tree (Ulmus davidiana var. japonica) induced by the aphid Tetraneura nigriabdominalis. Bioscience, Biotechnology and Biochemistry, 2017, 81, 1069-1077.	0.6	1
3753	Genome-Wide Survey of Genes Under Positive Selection in Avian Pathogenic<i>Escherichia coli</i>Strains. Foodborne Pathogens and Disease, 2017, 14, 245-252.	0.8	8

#	Article	IF	Citations
3754	Animal tracking meets migration genomics: transcriptomic analysis of a partially migratory bird species. Molecular Ecology, 2017, 26, 3204-3216.	2.0	48
3755	Genome-guided transcriptome analysis of miiuy croaker provides insights into pattern recognition receptors and cytokines in response to Vibrio anguillarum. Developmental and Comparative Immunology, 2017, 73, 72-78.	1.0	30
3756	Helminth secretomes reflect different lifestyles and parasitized hosts. International Journal for Parasitology, 2017, 47, 529-544.	1.3	50
3757	The regulation of lipid metabolism by a hypothetical P-loop NTPase and its impact on fecundity of the brown planthopper. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 1750-1758.	1.1	17
3758	Transcriptomic profiles of spring and summer populations of the Southern Ocean salp, Salpa thompsoni, in the Western Antarctic Peninsula region. Polar Biology, 2017, 40, 1261-1276.	0.5	17
3759	De novo transcriptome analysis of Fraxinus velutina using Illumina platform and development of EST-SSR markers. Biologia Plantarum, 2017, 61, 210-218.	1.9	11
3760	Transcriptomic profiles of striped snakehead fish cells (SSN-1) infected with red-spotted grouper nervous necrosis virus (RGNNV) with an emphasis on apoptosis pathway. Fish and Shellfish Immunology, 2017, 60, 346-354.	1.6	43
3761	Insights into bacterioplankton community structure from Sundarbans mangrove ecoregion using Sanger and Illumina MiSeq sequencing approaches: A comparative analysis. Genomics Data, 2017, 11, 39-42.	1.3	16
3762	RNA-seq for comparative transcript profiling of kenaf under salinity stress. Journal of Plant Research, 2017, 130, 365-372.	1.2	27
3763	Comparative transcriptomic analysis reveals phenol tolerance mechanism of evolved Chlorella strain. Bioresource Technology, 2017, 227, 266-272.	4.8	52
3764	Viral hemorrhagic septicemia virus (VHSV) infection-mediated sequential changes in microRNAs profile of Epithelioma papulosum cyprini (EPC) cells. Fish and Shellfish Immunology, 2017, 61, 93-99.	1.6	13
3765	Quantitative Trait Loci and Resistance Gene Analogs Associated with Maize White Spot Resistance. Plant Disease, 2017, 101, 200-208.	0.7	9
3766	Transcriptomic imprints of adaptation to fresh water: parallel evolution of osmoregulatory gene expression in the Alewife. Molecular Ecology, 2017, 26, 831-848.	2.0	54
3767	Association mapping reveals novel serpentine adaptation gene clusters in a population of symbiotic <i>Mesorhizobium</i>. ISME Journal, 2017, 11, 248-262.	4.4	69
3768	Defense peptide repertoire of Stellaria media predicted by high throughput next generation sequencing. Biochimie, 2017, 135, 15-27.	1.3	24
3769	The transcriptomic responses of small brown planthopper, Laodelphax striatellus upon juvenile hormone agonist and antagonist treatment. Journal of Asia-Pacific Entomology, 2017, 20, 529-534.	0.4	2
3770	De novo transcriptome assembly of the hydrocoral Millepora alcicornis (branching fire coral) from the Caribbean. Marine Genomics, 2017, 32, 27-30.	0.4	5
3771	Spliced leader-based analyses reveal the effects of polycyclic aromatic hydrocarbons on gene expression in the copepod Pseudodiaptomus poplesia. Aquatic Toxicology, 2017, 183, 114-126.	1.9	9

#	Article	IF	Citations
3772	Analysis of <i>de novo</i> sequencing and transcriptome assembly and lignocellulolytic enzymes gene expression of <i>Coriolopsis gallica</i> HTC. Bioscience, Biotechnology and Biochemistry, 2017, 81, 460-468.	0.6	3
3773	Comparative genome analysis of multiple vancomycin-resistant Enterococcus faecium isolated from two fatal cases. Infection, Genetics and Evolution, 2017, 49, 55-65.	1.0	3
3774	The transcriptional regulatory network mediated by banana (<i>Musa acuminata</i>) dehydrationâ€responsive element binding (MaDREB) transcription factors in fruit ripening. New Phytologist, 2017, 214, 762-781.	3.5	68
3775	Characterization of the global transcriptome and microsatellite marker information for spotted halibut Verasper variegatus. Genes and Genomics, 2017, 39, 307-316.	0.5	7
3776	Genetics and Genomics of Setaria. Plant Genetics and Genomics: Crops and Models, 2017, , .	0.3	18
3777	Transcript profiling in the milk of dairy ewes fed extruded linseed. Genomics Data, 2017, 11, 17-19.	1.3	4
3778	Proteome-wide identification of lysine propionylation in thermophilic and mesophilic bacteria: Geobacillus kaustophilus, Thermus thermophilus, Escherichia coli, Bacillus subtilis, and Rhodothermus marinus. Extremophiles, 2017, 21, 283-296.	0.9	18
3779	Jasmonic acidâ€mediated defense suppresses brassinosteroidâ€mediated susceptibility to <i>Rice black streaked dwarf virus</i> infection in rice. New Phytologist, 2017, 214, 388-399.	3.5	119
3780	Proteome-wide identification of lysine succinylation in thermophilic and mesophilic bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 232-242.	1.1	40
3781	Nuclear proteome analysis of apple cultivar â€˜Antonovkaâ€™ accessions in response to apple scab (Venturia inaequalis). European Journal of Plant Pathology, 2017, 148, 771-784.	0.8	6
3782	Draft Genome Sequence of Rhodococcus sp. Strain 66b. Genome Announcements, 2017, 5, .	0.8	2
3783	The maternalâ€zygotic transition and zygotic activation of the Mnemiopsis leidyi genome occurs within the first three cleavage cycles. Molecular Reproduction and Development, 2017, 84, 1218-1229.	1.0	8
3784	High infestation levels of Schizotetranychus oryzae severely affects rice metabolism. Journal of Plant Physiology, 2017, 219, 100-111.	1.6	23
3785	The Influence of a Cryptochrome on the Gene Expression Profile in the Diatom Phaeodactylum tricornutum under Blue Light and in Darkness. Plant and Cell Physiology, 2017, 58, 1914-1923.	1.5	14
3786	Genetics and Genomics of Cucurbitaceae. Plant Genetics and Genomics: Crops and Models, 2017, , .	0.3	22
3787	De novo transcriptome assembly and characterization of the 10-hydroxycamptothecin-producing Xylaria sp. M71 following salicylic acid treatment. Journal of Microbiology, 2017, 55, 871-876.	1.3	8
3788	Transcriptome analysis of immune response against Vibrio harveyi infection in orange-spotted grouper (Epinephelus coioides). Fish and Shellfish Immunology, 2017, 70, 628-637.	1.6	41
3789	Transcriptome analysis of Kuruma shrimp (Marsupenaeus japonicus) hepatopancreas in response to white spot syndrome virus (WSSV) under experimental infection. Fish and Shellfish Immunology, 2017, 70, 710-719.	1.6	60

#	ARTICLE	IF	CITATIONS
3790	Insights of Lr28 mediated wheat leaf rust resistance: Transcriptomic approach. Gene, 2017, 637, 72-89.	1.0	22
3791	Integrated analysis of mRNA and miRNA expression profiles in Ptychobarbus dipogon and Schizothorax oconnori , insight into genetic mechanisms of high altitude adaptation in the schizothoracine fishes. Gene Reports, 2017, 9, 74-80.	0.4	3
3792	Functions and substrates of NEDDylation during cell cycle in the silkworm, Bombyx mori. Insect Biochemistry and Molecular Biology, 2017, 90, 101-112.	1.2	10
3793	Transcriptomic responses to drought and salt stress in desert tree Prosopis juliflora. Plant Gene, 2017, 12, 114-122.	1.4	13
3794	Transcriptomic analysis reveals differentially expressed genes and a unique apoptosis pathway in channel catfish ovary cells after infection with the channel catfish virus. Fish and Shellfish Immunology, 2017, 71, 58-68.	1.6	14
3795	Parallel habitat acclimatization is realized by the expression of different genes in two closely related salamander species (genus Salamandra). Heredity, 2017, 119, 429-437.	1.2	15
3796	Architectural delineation and molecular identification of extracellular matrix in ascidian embryos and larvae. Biology Open, 2017, 6, 1383-1390.	0.6	16
3797	Transcriptomic analysis of juvenile wood formation during the growing season in <i>Pinus canariensis</i>. Holzforschung, 2017, 71, 919-937.	0.9	11
3798	Transcriptomic signature of Fusarium toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery. Physiological and Molecular Plant Pathology, 2017, 100, 163-177.	1.3	4
3799	Comparative transcriptome analysis of ovary and testis reveals potential sex-related genes and pathways in spotted knifejaw Oplegnathus punctatus. Gene, 2017, 637, 203-210.	1.0	51
3800	The dynamic landscape of gene regulation during Bombyx mori oogenesis. BMC Genomics, 2017, 18, 714.	1.2	11
3801	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
3802	Genetic diversity and structure of wild and cultivated Amorphophallus paeoniifolius populations in southwestern China as revealed by RAD-seq. Scientific Reports, 2017, 7, 14183.	1.6	22
3803	Genome sequencing of the winged midge, Parochlus steinenii, from the Antarctic Peninsula. GigaScience, 2017, 6, 1-8.	3.3	15
3804	Hybrid incompatibilities in interspecific crosses between tetraploid wheat and its wild diploid relative Aegilops umbellulata. Plant Molecular Biology, 2017, 95, 625-645.	2.0	20
3805	Complementary mechanisms for neurotoxin resistance in a copepod. Scientific Reports, 2017, 7, 14201.	1.6	11
3806	High throughput transcriptome analysis of coffee reveals prehaustorial resistance in response to Hemileia vastatrix infection. Plant Molecular Biology, 2017, 95, 607-623.	2.0	25
3807	Computational deciphering of biotic stress associated genes in tomato (Solanum lycopersicum). Genomics Data, 2017, 14, 82-90.	1.3	5

#	ARTICLE	IF	CITATIONS
3808	Signatures of polygenic adaptation associated with climate across the range of a threatened fish species with high genetic connectivity. Molecular Ecology, 2017, 26, 6253-6269.	2.0	34
3809	Transcriptome mining of immune-related genes in the muricid snail Concholepas concholepas. Fish and Shellfish Immunology, 2017, 71, 69-75.	1.6	4
3810	Signatures of positive selection and local adaptation to urbanization in whiteâ€footed mice (<i>Peromyscus leucopus</i>). Molecular Ecology, 2017, 26, 6336-6350.	2.0	61
3811	Temporal transcriptomic profiling of the ant-feeding assassin bug Acanthaspis cincticrus reveals a biased expression of genes associated with predation in nymphs. Scientific Reports, 2017, 7, 12691.	1.6	4
3813	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	9.4	150
3814	Natural product diversity associated with the nematode symbionts Photorhabdus and Xenorhabdus. Nature Microbiology, 2017, 2, 1676-1685.	5.9	136
3815	Ant-infecting Ophiocordyceps genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. Scientific Reports, 2017, 7, 12508.	1.6	52
3816	Mining and characterization of EST-SSR markers for Zingiber officinale Roscoe with transferability to other species of Zingiberaceae. Physiology and Molecular Biology of Plants, 2017, 23, 925-931.	1.4	9
3817	The other whiteâ€nose syndrome transcriptome: Tolerant and susceptible hosts respond differently to the pathogen <i>Pseudogymnoascus destructans</i>. Ecology and Evolution, 2017, 7, 7161-7170.	0.8	24
3818	Profiling of BABA-induced differentially expressed genes of Zea mays using suppression subtractive hybridization. RSC Advances, 2017, 7, 43849-43865.	1.7	2
3819	Both modular and singleâ€domain Type I polyketide synthases are expressed in the brevetoxinâ€producing dinoflagellate, <i>Karenia brevis</i> (Dinophyceae). Journal of Phycology, 2017, 53, 1325-1339.	1.0	28
3820	A Single Regulator Mediates Strategic Switching between Attachment/Spread and Growth/Virulence in the Plant Pathogen <i>Ralstonia solanacearum</i>. MBio, 2017, 8, .	1.8	66
3821	Transcriptome analysis of hepatopancraes of Procambarus clarkii challenged with polyriboinosinic polyribocytidylic acid (poly I:C). Fish and Shellfish Immunology, 2017, 71, 144-150.	1.6	28
3822	Effective purifying selection in ancient asexual oribatid mites. Nature Communications, 2017, 8, 873.	5.8	32
3823	Transcriptome sequencing and annotation of the halophytic microalga Dunaliella salina. Journal of Zhejiang University: Science B, 2017, 18, 833-844.	1.3	21
3824	Annotation of nerve cord transcriptome in earthworm Eisenia fetida. Genomics Data, 2017, 14, 91-105.	1.3	17
3825	Transcriptional response after exposure to domoic acid-producing Pseudo-nitzschia in the digestive gland of the mussel Mytilus galloprovincialis. Toxicon, 2017, 140, 60-71.	0.8	31
3826	Formation of Staphylococcus aureus Biofilm in the Presence of Sublethal Concentrations of Disinfectants Studied via a Transcriptomic Analysis Using Transcriptome Sequencing (RNA-seq). Applied and Environmental Microbiology, 2017, 83, .	1.4	33

#	Article	IF	Citations
3827	Identification of microRNAs and their target transcripts in the migratory locust adult brain revealed their roles in the epigenetic regulation of polyphenisms. Journal of Asia-Pacific Entomology, 2017, 20, 1396-1401.	0.4	2
3828	Revealing the Saline Adaptation Strategies of the Halophilic Bacterium Halomonas beimenensis through High-throughput Omics and Transposon Mutagenesis Approaches. Scientific Reports, 2017, 7, 13037.	1.6	35
3829	RNA-seq Analysis in Plantâ€"Fungus Interactions. , 2017, , 1-25.		0
3830	Structure of phycobilisome from the red alga Griffithsia pacifica. Nature, 2017, 551, 57-63.	13.7	183
3831	The effect of insecticide synergist treatment on genome-wide gene expression in a polyphagous pest. Scientific Reports, 2017, 7, 13440.	1.6	32
3832	Taxon-restricted genes at the origin of a novel trait allowing access to a new environment. Science, 2017, 358, 386-390.	6.0	87
3833	Comparative transcriptome analysis reveals whole-genome duplications and gene selection patterns in cultivated and wild Chrysanthemum species. Plant Molecular Biology, 2017, 95, 451-461.	2.0	21
3834	Identification of up-regulated genes from the metal-hyperaccumulator aquatic fern Salvinia minima Baker, in response to lead exposure. Aquatic Toxicology, 2017, 193, 86-96.	1.9	7
3835	Gill transcriptomes reveal involvement of cytoskeleton remodeling and immune defense in ammonia stress response in the banana shrimp Fenneropenaeus merguiensis. Fish and Shellfish Immunology, 2017, 71, 319-328.	1.6	51
3836	Distinct sources of gene flow produce contrasting population genetic dynamics at different range boundaries of a <i>Choristoneura</i> budworm. Molecular Ecology, 2017, 26, 6666-6684.	2.0	7
3837	Biofilm-Related Diseases and Omics: Global Transcriptional Profiling of<i>Enterococcus faecium</i>Reveals Different Gene Expression Patterns in the Biofilm and Planktonic Cells. OMICS A Journal of Integrative Biology, 2017, 21, 592-602.	1.0	29
3838	Comparative transcriptomic analysis of high and low egg-producing duck ovaries. Poultry Science, 2017, 96, 4378-4388.	1.5	48
3839	Comparative transcriptome analysis provides new insights into erect and prostrate growth in bermudagrass (Cynodon dactylon L.). Plant Physiology and Biochemistry, 2017, 121, 31-37.	2.8	14
3840	Chemosensing of honeybee parasite, Varroa destructor: Transcriptomic analysis. Scientific Reports, 2017, 7, 13091.	1.6	38
3841	Transcriptome profiling of red swamp crayfish (Procambarus clarkii) hepatopancreas in response to lipopolysaccharide (LPS) infection. Fish and Shellfish Immunology, 2017, 71, 423-433.	1.6	33
3842	Lateralized Feeding Behavior is Associated with Asymmetrical Neuroanatomy and Lateralized Gene Expressions in the Brain in Scale-Eating Cichlid Fish. Genome Biology and Evolution, 2017, 9, 3122-3136.	1.1	27
3843	Transcriptome-wide profiling and expression analysis of two accessions of Paulownia australis under salt stress. Tree Genetics and Genomes, 2017, 13, 1.	0.6	8
3844	Transcriptomic analysis of flower development in tea (Camellia sinensis (L.)). Gene, 2017, 631, 39-51.	1.0	48

#	Article	IF	Citations
3845	Genome-wide gene expression analysis of amphioxus (<i>Branchiostoma belcheri</i>) following lipopolysaccharide challenge using strand-specific RNA-seq. RNA Biology, 2017, 14, 1799-1809.	1.5	18
3846	Luxurious Nitrogen Fertilization of Two Sugar Cane Genotypes Contrasting for Lignin Composition Causes Changes in the Stem Proteome Related to Carbon, Nitrogen, and Oxidant Metabolism but Does Not Alter Lignin Content. Journal of Proteome Research, 2017, 16, 3688-3703.	1.8	12
3847	The molecular mechanism and post-transcriptional regulation characteristic of Tetragenococcus halophilus acclimation to osmotic stress revealed by quantitative proteomics. Journal of Proteomics, 2017, 168, 1-14.	1.2	23
3848	Advancing our understanding of the oxygen minimum zone microbial communities by an integrated metatranscriptomics approach. Meta Gene, 2017, 14, 85-90.	0.3	1
3849	Transcriptome analysis of the response of Burmese python to digestion. GigaScience, 2017, 6, 1-18.	3.3	17
3850	De novo transcriptomic and metabolomic analysis of docosahexaenoic acid (DHA)-producing Crypthecodinium cohnii during fed-batch fermentation. Algal Research, 2017, 26, 380-391.	2.4	38
3851	Draft genome of the Antarctic dragonfish, Parachaenichthys charcoti. GigaScience, 2017, 6, 1-6.	3.3	24
3852	Transcriptomic analysis of Camellia oleifera in response to drought stress using high throughput RNA-seq. Russian Journal of Plant Physiology, 2017, 64, 728-737.	0.5	6
3853	Growth on Chitin Impacts the Transcriptome and Metabolite Profiles of Antibiotic-Producing Vibrio coralliilyticus S2052 and Photobacterium galatheae S2753. MSystems, 2017, 2, .	1.7	21
3854	Transcriptomic Analysis of Olea europaea L. Roots during the Verticillium dahliae Early Infection Process. Plant Genome, 2017, 10, plantgenome2016.07.0060.	1.6	33
3855	Cellâ€typeâ€and tissueâ€specific transcriptomes of the white spruce (<i>Picea glauca</i>) bark unmask fineâ€scale spatial patterns of constitutive and induced conifer defense. Plant Journal, 2017, 92, 710-726.	2.8	47
3856	Exploring gene expression changes in the amphioxus gill after poly(I:C) challenge using digital expression profiling. Fish and Shellfish Immunology, 2017, 70, 57-65.	1.6	14
3857	Landscape genomics of Colorado potato beetle provides evidence of polygenic adaptation to insecticides. Molecular Ecology, 2017, 26, 6284-6300.	2.0	56
3858	Karyotype Stability and Unbiased Fractionation in the Paleo-Allotetraploid Cucurbita Genomes. Molecular Plant, 2017, 10, 1293-1306.	3.9	263
3859	Draft Genome Sequence of the Endophytic Bacillus aryabhattai Strain SQU-R12, Identified from <i>Phoenix dactylifera</i> L. Roots. Genome Announcements, 2017, 5, .	0.8	16
3860	Development of transcriptome based web genomic resources of yellow mosaic disease in Vigna mungo. Physiology and Molecular Biology of Plants, 2017, 23, 767-777.	1.4	11
3861	Communication via extracellular vesicles enhances viral infection of a cosmopolitan alga. Nature Microbiology, 2017, 2, 1485-1492.	5.9	56
3862	De novo transcriptome of the cosmopolitan dinoflagellate Amphidinium carterae to identify enzymes with biotechnological potential. Scientific Reports, 2017, 7, 11701.	1.6	52

#	Article	IF	Citations
3863	Transcriptional correlates of memory maintenance following long-term sensitization of <i>Aplysia californica</i>. Learning and Memory, 2017, 24, 502-515.	0.5	16
3864	Transcriptome analysis of the spleen of the darkbarbel catfish Pelteobagrus vachellii in response to Aeromonas hydrophila infection. Fish and Shellfish Immunology, 2017, 70, 498-506.	1.6	27
3865	Identification of secondary metabolite biosynthetic gene clusters associated with the infection of citrus fruit by Penicillium digitatum. Postharvest Biology and Technology, 2017, 134, 17-21.	2.9	28
3866	Transcriptome and phytohormone analysis reveals a comprehensive phytohormone and pathogen defence response in pear self-/cross-pollination. Plant Cell Reports, 2017, 36, 1785-1799.	2.8	32
3867	Comparative genomics of maize ear rot pathogens reveals expansion of carbohydrate-active enzymes and secondary metabolism backbone genes in Stenocarpella maydis. Fungal Biology, 2017, 121, 966-983.	1.1	8
3868	Transcriptome sequencing and estimation of DNA methylation level in the subsocial wood-feeding cockroach Cryptocercus punctulatus (Blattodea: Cryptocercidae). Applied Entomology and Zoology, 2017, 52, 643-651.	0.6	9
3869	Transcriptomics analysis of salt stress tolerance in the roots of the mangrove Avicennia officinalis. Scientific Reports, 2017, 7, 10031.	1.6	77
3870	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of Drosophila. Current Biology, 2017, 27, 2869-2877.e6.	1.8	37
3871	Genome-wide association study Identified multiple Genetic Loci on Chilling Resistance During Germination in Maize. Scientific Reports, 2017, 7, 10840.	1.6	49
3872	Integration of deep transcriptome and proteome analyses of salicylic acid regulation high temperature stress in Ulva prolifera. Scientific Reports, 2017, 7, 11052.	1.6	36
3873	Intracellular spectral recompositioning of light enhances algal photosynthetic efficiency. Science Advances, 2017, 3, e1603096.	4.7	42
3874	Genome-wide analysis of Phaseolus vulgaris C2C2-YABBY transcription factors under salt stress conditions. 3 Biotech, 2017, 7, 302.	1.1	21
3875	Transcriptomic analysis of the hepatopancreas induced by eyestalk ablation in shrimp, Litopenaeus vannamei. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 24, 99-110.	0.4	16
3876	De novo assembly of leaf transcriptome, functional annotation and genomic resources development in Prosopis cineraria , a multipurpose tree of Indian Thar Desert. Plant Gene, 2017, 12, 88-97.	1.4	12
3877	Transcriptomic and proteomic analysis of Locusta migratoria eggs at different embryonic stages: Comparison for diapause and non-diapause regimes. Journal of Integrative Agriculture, 2017, 16, 1777-1788.	1.7	36
3878	Analysis of the first Taraxacum kok-saghyz transcriptome reveals potential rubber yield related SNPs. Scientific Reports, 2017, 7, 9939.	1.6	50
3879	Comparative transcriptome analysis of the Pacific White Shrimp (Litopenaeus vannamei) muscle reveals the molecular basis of residual feed intake. Scientific Reports, 2017, 7, 10483.	1.6	19
3880	Transcriptomic Basis of Metamorphic Competence in the Salt-Marsh-Dwelling PolychaeteCapitella teleta. Biological Bulletin, 2017, 232, 158-170.	0.7	6

#	Article	IF	Citations
3881	Transcriptional responses to shortâ€term and longâ€term host plant experience and parasite load in an oligophagous beetle. Molecular Ecology, 2017, 26, 6370-6383.	2.0	28
3882	Comparative and population genomic landscape of <i>Phellinus noxius</i>: A hypervariable fungus causing root rot in trees. Molecular Ecology, 2017, 26, 6301-6316.	2.0	40
3883	De novo transcriptome sequencing of Camellia sasanqua and the analysis of major candidate genes related to floral traits. Plant Physiology and Biochemistry, 2017, 120, 103-111.	2.8	16
3884	Screening of miRNA profiles and construction of regulation networks in early and late lactation of dairy goat mammary glands. Scientific Reports, 2017, 7, 11933.	1.6	26
3885	Differential gene expression and SNP association between fast- and slow-growing turbot (Scophthalmus maximus). Scientific Reports, 2017, 7, 12105.	1.6	23
3886	Intergrative metabolomic and transcriptomic analyses unveil nutrient remobilization events in leaf senescence of tobacco. Scientific Reports, 2017, 7, 12126.	1.6	56
3887	The bottle gourd genome provides insights into Cucurbitaceae evolution and facilitates mapping of a <i>Papaya ringâ€spot virus</i> resistance locus. Plant Journal, 2017, 92, 963-975.	2.8	101
3888	Desiccation tolerance in bryophytes: The dehydration and rehydration transcriptomes in the desiccation-tolerant bryophyte Bryum argenteum. Scientific Reports, 2017, 7, 7571.	1.6	50
3889	Transcriptional transitions in Alphonso mango (Mangifera indica L.) during fruit development and ripening explain its distinct aroma and shelf life characteristics. Scientific Reports, 2017, 7, 8711.	1.6	42
3890	Aspergillus flavus infection triggered immune responses and host-pathogen cross-talks in groundnut during in-vitro seed colonization. Scientific Reports, 2017, 7, 9659.	1.6	38
3891	Differential evolutionary patterns and expression levels between sex-specific and somatic tissue-specific genes in peanut. Scientific Reports, 2017, 7, 9016.	1.6	9
3892	FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. Scientific Reports, 2017, 7, 10430.	1.6	29
3893	Multiple miRNAs jointly regulate the biosynthesis of ecdysteroid in the holometabolous insects, <i>Chilo suppressalis</i>. Rna, 2017, 23, 1817-1833.	1.6	35
3894	Hepatopancreas transcriptome analysis of Chinese mitten crab (Eriocheir sinensis) with white hepatopancreas syndrome. Fish and Shellfish Immunology, 2017, 70, 302-307.	1.6	27
3895	De novo assembly and analysis of the Heortia vitessoides transcriptome via high-throughput Illumina sequencing. Journal of Asia-Pacific Entomology, 2017, 20, 1241-1248.	0.4	15
3896	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
3897	Transcriptomic profiling of Tibetan highland fish (Gymnocypris przewalskii) in response to the infection of parasite ciliate Ichthyophthirius multifiliis. Fish and Shellfish Immunology, 2017, 70, 524-535.	1.6	23
3898	Apple genes involved in the response to Venturia inaequalis and salicylic acid treatment. Scientia Horticulturae, 2017, 226, 157-172.	1.7	10

#	ARTICLE	IF	CITATIONS
3899	Enhanced Biodegradation of Anthracene by <i>Bacillus Cereus</i> Strain JMG-01 Isolated from Hydrocarbon Contaminated Soils. Soil and Sediment Contamination, 2017, 26, 510-525.	1.1	10
3900	Comparative secretome analysis of Rhizoctonia solani isolates with different host ranges reveals unique secretomes and cell death inducing effectors. Scientific Reports, 2017, 7, 10410.	1.6	62
3901	Profiling methyl jasmonate-responsive transcriptome for understanding induced systemic resistance in whitebark pine (Pinus albicaulis). Plant Molecular Biology, 2017, 95, 359-374.	2.0	23
3902	An aldo-keto reductase is responsible for Fusarium toxin-degrading activity in a soil Sphingomonas strain. Scientific Reports, 2017, 7, 9549.	1.6	67
3903	Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild relative of sweet potato. Scientific Reports, 2017, 7, 9624.	1.6	22
3904	Comprehensive transcriptome profiling of Salvia miltiorrhiza for discovery of genes associated with the biosynthesis of tanshinones and phenolic acids. Scientific Reports, 2017, 7, 10554.	1.6	77
3905	A comparative integrated gene-based linkage and locus ordering by linkage disequilibrium map for the Pacific white shrimp, Litopenaeus vannamei. Scientific Reports, 2017, 7, 10360.	1.6	55
3906	Transcriptome Analysis Suggests That Chromosome Introgression Fragments from Sea Island Cotton (<i>Gossypium barbadense</i>) Increase Fiber Strength in Upland Cotton (<i>Gossypium hirsutum</i>). G3: Genes, Genomes, Genetics, 2017, 7, 3469-3479.	0.8	28
3907	RNA-seq of Rice Yellow Stem Borer<i>Scirpophaga incertulas</i>Reveals Molecular Insights During Four Larval Developmental Stages. G3: Genes, Genomes, Genetics, 2017, 7, 3031-3045.	0.8	12
3908	Transcriptome analysis of yellow catfish (Pelteobagrus fulvidraco) liver challenged with polyriboinosinic polyribocytidylic acid (poly I:C). Fish and Shellfish Immunology, 2017, 68, 395-403.	1.6	25
3909	Next Generation Sequencing to characterise the breaking of bud dormancy using a natural biostimulant in kiwifruit (Actinidia deliciosa). Scientia Horticulturae, 2017, 225, 252-263.	1.7	18
3910	Identification and comparison of RCMV ALL 03 open reading frame (ORF) among several different strains of cytomegalovirus worldwide. Infection, Genetics and Evolution, 2017, 54, 81-90.	1.0	6
3911	Physiological responses to fluctuating temperatures are characterized by distinct transcriptional profiles in a solitary bee. Journal of Experimental Biology, 2017, 220, 3372-3380.	0.8	20
3912	Revisiting venom of the sea anemone Stichodactyla haddoni : Omics techniques reveal the complete toxin arsenal of a well-studied sea anemone genus. Journal of Proteomics, 2017, 166, 83-92.	1.2	64
3913	Genomeâ€wide analysis of carbohydrateâ€active enzymes in <i>Pyramimonas parkeae</i> (Prasinophyceae). Journal of Phycology, 2017, 53, 1072-1086.	1.0	7
3914	Genetic architecture of wild soybean (Glycine soja) response to soybean cyst nematode (Heterodera) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	37
3915	Preliminary evidence for snail deformation from a Eutrophic lake. Environmental Toxicology and Pharmacology, 2017, 53, 219-226.	2.0	9
3916	De novo transcriptome assembly and its annotation for the aposematic wood tiger moth (Parasemia) Tj ETQq1 1 0.784314 rgBT /Overlo	1.3	7

#	Article	IF	Citations
3917	Cultivar-specific transcriptome prediction and annotation in Ficus carica L.. Genomics Data, 2017, 13, 64-66.	1.3	13
3918	A comparative genome analysis of Cercospora sojina with other members of the pathogen genus Mycosphaerella on different plant hosts. Genomics Data, 2017, 13, 54-63.	1.3	15
3919	First report of two complete Clostridium chauvoei genome sequences and detailed in silico genome analysis. Infection, Genetics and Evolution, 2017, 54, 287-298.	1.0	16
3920	Transcriptomic analysis of the larva Taenia multiceps. Research in Veterinary Science, 2017, 115, 407-411.	0.9	7
3921	Identification of long non-coding RNAs in two anthozoan species and their possible implications for coral bleaching. Scientific Reports, 2017, 7, 5333.	1.6	22
3922	Functional Analysis of Differentially Expressed MicroRNAs Associated with Drought Stress in Diploid and Tetraploid Paulownia fortunei. Plant Molecular Biology Reporter, 2017, 35, 389-398.	1.0	3
3923	Transcriptome analysis of female and male flower buds of Idesia polycarpa Maxim. var. vestita Diels. Electronic Journal of Biotechnology, 2017, 29, 39-46.	1.2	6
3924	The transcriptional response of the Pacific oyster Crassostrea gigas against acute heat stress. Fish and Shellfish Immunology, 2017, 68, 132-143.	1.6	47
3925	De novo transcriptome sequencing and analysis of Euphorbia pekinensis Rupr. and identification of genes involved in diterpenoid biosynthesis. Plant Gene, 2017, 12, 33-42.	1.4	5
3926	Dual RNAâ€Seq of <i>Lysobacter capsici</i> AZ78 â€" <i>Phytophthora infestans</i> interaction shows the implementation of attack strategies by the bacterium and unsuccessful oomycete defense responses. Environmental Microbiology, 2017, 19, 4113-4125.	1.8	30
3927	An in silico strategy for identification of novel drug targets against Plasmodium falciparum. Parasitology Research, 2017, 116, 2539-2559.	0.6	7
3928	Rapid evolution of female-biased genes among four species of <i>Anopheles</i> malaria mosquitoes. Genome Research, 2017, 27, 1536-1548.	2.4	60
3929	Genome-wide association mapping of latex yield and girth in Amazonian accessions of Hevea brasiliensis grown in a suboptimal climate zone. Genomics, 2017, 109, 475-484.	1.3	30
3930	Development of Genomic Simple Sequence Repeats (SSR) by Enrichment Libraries in Date Palm. Methods in Molecular Biology, 2017, 1638, 315-337.	0.4	6
3931	Genomic evidence for local adaptation in the ovoviviparous marine fish Sebastiscus marmoratus with a background of population homogeneity. Scientific Reports, 2017, 7, 1562.	1.6	32
3932	Genotyping-by-sequencing reveals three QTL for clubroot resistance to six pathotypes of Plasmodiophora brassicae in Brassica rapa. Scientific Reports, 2017, 7, 4516.	1.6	90
3933	RADseq provides evidence for parallel ecotypic divergence in the autotetraploid Cochlearia officinalis in Northern Norway. Scientific Reports, 2017, 7, 5573.	1.6	30
3934	Symbiont dynamics and strain diversity in the defensive mutualism between <i>Lagria</i> beetles and <i>Burkholderia</i>. Environmental Microbiology, 2017, 19, 3674-3688.	1.8	42

#	ARTICLE	IF	CITATIONS
3935	Analysis of Expressed Sequence Tags (EST) in Date Palm. Methods in Molecular Biology, 2017, 1638, 283-313.	0.4	3
3936	Date Fruit Proteomics During Development and Ripening Stages. Methods in Molecular Biology, 2017, 1638, 381-398.	0.4	4
3937	Polymorphisms in the LAC12 gene explain lactose utilisation variability in Kluyveromyces marxianus strains. FEMS Yeast Research, 2017, 17, .	1.1	46
3938	Identification and comparison of candidate odorant receptor genes in the olfactory and non-olfactory organs of Holotrichia oblita Faldermann by transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 24, 1-11.	0.4	28
3939	Differential expression patterns of MIKCC-type MADS-box genes in the endangered fern Vandenboschia speciosa. Plant Gene, 2017, 12, 50-56.	1.4	6
3940	Genomic and phenotypic signatures of climate adaptation in an <i>Anolis</i> lizard. Ecology and Evolution, 2017, 7, 6390-6403.	0.8	26
3941	Locally adapted populations of a copepod can evolve different gene expression patterns under the same environmental pressures. Ecology and Evolution, 2017, 7, 4312-4325.	0.8	19
3942	Unravelling the relationship between the tsetse fly and its obligate symbiont <i>Wigglesworthia</i> : transcriptomic and metabolomic landscapes reveal highly integrated physiological networks. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170360.	1.2	53
3943	Transcriptome analysis of terpene chemotypes of <i>Melaleuca alternifolia</i> across different tissues. Plant, Cell and Environment, 2017, 40, 2406-2425.	2.8	34
3944	Genome Sequence of Brevibacillus laterosporus UNISS 18, a Pathogen of Mosquitoes and Flies. Genome Announcements, 2017, 5, .	0.8	5
3945	De novo RNA sequencing and analysis of the transcriptome of signalgrass (Urochloa decumbens) roots exposed to aluminum. Plant Growth Regulation, 2017, 83, 157-170.	1.8	23
3946	Date Palm Biotechnology Protocols Volume II. Methods in Molecular Biology, 2017, , .	0.4	3
3947	Microbial Interspecies Interactions Affect Arsenic Fate in the Presence of MnII. Microbial Ecology, 2017, 74, 788-794.	1.4	5
3948	Workflow and web application for annotating NCBI BioProject transcriptome data. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
3949	In silico characterization of tandem repeats in Trichophyton rubrum and related dermatophytes provides new insights into their role in pathogenesis. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	4
3950	Adaptation of the pine fungal pathogen <i>Grosmannia clavigera</i> to monoterpenes: Biochemical mechanisms revealed by <scp>RNA</scp>â€seq analysis. Forest Pathology, 2017, 47, e12372.	0.5	4
3951	De novo transcriptome assembly and RNA-Seq expression analysis in blood from beluga whales of Bristol Bay, AK. Marine Genomics, 2017, 35, 77-92.	0.4	8
3952	Genome-wide characterization of the WRKY gene family in radish (Raphanus sativus L.) reveals its critical functions under different abiotic stresses. Plant Cell Reports, 2017, 36, 1757-1773.	2.8	41

#	Article	IF	Citations
3953	Graph repairing under neighborhood constraints. VLDB Journal, 2017, 26, 611-635.	2.7	10
3954	Transcriptome analysis of San Pedro-type fig (Ficus carica L.) parthenocarpic breba and non-parthenocarpic main crop reveals divergent phytohormone-related gene expression. Tree Genetics and Genomes, 2017, 13, 1.	0.6	21
3955	Transcriptome Analysis of Sclerotinia sclerotiorum at Different Infection Stages on Brassica napus. Current Microbiology, 2017, 74, 1237-1245.	1.0	12
3956	RNA-seq based transcriptomic analysis of CPPU treated grape berries and emission of volatile compounds. Journal of Plant Physiology, 2017, 218, 155-166.	1.6	32
3957	Complete Genome Sequence of Achromobacter denitrificans PR1. Genome Announcements, 2017, 5, .	0.8	12
3958	Gonad transcriptome of discus fish (Symphysodon haraldi) and discovery of sex-related genes. Aquaculture Research, 2017, 48, 5993-6000.	0.9	14
3959	Genomic, Network, and Phylogenetic Analysis of the Oomycete Effector Arsenal. MSphere, 2017, 2, .	1.3	64
3960	Drought and salt stress in Chrysopogon zizanioides leads to common and specific transcriptomic responses and may affect essential oil composition and benzylisoquinoline alkaloids metabolism. Current Plant Biology, 2017, 11-12, 12-22.	2.3	14
3961	The genome sequence of Bipolaris cookei reveals mechanisms of pathogenesis underlying target leaf spot of sorghum. Scientific Reports, 2017, 7, 17217.	1.6	29
3962	Comparative transcriptomic analysis of Tibetan Gynaephora to explore the genetic basis of insect adaptation to divergent altitude environments. Scientific Reports, 2017, 7, 16972.	1.6	15
3963	Molecular Mechanisms for Microbe Recognition and Defense by the Red Seaweed Laurencia dendroidea. MSphere, 2017, 2, .	1.3	19
3964	Transcription factor repertoire in Ashwagandha (Withania somnifera) through analytics of transcriptomic resources: Insights into regulation of development and withanolide metabolism. Scientific Reports, 2017, 7, 16649.	1.6	17
3965	De novo transcriptome assembly of Zanthoxylum bungeanum using Illumina sequencing for evolutionary analysis and simple sequence repeat marker development. Scientific Reports, 2017, 7, 16754.	1.6	38
3966	The KalanchoÃ« genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899.	5.8	159
3967	Transcriptome analysis of Brachypodium during fungal pathogen infection reveals both shared and distinct defense responses with wheat. Scientific Reports, 2017, 7, 17212.	1.6	27
3968	Strategy to Identify and Test Putative Light-Sensitive Non-Opsin G-Protein-Coupled Receptors: A Case Study. Biological Bulletin, 2017, 233, 70-82.	0.7	10
3969	Exposure to CO2 influences metabolism, calcification, and gene expression of the thecosome pteropod <i>Limacina retroversa</i>. Journal of Experimental Biology, 2018, 221, .	0.8	31
3970	Draft Genome Sequence of Arsenic-Resistant Microbacterium sp. Strain SZ1 Isolated from Arsenic-Bearing Gold Ores. Genome Announcements, 2017, 5, .	0.8	4

#	ARTICLE	IF	CITATIONS
3971	Physiological characterization, transcriptomic profiling, and microsatellite marker mining of Lycium ruthenicum. Journal of Zhejiang University: Science B, 2017, 18, 1002-1021.	1.3	12
3972	RNA-seq analysis provides insight into reprogramming of culm development in Zizania latifolia induced by Ustilago esculenta. Plant Molecular Biology, 2017, 95, 533-547.	2.0	43
3973	Transcriptomic response to thermal and salinity stress in introduced and native sympatric Palaemon caridean shrimps. Scientific Reports, 2017, 7, 13980.	1.6	14
3974	A novel miRNA analysis framework to analyze differential biological networks. Scientific Reports, 2017, 7, 14604.	1.6	13
3975	Transcriptome profiling and expression analysis of immune responsive genes in the liver of Golden mahseer (Tor putitora) challenged with Aeromonas hydrophila. Fish and Shellfish Immunology, 2017, 67, 655-666.	1.6	36
3976	Transcriptome changes between compatible and incompatible graft combination of Litchi chinensis by digital gene expression profile. Scientific Reports, 2017, 7, 3954.	1.6	46
3977	Large-scale SNP screenings identify markers linked with GCRV resistant traits through transcriptomes of individuals and cell lines in Ctenopharyngodon idella. Scientific Reports, 2017, 7, 1184.	1.6	18
3978	Analysis of culm elongation in photoheterotrophic status of Dendrocalamus sinicus by comparative proteomics. Trees - Structure and Function, 2017, 31, 687-704.	0.9	3
3979	Identification and comparative analysis of microRNAs in Pinus massoniana infected by Bursaphelenchus xylophilus. Plant Growth Regulation, 2017, 83, 223-232.	1.8	14
3980	Transcriptomes from the photogenic and non-photogenetic tissues and life stages of the Aspisoma lineatum firefly (Coleoptera: Lampyridae): Implications for the evolutionary origins of bioluminescence and its associated light organs. Gene Reports, 2017, 8, 150-159.	0.4	14
3981	Intrahost Genetic Diversity of Bacterial Symbionts Exhibits Evidence of Mixed Infections and Recombinant Haplotypes. Molecular Biology and Evolution, 2017, 34, 2747-2761.	3.5	31
3982	MeCP2 regulated glycogenes contribute to proliferation and apoptosis of gastric cancer cells. Glycobiology, 2017, 27, cwx006.	1.3	10
3983	Comparative transcriptional analysis of hop responses to infection with Verticillium nonalfalfae. Plant Cell Reports, 2017, 36, 1599-1613.	2.8	11
3984	SNP discovery from next-generation transcriptome sequencing data and their validation using KASP assay in wheat (Triticum aestivum L.). Molecular Breeding, 2017, 37, 1.	1.0	12
3985	Phosphorylation-mediated Regulatory Networks in Mycelia of Pyricularia oryzae Revealed by Phosphoproteomic Analyses. Molecular and Cellular Proteomics, 2017, 16, 1669-1682.	2.5	21
3986	Development of RNA-Seq SSR Markers and Application to Genetic Relationship Analysis among Sea Buckthorn Germplasm. Journal of the American Society for Horticultural Science, 2017, 142, 200-208.	0.5	9
3987	In-depth genome characterization of a Brazilian common bean core collection using DArTseq high-density SNP genotyping. BMC Genomics, 2017, 18, 423.	1.2	81
3988	Comparative proteomic analysis provides insight into the biological role of protein phosphatase inhibitor-2 from Arabidopsis. Journal of Proteomics, 2017, 165, 51-60.	1.2	3

#	ARTICLE	IF	CITATIONS
3989	Genome-wide analysis of gene expression and protein secretion of Babesia canis during virulent infection identifies potential pathogenicity factors. Scientific Reports, 2017, 7, 3357.	1.6	35
3990	Core features of triacylglyceride production in Ettlia oleoabundans revealed by lipidomic and gene expression profiling under distinct induction conditions. Algal Research, 2017, 26, 453-462.	2.4	3
3991	Comparative transcriptome analysis of molecular mechanism underlying gray-to-red body color formation in red crucian carp (Carassius auratus, red var.). Fish Physiology and Biochemistry, 2017, 43, 1387-1398.	0.9	64
3992	Estimates of linkage disequilibrium and effective population sizes in Chinese Merino (Xinjiang type) sheep by genome-wide SNPs. Genes and Genomics, 2017, 39, 733-745.	0.5	52
3993	The exceptionality of stress response in Magnaporthe oryzae: a set of â€œsalt stress-inducedâ€•genes unique to the rice blast fungus. Journal of Plant Diseases and Protection, 2017, 124, 399-402.	1.6	4
3994	Plant manipulation through gall formation constrains amino acid transporter evolution in sap-feeding insects. BMC Evolutionary Biology, 2017, 17, 153.	3.2	5
3995	The transcriptome of a â€œsleepingâ€•invader: de novo assembly and annotation of the transcriptome of aestivating Cornu aspersum. BMC Genomics, 2017, 18, 491.	1.2	17
3996	Transcriptome dynamics of Camellia sinensis in response to continuous salinity and drought stress. Tree Genetics and Genomes, 2017, 13, 1.	0.6	67
3997	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. Plant Journal, 2017, 91, 1108-1128.	2.8	109
3998	Genomic exaptation enables Lasius niger adaptation to urban environments. BMC Evolutionary Biology, 2017, 17, 39.	3.2	28
3999	Signatures of co-evolutionary host-pathogen interactions in the genome of the entomopathogenic nematode Steinernema carpocapsae. BMC Evolutionary Biology, 2017, 17, 108.	3.2	1
4000	De novo transcriptome assembly analysis of weed Apera spica-venti from seven tissues and growth stages. BMC Genomics, 2017, 18, 128.	1.2	30
4001	Cross-talk of the biotrophic pathogen Claviceps purpurea and its host Secale cereale. BMC Genomics, 2017, 18, 273.	1.2	19
4002	High-throughput sequencing of pituitary and hypothalamic microRNA transcriptome associated with high rate of egg production. BMC Genomics, 2017, 18, 255.	1.2	22
4003	Effects of cold-acclimation on gene expression in Fall field cricket (Gryllus pennsylvanicus) ionoregulatory tissues. BMC Genomics, 2017, 18, 357.	1.2	52
4004	Transcriptome analysis of smut fungi reveals widespread intergenic transcription and conserved antisense transcript expression. BMC Genomics, 2017, 18, 340.	1.2	30
4005	Statistical analysis of fractionation resistance by functional category and expression. BMC Genomics, 2017, 18, 366.	1.2	1
4006	Transcriptome profiling of litchi leaves in response to low temperature reveals candidate regulatory genes and key metabolic events during floral induction. BMC Genomics, 2017, 18, 363.	1.2	13

#	ARTICLE	IF	CITATIONS
4007	Genomic adaptation to agricultural environments: cabbage white butterflies (Pieris rapae) as a case study. BMC Genomics, 2017, 18, 412.	1.2	13
4008	Label-free quantitative proteomics of Corynebacterium pseudotuberculosis isolates reveals differences between Biovars ovis and equi strains. BMC Genomics, 2017, 18, 451.	1.2	17
4009	A high-quality annotated transcriptome of swine peripheral blood. BMC Genomics, 2017, 18, 479.	1.2	7
4010	Identification of microRNAs and their response to the stress of plant allelochemicals in Aphis gossypii (Hemiptera: Aphididae). BMC Molecular Biology, 2017, 18, 5.	3.0	23
4011	De novo sequencing and comparative transcriptome analysis of the male and hermaphroditic flowers provide insights into the regulation of flower formation in andromonoecious Taihangia rupestris. BMC Plant Biology, 2017, 17, 54.	1.6	29
4012	Transcriptome profiling of Elymus sibiricus, an important forage grass in Qinghai-Tibet plateau, reveals novel insights into candidate genes that potentially connected to seed shattering. BMC Plant Biology, 2017, 17, 78.	1.6	16
4013	Transcriptomic response of wolf spider, Pardosa pseudoannulata, to transgenic rice expressing Bacillus thuringiensis Cry1Ab protein. BMC Biotechnology, 2017, 17, 7.	1.7	11
4014	Identification of host cellular proteins that interact with the M protein of a highly pathogenic porcine reproductive and respiratory syndrome virus vaccine strain. Virology Journal, 2017, 14, 39.	1.4	6
4015	Identification of critical genes associated with lignin biosynthesis in radish (Raphanus sativus L.) by de novo transcriptome sequencing. Molecular Genetics and Genomics, 2017, 292, 1151-1163.	1.0	13
4016	Genome-wide comparative analysis of four Indian Drosophila species. Molecular Genetics and Genomics, 2017, 292, 1197-1208.	1.0	4
4017	Comparative transcriptome analysis of venom glands from Cotesia vestalis and Diadromus collaris, two endoparasitoids of the host Plutella xylostella. Scientific Reports, 2017, 7, 1298.	1.6	17
4018	Single-stranded RNA viruses infecting the invasive Argentine ant, Linepithema humile. Scientific Reports, 2017, 7, 3304.	1.6	39
4019	Transcriptome analysis explores genes related to shikonin biosynthesis in Lithospermeae plants and provides insights into Boraginalesâ€™ evolutionary history. Scientific Reports, 2017, 7, 4477.	1.6	26
4020	Profiling Diuraphis noxia (Hemiptera: Aphididae) Transcript Expression of the Biotypes SA1 and SAM Feeding on Various Triticum aestivum Varieties. Journal of Economic Entomology, 2017, 110, 692-701.	0.8	7
4021	De novo transcriptome analysis of the red seaweed Gracilaria chilensis and identification of linkers associated with phycobilisomes. Marine Genomics, 2017, 31, 17-19.	0.4	8
4022	Identification and characterization of genes on a single subgenome in the hexaploid wheat (<i>Triticum aestivum</i> L.) genotype â€˜Chinese Springâ€™. Genome, 2017, 60, 208-215.	0.9	4
4023	Investigating the mechanisms of glyphosate resistance in goosegrass (<i>Eleusine indica</i> (L.)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	44
4024	Proteomic and transcriptomic investigations on coldâ€responsive properties of the psychrophilic <scp>A</scp>ntarctic bacterium <scp><i>P</i></scp><i>sychrobacter</i> sp. PAMC 21119 at subzero temperatures. Environmental Microbiology, 2017, 19, 628-644.	1.8	58

#	ARTICLE	IF	CITATIONS
4025	Calmodulin as a downstream gene of octopamineâ€OAR Î±1 signalling mediates olfactory attraction in gregarious locusts. Insect Molecular Biology, 2017, 26, 1-12.	1.0	13
4027	Transcriptomic and proteomic analysis of yellow mosaic diseased soybean. Journal of Plant Biochemistry and Biotechnology, 2017, 26, 224-234.	0.9	17
4028	Transcriptomeâ€based phylogeny of endemic Lake Baikal amphipod species flock: fast speciation accompanied by frequent episodes of positive selection. Molecular Ecology, 2017, 26, 536-553.	2.0	55
4029	Drought stress-induced changes of microRNAs in diploid and autotetraploid Paulownia tomentosa. Genes and Genomics, 2017, 39, 77-86.	0.5	17
4030	Isolation and expression analysis of differentially expressed genes in stem tissue of the Greek lemon cv. Adamopoulou. Journal of Horticultural Science and Biotechnology, 2017, 92, 48-56.	0.9	3
4031	Expressed micro<scp>RNA</scp> associated with high rate of egg production in chicken ovarian follicles. Animal Genetics, 2017, 48, 205-216.	0.6	40
4032	The influence of dietary fatty acid and fasting on the hepatic lipid metabolism of barramundi (<i>Lates) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	14
4033	Novel seminal fluid proteins in the seed beetle <i>Callosobruchus maculatus</i> identified by a proteomic and transcriptomic approach. Insect Molecular Biology, 2017, 26, 58-73.	1.0	27
4034	Characterising genes associated with flowering time in carrot (<i>Daucus carota</i> L.) using transcriptome analysis. Plant Biology, 2017, 19, 286-297.	1.8	15
4035	Specific adjustments in grapevine leaf proteome discriminating resistant and susceptible grapevine genotypes to Plasmopara viticola. Journal of Proteomics, 2017, 152, 48-57.	1.2	41
4036	Adaptive genomic divergence under high gene flow between freshwater and brackishâ€water ecotypes of prickly sculpin (<i>Cottus asper</i>) revealed by Poolâ€Seq. Molecular Ecology, 2017, 26, 25-42.	2.0	58
4037	Comparative NGS Transcriptomics Unravels Molecular Components Associated with Mosaic Virus Infection in a Bioenergy Plant Species, Jatropha curcas L.. Bioenergy Research, 2017, 10, 129-145.	2.2	11
4038	Transcriptome analysis of mud crab (Scylla paramamosain) gills in response to Mud crab reovirus (MCRV). Fish and Shellfish Immunology, 2017, 60, 545-553.	1.6	39
4039	What distinguishes cyanobacteria able to revive after desiccation from those that cannot: the genome aspect. Environmental Microbiology, 2017, 19, 535-550.	1.8	49
4040	Whole genome sequence resource of Indian <i>Zaprionus indianus</i>. Molecular Ecology Resources, 2017, 17, 557-564.	2.2	12
4041	Microbeâ€"microbe interactions trigger Mn(II)-oxidizing gene expression. ISME Journal, 2017, 11, 67-77.	4.4	39
4042	Restriction site associated <scp>DNA</scp> (<scp>RAD</scp>) for de novo sequencing and marker discovery in sugarcane borer, <i>Diatraea saccharalis</i> Fab. (Lepidoptera: Crambidae). Molecular Ecology Resources, 2017, 17, 454-465.	2.2	5
4043	The defenceâ€associated transcriptome of hexaploid wheat displays homoeolog expression and induction bias. Plant Biotechnology Journal, 2017, 15, 533-543.	4.1	110

#	Article	IF	Citations
4044	New Insight Into Early Somatic Embryogenesis of Mangosteen (Garcinia mangostana) Through de Novo and Comparative Transcriptome Analyses. Tropical Plant Biology, 2017, 10, 30-44.	1.0	8
4045	Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. Environmental Microbiology, 2017, 19, 185-197.	1.8	32
4046	PceRBase: a database of plant competing endogenous RNA. Nucleic Acids Research, 2017, 45, D1009-D1014.	6.5	50
4047	Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity. Clinical and Experimental Allergy, 2017, 47, 577-592.	1.4	26
4048	Transcriptomic profile of Manila clam (Ruditapes philippinarum) haemocytes in response to Perkinsus olseni infection. Aquaculture, 2017, 467, 170-181.	1.7	15
4049	Adaptive evolution and segregating load contribute to the genomic landscape of divergence in two tree species connected by episodic gene flow. Molecular Ecology, 2017, 26, 59-76.	2.0	74
4050	MYB transcription factor gene involved in sex determination in <i>Asparagus officinalis</i>. Genes To Cells, 2017, 22, 115-123.	0.5	59
4051	Reâ€annotation, improved largeâ€scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga <i>Ectocarpus</i>. New Phytologist, 2017, 214, 219-232.	3.5	65
4052	Complete genome sequence of Stenotrophomonas sp. KACC 91585, an efficient bacterium for unsaturated fatty acid hydration. Journal of Biotechnology, 2017, 241, 108-111.	1.9	1
4053	Elucidation of the polyamine biosynthesis pathway during Brazilian pine (Araucaria angustifolia) seed development. Tree Physiology, 2017, 37, 116-130.	1.4	45
4054	Identification and characterization of the distinct expression profiles of candidate chemosensory membrane proteins in the antennal transcriptome of <i>Adelphocoris lineolatus</i> (Goeze). Insect Molecular Biology, 2017, 26, 74-91.	1.0	36
4055	SNP detection by parallel targeted sequencing from degraded DNA samples in Haliotis diversicolor. Conservation Genetics Resources, 2017, 9, 193-195.	0.4	1
4056	Transcriptome and physiological analysis of a lutein-producing alga Desmodesmus sp. reveals the molecular mechanisms for high lutein productivity. Algal Research, 2017, 21, 103-119.	2.4	19
4057	Estimation of long terminal repeat element content in the Helicoverpa zea genome from high-throughput sequencing of bacterial artificial chromosome pools. Genome, 2017, 60, 310-324.	0.9	7
4058	Transcriptome profiles of embryos before and after cleavage in Eriocheir sinensis: identification of developmental genes at the earliest stages. Chinese Journal of Oceanology and Limnology, 2017, 35, 770-781.	0.7	6
4059	Proteomic analysis of Toxocara canis excretory and secretory (TES) proteins. Molecular and Biochemical Parasitology, 2017, 211, 39-47.	0.5	31
4060	Computational analysis of the glutamate receptor gene family of <i>Arabidopsis thaliana</i>. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2454-2474.	2.0	13
4061	Genomic Scans across Three Eucalypts Suggest that Adaptation to Aridity is a Genome-Wide Phenomenon. Genome Biology and Evolution, 2017, 9, 253-265.	1.1	27

#	ARTICLE	IF	CITATIONS
4062	BdorOBP2 plays an indispensable role in the perception of methyl eugenol by mature males of Bactrocera dorsalis (Hendel). Scientific Reports, 2017, 7, 15894.	1.6	36
4063	Phytophthora megakarya and Phytophthora palmivora, Closely Related Causal Agents of Cacao Black Pod Rot, Underwent Increases in Genome Sizes and Gene Numbers by Different Mechanisms. Genome Biology and Evolution, 2017, 9, 536-557.	1.1	71
4064	Genome Expression Balance in a Triploid Trihybrid Vertebrate. Genome Biology and Evolution, 2017, 9, 968-980.	1.1	22
4065	Illumina-based de novo transcriptome sequencing and analysis of Chinese forest musk deer. Journal of Genetics, 2017, 96, 1033-1040.	0.4	11
4066	Proteome Analysis of Urticating Setae From Thaumetopoea pityocampa (Lepidoptera: Notodontidae). Journal of Medical Entomology, 2017, 54, 1560-1566.	0.9	7
4067	Whole-genome sequencing and SNV genotyping of â€˜Nebbioloâ€™ (Vitis vinifera L.) clones. Scientific Reports, 2017, 7, 17294.	1.6	72
4068	Environmental proteomics reveals taxonomic and functional changes in an enriched aquatic ecosystem. Ecosphere, 2017, 8, e01954.	1.0	12
4069	Transcriptomic profiling of Alternaria longipes invasion in tobacco reveals pathogenesis regulated by AlHK1, a group III histidine kinase. Scientific Reports, 2017, 7, 16083.	1.6	6
4070	Tree co-occurrence and transcriptomic response to drought. Nature Communications, 2017, 8, 1996.	5.8	21
4071	Into the Wild: Parallel Transcriptomics of the Tsetse-Wigglesworthia Mutualism within Kenyan Populations. Genome Biology and Evolution, 2017, 9, 2276-2291.	1.1	9
4072	Vitamin B₂(riboflavin) increases drought tolerance of<i>Agaricus bisporus</i>. Mycologia, 2017, 109, 860-873.	0.8	15
4073	Draft genome of the honey bee ectoparasitic mite, Tropilaelaps mercedesae, is shaped by the parasitic life history. GigaScience, 2017, 6, 1-17.	3.3	39
4074	Novel phosphate deficiency-responsive long non-coding RNAs in the legume model plant Medicago truncatula. Journal of Experimental Botany, 2017, 68, 5937-5948.	2.4	77
4075	Transcriptomic and metabolic responses of Calotropis procera to salt and drought stress. BMC Plant Biology, 2017, 17, 231.	1.6	30
4076	Transcriptome assembly in Suaeda aralocaspica to reveal the distinct temporal gene/miRNA alterations between the dimorphic seeds during germination. BMC Genomics, 2017, 18, 806.	1.2	11
4077	Differences in the genetic control of early egg development and reproduction between C. elegans and its parthenogenetic relative D. coronatus. EvoDevo, 2017, 8, 16.	1.3	4
4078	The Huperzia selago Shoot Tip Transcriptome Sheds New Light on the Evolution of Leaves. Genome Biology and Evolution, 2017, 9, 2444-2460.	1.1	22
4079	Gene expression atlas of pigeonpea and its application to gain insights into genes associated with pollen fertility implicated in seed formation. Journal of Experimental Botany, 2017, 68, 2037-2054.	2.4	55

#	ARTICLE	IF	CITATIONS
4080	Transcriptomic analysis, genic SSR development, and genetic diversity of proso millet (<i>Panicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	20
4081	Transcriptome profiles of Daphnia magna across to the different water chemistry of surface water of the Korean Demilitarized Zone. Toxicology and Environmental Health Sciences, 2017, 9, 188-198.	1.1	19
4082	Effect of HA330 resin-directed hemoadsorption on a porcine acute respiratory distress syndrome model. Annals of Intensive Care, 2017, 7, 84.	2.2	22
4083	An insight into structure and composition of the fig genome. Acta Horticulturae, 2017, , 69-74.	0.1	4
4084	Transcriptome Signatures of Selection, Drift, Introgression, and Gene Duplication in the Evolution of an Extremophile Endemic Plant. Genome Biology and Evolution, 2017, 9, 3478-3494.	1.1	4
4085	Complete genome sequence of lytic bacteriophage RG-2014 that infects the multidrug resistant bacterium Delftia tsuruhatensis ARB-1. Standards in Genomic Sciences, 2017, 12, 82.	1.5	5
4086	Orchidstra 2.0â€"A Transcriptomics Resource for the Orchid Family. Plant and Cell Physiology, 2017, 58, pcw220.	1.5	72
4087	Exploiting PubMed for Protein Molecular Function Prediction via NMF Based Multi-label Classification. , 2017, , .		4
4088	Molecular response of gall induction by aphid <i>Schlechtendalia chinensis</i> (Bell) attack on <i>Rhus chinensis</i> Mill. Journal of Plant Interactions, 2017, 12, 465-479.	1.0	22
4089	Genetic Environment of cry1 Genes Indicates Their Common Origin. Genome Biology and Evolution, 2017, 9, 2265-2275.	1.1	16
4091	In-silico analysis of marker genes from gene expression data of solanaceous plants responsible for various abiotic stresses. International Journal of Bioinformatics Research and Applications, 2017, 13, 329.	0.1	0
4092	Molecular Biomonitoring of Microbial Communities in Tannery Wastewater Treatment Plant for the Removal of Retanning Chemicals. , 0, , .		4
4093	Annotation transfer by homology among closely related genomes helps to identify protein function in Plasmodium species. International Journal of Bioinformatics Research and Applications, 2017, 13, 22.	0.1	0
4094	Recent expansion and adaptive evolution of the carcinoembryonic antigen family in bats of the Yangochiroptera subgroup. BMC Genomics, 2017, 18, 717.	1.2	14
4095	Sex and tissue specific gene expression patterns identified following de novo transcriptomic analysis of the Norway lobster, Nephrops norvegicus. BMC Genomics, 2017, 18, 622.	1.2	34
4096	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
4097	Identification and Expression Profiling of Chemosensory Genes in Dendrolimus punctatus Walker. Frontiers in Physiology, 2017, 8, 471.	1.3	37
4098	Identification and Characterization of Odorant Binding Proteins in the Forelegs of Adelphocoris lineolatus (Goeze). Frontiers in Physiology, 2017, 8, 735.	1.3	55

#	ARTICLE	IF	CITATIONS
4099	A Microarray Study of Carpet-Shell Clam (Ruditapes decussatus) Shows Common and Organ-Specific Growth-Related Gene Expression Differences in Gills and Digestive Gland. Frontiers in Physiology, 2017, 8, 943.	1.3	8
4100	Chemosensory Gene Families in Ectropis grisescens and Candidates for Detection of Type-II Sex Pheromones. Frontiers in Physiology, 2017, 8, 953.	1.3	40
4101	Transcriptome Analysis of Hamelia patens (Rubiaceae) Anthers Reveals Candidate Genes for Tapetum and Pollen Wall Development. Frontiers in Plant Science, 2017, 7, 1991.	1.7	8
4102	Cellular and Molecular Changes Associated with Onion Skin Formation Suggest Involvement of Programmed Cell Death. Frontiers in Plant Science, 2016, 07, 2031.	1.7	14
4103	Identification and Characterization of Segregation Distortion Loci on Cotton Chromosome 18. Frontiers in Plant Science, 2016, 7, 2037.	1.7	24
4104	Identification of Submergence-Responsive MicroRNAs and Their Targets Reveals Complex MiRNA-Mediated Regulatory Networks in Lotus (Nelumbo nucifera Gaertn). Frontiers in Plant Science, 2017, 8, 6.	1.7	25
4105	Transcriptome Analyses Reveal Candidate Genes Potentially Involved in Al Stress Response in Alfalfa. Frontiers in Plant Science, 2017, 8, 26.	1.7	27
4106	Overexpression of the Novel Arabidopsis Gene At5g02890 Alters Inflorescence Stem Wax Composition and Affects Phytohormone Homeostasis. Frontiers in Plant Science, 2017, 8, 68.	1.7	13
4107	Pistil Transcriptome Analysis to Disclose Genes and Gene Products Related to Aposporous Apomixis in Hypericum perforatum L.. Frontiers in Plant Science, 2017, 8, 79.	1.7	22
4108	RNA-Seq of Guar (Cyamopsis tetragonoloba, L. Taub.) Leaves: De novo Transcriptome Assembly, Functional Annotation and Development of Genomic Resources. Frontiers in Plant Science, 2017, 8, 91.	1.7	54
4109	Differential Gene Expression Analysis in Polygonum minus Leaf upon 24 h of Methyl Jasmonate Elicitation. Frontiers in Plant Science, 2017, 8, 109.	1.7	25
4110	De novo Transcriptome Assembly of Phomopsis liquidambari Provides Insights into Genes Associated with Different Lifestyles in Rice (Oryza sativa L.). Frontiers in Plant Science, 2017, 8, 121.	1.7	19
4111	RNA-seq Analysis of Cold and Drought Responsive Transcriptomes of Zea mays ssp. mexicana L.. Frontiers in Plant Science, 2017, 8, 136.	1.7	58
4112	Characterization of the Two-Speed Subgenomes of Fusarium graminearum Reveals the Fast-Speed Subgenome Specialized for Adaption and Infection. Frontiers in Plant Science, 2017, 8, 140.	1.7	56
4113	Phytophthora megakarya and P. palmivora, Causal Agents of Black Pod Rot, Induce Similar Plant Defense Responses Late during Infection of Susceptible Cacao Pods. Frontiers in Plant Science, 2017, 8, 169.	1.7	24
4114	Deep Sequencing of Suppression Subtractive Hybridisation Drought and Recovery Libraries of the Non-model Crop Trifolium repens L.. Frontiers in Plant Science, 2017, 8, 213.	1.7	6
4115	Global Transcriptome Analysis and Identification of Differentially Expressed Genes in Strawberry after Preharvest Application of Benzothiadiazole and Chitosan. Frontiers in Plant Science, 2017, 8, 235.	1.7	59
4116	Transcriptomic Analysis of Thermally Stressed Symbiodinium Reveals Differential Expression of Stress and Metabolism Genes. Frontiers in Plant Science, 2017, 8, 271.	1.7	94

#	Article	IF	Citations
4117	Transcriptome Analysis Reveals Candidate Genes Related to Color Fading of â€˜Red Bartlettâ€™ (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10	1.7	49
4118	Genome-Wide Identification, Characterization, and Expression Analysis of Small RNA Biogenesis Purveyors Reveal Their Role in Regulation of Biotic Stress Responses in Three Legume Crops. Frontiers in Plant Science, 2017, 8, 488.	1.7	15
4119	Modular Design of Picroside-II Biosynthesis Deciphered through NGS Transcriptomes and Metabolic Intermediates Analysis in Naturally Variant Chemotypes of a Medicinal Herb, Picrorhiza kurroa. Frontiers in Plant Science, 2017, 8, 564.	1.7	23
4120	Transcriptomic Comparison Reveals Candidate Genes for Triterpenoid Biosynthesis in Two Closely Related Ilex Species. Frontiers in Plant Science, 2017, 8, 634.	1.7	10
4121	Grapevine Grafting: Scion Transcript Profiling and Defense-Related Metabolites Induced by Rootstocks. Frontiers in Plant Science, 2017, 8, 654.	1.7	72
4122	Insights into the Mechanism of Proliferation on the Special Microbes Mediated by Phenolic Acids in the Radix pseudostellariae Rhizosphere under Continuous Monoculture Regimes. Frontiers in Plant Science, 2017, 8, 659.	1.7	29
4123	Time-Course Transcriptome Analysis of Compatible and Incompatible Pollen-Stigma Interactions in Brassica napus L.. Frontiers in Plant Science, 2017, 8, 682.	1.7	19
4124	Genome-Wide Analysis of Gene Expression Provides New Insights into Cold Responses in Thellungiella salsuginea. Frontiers in Plant Science, 2017, 8, 713.	1.7	59
4125	Comparative Analysis of Transcriptomes in Rhizophoraceae Provides Insights into the Origin and Adaptive Evolution of Mangrove Plants in Intertidal Environments. Frontiers in Plant Science, 2017, 8, 795.	1.7	39
4126	Molecular Link between Leaf Coloration and Gene Expression of Flavonoid and Carotenoid Biosynthesis in Camellia sinensis Cultivar â€˜Huangjinyaâ€™. Frontiers in Plant Science, 2017, 8, 803.	1.7	103
4127	Comparative Transcriptome Analysis Reveals Critical Function of Sucrose Metabolism Related-Enzymes in Starch Accumulation in the Storage Root of Sweet Potato. Frontiers in Plant Science, 2017, 8, 914.	1.7	52
4128	Identification, Characterization, and Functional Validation of Drought-responsive MicroRNAs in Subtropical Maize Inbreds. Frontiers in Plant Science, 2017, 8, 941.	1.7	74
4129	Generation, Annotation, and Analysis of a Large-Scale Expressed Sequence Tag Library from Arabidopsis pumila to Explore Salt-Responsive Genes. Frontiers in Plant Science, 2017, 8, 955.	1.7	16
4130	Transcriptome Analysis of Genes Associated with the Artemisinin Biosynthesis by Jasmonic Acid Treatment under the Light in Artemisia annua. Frontiers in Plant Science, 2017, 8, 971.	1.7	69
4131	Identification of Genes Associated with Lemon Floral Transition and Flower Development during Floral Inductive Water Deficits: A Hypothetical Model. Frontiers in Plant Science, 2017, 8, 1013.	1.7	32
4132	Comparative Transcriptome Analysis Reveal Candidate Genes Potentially Involved in Regulation of Primocane Apex Rooting in Raspberry (Rubus spp.). Frontiers in Plant Science, 2017, 8, 1036.	1.7	14
4133	Molecular Mechanisms behind the Physiological Resistance to Intense Transient Warming in an Iconic Marine Plant. Frontiers in Plant Science, 2017, 8, 1142.	1.7	59
4134	DNA Methylation Influences Chlorogenic Acid Biosynthesis in Lonicera japonica by Mediating LjbZIP8 to Regulate Phenylalanine Ammonia-Lyase 2 Expression. Frontiers in Plant Science, 2017, 8, 1178.	1.7	20

#	Article	IF	Citations
4135	Transcriptome Profiling Using Single-Molecule Direct RNA Sequencing Approach for In-depth Understanding of Genes in Secondary Metabolism Pathways of Camellia sinensis. Frontiers in Plant Science, 2017, 8, 1205.	1.7	74
4136	Transcriptome Analysis of Calcium- and Hormone-Related Gene Expressions during Different Stages of Peanut Pod Development. Frontiers in Plant Science, 2017, 8, 1241.	1.7	19
4137	Uncovering Male Fertility Transition Responsive miRNA in a Wheat Photo-Thermosensitive Genic Male Sterile Line by Deep Sequencing and Degradome Analysis. Frontiers in Plant Science, 2017, 8, 1370.	1.7	38
4138	Phenotypic and Comparative Transcriptome Analysis of Different Ploidy Plants in Dendrocalamus latiflorus Munro. Frontiers in Plant Science, 2017, 8, 1371.	1.7	14
4139	Transcriptome Profiling to Identify Genes Involved in Mesosulfuron-Methyl Resistance in Alopecurus aequalis. Frontiers in Plant Science, 2017, 8, 1391.	1.7	66
4140	Identification of Genes under Positive Selection Reveals Differences in Evolutionary Adaptation between Brown-Algal Species. Frontiers in Plant Science, 2017, 8, 1429.	1.7	17
4141	Molecular Resources from Transcriptomes in the Brassicaceae Family. Frontiers in Plant Science, 2017, 8, 1488.	1.7	11
4142	Identification and Expression Profile of CYPome in Perennial Ryegrass and Tall Fescue in Response to Temperature Stress. Frontiers in Plant Science, 2017, 8, 1519.	1.7	39
4143	De novo Assembly of the Camellia nitidissima Transcriptome Reveals Key Genes of Flower Pigment Biosynthesis. Frontiers in Plant Science, 2017, 8, 1545.	1.7	43
4144	Comparative Genomics of Ralstonia solanacearum Identifies Candidate Genes Associated with Cool Virulence. Frontiers in Plant Science, 2017, 8, 1565.	1.7	25
4145	Identification and Functional Annotation of Genes Differentially Expressed in the Reproductive Tissues of the Olive Tree (Olea europaea L.) through the Generation of Subtractive Libraries. Frontiers in Plant Science, 2017, 8, 1576.	1.7	5
4146	Transcriptome and Differential Expression Profiling Analysis of the Mechanism of Ca2+ Regulation in Peanut (Arachis hypogaea) Pod Development. Frontiers in Plant Science, 2017, 8, 1609.	1.7	30
4147	De Novo Assembly of Transcriptome and Development of Novel EST-SSR Markers in Rhododendron rex LÃ©vl. through Illumina Sequencing. Frontiers in Plant Science, 2017, 8, 1664.	1.7	66
4148	Strigolactones Improve Plant Growth, Photosynthesis, and Alleviate Oxidative Stress under Salinity in Rapeseed (Brassica napus L.) by Regulating Gene Expression. Frontiers in Plant Science, 2017, 8, 1671.	1.7	134
4149	Transcriptomic Analysis of Seed Coats in Yellow-Seeded Brassica napus Reveals Novel Genes That Influence Proanthocyanidin Biosynthesis. Frontiers in Plant Science, 2017, 8, 1674.	1.7	55
4150	An RNA Sequencing Transcriptome Analysis of Grasspea (Lathyrus sativus L.) and Development of SSR and KASP Markers. Frontiers in Plant Science, 2017, 8, 1873.	1.7	30
4151	Transcriptome and Metabolome Analyses Provide Insights into the Occurrence of Peel Roughing Disorder on Satsuma Mandarin (Citrus unshiu Marc.) Fruit. Frontiers in Plant Science, 2017, 8, 1907.	1.7	10
4152	Arbuscular Mycorrhizal Fungus Enhances Lateral Root Formation in Poncirus trifoliata (L.) as Revealed by RNA-Seq Analysis. Frontiers in Plant Science, 2017, 8, 2039.	1.7	36

#	Article	IF	Citations
4153	Transcriptome Analyses to Reveal Genes Involved in Terpene Biosynthesis in Resin Producing Pine Tree Pinus kesiya var. langbianensis. BioResources, 2017, 13, .	0.5	3
4154	Isoform Sequencing Provides a More Comprehensive View of the Panax ginseng Transcriptome. Genes, 2017, 8, 228.	1.0	42
4155	Estrogen exposure overrides the masculinizing effect of elevated temperature by a downregulation of the key genes implicated in sexual differentiation in a fish with mixed genetic and environmental sex determination. BMC Genomics, 2017, 18, 973.	1.2	33
4156	Genomic signature of highland adaptation in fish: a case study in Tibetan Schizothoracinae species. BMC Genomics, 2017, 18, 948.	1.2	26
4157	Gut transcriptome analysis on females of Ornithodoros mimon (Acari: Argasidae) and phylogenetic inference of ticks. Brazilian Journal of Veterinary Parasitology, 2017, 26, 185-204.	0.2	13
4158	Comparative Transcriptomic Analysis Reveals Candidate Genes and Pathways Involved in Larval Settlement of the Barnacle Megabalanus volcano. International Journal of Molecular Sciences, 2017, 18, 2253.	1.8	11
4159	Using Next-Generation Sequencing to Detect Differential Expression Genes in Bradysia odoriphaga after Exposure to Insecticides. International Journal of Molecular Sciences, 2017, 18, 2445.	1.8	12
4160	RNAâ€seq: Applications and Best Practices. , 0, , .		17
4161	De novo metatranscriptome assembly and coral gene expression profile of Montipora capitata with growth anomaly. BMC Genomics, 2017, 18, 710.	1.2	22
4162	Chemosensory genes in the antennal transcriptome of two syrphid species, Episyrphus balteatus and Eupeodes corollae (Diptera: Syrphidae). BMC Genomics, 2017, 18, 586.	1.2	64
4163	RNA Sequencing and Coexpression Analysis Reveal Key Genes Involved in Î±-Linolenic Acid Biosynthesis in Perilla frutescens Seed. International Journal of Molecular Sciences, 2017, 18, 2433.	1.8	27
4164	A Transcriptomic Survey of Ion Channel-Based Conotoxins in the Chinese Tubular Cone Snail (Conus) Tj ETQq1 1 0.784314 rgBT /Overlo	2.2	5
4165	Using Network Extracted Ontologies to Identify Novel Genes with Roles in Appressorium Development in the Rice Blast Fungus Magnaporthe oryzae. Microorganisms, 2017, 5, 3.	1.6	12
4166	Genome-Wide Identification and Evolutionary Analysis of Sarcocystis neurona Protein Kinases. Pathogens, 2017, 6, 12.	1.2	4
4167	A Proteomic Approach to Investigate the Drought Response in the Orphan Crop Eragrostis tef. Proteomes, 2017, 5, 32.	1.7	18
4168	Patterns of Gene Expression in Western Corn Rootworm (Diabrotica virgifera virgifera) Neonates, Challenged with Cry34Ab1, Cry35Ab1 and Cry34/35Ab1, Based on Next-Generation Sequencing. Toxins, 2017, 9, 124.	1.5	14
4169	Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis in Lepidoptera. BMC Genomics, 2017, 18, 931.	1.2	18
4170	Diatom flagellar genes and their expression during sexual reproduction in Leptocylindrus danicus. BMC Genomics, 2017, 18, 813.	1.2	12

#	Article	IF	Citations
4171	Expression of proteins in intestinal middle villus epithelial cells of weanling piglets. Frontiers in Bioscience - Landmark, 2017, 22, 539-557.	3.0	6
4172	Weighted Gene Co-expression Network Analysis of the Dioscin Rich Medicinal Plant Dioscorea nipponica. Frontiers in Plant Science, 2017, 8, 789.	1.7	21
4173	Generation and Characterisation of a Reference Transcriptome for Phalaris (Phalaris aquatica L.). Agronomy, 2017, 7, 14.	1.3	8
4174	Characterisation of Faba Bean (Vicia faba L.) Transcriptome Using RNA-Seq: Sequencing, De Novo Assembly, Annotation, and Expression Analysis. Agronomy, 2017, 7, 53.	1.3	10
4175	Transcriptome Sequencing and Comparative Analysis of Piptoporus betulinus in Response to Birch Sawdust Induction. Forests, 2017, 8, 374.	0.9	4
4176	Identification and Characterization of TALE Homeobox Genes in the Endangered Fern Vandenboschia speciosa. Genes, 2017, 8, 275.	1.0	12
4177	Integrative RNA- and miRNA-Profile Analysis Reveals a Likely Role of BR and Auxin Signaling in Branch Angle Regulation of B. napus. International Journal of Molecular Sciences, 2017, 18, 887.	1.8	23
4178	Comparative Proteomic Profiling Reveals Molecular Characteristics Associated with Oogenesis and Oocyte Maturation during Ovarian Development of Bactrocera dorsalis (Hendel). International Journal of Molecular Sciences, 2017, 18, 1379.	1.8	18
4179	Different Phenotypes of Mature Biofilm in Flavobacterium psychrophilum Share a Potential for Virulence That Differs from Planktonic State. Frontiers in Cellular and Infection Microbiology, 2017, 7, 76.	1.8	33
4180	Genomics and Comparative Genomic Analyses Provide Insight into the Taxonomy and Pathogenic Potential of Novel Emmonsia Pathogens. Frontiers in Cellular and Infection Microbiology, 2017, 7, 105.	1.8	6
4181	Gene Duplication Analysis Reveals No Ancient Whole Genome Duplication but Extensive Small-Scale Duplications during Genome Evolution and Adaptation of Schistosoma mansoni. Frontiers in Cellular and Infection Microbiology, 2017, 7, 412.	1.8	9
4182	Comparative Pan-Genome Analysis of Piscirickettsia salmonis Reveals Genomic Divergences within Genogroups. Frontiers in Cellular and Infection Microbiology, 2017, 7, 459.	1.8	52
4183	Transcriptomes of the Premature and Mature Ovaries of an Ascidian, Ciona intestinalis. Frontiers in Endocrinology, 2017, 8, 88.	1.5	9
4184	Comparing the Expression of Olfaction-Related Genes in Gypsy Moth (Lymantria dispar) Adult Females and Larvae from One Flightless and Two Flight-Capable Populations. Frontiers in Ecology and Evolution, 2017, 5, .	1.1	10
4185	Draft of Zucchini (Cucurbita pepo L.) Proteome: A Resource for Genetic and Genomic Studies. Frontiers in Genetics, 2017, 8, 181.	1.1	18
4186	Single-Molecule Long-Read Transcriptome Dataset of Halophyte Halogeton glomeratus. Frontiers in Genetics, 2017, 8, 197.	1.1	6
4187	Genomic Characterization of Dairy Associated Leuconostoc Species and Diversity of Leuconostocs in Undefined Mixed Mesophilic Starter Cultures. Frontiers in Microbiology, 2017, 8, 132.	1.5	43
4188	The Histidine Decarboxylase Gene Cluster of Lactobacillus parabuchneri Was Gained by Horizontal Gene Transfer and Is Mobile within the Species. Frontiers in Microbiology, 2017, 8, 218.	1.5	40

#	ARTICLE	IF	CITATIONS
4189	Association Mapping Reveals Genetic Loci Associated with Important Agronomic Traits in Lentinula edodes, Shiitake Mushroom. Frontiers in Microbiology, 2017, 8, 237.	1.5	13
4190	New Insights into the Anti-pathogenic Potential of Lactococcus garvieae against Staphylococcus aureus Based on RNA Sequencing Profiling. Frontiers in Microbiology, 2017, 08, 359.	1.5	10
4191	Responses of the Housefly, Musca domestica, to the Hytrosavirus Replication: Impacts on Host's Vitellogenesis and Immunity. Frontiers in Microbiology, 2017, 8, 583.	1.5	21
4192	Comparative Genomics and Transcriptional Analysis of Flavobacterium columnare Strain ATCC 49512. Frontiers in Microbiology, 2017, 8, 588.	1.5	46
4193	Morphological and Transcriptomic Analysis Reveals the Osmoadaptive Response of Endophytic Fungus Aspergillus montevidensis ZYD4 to High Salt Stress. Frontiers in Microbiology, 2017, 8, 1789.	1.5	33
4194	Arbuscular Mycorrhizal Fungal Community Composition in Carludovica palmata, Costus scaber and Euterpe precatoria from Weathered Oil Ponds in the Ecuadorian Amazon. Frontiers in Microbiology, 2017, 8, 2134.	1.5	22
4195	Secretome Characterization and Correlation Analysis Reveal Putative Pathogenicity Mechanisms and Identify Candidate Avirulence Genes in the Wheat Stripe Rust Fungus Puccinia striiformis f. sp. tritici. Frontiers in Microbiology, 2017, 8, 2394.	1.5	29
4196	Genome Characterization of the First Mimiviruses of Lineage C Isolated in Brazil. Frontiers in Microbiology, 2017, 8, 2562.	1.5	16
4197	Gene Expression Profiling in the Injured Spinal Cord of Trachemys scripta elegans: An Amniote with Self-Repair Capabilities. Frontiers in Molecular Neuroscience, 2017, 10, 17.	1.4	5
4198	The Draft Genome and Transcriptome of the Atlantic Horseshoe Crab,<i>Limulus polyphemus</i>. International Journal of Genomics, 2017, 2017, 1-14.	0.8	19
4199	Integrating miRNA and mRNA Expression Profiling Uncovers miRNAs Underlying Fat Deposition in Sheep. BioMed Research International, 2017, 2017, 1-11.	0.9	38
4200	Transcriptome Analysis of Two Different Developmental Stages of <i>Paeonia lactiflora</i> Seeds. International Journal of Genomics, 2017, 2017, 1-10.	0.8	8
4201	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. Advances in Genetics, 2017, 100, 73-140.	0.8	17
4202	Enriching Genomic Resources and Marker Development from Transcript Sequences of<i>Jatropha curcas</i>for Microgravity Studies. International Journal of Genomics, 2017, 2017, 1-14.	0.8	7
4203	The genome of the Antarctic-endemic copepod, Tigriopus kingsejongensis. GigaScience, 2017, 6, 1-9.	3.3	12
4204	Identification of differentially expressed genes in flower, leaf and bulb scale of Lilium oriental hybrid â€˜Sorbonneâ€™ and putative control network for scent genes. BMC Genomics, 2017, 18, 899.	1.2	18
4205	Transcriptomic response of the Antarctic pteropod Limacina helicina antarctica to ocean acidification. BMC Genomics, 2017, 18, 812.	1.2	43
4206	Down-regulation of aminopeptidase N and ABC transporter subfamily G transcripts in Cry1Ab and Cry1Ac resistant Asian corn borer, <i>Ostrinia furnacalis</i> (Lepidoptera: Crambidae). International Journal of Biological Sciences, 2017, 13, 835-851.	2.6	43

#	Article	IF	Citations
4207	Distinct herpesvirus resistances and immune responses of three gynogenetic clones of gibel carp revealed by comprehensive transcriptomes. BMC Genomics, 2017, 18, 561.	1.2	56
4208	Use of genotyping-by-sequencing to determine the genetic structure in the medicinal plant chamomile, and to identify flowering time and alpha-bisabolol associated SNP-loci by genome-wide association mapping. BMC Genomics, 2017, 18, 599.	1.2	29
4209	Transcriptome profiling of antiviral immune and dietary fatty acid dependent responses of Atlantic salmon macrophage-like cells. BMC Genomics, 2017, 18, 706.	1.2	62
4210	Dehydration induced transcriptomic responses in two Tibetan hulless barley (Hordeum vulgare var.) Tj ETQq1 1 0.784314 rgBT /Overloc	1.2	25
4211	Wound healing, calcium signaling, and other novel pathways are associated with the formation of butterfly eyespots. BMC Genomics, 2017, 18, 788.	1.2	45
4212	Structure of Pigment Metabolic Pathways and Their Contributions to White Tepal Color Formation of Chinese Narcissus tazetta var. chinensis cv Jinzhanyintai. International Journal of Molecular Sciences, 2017, 18, 1923.	1.8	17
4213	Whole Transcriptomic Analysis Provides Insights into Molecular Mechanisms for Toxin Biosynthesis in a Toxic Dinoflagellate Alexandrium catenella (ACHK-T). Toxins, 2017, 9, 213.	1.5	33
4214	De novo transcriptome analysis shows differential expression of genes in salivary glands of edible birdâ€™s nest producing swiftlets. BMC Genomics, 2017, 18, 504.	1.2	9
4215	Evaluation of a Bead-Free Coimmunoprecipitation Technique for Identification of Virusâ€"Host Protein Interactions Using High-Resolution Mass Spectrometry. Journal of Biomolecular Techniques, 2017, 28, 111-121.	0.8	4
4216	Comparative Transcriptome Analysis Reveals Adaptive Evolution of Notopterygium incisum and Notopterygium franchetii, Two High-Alpine Herbal Species Endemic to China. Molecules, 2017, 22, 1158.	1.7	21
4217	Transcriptome Analysis of Taxillusi chinensis (DC.) Danser Seeds in Response to Water Loss. PLoS ONE, 2017, 12, e0169177.	1.1	31
4218	Transcriptome Analysis of Leaves, Flowers and Fruits Perisperm of Coffea arabica L. Reveals the Differential Expression of Genes Involved in Raffinose Biosynthesis. PLoS ONE, 2017, 12, e0169595.	1.1	35
4219	Uncovering stem cell differentiation factors for salivary gland regeneration by quantitative analysis of differential proteomes. PLoS ONE, 2017, 12, e0169677.	1.1	7
4220	First Insights into the Subterranean Crustacean Bathynellacea Transcriptome: Transcriptionally Reduced Opsin Repertoire and Evidence of Conserved Homeostasis Regulatory Mechanisms. PLoS ONE, 2017, 12, e0170424.	1.1	11
4221	A novel hypothesis-unbiased method for Gene Ontology enrichment based on transcriptome data. PLoS ONE, 2017, 12, e0170486.	1.1	48
4222	Transcriptome Analysis and Differential Gene Expression on the Testis of Orange Mud Crab, Scylla olivacea, during Sexual Maturation. PLoS ONE, 2017, 12, e0171095.	1.1	58
4223	Transcriptomic analysis of Crassostrea sikamea Ã— Crassostrea angulata hybrids in response to low salinity stress. PLoS ONE, 2017, 12, e0171483.	1.1	40
4224	De novo assembly of the sea trout (Salmo trutta m. trutta) skin transcriptome to identify putative genes involved in the immune response and epidermal mucus secretion. PLoS ONE, 2017, 12, e0172282.	1.1	34

#	Article	IF	Citations
4225	Genome-wide analysis of brain and gonad transcripts reveals changes of key sex reversal-related genes expression and signaling pathways in three stages of Monopterus albus. PLoS ONE, 2017, 12, e0173974.	1.1	40
4226	Identification of candidate chemosensory genes by transcriptome analysis in Loxostege sticticalis Linnaeus. PLoS ONE, 2017, 12, e0174036.	1.1	20
4227	Comparative transcriptomics of Entelegyne spiders (Araneae, Entelegynae), with emphasis on molecular evolution of orphan genes. PLoS ONE, 2017, 12, e0174102.	1.1	8
4228	Differential transcriptome analysis supports Rhodnius montenegrensis and Rhodnius robustus (Hemiptera, Reduviidae, Triatominae) as distinct species. PLoS ONE, 2017, 12, e0174997.	1.1	15
4229	Bruchid egg induced transcript dynamics in developing seeds of black gram (Vigna mungo). PLoS ONE, 2017, 12, e0176337.	1.1	6
4230	De novo assembly and comparative transcriptome analysis of the foot from Chinese green mussel (Perna viridis) in response to cadmium stimulation. PLoS ONE, 2017, 12, e0176677.	1.1	18
4231	Biomolecular changes that occur in the antennal gland of the giant freshwater prawn (Machrobrachium rosenbergii). PLoS ONE, 2017, 12, e0177064.	1.1	13
4232	The Rhizoctonia solani AG1-IB (isolate 7/3/14) transcriptome during interaction with the host plant lettuce (Lactuca sativa L.). PLoS ONE, 2017, 12, e0177278.	1.1	28
4233	Transcriptome profiling of ontogeny in the acridid grasshopper Chorthippus biguttulus. PLoS ONE, 2017, 12, e0177367.	1.1	4
4234	Transcriptome profiling revealed novel transcriptional regulators in maize responses to Ostrinia furnacalis and jasmonic acid. PLoS ONE, 2017, 12, e0177739.	1.1	16
4235	De novo transcriptome of the mayfly Cloeon viridulum and transcriptional signatures of Prometabola. PLoS ONE, 2017, 12, e0179083.	1.1	13
4236	The mitochondrial genome of the terrestrial carnivorous plant Utricularia reniformis (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. PLoS ONE, 2017, 12, e0180484.	1.1	24
4237	Effects of dietary lipids on the hepatopancreas transcriptome of Chinese mitten crab (Eriocheir) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26	1.1	25
4238	A comparative transcriptomic analysis reveals the core genetic components of salt and osmotic stress responses in Braya humilis. PLoS ONE, 2017, 12, e0183778.	1.1	2
4239	The transcriptional landscape of Rhizoctonia solani AG1-IA during infection of soybean as defined by RNA-seq. PLoS ONE, 2017, 12, e0184095.	1.1	16
4240	Development of hop transcriptome to support research into host-viroid interactions. PLoS ONE, 2017, 12, e0184528.	1.1	26
4241	Transcriptome analysis of sex-related genes in the blood clam Tegillarca granosa. PLoS ONE, 2017, 12, e0184584.	1.1	16
4242	Gene expression analysis of primordial shoot explants collected from mature white spruce (Picea) Tj ETQq1 1 0.784314 rgBT /Overloc 12, e0185015.	1.1	24

#	Article	IF	Citations
4243	The mitochondrial genome of the plant-pathogenic fungus Stemphylium lycopersici uncovers a dynamic structure due to repetitive and mobile elements. PLoS ONE, 2017, 12, e0185545.	1.1	52
4244	Integrating transcriptomics and metabolomics to characterize the regulation of EPA biosynthesis in response to cold stress in seaweed Bangia fuscopurpurea. PLoS ONE, 2017, 12, e0186986.	1.1	26
4245	Comparison of the transcriptomic analysis between two Chinese white pear (Pyrus bretschneideri) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	34
4246	De novo sequencing and analysis of the transcriptome during the browning of fresh-cut Luffa cylindrica 'Fusi-3' fruits. PLoS ONE, 2017, 12, e0187117.	1.1	19
4247	Identification of Viscum album L. miRNAs and prediction of their medicinal values. PLoS ONE, 2017, 12, e0187776.	1.1	18
4248	Positive selection and comparative molecular evolution of reproductive proteins from New Zealand tree weta (Orthoptera, Hemideina). PLoS ONE, 2017, 12, e0188147.	1.1	4
4249	Genome-wide recombination rate variation in a recombination map of cotton. PLoS ONE, 2017, 12, e0188682.	1.1	26
4250	Transcriptional profiling of sugarcane leaves and roots under progressive osmotic stress reveals a regulated coordination of gene expression in a spatiotemporal manner. PLoS ONE, 2017, 12, e0189271.	1.1	28
4251	Isolation and characterization of a N4-like lytic bacteriophage infecting Vibrio splendidus, a pathogen of fish and bivalves. PLoS ONE, 2017, 12, e0190083.	1.1	33
4252	Activated entomopathogenic nematode infective juveniles release lethal venom proteins. PLoS Pathogens, 2017, 13, e1006302.	2.1	95
4253	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. PLoS Biology, 2017, 15, e2003790.	2.6	202
4254	Transcriptomic analyses on muscle tissues of Litopenaeus vannamei provide the first profile insight into the response to low temperature stress. PLoS ONE, 2017, 12, e0178604.	1.1	39
4255	Investigation of the Fusarium virguliforme Transcriptomes Induced during Infection of Soybean Roots Suggests that Enzymes with Hydrolytic Activities Could Play a Major Role in Root Necrosis. PLoS ONE, 2017, 12, e0169963.	1.1	11
4256	Transcriptome Analysis Reveals Comprehensive Insights into the Early Immune Response of Large Yellow Croaker (Larimichthys crocea) Induced by Trivalent Bacterial Vaccine. PLoS ONE, 2017, 12, e0170958.	1.1	26
4257	Development of EST-SSR markers in flowering Chinese cabbage (Brassica campestris L. ssp. chinensis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	36
4258	Parallel evolution of the POQR prolyl oligo peptidase gene conferring plant quantitative disease resistance. PLoS Genetics, 2017, 13, e1007143.	1.5	38
4259	The Biomphalaria glabrata DNA methylation machinery displays spatial tissue expression, is differentially active in distinct snail populations and is modulated by interactions with Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2017, 11, e0005246.	1.3	39
4260	Molecular characterization of tsetseâ€™s proboscis and its response to Trypanosoma congolense infection. PLoS Neglected Tropical Diseases, 2017, 11, e0006057.	1.3	8

#	Article	IF	Citations
4261	Analysis of the interactome of Schistosoma mansoni histone deacetylase 8. PLoS Neglected Tropical Diseases, 2017, 11, e0006089.	1.3	8
4262	A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. BMC Plant Biology, 2017, 17, 232.	1.6	21
4263	Comparative analysis of lincRNA in insect species. BMC Evolutionary Biology, 2017, 17, 155.	3.2	22
4264	Evidence of high-altitude adaptation in the glyptosternoid fish, Creteuchiloglanis macropterus from the Nujiang River obtained through transcriptome analysis. BMC Evolutionary Biology, 2017, 17, 229.	3.2	33
4265	De novo transcriptomic analysis of cowpea (Vigna unguiculata L. Walp.) for genic SSR marker development. BMC Genetics, 2017, 18, 65.	2.7	28
4266	Genetic variation in populations of the earthworm, Lumbricus rubellus, across contaminated mine sites. BMC Genetics, 2017, 18, 97.	2.7	29
4267	Identification and integrated analysis of differentially expressed lncRNAs and circRNAs reveal the potential ceRNA networks during PDLSC osteogenic differentiation. BMC Genetics, 2017, 18, 100.	2.7	137
4268	RNA-Seq analysis of resistant and susceptible sub-tropical maize lines reveals a role for kauralexins in resistance to grey leaf spot disease, caused by Cercospora zeina. BMC Plant Biology, 2017, 17, 197.	1.6	43
4269	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. BMC Biology, 2017, 15, 86.	1.7	114
4270	Malaria vectors in the Democratic Republic of the Congo: the mechanisms that confer insecticide resistance in Anopheles gambiae and Anopheles funestus. Malaria Journal, 2017, 16, 448.	0.8	36
4271	Abundant expression of somatic transposon-derived piRNAs throughout Tribolium castaneum embryogenesis. Genome Biology, 2017, 18, 184.	3.8	19
4272	Time-resolved transcriptome analysis and lipid pathway reconstruction of the oleaginous green microalga Monoraphidium neglectum reveal a model for triacylglycerol and lipid hyperaccumulation. Biotechnology for Biofuels, 2017, 10, 197.	6.2	35
4273	Transcriptomic characterization of Caecomyces churrovis: a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus. Biotechnology for Biofuels, 2017, 10, 305.	6.2	70
4274	Sialotranscriptomics of Rhipicephalus zambeziensis reveals intricate expression profiles of secretory proteins and suggests tight temporal transcriptional regulation during blood-feeding. Parasites and Vectors, 2017, 10, 384.	1.0	28
4275	Tsetse fly (Glossina pallidipes) midgut responses to Trypanosoma brucei challenge. Parasites and Vectors, 2017, 10, 614.	1.0	8
4276	High-throughput SuperSAGE for gene expression analysis of Nicotiana tabacumâ€"Rhizoctonia solani interaction. BMC Research Notes, 2017, 10, 603.	0.6	2
4277	Huanglongbing impairs the rhizosphere-to-rhizoplane enrichment process of the citrus root-associated microbiome. Microbiome, 2017, 5, 97.	4.9	177
4278	Comparative Transcriptome and DNA methylation analyses of the molecular mechanisms underlying skin color variations in Crucian carp (Carassius carassius L.). BMC Genetics, 2017, 18, 95.	2.7	43

#	ARTICLE	IF	CITATIONS
4279	Carbohydrate-active enzymes in Trichoderma harzianum: a bioinformatic analysis bioprospecting for key enzymes for the biofuels industry. BMC Genomics, 2017, 18, 779.	1.2	48
4280	Genome of Russian wheat aphid an economically important cereal aphid. Standards in Genomic Sciences, 2017, 12, 90.	1.5	25
4281	Genome overview of eight Candida boidinii strains isolated from human activities and wild environments. Standards in Genomic Sciences, 2017, 12, 70.	1.5	13
4282	The genomic study of an environmental isolate of Scedosporium apiospermum shows its metabolic potential to degrade hydrocarbons. Standards in Genomic Sciences, 2017, 12, 71.	1.5	25
4283	Identification of candidate genes involved in isoquinoline alkaloids biosynthesis in Dactylicapnos scandens by transcriptome analysis. Scientific Reports, 2017, 7, 9119.	1.6	26
4284	Whole-genome assembly of Babesia ovata and comparative genomics between closely related pathogens. BMC Genomics, 2017, 18, 832.	1.2	30
4285	Whole Genome Sequencing and Analysis of Godawee, a Salt Tolerant Indica Rice Variety. Rice Research Open Access, 2017, 05, .	0.4	10
4286	The Grass Carp Genome Database (GCGD): an online platform for genome features and annotations. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	14
4287	GOstruct 2.0. , 2017, , .		8
4288	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
4289	De novo transcriptome assembly and SSR markerdevelopment in apricot (Prunus armeniaca). Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2017, 41, 305-315.	0.8	6
4290	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
4291	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
4292	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
4293	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
4294	Genome-wide characterization of non-reference transposable element insertion polymorphisms reveals genetic diversity in tropical and temperate maize. BMC Genomics, 2017, 18, 702.	1.2	18
4295	High Quality Unigenes and Microsatellite Markers from Tissue Specific Transcriptome and Development of a Database in Clusterbean (Cyamopsis tetragonoloba, L. Taub). Genes, 2017, 8, 313.	1.0	33
4296	Transcriptomic profiling of genes in matured dimorphic seeds of euhalophyte Suaeda salsa. BMC Genomics, 2017, 18, 727.	1.2	27

#	ARTICLE	IF	CITATIONS
4297	Evidence for a Saponin Biosynthesis Pathway in the Body Wall of the Commercially Significant Sea Cucumber Holothuria scabra. Marine Drugs, 2017, 15, 349.	2.2	26
4298	The transcriptome of the developing grain: a resource for understanding seed development and the molecular control of the functional and nutritional properties of wheat. BMC Genomics, 2017, 18, 766.	1.2	46
4299	Analysis of the genome of the New Zealand giant collembolan (Holacanthella duospinosa) sheds light on hexapod evolution. BMC Genomics, 2017, 18, 795.	1.2	28
4300	Sequencing flow-sorted short arm of Haynaldia villosa chromosome 4V provides insights into its molecular structure and virtual gene order. BMC Genomics, 2017, 18, 791.	1.2	10
4301	Surviving a Genome Collision: Genomic Signatures of Allopolyploidization in the Recent Crop Species <i>Brassica napus</i>. Plant Genome, 2017, 10, plantgenome2017.02.0013.	1.6	86
4302	Transcriptome sequencing and analysis of zinc-uptake-related genes in Trichophyton mentagrophytes. BMC Genomics, 2017, 18, 888.	1.2	7
4303	Codon optimization underpins generalist parasitism in fungi. ELife, 2017, 6, .	2.8	36
4304	De Novo Assembly and Analysis of the Testes Transcriptome from the Menhaden, Bervoortia tyrannus. Fisheries and Aquaculture Journal, 2017, 08, .	0.2	0
4305	Transcriptome-wide analysis of immune-responsive microRNAs against poly (I:C) challenge in <i>Branchiostoma belcheri</i> by deep sequencing and bioinformatics. Oncotarget, 2017, 8, 73590-73602.	0.8	11
4306	Identification of putative CONSTANS-like genes from the de novo assembled transcriptome of leek. Biologia Plantarum, 2018, 62, 269-276.	1.9	4
4307	Enrichment of genomic resources and identification of simple sequence repeats from medicinally important Clausena excavata. 3 Biotech, 2018, 8, 133.	1.1	6
4308	Parent-of-Origin-Dependent Gene Expression in Male and Female Schistosome Parasites. Genome Biology and Evolution, 2018, 10, 840-856.	1.1	2
4309	Transcriptomic analysis of boron hyperaccumulation mechanisms in Puccinellia distans. Chemosphere, 2018, 199, 390-401.	4.2	17
4310	Mating-Induced Differential Peptidomics of Neuropeptides and Protein Hormones in <i>Agrotis ipsilon</i> Moths. Journal of Proteome Research, 2018, 17, 1397-1414.	1.8	13
4311	The Use of RNA Sequencing and Correlation Network Analysis to Study Potential Regulators of Crabapple Leaf Color Transformation. Plant and Cell Physiology, 2018, 59, 1027-1042.	1.5	28
4312	Deciphering droughtâ€induced metabolic responses and regulation in developing maize kernels. Plant Biotechnology Journal, 2018, 16, 1616-1628.	4.1	70
4313	Characterizing Physiological and Proteomic Analysis of the Action of H2S to Mitigate Drought Stress in Young Seedling of Wheat. Plant Molecular Biology Reporter, 2018, 36, 45-57.	1.0	29
4314	Characterization of lipid metabolism genes and the influence of fatty acid supplementation in the hepatic lipid metabolism of dusky grouper (Epinephelus marginatus). Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2018, 219-220, 1-9.	0.8	13

#	Article	IF	Citations
4315	Transcription profile analysis of Lycopersicum esculentum leaves, unravels volatile emissions and gene expression under salinity stress. Plant Physiology and Biochemistry, 2018, 126, 11-21.	2.8	20
4316	Vesicle-based secretion in schistosomes: Analysis of protein and microRNA (miRNA) content of exosome-like vesicles derived from Schistosoma mansoni. Scientific Reports, 2018, 8, 3286.	1.6	122
4317	De Novo Transcriptome Assembly of Isatis indigotica 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
4318	Morphological and transcriptomic analyses reveal three discrete primary stages of postembryonic development in the common fire salamander, <i>Salamandra salamandra</i>. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 96-108.	0.6	10
4319	Genome-wide identification and analysis of elongase of very long chain fatty acid genes in the silkworm, <i>Bombyx mori</i>. Genome, 2018, 61, 167-176.	0.9	14
4320	Use of a draft genome of coffee (C<i>offea arabica</i>) to identify <scp>SNP</scp>s associated with caffeine content. Plant Biotechnology Journal, 2018, 16, 1756-1766.	4.1	48
4321	Bivalve transcriptomics reveal pathogen sequences and a powerful immune response of the Mediterranean mussel (Mytilus galloprovincialis). Marine Biology, 2018, 165, 1.	0.7	22
4322	De novo transcriptomics reveal distinct phototransduction signaling components in the retina and skin of a color-changing vertebrate, the hogfish (Lachnolaimus maximus). Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology, 2018, 204, 475-485.	0.7	7
4323	Characterization of Spleen Transcriptome of Schizothorax prenanti during Aeromonas hydrophila Infection. Marine Biotechnology, 2018, 20, 246-256.	1.1	34
4324	Identification of microRNAs involved in lipid biosynthesis and seed size in developing sea buckthorn seeds using high-throughput sequencing. Scientific Reports, 2018, 8, 4022.	1.6	22
4325	Gene expression of indoor fungal communities under damp building conditions: Implications for human health. Indoor Air, 2018, 28, 548-558.	2.0	34
4326	Collective transcriptomic deregulation of hypertrophic and dilated cardiomyopathy â€“ Importance of fibrotic mechanism in heart failure. Computational Biology and Chemistry, 2018, 73, 85-94.	1.1	7
4327	Differential Metabolic Pathway Analysis of the Proteomes of <i>Leishmania donovani</i> and <i>Leptomonas seymouri</i>. Proteomics - Clinical Applications, 2018, 12, e1600087.	0.8	2
4328	Comparative Study of Withanolide Biosynthesis-Related miRNAs in Root and Leaf Tissues of Withania somnifera. Applied Biochemistry and Biotechnology, 2018, 185, 1145-1159.	1.4	25
4329	Hypothalamus and pituitary transcriptome profiling of male and female Hong Kong grouper () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	1.0	8
4330	Comparative transcriptomics of multidrug-resistant Acinetobacter baumannii in response to antibiotic treatments. Scientific Reports, 2018, 8, 3515.	1.6	53
4331	Transcriptome-sequencing analyses reveal putative genes related to flower color variation in Chinese Rosa rugosa. Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	10
4332	Revealing Mytilus galloprovincialis transcriptomic profiles during ontogeny. Developmental and Comparative Immunology, 2018, 84, 292-306.	1.0	18

#	Article	IF	Citations
4333	Disentangling thermal stress responses in a reef-calcifier and its photosymbionts by shotgun proteomics. Scientific Reports, 2018, 8, 3524.	1.6	24
4334	The transcriptomic signature of different sexes in two protogynous hermaphrodites: Insights into the molecular network underlying sex phenotype in fish. Scientific Reports, 2018, 8, 3564.	1.6	32
4335	Draft Genome Assemblies of Xylose-Utilizing Candida tropicalis and Candida boidinii with Potential Application in Biochemical and Biofuel Production. Genome Announcements, 2018, 6, .	0.8	3
4336	De novo transcriptome analysis and gene expression profiling of an oleaginous microalga Scenedesmus acutus TISTR8540 during nitrogen deprivation-induced lipid accumulation. Scientific Reports, 2018, 8, 3668.	1.6	35
4337	Investigation of Cry3Bb1 resistance and intoxication in western corn rootworm by RNA sequencing. Journal of Applied Entomology, 2018, 142, 921-936.	0.8	11
4338	Genome-wide genetic variation and comparison of fruit-associated traits between kumquat (Citrus) Tj ETQq1 1 0.784314 rgBT /Overloc	2.0	10
4339	RNA-seq data of control and powdery mildew pathogen (Golovinomyces orontii) treated transcriptomes of Helianthus niveus. Data in Brief, 2018, 17, 210-217.	0.5	2
4340	Comparative transcriptomic analysis provides insights into antibacterial mechanisms of Branchiostoma belcheri under Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2018, 76, 196-205.	1.6	17
4341	Transcriptome response of Atlantic salmon (<i>Salmo salar</i>) to competition with ecologically similar nonâ€native species. Ecology and Evolution, 2018, 8, 1769-1777.	0.8	8
4342	Transcriptome analysis of flax (Linum usitatissimum L.) undergoing osmotic stress. Industrial Crops and Products, 2018, 116, 215-223.	2.5	22
4343	Histological, Physiological, and Comparative Proteomic Analyses Provide Insights into Leaf Rolling in <i>Brassica napus</i>. Journal of Proteome Research, 2018, 17, 1761-1772.	1.8	6
4344	Transcriptome, Biochemical and Growth Responses of the Marine Phytoplankter Phaeodactylum Tricornutum Bohlin (Bacillariophyta) to Copepod Grazer Presence. Cellular Physiology and Biochemistry, 2018, 46, 1091-1111.	1.1	9
4345	Transcriptome profiling of genes involved in photosynthesis in Elaeagnus angustifolia L. under salt stress. Photosynthetica, 2018, 56, 998-1009.	0.9	56
4346	Transcriptome analysis of alternative splicing in different moso bamboo tissues. Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	7
4347	Draft Genome Assembly of the Sheep Scab Mite, Psoroptes ovis. Genome Announcements, 2018, 6, .	0.8	15
4348	VEGF and VEGFB Play Balancing Roles in Adipose Differentiation, Gene Expression, and Function. Endocrinology, 2018, 159, 2036-2049.	1.4	26
4349	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 107 Td 519-531.	1.4	21
4350	Avian transcriptomics: opportunities and challenges. Journal of Ornithology, 2018, 159, 599-629.	0.5	31

#	ARTICLE	IF	CITATIONS
4351	Skin Transcriptomes of common bottlenose dolphins (Tursiops truncatus) from the northern Gulf of Mexico and southeastern U.S. Atlantic coasts. Marine Genomics, 2018, 38, 45-58.	0.4	12
4352	Food Spoilage-Associated Leuconostoc, Lactococcus, and Lactobacillus Species Display Different Survival Strategies in Response to Competition. Applied and Environmental Microbiology, 2018, 84, .	1.4	50
4353	Draft Genome Sequence of the Yeast Vanrija humicola (Formerly Cryptococcus humicola) Strain UJ1, a Producer of <scp>d</scp> -Aspartate Oxidase. Genome Announcements, 2018, 6, .	0.8	5
4354	Genome Annotation Generator: a simple tool for generating and correcting WGS annotation tables for NCBI submission. GigaScience, 2018, 7, 1-5.	3.3	41
4355	Identification of genes associated with stress tolerance in moth bean [Vigna aconitifolia (Jacq.) Marechal], a stress hardy crop. Physiology and Molecular Biology of Plants, 2018, 24, 551-561.	1.4	10
4356	RNA-Seq analysis of interferon inducible p204-mediated network in anti-tumor immunity. Scientific Reports, 2018, 8, 6495.	1.6	6
4357	Characterization of <i>Heterobasidion occidentale</i> transcriptomes reveals candidate genes and <scp>DNA</scp> polymorphisms for virulence variations. Microbial Biotechnology, 2018, 11, 537-550.	2.0	5
4358	Parallel evolution and adaptation to environmental factors in a marine flatfish: Implications for fisheries and aquaculture management of the turbot (<i>Scophthalmus maximus</i>). Evolutionary Applications, 2018, 11, 1322-1341.	1.5	54
4359	Temperature gradient affects differentiation of gene expression and SNP allele frequencies in the dominant Lake Baikal zooplankton species. Molecular Ecology, 2018, 27, 2544-2559.	2.0	15
4360	The comparison of alternative splicing among the multiple tissues in cucumber. BMC Plant Biology, 2018, 18, 5.	1.6	18
4361	Genomewide evidence of environmentally mediated secondary contact of European green crab (<i>Carcinus maenas</i>) lineages in eastern North America. Evolutionary Applications, 2018, 11, 869-882.	1.5	22
4362	Systemic and sex-biased regulation of OBP expression under semiochemical stimuli. Scientific Reports, 2018, 8, 6035.	1.6	12
4363	The Mycoheterotrophic Symbiosis Between Orchids and Mycorrhizal Fungi Possesses Major Components Shared with Mutualistic Plant-Mycorrhizal Symbioses. Molecular Plant-Microbe Interactions, 2018, 31, 1032-1047.	1.4	32
4364	Fish red blood cells express immune genes and responses. Aquaculture and Fisheries, 2018, 3, 14-21.	1.2	63
4365	Transcriptome analysis of Pinus halepensis under drought stress and during recovery. Tree Physiology, 2018, 38, 423-441.	1.4	96
4366	Genome-wide single nucleotide polymorphism scan suggests adaptation to urbanization in an important pollinator, the red-tailed bumblebee (<i>Bombus lapidarius</i> L.). Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172806.	1.2	57
4367	Transcriptomic identification of salt-related genes and de novo assembly in common buckwheat (F.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	11
4368	Putative resistance-associated genes induced in sugarcane in response to the brown rust fungus, Puccinia melanocephala and their use in genetic diversity analysis of Louisiana sugarcane clones. Plant Gene, 2018, 14, 20-28.	1.4	10

#	Article	IF	Citations
4369	Transcriptome profiling of genes involving in carotenoid biosynthesis and accumulation between leaf and root of carrot (&lt;italic&gt;Daucus carota&lt;/italic&gt; L.). Acta Biochimica Et Biophysica Sinica, 2018, 50, 481-490.	0.9	34
4370	Identification of salinity-related genes in ENO2 mutant (eno2) of Arabidopsis thaliana. Journal of Integrative Agriculture, 2018, 17, 94-110.	1.7	12
4371	Groupâ€specific environmental sequencing reveals high levels of ecological heterogeneity across the microsporidian radiation. Environmental Microbiology Reports, 2018, 10, 328-336.	1.0	28
4372	Gonadal Transcriptome Analysis of Pacific Abalone Haliotis discus discus: Identification of Genes Involved in Germ Cell Development. Marine Biotechnology, 2018, 20, 467-480.	1.1	31
4373	GraphR: Accelerating Graph Processing Using ReRAM. , 2018, , .		169
4374	Comparison of closely related, uncultivated <i>Coxiella</i> tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. Environmental Microbiology, 2018, 20, 1751-1764.	1.8	33
4375	De novo transcriptomic analysis to identify differentially expressed genes during the process of aerenchyma formation in Typha angustifolia leaves. Gene, 2018, 662, 66-75.	1.0	8
4376	Mining and comparative survey of ESTâ€"SSR markers among members of Euphorbiaceae family. Molecular Biology Reports, 2018, 45, 453-468.	1.0	5
4377	Genomic signatures of parasite-driven natural selection in north European Atlantic salmon (Salmo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.4	15
4378	Genomewide signatures of selection in <i>EpichloÃ«</i> reveal candidate genes for host specialization. Molecular Ecology, 2018, 27, 3070-3086.	2.0	28
4379	The RNA-Seq-based high resolution gene expression atlas of chickpea (<i>Cicer arietinum</i> L.) reveals dynamic spatio-temporal changes associated with growth and development. Plant, Cell and Environment, 2018, 41, 2209-2225.	2.8	72
4380	Hostâ€and stageâ€dependent secretome of the arbuscular mycorrhizal fungus <i>Rhizophagus irregularis</i>. Plant Journal, 2018, 94, 411-425.	2.8	88
4381	Comprehensive transcriptome profiling of soybean leaves in response to simulated acid rain. Ecotoxicology and Environmental Safety, 2018, 158, 18-27.	2.9	11
4382	Transcriptome-wide identification and expression profile analysis of the bHLH family genes in Camellia sinensis. Functional and Integrative Genomics, 2018, 18, 489-503.	1.4	47
4383	Bioinformatics characterization of a cathepsin B transcript from the giant river prawn, Macrobrachium rosenbergii : Homology modeling and expression analysis after Aeromonas hydrophila infection. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2018, 221-222, 18-28.	0.7	8
4384	De novo assembly and analysis of the Artemisia argyi transcriptome and identification of genes involved in terpenoid biosynthesis. Scientific Reports, 2018, 8, 5824.	1.6	30
4385	Effects of two-hour exposure to environmental and high concentrations of methylmercury on the transcriptome of the macrophyte Elodea nuttallii. Aquatic Toxicology, 2018, 194, 103-111.	1.9	10
4386	Effect of dietary chitosan oligosaccharide supplementation on the pig ovary transcriptome. RSC Advances, 2018, 8, 13266-13273.	1.7	6

#	Article	IF	Citations
4387	De novo transcriptome assembly and analysis of differential gene expression following peptidoglycan (PGN) challenge in Antheraea pernyi. International Journal of Biological Macromolecules, 2018, 112, 1199-1207.	3.6	8
4388	The R2R3 transcription factor HlMYB8 and its role in flavonoid biosynthesis in hop (Humulus lupulus) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	24
4389	Genomic and transcriptomic alterations following intergeneric hybridization and polyploidization in the Chrysanthemum nankingenseÃ—Tanacetum vulgare hybrid and allopolyploid (Asteraceae). Horticulture Research, 2018, 5, 5.	2.9	17
4390	Transcriptome analysis reveals carbohydrate-mediated liver immune responses in Epinephelus akaara. Scientific Reports, 2018, 8, 639.	1.6	29
4391	GO FEAT: a rapid web-based functional annotation tool for genomic and transcriptomic data. Scientific Reports, 2018, 8, 1794.	1.6	99
4392	Analyses of the molecular mechanisms associated with salinity adaption of Trachidermus fasciatus through combined iTRAQ-based proteomics and RNA sequencing-based transcriptomics. Progress in Biophysics and Molecular Biology, 2018, 136, 40-53.	1.4	19
4393	Effect of CO2 on NADH production of denitrifying microbes via inhibiting carbon source transport and its metabolism. Science of the Total Environment, 2018, 627, 896-904.	3.9	40
4394	microRNA profiling between <i>Bacillus thuringiensis</i> Cry1Abâ€susceptible and â€resistant European corn borer, <i>Ostrinia nubilalis</i> (HÃ¼bner). Insect Molecular Biology, 2018, 27, 279-294.	1.0	13
4395	RNA-Seq Analysis of the Transcriptome of Leaf Senescence in Tobacco. Methods in Molecular Biology, 2018, 1744, 331-337.	0.4	17
4396	Comprehensive analysis of the lysine acetylome and its potential regulatory roles in the virulence of Streptococcus pneumoniae. Journal of Proteomics, 2018, 176, 46-55.	1.2	37
4397	Genomic resequencing combined with quantitative proteomic analyses elucidate the survival mechanisms of Lactobacillus plantarum P-8 in a long-term glucose-limited experiment. Journal of Proteomics, 2018, 176, 37-45.	1.2	9
4398	Behavioural tactic predicts preoptic-hypothalamic gene expression more strongly than developmental morph in fish with alternative reproductive tactics. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172742.	1.2	20
4400	Skin and scale regeneration after mechanical damage in a teleost. Molecular Immunology, 2018, 95, 73-82.	1.0	15
4401	De novo transcriptome of the pallial gland of the date mussel (Lithophaga lithophaga). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 26, 1-9.	0.4	4
4402	MicroRNA profile of silk gland reveals different silk yields of three silkworm strains. Gene, 2018, 653, 1-9.	1.0	10
4403	Cellulomonas fimi secretomes: In vivo and in silico approaches for the lignocellulose bioconversion. Journal of Biotechnology, 2018, 270, 21-29.	1.9	13
4404	Comparative transcriptome analysis of a Trichoplusia ni cell line reveals distinct host responses to intracellular and secreted protein products expressed by recombinant baculoviruses. Journal of Biotechnology, 2018, 270, 61-69.	1.9	23
4405	Muscle and liver transcriptome characterization and genetic marker discovery in the farmed meagre, Argyrosomus regius. Marine Genomics, 2018, 39, 39-44.	0.4	4

#	ARTICLE	IF	CITATIONS
4406	An unusual strategy of stomatal control in the desert shrub Ammopiptanthus mongolicus. Plant Physiology and Biochemistry, 2018, 125, 13-26.	2.8	7
4407	New insight into ovary abortion during ovary development of hazelnut through a combined proteomic and transcriptomic analysis. Scientia Horticulturae, 2018, 234, 36-48.	1.7	8
4408	Integrative Genomic and Proteomic Analysis of the Response ofLactobacillus caseiZhang to Glucose Restriction. Journal of Proteome Research, 2018, 17, 1290-1299.	1.8	5
4409	Evolution of the Quorum network and the mobilome (plasmids and bacteriophages) in clinical strains of Acinetobacter baumannii during a decade. Scientific Reports, 2018, 8, 2523.	1.6	28
4410	Elevated CO2 delays the early development of scleractinian coral Acropora gemmifera. Scientific Reports, 2018, 8, 2787.	1.6	19
4411	Comparative Analysis of Differential Gene Expression Profiling of Sex-Bias Fat Body of Bactrocera dorsalis (Diptera: Tephritidae) Identifying a New Vitellogenin Gene. Annals of the Entomological Society of America, 2018, 111, 43-54.	1.3	11
4412	Genomic Architecture of the Two Cold-Adapted Genera Exiguobacterium and Psychrobacter: Evidence of Functional Reduction in the Exiguobacterium antarcticum B7 Genome. Genome Biology and Evolution, 2018, 10, 731-741.	1.1	17
4413	Increased socially mediated plasticity in gene expression accompanies rapid adaptive evolution. Ecology Letters, 2018, 21, 546-556.	3.0	21
4414	Transcriptome analysis in tissue sectors with contrasting crocins accumulation provides novel insights into apocarotenoid biosynthesis and regulation during chromoplast biogenesis. Scientific Reports, 2018, 8, 2843.	1.6	41
4415	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. Genome Research, 2018, 28, 396-411.	2.4	299
4416	Evolutionary diversification of galactinol synthases in Rosaceae: adaptive roles of galactinol and raffinose during apple bud dormancy. Journal of Experimental Botany, 2018, 69, 1247-1259.	2.4	33
4417	Unmapped sequencing reads identify additional candidate genes linked to magnetoreception in rainbow trout. Environmental Biology of Fishes, 2018, 101, 711-721.	0.4	5
4418	Transcriptomic insight into pathogenicityâ€associated factors of <i>Conidiobolus obscurus</i>, an obligate aphidâ€pathogenic fungus belonging to Entomopthoromycota. Pest Management Science, 2018, 74, 1677-1686.	1.7	12
4419	Plant Senescence. Methods in Molecular Biology, 2018, , .	0.4	3
4420	Migration-Selection Balance Drives Genetic Differentiation in Genes Associated with High-Altitude Function in the Speckled Teal (Anas flavirostris) in the Andes. Genome Biology and Evolution, 2018, 10, 14-32.	1.1	18
4421	Partial Proteome of the Corynetoxinâ€Producing Gramâ€Positive Bacterium, Rathayibacter toxicus. Proteomics, 2018, 18, 1700350.	1.3	2
4422	Blood transcriptomics of captive forest musk deer (Moschus berezovskii) and possible associations with the immune response to abscesses. Scientific Reports, 2018, 8, 599.	1.6	17
4423	Evidence of Adaptive Evolution and Relaxed Constraints in Sex-Biased Genes of South American and West Indies Fruit Flies (Diptera: Tephritidae). Genome Biology and Evolution, 2018, 10, 380-395.	1.1	11

#	ARTICLE	IF	CITATIONS
4424	The root transcriptome of Achyranthes bidentata and the identification of the genes involved in the replanting benefit. Plant Cell Reports, 2018, 37, 611-625.	2.8	10
4425	Evolution of resistance to chytridiomycosis is associated with a robust early immune response. Molecular Ecology, 2018, 27, 919-934.	2.0	50
4426	Comparative transcriptomics uncovers differences in photoautotrophic versus photoheterotrophic modes of nutrition in relation to secondary metabolites biosynthesis in Swertia chirayita. Molecular Biology Reports, 2018, 45, 77-98.	1.0	12
4427	Transcriptome sequence analysis and mining of SSRs in Jhar Ber (Ziziphus nummularia (Burm.f.) Wight) Tj ETQq1 1 0.784314 rgBT /Over	1.6	10
4428	Shigella Phages Isolated during a Dysentery Outbreak Reveal Uncommon Structures and Broad Species Diversity. Journal of Virology, 2018, 92, .	1.5	33
4429	Transcriptome profiles of sunflower reveal the potential role of microsatellites in gene expression divergence. Molecular Ecology, 2018, 27, 1188-1199.	2.0	10
4430	Transcriptome Analysis of Hepatopancreas from the Cr (VI)-Stimulated Mantis Shrimp (<i>Oratosquilla) Tj ETQq0 0 0 rgBT /Overlock 10 Journal of Agricultural and Food Chemistry, 2018, 66, 2598-2606.	2.4	17
4431	Root transcripts associated with arsenic accumulation in hyperaccumulator Pteris vittata. Journal of Biosciences, 2018, 43, 105-115.	0.5	10
4432	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. Molecular Ecology Resources, 2018, 18, 639-645.	2.2	46
4433	Transcriptome Analyses of Mosaic (MSC) Mitochondrial Mutants of Cucumber in a Highly Inbred Nuclear Background. G3: Genes, Genomes, Genetics, 2018, 8, 953-965.	0.8	5
4434	Identification of candidate effector genes of <i>Pratylenchus penetrans</i>. Molecular Plant Pathology, 2018, 19, 1887-1907.	2.0	36
4435	Vernalization can regulate flowering time through microRNA mechanism in <i>Brassica rapa</i>. Physiologia Plantarum, 2018, 164, 204-215.	2.6	11
4436	Proteotranscriptomic Analysis and Discovery of the Profile and Diversity of Toxin-like Proteins in Centipede. Molecular and Cellular Proteomics, 2018, 17, 709-720.	2.5	13
4437	Draft genome and reference transcriptomic resources for the urticating pine defoliator <i>Thaumetopoea pityocampa</i> (Lepidoptera: Notodontidae). Molecular Ecology Resources, 2018, 18, 602-619.	2.2	23
4438	Patterns of Genome-Wide Nucleotide Diversity in the Gynodioecious Plant Thymus vulgaris Are Compatible with Recent Sweeps of Cytoplasmic Genes. Genome Biology and Evolution, 2018, 10, 239-248.	1.1	8
4439	Demography and selection shape transcriptomic divergence in field crickets. Evolution; International Journal of Organic Evolution, 2018, 72, 553-567.	1.1	6
4440	microRNA regulation in an ancient obligate endosymbiosis. Molecular Ecology, 2018, 27, 1777-1793.	2.0	25
4441	Development of microsatellite markers using next-generation sequencing for the fish Colossoma macropomum. Molecular Biology Reports, 2018, 45, 9-18.	1.0	11

#	ARTICLE	IF	CITATIONS
4442	6.0â€‰K microarray reveals differential transcriptomic responses in the dinoflagellate Prorocentrum minimum exposed to polychlorinated biphenyl (PCB). Chemosphere, 2018, 195, 398-409.	4.2	19
4443	Comparative transcriptomic analysis of shrimp hemocytes in response to acute hepatopancreas necrosis disease (AHPND) causing Vibrio parahemolyticus infection. Fish and Shellfish Immunology, 2018, 74, 10-18.	1.6	47
4444	Transcriptome analysis provides insights into the mechanism of albinism during different pigmentation stages of the albino sea cucumber Apostichopus japonicus. Aquaculture, 2018, 486, 148-160.	1.7	13
4445	De novo transcriptome assembly and comparative analysis between male and benzyladenine-induced female inflorescence buds of Plukenetia volubilis. Journal of Plant Physiology, 2018, 221, 107-118.	1.6	16
4446	Asymmetrical changes of gene expression, small <scp>RNA</scp>s and chromatin in two resynthesized wheat allotetraploids. Plant Journal, 2018, 93, 828-842.	2.8	40
4447	Signatures of protein expression revealed by secretome analyses of cancer associated fibroblasts and melanoma cell lines. Journal of Proteomics, 2018, 174, 1-8.	1.2	20
4448	Human resource optimisation through semanticallyÂenriched data. International Journal of Production Research, 2018, 56, 2855-2877.	4.9	14
4449	Comparative Genomics for Prokaryotes. Methods in Molecular Biology, 2018, 1704, 55-78.	0.4	15
4450	Coding and long non-coding RNAs regulating adult migratory locust (Locusta migratoria) brain polyphenism revealed via whole transcriptome analyses. Journal of Asia-Pacific Entomology, 2018, 21, 58-68.	0.4	4
4451	De novo transcriptome sequencing of an estuarine amphipod Grandidierella japonica exposed to zinc. Marine Genomics, 2018, 39, 11-14.	0.4	6
4452	Transcriptomic responses of the freshwater snail (Parafossarulus striatulus) following dietary exposure to cyanobacteria. Science of the Total Environment, 2018, 624, 153-161.	3.9	19
4453	The Long Intergenic Noncoding RNA (LincRNA) Landscape of the Soybean Genome. Plant Physiology, 2018, 176, 2133-2147.	2.3	88
4454	Mechanisms of thermal adaptation and evolutionary potential of conspecific populations to changing environments. Molecular Ecology, 2018, 27, 659-674.	2.0	72
4455	An interplay between plasticity and parental phenotype determines impacts of ocean acidification on a reef fish. Nature Ecology and Evolution, 2018, 2, 334-342.	3.4	75
4456	The physiological differentiation along the midgut of <i>Bombyx mori</i> â€“ inspirations from proteomics and gene expression patterns of the secreted proteins in the ectoperitrophic space. Insect Molecular Biology, 2018, 27, 247-259.	1.0	11
4457	Genome re-annotation of the wild strawberry Fragaria vesca using extensive Illumina- and SMRT-based RNA-seq datasets. DNA Research, 2018, 25, 61-70.	1.5	67
4458	Genome-wide characterization of differentially expressed genes provides insights into regulatory network of heat stress response in radish (Raphanus sativus L.). Functional and Integrative Genomics, 2018, 18, 225-239.	1.4	33
4459	Whole transcriptome analysis reveals potential novel mechanisms of low-level linezolid resistance in Enterococcus faecalis. Gene, 2018, 647, 143-149.	1.0	22

#	ARTICLE	IF	CITATIONS
4460	Transcriptome profiling during mangrove viviparity in response to abscisic acid. Scientific Reports, 2018, 8, 770.	1.6	48
4461	Transcriptome changes induced by arbuscular mycorrhizal fungi in sunflower (Helianthus annuus L.) roots. Scientific Reports, 2018, 8, 4.	1.6	170
4462	Identification of transcription factors involved in the phenotype of a domesticated oleaginous microalgae strain of Tisochrysis lutea. Algal Research, 2018, 30, 59-72.	2.4	19
4464	Genererating a core cluster of Fasciola hepatica virulence and immunomodulation-related genes using a comparative in silico approach. Research in Veterinary Science, 2018, 117, 271-276.	0.9	3
4465	Genome characterization of piscine â€˜Scale drop and Muscle Necrosis syndromeâ€™-associated strain of<i>Vibrio harveyi</i>focusing on bacterial virulence determinants. Journal of Applied Microbiology, 2018, 124, 652-666.	1.4	9
4466	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. Bioinformatics, 2018, 34, 1697-1704.	1.8	3
4467	Transcriptome assembly and expression profiling of the molecular responses to cadmium toxicity in cerebral ganglia of wolf spider Pardosa pseudoannulata (Araneae: Lycosidae). Ecotoxicology, 2018, 27, 198-208.	1.1	18
4468	Lysine Succinylation Contributes to Aflatoxin Production and Pathogenicity in Aspergillus flavus. Molecular and Cellular Proteomics, 2018, 17, 457-471.	2.5	59
4469	Transcriptional responses of Acropora hyacinthus embryo under the benzo(a)pyrene stress by deep sequencing. Chemosphere, 2018, 206, 387-397.	4.2	16
4470	AmpuBase: a transcriptome database for eight species of apple snails (Gastropoda: Ampullariidae). BMC Genomics, 2018, 19, 179.	1.2	20
4471	Larval transcriptomic response to host plants in two related phytophagous lepidopteran species: implications for host specialization and species divergence. BMC Genomics, 2018, 19, 265.	1.2	22
4472	Transcriptomic analysis of Perilla frutescens seed to insight into the biosynthesis and metabolic of unsaturated fatty acids. BMC Genomics, 2018, 19, 213.	1.2	31
4473	Divergent transcriptomic responses underlying the ranaviruses-amphibian interaction processes on interspecies infection of Chinese giant salamander. BMC Genomics, 2018, 19, 211.	1.2	15
4474	Intraspecific comparative genomics of isolates of the Norway spruce pathogen (Heterobasidion) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.2	37
4475	Diapause in a tropical oil-collecting bee: molecular basis unveiled by RNA-Seq. BMC Genomics, 2018, 19, 305.	1.2	39
4476	SSR marker development and intraspecific genetic divergence exploration of Chrysanthemum indicum based on transcriptome analysis. BMC Genomics, 2018, 19, 291.	1.2	40
4477	Ginseng Genome Database: an open-access platform for genomics of Panax ginseng. BMC Plant Biology, 2018, 18, 62.	1.6	73
4478	Transcriptome analysis of the digestive system of a wood-feeding termite (Coptotermes formosanus) revealed a unique mechanism for effective biomass degradation. Biotechnology for Biofuels, 2018, 11, 24.	6.2	37

#	Article	IF	Citations
4479	Genome-wide expression analysis suggests a role for jasmonates in the resistance to blue mold in apple. Plant Growth Regulation, 2018, 85, 375-387.	1.8	8
4480	The identification of growth, immune related genes and marker discovery through transcriptome in the yellow drum (Nibea albiflora). Genes and Genomics, 2018, 40, 881-891.	0.5	19
4481	Comparative transcriptomic analysis reveals the mechanism of leech environmental adaptation. Gene, 2018, 664, 70-77.	1.0	10
4482	Expression of hydroxytyrosol and oleuropein biosynthetic genes are correlated with metabolite accumulation during fruit development in olive, Olea europaea , cv. Koroneiki. Plant Physiology and Biochemistry, 2018, 128, 41-49.	2.8	25
4483	Analysis of Theileria orientalis draft genome sequences reveals potential species-level divergence of the Ikeda, Chitose and Buffeli genotypes. BMC Genomics, 2018, 19, 298.	1.2	24
4484	Transcriptome analysis of different growth stages of Aspergillus oryzae reveals dynamic changes of distinct classes of genes during growth. BMC Microbiology, 2018, 18, 12.	1.3	23
4485	Tissue-Specific Transcriptome for <i>Poeciliopsis prolifica</i> Reveals Evidence for Genetic Adaptation Related to the Evolution of a Placental Fish. G3: Genes, Genomes, Genetics, 2018, 8, 2181-2192.	0.8	10
4486	Transcriptome analysis reveals enrichment of genes associated with auditory system in swimbladder of channel catfish. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 30-39.	0.4	8
4487	De novo transcriptome assembly and identification of salt-responsive genes in sugar beet M14. Computational Biology and Chemistry, 2018, 75, 1-10.	1.1	21
4488	Proteomic analysis and food-grade enzymes of Moringa oleifer Lam. a Lam. flower. International Journal of Biological Macromolecules, 2018, 115, 883-890.	3.6	29
4489	Dehydration prompts increased activity and blood feeding by mosquitoes. Scientific Reports, 2018, 8, 6804.	1.6	69
4490	Transcriptome analysis reveals hybridization-induced genome shock in an interspecific F₁hybrid from<i>Camellia</i>. Genome, 2018, 61, 477-485.	0.9	7
4491	Oceanographic variation influences spatial genomic structure in the sea scallop, <i>Placopecten magellanicus</i>. Ecology and Evolution, 2018, 8, 2824-2841.	0.8	12
4492	Genome sequence and comparative analyses of atoxigenic <i>Aspergillus flavus</i> WRRL 1519. Mycologia, 2018, 110, 482-493.	0.8	10
4493	Symbiotic polydnavirus and venom reveal parasitoid to its hyperparasitoids. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5205-5210.	3.3	54
4494	Signatures of local adaptation along environmental gradients in a rangeâ€expanding damselfly (<i>Ischnura elegans</i>). Molecular Ecology, 2018, 27, 2576-2593.	2.0	82
4495	Comparative transcriptomics and genomic patterns of discordance in Capsiceae (Solanaceae). Molecular Phylogenetics and Evolution, 2018, 126, 293-302.	1.2	15
4496	Integrative network analyses of wilt transcriptome in chickpea reveal genotype dependent regulatory hubs in immunity and susceptibility. Scientific Reports, 2018, 8, 6528.	1.6	14

#	Article	IF	Citations
4497	RNA Sequencing, <i>De novo</i> assembly, functional annotation and SSR analysis of the endangered diving beetle <scp><i>Cybister chinensis</i></scp> (= <scp><i>Cybister japonicus</i></scp>) using the Illumina platform. Entomological Research, 2018, 48, 60-72.	0.6	3
4498	Populations of doubled haploids for genetic mapping in hexaploid winter triticale. Molecular Breeding, 2018, 38, 46.	1.0	21
4499	Deep sequencing-based characterization of transcriptome of Pyrus ussuriensis in response to cold stress. Gene, 2018, 661, 109-118.	1.0	30
4500	Identification of candidate resistance genes of cotton against Aspergillus flavus infection using a comparative transcriptomics approach. Physiology and Molecular Biology of Plants, 2018, 24, 513-519.	1.4	3
4501	Identification of DFR as a promoter of anthocyanin accumulation in poinsettia (Euphorbia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td 158-165.	1.7	18
4502	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. Scientific Reports, 2018, 8, 4473.	1.6	28
4503	The transcriptome analyses of Tagetes erecta provides novel insights into secondary metabolite biosynthesis during flower development. Gene, 2018, 660, 18-27.	1.0	16
4504	Discovering microRNAs and their targets in the red flour beetle Tribolium castaneum from expressed sequence tags. Meta Gene, 2018, 17, 61-67.	0.3	0
4505	Oyster transcriptome response to Alexandrium exposure is related to saxitoxin load and characterized by disrupted digestion, energy balance, and calcium and sodium signaling. Aquatic Toxicology, 2018, 199, 127-137.	1.9	19
4506	Survival, gene and metabolite responses of Litoria verreauxii alpina frogs to fungal disease chytridiomycosis. Scientific Data, 2018, 5, 180033.	2.4	9
4507	Comprehensive analysis of differentially expressed genes reveals the molecular response to elevated CO 2 levels in two sea buckthorn cultivars. Gene, 2018, 660, 120-127.	1.0	17
4508	Genomic Signatures of Selection between Urban and Rural Populations of Black Garden Ant Lasius niger. Russian Journal of Genetics, 2018, 54, 218-225.	0.2	4
4509	Probing the Phylogenomics and Putative Pathogenicity Genes of Pythium insidiosum by Oomycete Genome Analyses. Scientific Reports, 2018, 8, 4135.	1.6	35
4510	Differential gene expression revealed with RNA-Seq and parallel genotype selection of the ornithine decarboxylase gene in fish inhabiting polluted areas. Scientific Reports, 2018, 8, 4820.	1.6	12
4511	Unravelling the adaptation strategies employed by Glaciozyma antarctica PI12 on Antarctic sea ice. Marine Environmental Research, 2018, 137, 169-176.	1.1	14
4512	Comparative transcriptome analysis reveals phytohormone signalings, heat shock module and ROS scavenger mediate the cold-tolerance of rubber tree. Scientific Reports, 2018, 8, 4931.	1.6	36
4513	Identification of proteins in response to terminal drought stress in sorghum (Sorghum bicolor (L.)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Plant Physiology, 2018, 23, 24-39.	0.8	13
4514	De novo transcriptome analysis of immune response on cobia (Rachycentron canadum) infected with Photobacterium damselae subsp. piscicida revealed inhibition of complement components and involvement of MyD88-independent pathway. Fish and Shellfish Immunology, 2018, 77, 120-130.	1.6	16

#	ARTICLE	IF	CITATIONS
4515	Differential carbohydrate gene expression during preplanting temperature treatments controls meristem termination and bulbing in garlic. Environmental and Experimental Botany, 2018, 150, 280-291.	2.0	16
4516	Molecular characterization and evolution of a chemosensory receptor gene family in three notorious rice planthoppers, <scp><i>Nilaparvata lugens</i></scp>, <scp><i>Sogatella furcifera</i></scp> and <scp><i>Laodelphax striatellus</i></scp>, based on genome and transcriptome analyses. Pest Management Science, 2018, 74, 2156-2167.	1.7	54
4517	Two transcription factors TaPpm1 and TaPpb1 co-regulate anthocyanin biosynthesis in purple pericarps of wheat. Journal of Experimental Botany, 2018, 69, 2555-2567.	2.4	71
4518	Uncovering tea-specific secondary metabolism using transcriptomic and metabolomic analyses in grafts of Camellia sinensis and C. oleifera. Tree Genetics and Genomes, 2018, 14, 1.	0.6	17
4519	Low pH stress responsive transcriptome of seedling roots in wheat (Triticum aestivum L.). Genes and Genomics, 2018, 40, 1199-1211.	0.5	15
4520	Reconstructing the suberin pathway in poplar by chemical and transcriptomic analysis of bark tissues. Tree Physiology, 2018, 38, 340-361.	1.4	51
4521	Inferring the Functions of Proteins from the Interrelationships between Functional Categories. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 157-167.	1.9	4
4522	Quantitative trait locus mapping reveals complex genetic architecture of quantitative virulence in the wheat pathogen <i>Zymoseptoria tritici</i>. Molecular Plant Pathology, 2018, 19, 201-216.	2.0	76
4523	Transcriptome analysis in the beet webworm, <i>Spoladea recurvalis</i> (Lepidoptera: Crambidae). Insect Science, 2018, 25, 33-44.	1.5	11
4524	Next-generation sequencing of Dreissena polymorpha transcriptome sheds light on its mitochondrial DNA. Hydrobiologia, 2018, 810, 255-263.	1.0	8
4525	Large-scale label-free proteomics analysis of occupational poisoned patients of 1-bromopropane, workers exposed to 1-bromopropane and healthy individuals. Human and Experimental Toxicology, 2018, 37, 3-12.	1.1	1
4526	Genome-wide identification, phylogenetic analysis, and expression profiling of the BBX family genes in pear. Journal of Horticultural Science and Biotechnology, 2018, 93, 37-50.	0.9	24
4527	Strand-specific RNA-Seq analysis provides first insight into transcriptome response of Vibrio alginolyticus to phage infection. Marine Genomics, 2018, 38, 5-8.	0.4	4
4528	Antennal transcriptome and odorant binding protein expression profiles of an invasive mealybug and its parasitoid. Journal of Applied Entomology, 2018, 142, 149-161.	0.8	19
4529	Comparative RNA-sequencing analysis of ER-based HSP90 functions and signal pathways in Tribolium castaneum. Cell Stress and Chaperones, 2018, 23, 29-43.	1.2	10
4530	De novo assembly and annotation of the Avicennia officinalis L. transcriptome. Marine Genomics, 2018, 39, 3-6.	0.4	3
4531	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
4532	Ultraviolet filters and heat shock proteins: effects in Chironomus riparius by benzophenone-3 and 4-methylbenzylidene camphor. Environmental Science and Pollution Research, 2018, 25, 333-344.	2.7	18

#	Article	IF	Citations
4533	Profiling of secondary metabolite gene clusters regulated by LaeA in Aspergillus niger FGSC A1279 based on genome sequencing and transcriptome analysis. Research in Microbiology, 2018, 169, 67-77.	1.0	40
4534	Identification of new proteinâ€"protein and proteinâ€"DNA interactions linked with wood formation in Populus trichocarpa. Tree Physiology, 2018, 38, 362-377.	1.4	17
4535	Sequencing, de novo assembly and characterization of the spotted scat Scatophagus argus (Linnaeus) Tj ETQq0 0 0 rgBT /Overlock 10 T Limnology, 2018, 36, 1329-1341.	0.6	15
4536	Label-free based quantitative proteomic analysis identifies proteins involved in the testis maturation of Bactrocera dorsalis (Hendel). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 25, 9-18.	0.4	6
4537	Successive evolutionary steps drove Pooideae grasses from tropical to temperate regions. New Phytologist, 2018, 217, 925-938.	3.5	27
4538	Drought and salt stress in Macrotyloma uniflorum leads to common and specific transcriptomic responses and reveals importance of raffinose family oligosaccharides in stress tolerance. Gene Reports, 2018, 10, 7-16.	0.4	10
4539	Proteomics analysis of the germinating seeds of Cariniana legalis (Mart.) Kuntze (Meliaceae): an endangered species of the Brazilian Atlantic Rainforest. Revista Brasileira De Botanica, 2018, 41, 117-128.	0.5	1
4540	Transcriptional profile of the human skin pathogenic fungus Mucor irregularis in response to low oxygen. Medical Mycology, 2018, 56, 631-644.	0.3	11
4541	Planctomycetes attached to algal surfaces: Insight into their genomes. Genomics, 2018, 110, 231-238.	1.3	39
4542	Comparative transcriptomics of cyprinid minnows and carp in a common wild setting: a resource for ecological genomics in freshwater communities. DNA Research, 2018, 25, 11-23.	1.5	2
4543	Using RNA-seq to determine patterns of sex-bias in gene expression in the brain of the sex-role reversed Gulf Pipefish (Syngnathus scovelli). Marine Genomics, 2018, 37, 120-127.	0.4	10
4544	Comparative transcriptome profiling of genes and pathways related to resistance against powdery mildew in two contrasting melon genotypes. Scientia Horticulturae, 2018, 227, 169-180.	1.7	38
4545	Transcriptome analysis reveals the molecular mechanism of hepatic fat metabolism disorder caused by Muscovy duck reovirus infection. Avian Pathology, 2018, 47, 127-139.	0.8	20
4546	Tolerance of olive (<i>Olea europaea</i>) cv Frantoio to <i>Verticillium dahliae</i> relies on both basal and pathogenâ€induced differential transcriptomic responses. New Phytologist, 2018, 217, 671-686.	3.5	56
4547	Comparative transcriptome analysis reveals networks of genes activated in the whitefly, Bemisia tabaci when fed on tomato plants infected with Tomato yellow leaf curl virus. Virology, 2018, 513, 52-64.	1.1	48
4548	Comprehensive analysis of transcriptional and proteomic profiling reveals silver nanoparticles-induced toxicity to bacterial denitrification. Journal of Hazardous Materials, 2018, 344, 291-298.	6.5	58
4549	Genes coding for transporters showed a rapid and sharp increase in their expression in response to lead, in the aquatic fern (Salvinia minima Baker). Ecotoxicology and Environmental Safety, 2018, 147, 1056-1064.	2.9	14
4550	De novo assembly and transcriptome characterization of the freshwater prawn Palaemonetes argentinus: Implications for a detoxification response. Marine Genomics, 2018, 37, 74-81.	0.4	6

#	Article	IF	Citations
4551	Proteome-wide prediction and annotation of mitochondrial and sub-mitochondrial proteins by incorporating domain information. Mitochondrion, 2018, 42, 11-22.	1.6	28
4552	Intergenerational environmental effects: functional signals in offspring transcriptomes and metabolomes after parental jasmonic acid treatment in apomictic dandelion. New Phytologist, 2018, 217, 871-882.	3.5	36
4553	The genetic architecture of photosynthesis and plant growthâ€related traits in tomato. Plant, Cell and Environment, 2018, 41, 327-341.	2.8	59
4554	Genotoxic effects of vinclozolin on the aquatic insect Chironomus riparius (Diptera, Chironomidae). Environmental Pollution, 2018, 232, 563-570.	3.7	14
4555	De novo assembly, characterization and annotation for the transcriptome of Sphaeroma terebrans and microsatellite marker discovery. Genes and Genomics, 2018, 40, 167-176.	0.5	2
4556	Molecular dissection of nuptial gifts in divergent strains of O strinia moths. Physiological Entomology, 2018, 43, 10-19.	0.6	7
4557	Characterization of Putative Effectors from the Cereal Cyst Nematode <i>Heterodera avenae</i>. Phytopathology, 2018, 108, 264-274.	1.1	8
4558	De novo assembly and annotation of the whole transcriptome of Oratosquilla oratoria. Marine Genomics, 2018, 38, 17-20.	0.4	14
4559	Development and evaluation of highâ€density Axiom^{Â®}<i>Cicer<scp>SNP</scp></i>ÂArray for highâ€resolution genetic mapping and breeding applications in chickpea. Plant Biotechnology Journal, 2018, 16, 890-901.	4.1	76
4560	Multiple Nodulation Genes Are Up-Regulated During Establishment of Reniform Nematode Feeding Sites in Soybean. Phytopathology, 2018, 108, 275-291.	1.1	8
4561	Transcriptome analysis, using <scp>RNA</scp>â€Seq of <i>Lomandra longifolia</i> roots infected with <i>Phytophthora cinnamomi</i> reveals the complexity of the resistance response. Plant Biology, 2018, 20, 130-142.	1.8	27
4562	Transcriptome sequencing and characterization of Symbiodinium muscatinei and Elliptochloris marina, symbionts found within the aggregating sea anemone Anthopleura elegantissima. Marine Genomics, 2018, 37, 82-91.	0.4	4
4563	Transcriptomics reveals tissue/organ-specific differences in gene expression in the starfish Patiria pectinifera. Marine Genomics, 2018, 37, 92-96.	0.4	8
4564	A transcriptomic resource for the northern krill Meganyctiphanes norvegica based on a short-term temperature exposure experiment. Marine Genomics, 2018, 38, 25-32.	0.4	6
4565	Changes in fenugreek transcriptome induced by methyl jasmonate and steroid precursors revealed by RNA-Seq. Genomics, 2018, 110, 267-276.	1.3	16
4566	Acetylome Profiling Reveals Extensive Lysine Acetylation of the Fatty Acid Metabolism Pathway in the Diatom Phaeodactylum tricornutum. Molecular and Cellular Proteomics, 2018, 17, 399-412.	2.5	26
4567	A multiple near isogenic line (multi-NIL) RNA-seq approach to identify candidate genes underpinning QTL. Theoretical and Applied Genetics, 2018, 131, 613-624.	1.8	30
4568	Gene expression analysis of Ruditapes philippinarum haemocytes after experimental Perkinsus olseni zoospore challenge and infection in the wild. Fish and Shellfish Immunology, 2018, 72, 611-621.	1.6	5

#	ARTICLE	IF	CITATIONS
4569	Proteomic profiling of integral membrane proteins associated to pathogenicity in <i>Vibrio parahaemolyticus</i> strains. Microbiology and Immunology, 2018, 62, 14-23.	0.7	26
4570	Comparative transcriptome analysis reveals conserved branching morphogenesis related genes involved in chamber formation of catfish swimbladder. Physiological Genomics, 2018, 50, 67-76.	1.0	6
4571	Genome sequences of <i>Chlorella sorokiniana </i><scp>UTEX</scp> 1602 and <i>Micractinium conductrix </i><scp>SAG</scp> 241.80: implications to maltose excretion by a green alga. Plant Journal, 2018, 93, 566-586.	2.8	68
4572	Sex-specific transcript expression in the hepatopancreas of the banana shrimp (Fenneropenaeus) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	5
4573	Fantastic Beasts and How To Sequence Them: Ecological Genomics for Obscure Model Organisms. Trends in Genetics, 2018, 34, 121-132.	2.9	64
4574	Transcriptome and defence response in <scp><i>Eucalyptus camaldulensis</i></scp> leaves to feeding by <i>Glycaspis brimblecombei</i> Moore (Hemiptera: Aphalaridae): a stealthy psyllid does not go unnoticed. Austral Entomology, 2018, 57, 247-254.	0.8	23
4575	Transcriptome analysis reveals novel insights into the response to Pb exposure in Phanerochaete chrysosporium. Chemosphere, 2018, 194, 657-665.	4.2	12
4576	De novo assembly and functional annotations of the transcriptome of Metorchis orientalis (trematoda: Opisthorchiidae). Experimental Parasitology, 2018, 184, 90-96.	0.5	7
4577	Genotyping-by-sequencing for construction of a new genetic linkage map and QTL analysis of growth-related traits in Pacific bluefin tuna. Aquaculture Research, 2018, 49, 1293-1301.	0.9	6
4578	Assembly and analysis of a <i>qingke</i> reference genome demonstrate its close genetic relation to modern cultivated barley. Plant Biotechnology Journal, 2018, 16, 760-770.	4.1	50
4579	Transcriptome sequencing of Paeonia suffruticosa â€˜Shima Nishikiâ€™ to identify differentially expressed genes mediating double-color formation. Plant Physiology and Biochemistry, 2018, 123, 114-124.	2.8	23
4580	Transcriptional activity of detoxification genes is altered by ultraviolet filters in Chironomus riparius. Ecotoxicology and Environmental Safety, 2018, 149, 64-71.	2.9	28
4581	Blue Native/SDSâ€PAGE and iTRAQâ€Based Chloroplasts Proteomics Analysis of <i>Nicotiana tabacum</i> Leaves Infected with M Strain of Cucumber Mosaic Virus Reveals Several Proteins Involved in Chlorosis Symptoms. Proteomics, 2018, 18, 1700359.	1.3	6
4582	Hygrocin C from marine-derived Streptomyces sp. SCSGAA 0027 inhibits biofilm formation in Bacillus amyloliquefaciens SCSGAB0082 isolated from South China Sea gorgonian. Applied Microbiology and Biotechnology, 2018, 102, 1417-1427.	1.7	20
4583	Transcriptome analysis of the threatened snail Ellobium chinense reveals candidate genes for adaptation and identifies SSRs for conservation genetics. Genes and Genomics, 2018, 40, 333-347.	0.5	6
4584	<i>Pas de deux</i>: An Intricate Dance of Anther Smut and Its Host. G3: Genes, Genomes, Genetics, 2018, 8, 505-518.	0.8	6
4585	Refining Transcriptome Gene Catalogs by MSâ€Validation of Expressed Proteins. Proteomics, 2018, 18, 1700271.	1.3	6
4586	RNA-Seq-derived identification of differential transcription in the eggplant (Solanum melongena) following inoculation with bacterial wilt. Gene, 2018, 644, 137-147.	1.0	9

#	ARTICLE	IF	CITATIONS
4587	Landscape features along migratory routes influence adaptive genomic variation in anadromous steelhead (<i>Oncorhynchus mykiss</i>). Molecular Ecology, 2018, 27, 128-145.	2.0	36
4588	Identification of novel Est-ssr markers by transcriptome sequencing in ridgetail white prawn Exopalaemon carinicauda. Genes and Genomics, 2018, 40, 207-215.	0.5	16
4589	Transcriptional profiling of antioxidant defense system and heat shock protein (Hsp) families in the cadmium- and copper-exposed marine ciliate Euplotes crassu. Genes and Genomics, 2018, 40, 85-98.	0.5	13
4590	An integrated metabolic consequence of Hepatospora eriocheir infection in the Chinese mitten crab Eriocheir sinensis. Fish and Shellfish Immunology, 2018, 72, 443-451.	1.6	27
4591	Transcriptome Analysis Reveals the Mechanism of Fungicidal of Thymol Against Fusarium oxysporum f. sp. niveum. Current Microbiology, 2018, 75, 410-419.	1.0	30
4592	Resistance mechanisms and their difference between the root and leaf of Microsorum pteropus â€" A novel potential aquatic cadmium hyperaccumulator. Science of the Total Environment, 2018, 616-617, 480-490.	3.9	12
4593	<scp>RNA</scp>â€Seq of <i>Agropyron mongolicum</i> Keng in response to drought stress. Grassland Science, 2018, 64, 3-15.	0.6	4
4594	Ecological disturbance influences adaptive divergence despite high gene flow in golden perch (<i>Macquaria ambigua</i>): Implications for management and resilience to climate change. Molecular Ecology, 2018, 27, 196-215.	2.0	24
4595	Insights into the conversion potential of Theobroma cacao L. somatic embryos using quantitative proteomic analysis. Scientia Horticulturae, 2018, 229, 65-76.	1.7	17
4596	Temporal variation in brain transcriptome is associated with the expression of female mimicry as a sequential male alternative reproductive tactic in fish. Molecular Ecology, 2018, 27, 789-803.	2.0	7
4597	Metaproteomics reveals major microbial players and their metabolic activities during the blooming period of a marine dinoflagellate <i>Prorocentrum donghaiense</i>. Environmental Microbiology, 2018, 20, 632-644.	1.8	35
4598	Identification and characterization of a calcium-dependent lily-type lectin from black rockfish (Sebastes schlegelii): Molecular antennas are involved in host defense via pathogen recognition. Developmental and Comparative Immunology, 2018, 81, 54-62.	1.0	18
4599	Transcriptome â€" Scale characterization of salt responsive bean TCP transcription factors. Gene, 2018, 642, 64-73.	1.0	24
4600	Transcriptome profiling analysis of Mactra veneriformis by deep sequencing after exposure to 2,2â€²,4,4â€²-tetrabromodiphenyl ether. Journal of Oceanology and Limnology, 2018, 36, 490-507.	0.6	4
4601	Design for an in silico Platform of Precision Medicine on Cancer Therapy. , 2018, , .		0
4602	<i>De novo</i> male gonad transcriptome draft for the marine mussel <i>Perumytilus purpuratus</i> with a focus on its reproductive-related proteins. Journal of Genomics, 2018, 6, 127-132.	0.6	10
4603	The Population Genetics of Alternaria tenuissima in Four Regions of China as Determined by Microsatellite Markers Obtained by Transcriptome Sequencing. Frontiers in Microbiology, 2018, 9, 2904.	1.5	11
4604	Genetics of a de novo origin of undifferentiated multicellularity. Royal Society Open Science, 2018, 5, 180912.	1.1	9

#	ARTICLE	IF	CITATIONS
4605	Pathogenic variability in Phytophthora capsici from black pepper (Piper nigrum L.) as revealed by transcriptome analysis. Indian Phytopathology, 2018, 71, 495-503.	0.7	2
4606	Identification of cordycepin biosynthesis-related genes through de novo transcriptome assembly and analysis in <i>Cordyceps cicadae</i>. Royal Society Open Science, 2018, 5, 181247.	1.1	21
4607	Survival, Virulent Characteristics, and Transcriptomic Analyses of the Pathogenic Vibrio anguillarum Under Starvation Stress. Frontiers in Cellular and Infection Microbiology, 2018, 8, 389.	1.8	21
4608	How Quercus ilex L. saplings face combined salt and ozone stress: a transcriptome analysis. BMC Genomics, 2018, 19, 872.	1.2	15
4609	Yerba mate (Ilex paraguariensis, A. St.-Hil.) de novo transcriptome assembly based on tissue specific genomic expression profiles. BMC Genomics, 2018, 19, 891.	1.2	9
4610	Cell Wall Synthesis, Development of Hyphae and Metabolic Pathways Are Processes Potentially Regulated by MicroRNAs Produced Between the Morphological Stages of Paracoccidioides brasiliensis. Frontiers in Microbiology, 2018, 9, 3057.	1.5	5
4611	Draft Genome Sequences of Sporulating (CIDEFI-213) and Nonsporulating (CIDEFI-212) Strains of Stemphylium lycopersici. Microbiology Resource Announcements, 2018, 7, .	0.3	5
4612	Tracking a serial killer: Integrating phylogenetic relationships, epidemiology, and geography for two invasive meningococcal disease outbreaks. PLoS ONE, 2018, 13, e0202615.	1.1	8
4613	Voltage-dependent calcium channels in the neurosecretory cells of cerebral ganglia of the mud crab, Scylla paramamosain. NeuroReport, 2018, 29, 1068-1074.	0.6	1
4614	Effects of glucose on biochemical immune responses and hepatic gene expression in common carp, <i>Cyprinus carpio</i> L. Biotechnology and Biotechnological Equipment, 2018, 32, 1440-1446.	0.5	1
4615	Transcriptome-wide responses of adult melon thrips (Thrips palmi) associated with capsicum chlorosis virus infection. PLoS ONE, 2018, 13, e0208538.	1.1	20
4616	Genotype-dependent changes of gene expression during somatic embryogenesis in oil palm hybrids (Elaeis oleifera x E. guineensis). PLoS ONE, 2018, 13, e0209445.	1.1	16
4617	De novo transcriptome analyses provide insights into opsin-based photoreception in the lanternshark Etmopterus spinax. PLoS ONE, 2018, 13, e0209767.	1.1	37
4618	High Throughput Identification of Novel Conotoxins from the Vermivorous Oak Cone Snail (Conus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	21
4619	Transcriptome Analysis and Functional Identification of Xa13 and Piâ€ta Orthologs in Oryza granulata. Plant Genome, 2018, 11, 170097.	1.6	2
4620	De novo transcriptome sequencing and SSR markers development for Cedrela balansae C.DC., a native tree species of northwest Argentina. PLoS ONE, 2018, 13, e0203768.	1.1	5
4621	Genome Scans Reveal Homogenization and Local Adaptations in Populations of the Soybean Cyst Nematode. Frontiers in Plant Science, 2018, 9, 987.	1.7	6
4622	De novo transcriptomic profiling of the clonal Leymus chinensis response to long-term overgrazing-induced memory. Scientific Reports, 2018, 8, 17912.	1.6	5

#	Article	IF	Citations
4623	Transcriptome sequencing and molecular markers discovery in the gonads of Portunus sanguinolentus. Scientific Data, 2018, 5, 180131.	2.4	18
4624	Biosorption of Cr(<scp>vi</scp>) from aqueous solution using dormant spores of<i>Aspergillus niger</i>. RSC Advances, 2018, 8, 38157-38165.	1.7	42
4625	Identification of the Genetic Variation and Gene Exchange between Citrus Trifoliata and Citrus Clementina. Biomolecules, 2018, 8, 182.	1.8	4
4626	Toxicity of <i>Melaleuca alternifolia</i> essential oil to the mitochondrion and NAD⁺/NADH dehydrogenase in <i>Tribolium confusum</i>. PeerJ, 2018, 6, e5693.	0.9	15
4627	Transcriptome analysis of hsp18.3 functions and regulatory systems using RNA-sequencing in the red flour beetle, Tribolium castaneum. Journal of Integrative Agriculture, 2018, 17, 1040-1056.	1.7	5
4628	De Novo Analysis Reveals Transcriptomic Responses in Eriobotrya japonica Fruits during Postharvest Cold Storage. Genes, 2018, 9, 639.	1.0	19
4629	Development of polymorphic microsatellite markers by using de novo transcriptome assembly of Calanthe masuca and C. sinica (Orchidaceae). BMC Genomics, 2018, 19, 800.	1.2	3
4630	MaMADS2 repression in banana fruits modifies hormone synthesis and signalling pathways prior to climacteric stage. BMC Plant Biology, 2018, 18, 267.	1.6	7
4631	Genome-wide transcriptome analysis reveals small RNA profiles involved in early stages of stolon-to-tuber transitions in potato under photoperiodic conditions. BMC Plant Biology, 2018, 18, 284.	1.6	22
4632	Comprehensive Analysis of Carbohydrate-Active Enzymes from the Filamentous Fungus Scytalidium candidum 3C. Biochemistry (Moscow), 2018, 83, 1399-1410.	0.7	0
4633	Copper-induced increased expression of genes involved in photosynthesis, carotenoid synthesis and C assimilation in the marine alga Ulva compressa. BMC Genomics, 2018, 19, 829.	1.2	18
4634	Transcriptomes Divergence of Ricotia lunaria Between the Two Micro-Climatic Divergent Slopes at â€œEvolution Canyonâ€•l, Israel. Frontiers in Genetics, 2018, 9, 506.	1.1	12
4635	Characterization of drought stress-responsive root transcriptome of faba bean (Vicia faba L.) using RNA sequencing. 3 Biotech, 2018, 8, 502.	1.1	15
4636	Physiological Analysis and Transcriptome Profiling of Inverted Cuttings of Populus yunnanensis Reveal That Cell Wall Metabolism Plays a Crucial Role in Responding to Inversion. Genes, 2018, 9, 572.	1.0	3
4637	Single-molecule long-read sequencing facilitates shrimp transcriptome research. Scientific Reports, 2018, 8, 16920.	1.6	37
4638	Genomic Analysis of Colombian Leishmania panamensis strains with different level of virulence. Scientific Reports, 2018, 8, 17336.	1.6	25
4639	Proteomic Analysis of Plasmodesmata From Populus Cell Suspension Cultures in Relation With Callose Biosynthesis. Frontiers in Plant Science, 2018, 9, 1681.	1.7	32
4640	Identification and characterization of Loa loa antigens responsible for cross-reactivity with rapid diagnostic tests for lymphatic filariasis. PLoS Neglected Tropical Diseases, 2018, 12, e0006963.	1.3	21

#	Article	IF	Citations
4641	Genomes of trombidid mites reveal novel predicted allergens and laterally transferred genes associated with secondary metabolism. GigaScience, 2018, 7, .	3.3	32
4642	Transcriptomic time-series analysis of early development in olive from germinated embryos to juvenile tree. BMC Genomics, 2018, 19, 824.	1.2	10
4643	Improved xylose tolerance and 2,3-butanediol production of Klebsiella pneumoniae by directed evolution of rpoD and the mechanisms revealed by transcriptomics. Biotechnology for Biofuels, 2018, 11, 307.	6.2	18
4644	Trypanosoma cruzi transcriptome during axenic epimastigote growth curve. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e170404.	0.8	15
4645	Transcriptome Analysis of Cinnamomum chago: A Revelation of Candidate Genes for Abiotic Stress Response and Terpenoid and Fatty Acid Biosyntheses. Frontiers in Genetics, 2018, 9, 505.	1.1	14
4646	Nezara viridula (Hemiptera: Pentatomidae) transcriptomic analysis and neuropeptidomics. Scientific Reports, 2018, 8, 17244.	1.6	22
4647	Endangered PÃ¨re Davidâ€™s deer genome provides insights into population recovering. Evolutionary Applications, 2018, 11, 2040-2053.	1.5	19
4648	Genome-Wide Association Studies Reveal Genomic Regions Associated With the Response of Wheat (Triticum aestivum L.) to Mycorrhizae Under Drought Stress Conditions. Frontiers in Plant Science, 2018, 9, 1728.	1.7	48
4649	Uncovering the Changing Gene Expression Profile of Honeybee (Apis mellifera) Worker Larvae Transplanted to Queen Cells. Frontiers in Genetics, 2018, 9, 416.	1.1	12
4650	SSR-Linkage map of interspecific populations derived from Gossypium trilobum and Gossypium thurberi and determination of genes harbored within the segregating distortion regions. PLoS ONE, 2018, 13, e0207271.	1.1	6
4651	Genome-wide identification and characterization of long non-coding RNAs involved in the early somatic embryogenesis in Dimocarpus longan Lour. BMC Genomics, 2018, 19, 805.	1.2	45
4652	Transcriptomic analysis reveals similarities in genetic activation of detoxification mechanisms resulting from imidacloprid and chlorothalonil exposure. PLoS ONE, 2018, 13, e0205881.	1.1	18
4653	Parasitic Nematodes Exert Antimicrobial Activity and Benefit From Microbiota-Driven Support for Host Immune Regulation. Frontiers in Immunology, 2018, 9, 2282.	2.2	57
4654	Linkage fine-mapping and QTLs affecting morpho-agronomic traits of a Mesoamericanâ€‰Ã—â€‰Andean RIL common bean population. Euphytica, 2018, 214, 1.	0.6	7
4655	A rice Serine/Threonine receptor-like kinase regulates arbuscular mycorrhizal symbiosis at the peri-arbuscular membrane. Nature Communications, 2018, 9, 4677.	5.8	45
4656	Draft Macronuclear Genome Sequence of the Ruminal Ciliate Entodinium caudatum. Microbiology Resource Announcements, 2018, 7, .	0.3	18
4657	iTRAQ-based quantitative tissue proteomic analysis of differentially expressed proteins (DEPs) in non-transgenic and transgenic soybean seeds. Scientific Reports, 2018, 8, 17681.	1.6	48
4658	Comparative analysis of microsatellite, SNP, and InDel markers in four <i>Rhododendron</i> species based on RNA-seq. Breeding Science, 2018, 68, 536-544.	0.9	11

#	Article	IF	Citations
4659	Identifying Differential Gene Expression in Wing Polymorphism of Adult Males of the Largest Water Strider: De novo Transcriptome Assembly forGigantometra gigas(Hemiptera: Gerridae). Journal of Insect Science, 2018, 18, .	0.6	4
4660	Transcriptome reprogramming during severe dehydration contributes to physiological and metabolic changes in the resurrection plant Haberlea rhodopensis. BMC Plant Biology, 2018, 18, 351.	1.6	40
4661	Genomic insights into multidrug-resistance, mating and virulence in Candida auris and related emerging species. Nature Communications, 2018, 9, 5346.	5.8	298
4662	Transcriptome analysis of the anhydrobiotic cell line Pv11 infers the mechanism of desiccation tolerance and recovery. Scientific Reports, 2018, 8, 17941.	1.6	14
4663	Transcriptome analysis of Aeromonas hydrophila infected hybrid sturgeon (Huso dauricusÃ—Acipenser) Tj ETQq0 0 0 rgBT /Overlock 10	1.6	29
4664	Draft Genome Sequence of Bacillus thuringiensis Strain m401, Isolated from Honey in Argentina. Microbiology Resource Announcements, 2018, 7, .	0.3	3
4665	Comparative transcriptome and metabolome analysis suggests bottlenecks that limit seed and oil yields in transgenic Camelina sativa expressing diacylglycerol acyltransferase 1 and glycerol-3-phosphate dehydrogenase. Biotechnology for Biofuels, 2018, 11, 335.	6.2	12
4666	Transcriptomic and proteomic analyses of drought responsive genes and proteins in Agropyron mongolicum Keng. Current Plant Biology, 2018, 14, 19-29.	2.3	12
4667	Draft Genome Sequence of Lactococcus lactis subsp. lactis W8, a Potential Nisin-Producing Starter Culture for Indian Traditional Fermented Milk (Dahi). Microbiology Resource Announcements, 2018, 7, .	0.3	4
4668	Comprehensive assembly and analysis of the transcriptome of maritime pine developing embryos. BMC Plant Biology, 2018, 18, 379.	1.6	17
4669	Transciptome profiling at early infection of Elaeis guineensis by Ganoderma boninense provides novel insights on fungal transition from biotrophic to necrotrophic phase. BMC Plant Biology, 2018, 18, 377.	1.6	30
4670	De novo transcriptome assembly of brackish water flea Diaphanosoma celebensis based on short-term cadmium and benzo[a]pyrene exposure experiments. Hereditas, 2018, 155, 36.	0.5	22
4671	Genomic signatures of local adaptation to the degree of environmental predictability in rotifers. Scientific Reports, 2018, 8, 16051.	1.6	22
4672	A Phylogenomic Framework and Divergence History of Cephalochordata Amphioxus. Frontiers in Physiology, 2018, 9, 1833.	1.3	11
4673	Effect of Sublethal Doses of Imidacloprid on the Biological Performance of Aphid Endoparasitoid Aphidius gifuensis (Hymenoptera: Aphidiidae) and Influence on Its Related Gene Expression. Frontiers in Physiology, 2018, 9, 1729.	1.3	35
4674	Primula vulgaris (primrose) genome assembly, annotation and gene expression, with comparative genomics on the heterostyly supergene. Scientific Reports, 2018, 8, 17942.	1.6	40
4675	Using Transcriptome Analysis to Identify Genes Involved in Switchgrass Flower Reversion. Frontiers in Plant Science, 2018, 9, 1805.	1.7	5
4676	Genome sequence of walking catfish (Clarias batrachus) provides insights into terrestrial adaptation. BMC Genomics, 2018, 19, 952.	1.2	36

#	ARTICLE	IF	CITATIONS
4677	Comparative Transcriptome Analysis between Fertile and CMS Flower Buds in Wucai (Brassica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.2	35
4678	Genome-wide identification and functional analysis of circRNAs in Zea mays. PLoS ONE, 2018, 13, e0202375.	1.1	32
4679	Comparative cochlear transcriptomics of echolocating bats provides new insights into different nervous activities of CF bat species. Scientific Reports, 2018, 8, 15934.	1.6	9
4680	Differential responses of Lasiopodomys mandarinus and Lasiopodomys brandtii to chronic hypoxia: a cross-species brain transcriptome analysis. BMC Genomics, 2018, 19, 901.	1.2	14
4681	Effect of Aspergillus flavus Fungal Elicitor on the Production of Terpenoid Indole Alkaloids in Catharanthus roseus Cambial Meristematic Cells. Molecules, 2018, 23, 3276.	1.7	20
4682	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. Ecology and Evolution, 2018, 8, 11273-11292.	0.8	9
4683	Combination of transcriptome sequencing and iTRAQ proteome reveals the molecular mechanisms determining petal shape in herbaceous peony (<i>Paeonia lactiflora</i> Pall.). Bioscience Reports, 2018, 38, .	1.1	15
4684	Genomic identification and functional analysis of essential genes in Caenorhabditis elegans. BMC Genomics, 2018, 19, 871.	1.2	10
4685	Comparative transcriptomics between high and low rubber producing Taraxacum kok-saghyz R. plants. BMC Genomics, 2018, 19, 875.	1.2	13
4686	Analysis of the transcriptome data in Litopenaeus vannamei reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. PLoS ONE, 2018, 13, e0207771.	1.1	20
4687	Dual RNA-Seq Uncovers Metabolic Amino Acids Dependency of the Intracellular Bacterium Piscirickettsia salmonis Infecting Atlantic Salmon. Frontiers in Microbiology, 2018, 9, 2877.	1.5	53
4688	Identification and Comparison of Chemosensory Genes in the Antennal Transcriptomes of Eucryptorrhynchus scrobiculatus and E. brandti Fed on Ailanthus altissima. Frontiers in Physiology, 2018, 9, 1652.	1.3	14
4689	De novo sequencing and transcriptome assembly of Arisaema heterophyllum Blume and identification of genes involved in isoflavonoid biosynthesis. Scientific Reports, 2018, 8, 17643.	1.6	19
4690	Analysis of genome-wide variants through bulked segregant RNA sequencing reveals a major gene for resistance to Plasmodiophora brassicae in Brassica oleracea. Scientific Reports, 2018, 8, 17657.	1.6	40
4691	Population genomics of parallel evolution in gene expression and gene sequence during ecological adaptation. Scientific Reports, 2018, 8, 16147.	1.6	12
4692	De Novo Transcriptomic Analysis and Development of ESTâ€“SSRs for Styrax japonicus. Forests, 2018, 9, 748.	0.9	18
4693	Introduction to Bioinformatics in Microbiology. Learning Materials in Biosciences, 2018, , .	0.2	5
4694	Full Shotgun DNA Metagenomics. Learning Materials in Biosciences, 2018, , 163-175.	0.2	1

#	Article	IF	Citations
4695	Generation and classification of transcriptomes in two Croomia species and molecular evolution of CYC/TB1 genes in Stemonaceae. Plant Diversity, 2018, 40, 253-264.	1.8	1
4696	Unique Diversity of Sting-Related Toxins Based on Transcriptomic and Proteomic Analysis of the Jellyfish Cyanea capillata and Nemopilema nomurai (Cnidaria: Scyphozoa). Journal of Proteome Research, 2018, 18, 436-448.	1.8	27
4697	Molecular genotyping, diversity studies and high-resolution molecular markers unveiled by microsatellites in Giardia duodenalis. PLoS Neglected Tropical Diseases, 2018, 12, e0006928.	1.3	7
4698	Detoxification and Immune Transcriptomic Response of the Gill Tissue of Bay Scallop (Argopecten) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	6
4699	Transcriptome Analysis Provides Insights into Gingerol Biosynthesis in Ginger (<i>Zingiber) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 Td	1.6	19
4700	Comparison of Olfactory Genes in Two Ectropis Species: Emphasis on Candidates Involved in the Detection of Type-II Sex Pheromones. Frontiers in Physiology, 2018, 9, 1602.	1.3	5
4701	Genome-wide exploration of C2H2 zinc finger family in durum wheat (Triticum turgidum ssp. Durum): insights into the roles in biological processes especially stress response. BioMetals, 2018, 31, 1019-1042.	1.8	37
4702	Transcriptome analysis reveals the molecular response to cadmium toxicity in P. pseudoannulata. Environmental Science and Pollution Research, 2018, 25, 34294-34305.	2.7	15
4703	RNA-seq data from mature male gonads of marine mussels Mytilus edulis and M. galloprovincialis. Data in Brief, 2018, 21, 167-175.	0.5	7
4704	A draft genome of the striped catfish, Pangasianodon hypophthalmus, for comparative analysis of genes relevant to development and a resource for aquaculture improvement. BMC Genomics, 2018, 19, 733.	1.2	34
4705	Deletions linked to PROG1 gene participate in plant architecture domestication in Asian and African rice. Nature Communications, 2018, 9, 4157.	5.8	63
4706	Allele-defined genome of the autopolyploid sugarcane Saccharum spontaneum L.. Nature Genetics, 2018, 50, 1565-1573.	9.4	463
4707	Catfish Mucus Alters the Flavobacterium columnare Transcriptome. FEMS Microbiology Letters, 2018, 365, .	0.7	17
4708	Proteome of olive non-glandular trichomes reveals protective protein network against (a)biotic challenge. Journal of Plant Physiology, 2018, 231, 210-218.	1.6	17
4709	Comparative in depth RNA sequencing of P. tricornutumâ€™s morphotypes reveals specific features of the oval morphotype. Scientific Reports, 2018, 8, 14340.	1.6	19
4710	Chromosomal-level assembly of yellow catfish genome using third-generation DNA sequencing and Hi-C analysis. GigaScience, 2018, 7, .	3.3	75
4711	Evolutionary insights from comparative transcriptome and transcriptome-wide coalescence analyses in Tetrastigma hemsleyanum. BMC Plant Biology, 2018, 18, 208.	1.6	11
4712	Complex gene response of herbicide-resistant Enterobacter strain NRS-1 under different glyphosate stresses. 3 Biotech, 2018, 8, 422.	1.1	1

#	Article	IF	Citations
4713	Genetic mapping of psl locus and quantitative trait loci for angular leaf spot resistance in cucumber (Cucumis sativus L.). Molecular Breeding, 2018, 38, 111.	1.0	13
4714	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. Genome Biology and Evolution, 2018, 10, 2785-2800.	1.1	42
4715	Conserved Genes Underlie Phenotypic Plasticity in an Incipiently Social Bee. Genome Biology and Evolution, 2018, 10, 2749-2758.	1.1	24
4716	A functional transcriptomic analysis in the relict marsupial <i>Dromiciops gliroides</i> reveals adaptive regulation of protective functions during hibernation. Molecular Ecology, 2018, 27, 4489-4500.	2.0	24
4717	Microsynteny analysis to understand evolution and impact of polyploidization on MIR319 family within Brassicaceae. Development Genes and Evolution, 2018, 228, 227-242.	0.4	6
4718	Full-length transcriptome sequences of ephemeral plant Arabidopsis pumila provides insight into gene expression dynamics during continuous salt stress. BMC Genomics, 2018, 19, 717.	1.2	54
4719	Transcriptome analysis of Macrobrachium rosenbergii intestines under the white spot syndrome virus and poly (I:C) challenges. PLoS ONE, 2018, 13, e0204626.	1.1	12
4720	Tamanu oil and skin active properties: from traditional to modern cosmetic uses. OCL - Oilseeds and Fats, Crops and Lipids, 2018, 25, D504.	0.6	9
4721	Phenotypic and molecular consequences of stepwise temperature increase across generations in a coral reef fish. Molecular Ecology, 2018, 27, 4516-4528.	2.0	37
4722	Dynamics of the Methylome and Transcriptome during the Regeneration of Rice. Epigenomes, 2018, 2, 14.	0.8	15
4723	Genotypic response of pollen germination in Dura, Pisifera and Tenera oil palm (Elaeis guineensis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.6	1
4724	A highâ€resolution einkorn (<i>Triticum monococcum</i> L.) linkage map involving wild, domesticated and feral einkorn genotypes. Plant Breeding, 2018, 137, 682-690.	1.0	7
4725	Transcriptomic response to parasite infection in Nile tilapia (Oreochromis niloticus) depends on rearing density. BMC Genomics, 2018, 19, 723.	1.2	44
4726	Quantitative Proteomics Analysis of Lettuce (Lactuca sativa L.) Reveals Molecular Basis-Associated Auxin and Photosynthesis with Bolting Induced by High Temperature. International Journal of Molecular Sciences, 2018, 19, 2967.	1.8	22
4727	Comparative genome analyses reveal sequence features reflecting distinct modes of host-adaptation between dicot and monocot powdery mildew. BMC Genomics, 2018, 19, 705.	1.2	39
4728	Transcriptome sequencing of Pinus kesiya var. langbianensis and comparative analysis in the Pinus phylogeny. BMC Genomics, 2018, 19, 725.	1.2	13
4729	Specific LTR-Retrotransposons Show Copy Number Variations between Wild and Cultivated Sunflowers. Genes, 2018, 9, 433.	1.0	16
4730	Comprehensive Transcriptome Profiling and Identification of Potential Genes Responsible for Salt Tolerance in Tall Fescue Leaves under Salinity Stress. Genes, 2018, 9, 466.	1.0	5

#	ARTICLE	IF	CITATIONS
4731	Characterization, homology modeling and expression of the putative translationally controlled tumor protein gene from giant river prawn Macrobrachium rosenbergii (de Man). Agriculture and Natural Resources, 2018, 52, 182-189.	0.4	0
4732	Energy metabolism in the intestinal crypt epithelial cells of piglets during the suckling period. Scientific Reports, 2018, 8, 12948.	1.6	7
4733	Draft Genome Sequence of Streptomyces cavourensis YBQ59, an Endophytic Producer of Antibiotics Bafilomycin D, Nonactic Acid, Prelactone B, and 5,11-Epoxy-10-Cadinanol. Microbiology Resource Announcements, 2018, 7, .	0.3	4
4734	DNA barcoding reveals seasonal shifts in diet and consumption of deep-sea fishes in wedge-tailed shearwaters. PLoS ONE, 2018, 13, e0195385.	1.1	14
4735	Expression Profile of Glossina pallidipes MicroRNAs During Symptomatic and Asymptomatic Infection With Glossina pallidipes Salivary Gland Hypertrophy Virus (Hytrosavirus). Frontiers in Microbiology, 2018, 9, 2037.	1.5	7
4736	Ceratocystidaceae exhibit high levels of recombination at the mating-type (MAT) locus. Fungal Biology, 2018, 122, 1184-1191.	1.1	10
4737	Transcriptomic and metabolic response to chronic and acute thermal exposure of juvenile geoduck clams Panopea globosa. Marine Genomics, 2018, 42, 1-13.	0.4	21
4738	The Duality of the MAPK Signaling Pathway in the Control of Metabolic Processes and Cellulase Production in Trichoderma reesei. Scientific Reports, 2018, 8, 14931.	1.6	31
4739	Transcriptome Analysis Provides Insights Into the Adaptive Responses to Hypoxia of a Schizothoracine Fish (Gymnocypris eckloni). Frontiers in Physiology, 2018, 9, 1326.	1.3	35
4740	De Novo assembly and comparative transcriptome analyses of purple and green morphs of Apostichopus japonicus during body wall pigmentation process. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 151-161.	0.4	11
4741	Transcriptome analysis provides novel insights into high-soil-moisture-elevated susceptibility to Ralstonia solanacearum infection in ginger (Zingiber officinale Roscoe cv. Southwest). Plant Physiology and Biochemistry, 2018, 132, 547-556.	2.8	15
4742	Acute toxic effects of zinc oxide nanoparticles on Hydra magnipapillata. Aquatic Toxicology, 2018, 205, 130-139.	1.9	24
4743	Quantitative analysis of the grain amyloplast proteome reveals differences in metabolism between two wheat cultivars at two stages of grain development. BMC Genomics, 2018, 19, 768.	1.2	10
4744	Landscape of alternative splicing in Capra_hircus. Scientific Reports, 2018, 8, 15128.	1.6	3
4745	Transcriptome Dynamics During Turbot Spermatogenesis Predicting the Potential Key Genes Regulating Male Germ Cell Proliferation and Maturation. Scientific Reports, 2018, 8, 15825.	1.6	17
4746	Genomic regions underlying uniformity of yearling weight in Nellore cattle evaluated under different response variables. BMC Genomics, 2018, 19, 619.	1.2	11
4747	Evidence of peripheral olfactory impairment in the domestic silkworms: insight from the comparative transcriptome and population genetics. BMC Genomics, 2018, 19, 788.	1.2	14
4748	RNA-Seq-based transcriptome analysis of reproduction- and growth-related genes in Lateolabrax japonicus ovaries at four different ages. Molecular Biology Reports, 2018, 45, 2213-2225.	1.0	3

#	ARTICLE	IF	CITATIONS
4749	Comparative proteomic analysis of Ulva prolifera response to high temperature stress. Proteome Science, 2018, 16, 17.	0.7	18
4750	Genetic diversity and phylogeny of South African Meloidogyne populations using genotyping by sequencing. Scientific Reports, 2018, 8, 13816.	1.6	21
4751	Pathways and Network Based Analysis of Candidate Genes to Reveal Cross-Talk and Specificity in the Sorghum (Sorghum bicolor (L.) Moench) Responses to Drought and It's Co-occurring Stresses. Frontiers in Genetics, 2018, 9, 557.	1.1	22
4752	Non-target site-based resistance to tribenuron-methyl and essential involved genes in Myosoton aquaticum (L.). BMC Plant Biology, 2018, 18, 225.	1.6	37
4753	Characterization of candidate genes involved in halotolerance using high-throughput omics in the halotolerant bacterium Virgibacillus chiguensis. PLoS ONE, 2018, 13, e0201346.	1.1	7
4754	Identification of water use efficiency related genes in â€˜Garnemâ€™ almond-peach rootstock using time-course transcriptome analysis. PLoS ONE, 2018, 13, e0205493.	1.1	24
4755	Identification of differentially expressed immunityâ€•related genes in <i>Monochamus alternatus</i> Hope (Coleoptera: Cerambycidae) larvae parasitized by <i>Dastarcus helophoroides</i> (Fairmaire) (Coleoptera: Bothrideridae). Entomological Research, 2018, 48, 248-261.	0.6	1
4756	A Wor1-Like Transcription Factor Is Essential for Virulence of Cryptococcus neoformans. Frontiers in Cellular and Infection Microbiology, 2018, 8, 369.	1.8	3
4757	Unraveling Rice Tolerance Mechanisms Against Schizotetranychus oryzae Mite Infestation. Frontiers in Plant Science, 2018, 9, 1341.	1.7	9
4758	Social environment affects the transcriptomic response to bacteria in ant queens. Ecology and Evolution, 2018, 8, 11031-11070.	0.8	6
4759	High-throughput sequencing analysis of Euphorbia fischeriana Steud provides insights into the molecular mechanism of pharmaceutical ingredient biosynthesis. 3 Biotech, 2018, 8, 449.	1.1	2
4760	Metaproteomic characterization of Vitis vinifera rhizosphere. FEMS Microbiology Ecology, 2019, 95, .	1.3	26
4761	Immune-suppression by OsHV-1 viral infection causes fatal bacteraemia in Pacific oysters. Nature Communications, 2018, 9, 4215.	5.8	217
4762	Reticulate evolution within a spruce (<i>Picea</i>) species complex revealed by population genomic analysis. Evolution; International Journal of Organic Evolution, 2018, 72, 2669-2681.	1.1	22
4763	Development, characterization, and transferability of <scp>SSR</scp> markers for <i>Vriesea carinata</i> (Bromeliaceae) based on <scp>RNA</scp> sequencing. Applications in Plant Sciences, 2018, 6, e01184.	0.8	2
4764	Three new genome assemblies support a rapid radiation in Musa acuminata (wild banana). Genome Biology and Evolution, 2018, 10, 3129-3140.	1.1	29
4765	Draft Genome Sequence of Escherichia coli Phage CMSTMSU, Isolated from Shrimp Farm Effluent Water. Microbiology Resource Announcements, 2018, 7, .	0.3	6
4766	RNA-Seq Analysis for Assessing the Early Response to DSP Toxins in Mytilus galloprovincialis Digestive Gland and Gill. Toxins, 2018, 10, 417.	1.5	29

#	ARTICLE	IF	CITATIONS
4767	The Defense Response of Nicotiana benthamiana to Peanut Stunt Virus Infection in the Presence of Symptom Exacerbating Satellite RNA. Viruses, 2018, 10, 449.	1.5	7
4768	De novo genome and transcriptome analyses provide insights into the biology of the trematode human parasite Fasciolopsis buski. PLoS ONE, 2018, 13, e0205570.	1.1	4
4769	A distinct strain of Arsenophonus symbiont decreases insecticide resistance in its insect host. PLoS Genetics, 2018, 14, e1007725.	1.5	88
4770	Transcriptome sequencing, de novo assembly and annotation of the freeze tolerant earthworm, Dendrobaena octaedra. Gene Reports, 2018, 13, 180-191.	0.4	8
4771	Prey Range and Genome Evolution of Halobacteriovorax marinus Predatory Bacteria from an Estuary. MSphere, 2018, 3, .	1.3	10
4772	De novo transcriptome based on next-generation sequencing reveals candidate genes with sex-specific expression in Arapaima gigas (Schinz, 1822), an ancient Amazonian freshwater fish. PLoS ONE, 2018, 13, e0206379.	1.1	13
4773	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. PLoS ONE, 2018, 13, e0205295.	1.1	33
4774	Persistent Interactions with Bacterial Symbionts Direct Mature-Host Cell Morphology and Gene Expression in the Squid-Vibrio Symbiosis. MSystems, 2018, 3, .	1.7	17
4775	A Genome-wide View of Transcriptome Dynamics During Early Spike Development in Bread Wheat. Scientific Reports, 2018, 8, 15338.	1.6	45
4776	Transcriptome analysis reveals crucial genes involved in the biosynthesis of nervonic acid in woody Malania oleifera oilseeds. BMC Plant Biology, 2018, 18, 247.	1.6	31
4777	RNA-Seq analysis of differentially expressed genes relevant to innate and adaptive immunity in cecropin P1 transgenic rainbow trout (Oncorhynchus mykiss). BMC Genomics, 2018, 19, 760.	1.2	13
4778	An integration of phenotypic and transcriptomic data analysis reveals yield-related hub genes in Jatropha curcas inflorescence. PLoS ONE, 2018, 13, e0203441.	1.1	4
4779	Comparative transcriptome analysis two genotypes of Acer truncatum Bunge seeds reveals candidate genes that influences seed VLCFAs accumulation. Scientific Reports, 2018, 8, 15504.	1.6	20
4780	Transcriptomic Plasticity in the Arthropod Generalist Tetranychus urticae Upon Long-Term Acclimation to Different Host Plants. G3: Genes, Genomes, Genetics, 2018, 8, 3865-3879.	0.8	36
4781	Effects of single exposure and binary mixtures of ultraviolet filters octocrylene and 2-ethylhexyl 4-(dimethylamino) benzoate on gene expression in the freshwater insect Chironomus riparius. Environmental Science and Pollution Research, 2018, 25, 35501-35514.	2.7	21
4782	Differential Expression Analysis of RNA-seq Reads: Overview, Taxonomy and Tools. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	1.9	14
4783	Major ampullate silk gland transcriptomes and fibre proteomes of the golden orb-weavers, Nephila plumipes and Nephila pilipes (Araneae: Nephilidae). PLoS ONE, 2018, 13, e0204243.	1.1	13
4784	Endochondral ossification in hindlimbs during <i>bufo gargarizans</i> metamorphosis: A model of studying skeletal development in vertebrates. Developmental Dynamics, 2018, 247, 1121-1134.	0.8	13

#	ARTICLE	IF	CITATIONS
4785	CeleryDB: a genomic database for celery. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	27
4786	Transcriptome analysis of the critically endangered Dabry's sturgeon (Acipenser dabryanus) head kidney response to Aeromonas hydrophila. Fish and Shellfish Immunology, 2018, 83, 249-261.	1.6	31
4787	The genome of Naegleria lovaniensis, the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba N. fowleri. BMC Genomics, 2018, 19, 654.	1.2	23
4788	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. Genome Biology and Evolution, 2018, 10, 2716-2733.	1.1	53
4789	Quantitative Trait Loci Controlling Fruit Size and Other Horticultural Traits in Bell Pepper (Capsicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	66
4790	Brazilin induces T24 cell death through <i>câ€Fos</i> and <i>GADD45Î²</i> independently regulated genes and pathways. IUBMB Life, 2018, 70, 1101-1110.	1.5	12
4791	An Adult Zebrafish Model Reveals that Mucormycosis Induces Apoptosis of Infected Macrophages. Scientific Reports, 2018, 8, 12802.	1.6	33
4792	Expansion of cytochrome P450 and cathepsin genes in the generalist herbivore brown marmorated stink bug. BMC Genomics, 2018, 19, 60.	1.2	18
4793	Transcriptomic Profiling and Gene Disruption Revealed that Two Genes Related to PUFAs/DHA Biosynthesis May be Essential for Cell Growth of Aurantiochytrium sp.. Marine Drugs, 2018, 16, 310.	2.2	19
4794	The assembled transcriptome of the adult horn fly, Haematobia irritans. Data in Brief, 2018, 19, 1933-1940.	0.5	6
4795	SNP in the Coffea arabica genome associated with coffee quality. Tree Genetics and Genomes, 2018, 14, 1.	0.6	19
4796	Data on genome annotation and analysis of earthworm Eisenia fetida. Data in Brief, 2018, 20, 525-534.	0.5	6
4797	Whole Genome Sequencing of the Pirarucu (Arapaima gigas) Supports Independent Emergence of Major Teleost Clades. Genome Biology and Evolution, 2018, 10, 2366-2379.	1.1	33
4798	De novo sequencing of the Freesia hybrida petal transcriptome to discover putative anthocyanin biosynthetic genes and develop ESTâ€“SSR markers. Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	6
4799	Analysis of the hybrid genomes of two field isolates of the soil-borne fungal species Verticillium longisporum. BMC Genomics, 2018, 19, 14.	1.2	23
4800	De novo assembly, characterization, functional annotation and expression patterns of the black tiger shrimp (Penaeus monodon) transcriptome. Scientific Reports, 2018, 8, 13553.	1.6	48
4801	Hemolymph protein profiles of subterranean termite Reticulitermes flavipes challenged with methicillin resistant Staphylococcus aureus or Pseudomonas aeruginosa. Scientific Reports, 2018, 8, 13251.	1.6	3
4802	A draft genome assembly of the Chinese sillago (Sillago sinica), the first reference genome for Sillaginidae fishes. GigaScience, 2018, 7, .	3.3	30

#	ARTICLE	IF	CITATIONS
4803	Research Article Preliminary analysis on the developmental transcriptomes of swallowtail butterfly Papilio polytes (Lepidoptera: Papilioidae). Genetics and Molecular Research, 2018, 17, .	0.3	0
4804	Identification and functional analyses of new sesame miRNAs (Sesamum indicum L.) and their targets. Molecular Biology Reports, 2018, 45, 2145-2155.	1.0	9
4805	Suckling Piglet Intestinal Enterocyte Nutrient Metabolism Changes. Cellular Physiology and Biochemistry, 2018, 48, 2103-2113.	1.1	4
4806	Analysis of evolution and genetic diversity of sweetpotato and its related different polyploidy wild species I. trifida using RAD-seq. BMC Plant Biology, 2018, 18, 181.	1.6	27
4807	Characterization of Laguncularia racemosa transcriptome and molecular response to oil pollution. Aquatic Toxicology, 2018, 205, 36-50.	1.9	5
4808	RNA-Seq-based transcriptome profiling and expression of 16 cytochrome P450 genes in the benzo[Î±]pyrene-exposed estuarine copepod Eurytemora affinis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 142-150.	0.4	7
4809	Genome-wide transcriptome analysis of the salt stress tolerance mechanism in Rosa chinensis. PLoS ONE, 2018, 13, e0200938.	1.1	30
4810	Comparative transcriptome analysis of Eriocheir japonica sinensis response to environmental salinity. PLoS ONE, 2018, 13, e0203280.	1.1	9
4811	New insights into Phakopsora pachyrhizi infection based on transcriptome analysis in planta. Genetics and Molecular Biology, 2018, 41, 671-691.	0.6	4
4812	Transcriptome assembly and annotation of johnsongrass (<i>Sorghum halepense</i>) rhizomes identify candidate rhizomeâ€specific genes. Plant Direct, 2018, 2, e00065.	0.8	8
4813	Small RNAs from cereal powdery mildew pathogens may target host plant genes. Fungal Biology, 2018, 122, 1050-1063.	1.1	41
4814	Mining and analysis of simple sequence repeats in the chloroplast genomes of genus Vigna. Biotechnology Research and Innovation, 2018, 2, 9-18.	0.3	15
4815	Transcriptome profiling uncovers Î²-galactosidases of diverse domain classes influencing hypocotyl development in jute (Corchorus capsularis L.). Phytochemistry, 2018, 156, 20-32.	1.4	8
4816	Genomic Analysis of Picochlorum Species Reveals How Microalgae May Adapt to Variable Environments. Molecular Biology and Evolution, 2018, 35, 2702-2711.	3.5	30
4817	De novo transcriptome assembly of the lobster cockroach Nauphoeta cinerea (Blaberidae). Genetics and Molecular Biology, 2018, 41, 713-721.	0.6	8
4818	Comparative transcriptomics analysis of the river pufferfish (Takifugu obscurus) by tributyltin exposure: Clues for revealing its toxic injury mechanism. Fish and Shellfish Immunology, 2018, 82, 536-543.	1.6	3
4819	Opposite Polarity Monospore Genome De Novo Sequencing and Comparative Analysis Reveal the Possible Heterothallic Life Cycle of Morchella importuna. International Journal of Molecular Sciences, 2018, 19, 2525.	1.8	31
4820	Transcriptome analysis and identification of genes associated with flower development in Rhododendron pulchrum Sweet (Ericaceae). Gene, 2018, 679, 108-118.	1.0	22

#	ARTICLE	IF	CITATIONS
4821	Development and characterization of Novel Microsatellite markers in great snakehead, Channa marulia ( ). Meta Gene, 2018, 18, 143-148.	0.3	3
4822	Transcriptomic changes in Cucurbita pepo fruit after cold storage: differential response between two cultivars contrasting in chilling sensitivity. BMC Genomics, 2018, 19, 125.	1.2	24
4823	Organism-environment interactions and differential gene expression patterns among open-coastal and estuarine populations of Porphyra umbilicalis KÃ¼tzing (Rhodophyta) in the Northwest Atlantic. Fisheries and Aquatic Sciences, 2018, 21, .	0.3	3
4824	Comparative Analysis of Impatiens Leaf Transcriptomes Reveal Candidate Genes for Resistance to Downy Mildew Caused by Plasmopara obducens. International Journal of Molecular Sciences, 2018, 19, 2057.	1.8	13
4825	Differential gene expression in the evolution of sex pheromone communication in New Zealandâ€™s endemic leafroller moths of the genera Ctenopseustis and Planotortrix. BMC Genomics, 2018, 19, 94.	1.2	18
4826	A comprehensive comparison of four species of Onchidiidae provides insights on the morphological and molecular adaptations of invertebrates from shallow seas to wetlands. PLoS ONE, 2018, 13, e0196252.	1.1	7
4827	BdorOR88a Modulates the Responsiveness to Methyl Eugenol in Mature Males of Bactrocera dorsalis (Hendel). Frontiers in Physiology, 2018, 9, 987.	1.3	29
4828	Transcriptome analysis and physiological responses of the potato plantlets in vitro under red, blue, and white light conditions. 3 Biotech, 2018, 8, 394.	1.1	9
4829	Identification of candidate olfactory genes in cicada Subpsaltria yangi by antennal transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 122-133.	0.4	7
4830	Coordinated RNA-Seq and peptidomics identify neuropeptides and G-protein coupled receptors (GPCRs) in the large pine weevil Hylobius abietis, a major forestry pest. Insect Biochemistry and Molecular Biology, 2018, 101, 94-107.	1.2	39
4831	Transcriptional profiling and genes involved in acquired thermotolerance in Banana: a non-model crop. Scientific Reports, 2018, 8, 10683.	1.6	14
4832	A gene-rich fraction analysis of the Passiflora edulis genome reveals highly conserved microsyntenic regions with two related Malpighiales species. Scientific Reports, 2018, 8, 13024.	1.6	18
4833	Transcriptome analysis of Valsa mali reveals its response mechanism to the biocontrol actinomycete Saccharothrix yanglingensis Hhs.015. BMC Microbiology, 2018, 18, 90.	1.3	9
4834	Draft genome of Dugesia japonica provides insights into conserved regulatory elements of the brain restriction gene nou-darake in planarians. Zoological Letters, 2018, 4, 24.	0.7	38
4835	Transcriptome sequencing analysis of two different genotypes of Asian pear reveals potential drought stress genes. Tree Genetics and Genomes, 2018, 14, 1.	0.6	9
4836	Transcriptome sequencing for identification of diapause-associated genes in fall webworm, Hyphantria cunea Drury. Gene, 2018, 668, 229-236.	1.0	15
4837	Gene Expression Analysis. Methods in Molecular Biology, 2018, , .	0.4	3
4838	De novo assembly and annotation of the blood transcriptome of the southern giant petrel Macronectes giganteus from the South Shetland Islands, Antarctica. Marine Genomics, 2018, 42, 63-66.	0.4	2

#	Article	IF	Citations
4839	Probing the transcriptome of Aconitum carmichaelii reveals the candidate genes associated with the biosynthesis of the toxic aconitine-type C19-diterpenoid alkaloids. Phytochemistry, 2018, 152, 113-124.	1.4	20
4840	Transcriptome profiling reveals differential gene expression of detoxification enzymes in Sitophilus zeamais responding to terpinen-4-ol fumigation. Pesticide Biochemistry and Physiology, 2018, 149, 44-53.	1.6	36
4841	Draft Genome Sequences of Streptomyces sp. Strains MH60 and 111WW2. Genome Announcements, 2018, 6, .	0.8	1
4842	WEGO 2.0: a web tool for analyzing and plotting GO annotations, 2018 update. Nucleic Acids Research, 2018, 46, W71-W75.	6.5	473
4843	Transcriptome profiling analysis reveals the role of latrophilin in controlling development, reproduction and insecticide susceptibility in Tribolium castaneum. Genetica, 2018, 146, 287-302.	0.5	17
4844	Metagenomic and metatranscriptomic analysis of the microbial community in Swiss-type Maasdam cheese during ripening. International Journal of Food Microbiology, 2018, 281, 10-22.	2.1	63
4845	RNA-Seq and UHPLC-Q-TOF/MS Based Lipidomics Study in Lysiphlebia japonica. Scientific Reports, 2018, 8, 7802.	1.6	6
4846	Differential response to heat stress in outer and inner onion bulb scales. Journal of Experimental Botany, 2018, 69, 4047-4064.	2.4	16
4847	Comparative Genomics Reveals the Core Gene Toolbox for the Fungus-Insect Symbiosis. MBio, 2018, 9, .	1.8	17
4848	High Throughput Sequencing-Based Approaches for Gene Expression Analysis. Methods in Molecular Biology, 2018, 1783, 299-323.	0.4	8
4849	Identification of genes involved in gonadal sex differentiation and the dimorphic expression pattern in Takifugu rubripes gonad at the early stage of sex differentiation. Fish Physiology and Biochemistry, 2018, 44, 1275-1290.	0.9	31
4850	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in Ettlia oleoabundans. Algal Research, 2018, 33, 142-155.	2.4	21
4851	Transcriptomic profiling and identification of candidate genes in two Phoebe bournei ecotypes with contrasting cold stress responses. Trees - Structure and Function, 2018, 32, 1315-1333.	0.9	15
4852	Extrapolation of significant genes and transcriptional regulatory networks involved in Zea mays in response in UV-B stress. Genes and Genomics, 2018, 40, 973-990.	0.5	22
4853	Transcriptome analysis of the Yesso scallop, Patinopecten yessoensis gills in response to water temperature fluctuations. Fish and Shellfish Immunology, 2018, 80, 133-140.	1.6	30
4854	Draft genome sequence of Xylaria sp., the causal agent of taproot decline of soybean in the southern United States. Data in Brief, 2018, 17, 129-133.	0.5	1
4855	Genome-wide DNA methylation profile of prepubertal porcine testis. Reproduction, Fertility and Development, 2018, 30, 349.	0.1	16
4856	Transcriptome and Expression Profiling Analysis of Recalcitrant Tea (Camellia sinensis L.) Seeds Sensitive to Dehydration. International Journal of Genomics, 2018, 2018, 1-11.	0.8	7

#	ARTICLE	IF	CITATIONS
4857	Genome-Wide Investigation and Expression Profiling of HD-Zip Transcription Factors in Foxtail Millet (<i>Setaria italica</i>L.). BioMed Research International, 2018, 2018, 1-18.	0.9	25
4858	The genome of the Hi5 germ cell line from Trichoplusia ni, an agricultural pest and novel model for small RNA biology. ELife, 2018, 7, .	2.8	68
4859	Comparative proteomic analysis of foodborne Salmonella Enteritidis SE86 subjected to cold plasma treatment. Food Microbiology, 2018, 76, 310-318.	2.1	16
4860	Interrogation of the Gulf toadfish intestinal proteome response to hypersalinity exposure provides insights into osmoregulatory mechanisms and regulation of carbonate mineral precipitation. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 66-76.	0.4	4
4861	Comparative analysis of distinctive transcriptome profiles with biochemical evidence in bisphenol S- and benzo[a]pyrene-exposed liver tissues of the olive flounder Paralichthys olivaceus. PLoS ONE, 2018, 13, e0196425.	1.1	17
4862	A fine-tuned vector-parasite dialogue in tsetse's cardia determines peritrophic matrix integrity and trypanosome transmission success. PLoS Pathogens, 2018, 14, e1006972.	2.1	23
4863	De novo assembly and annotation of Didymium iridis transcriptome and identification of stage-specfic genes. Biologia (Poland), 2018, 73, 393-402.	0.8	4
4864	Identification of candidate chemosensory receptors in the antennal transcriptome of the large black chafer Holotrichia parallela Motschulsky (Coleoptera: Scarabaeidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 63-71.	0.4	17
4865	l-arginine alters the proteome of frozen-thawed bovine sperm during inÂvitro capacitation. Theriogenology, 2018, 119, 1-9.	0.9	18
4866	Genome-Wide Expression Profiles of Hemp (Cannabis sativa L.) in Response to Drought Stress. International Journal of Genomics, 2018, 2018, 1-13.	0.8	23
4867	Uncaria rhynchophylla Ameliorates Parkinsonâ€™s Disease by Inhibiting HSP90 Expression: Insights from Quantitative Proteomics. Cellular Physiology and Biochemistry, 2018, 47, 1453-1464.	1.1	40
4868	Transcriptome analysis of differentially expressed genes involved in selenium accumulation in tea plant (Camellia sinensis). PLoS ONE, 2018, 13, e0197506.	1.1	44
4869	Transcriptome-wide survey, gene expression profiling and exogenous chemical-induced transcriptional responses of cytochrome P450 superfamily genes in migratory locust (Locusta) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 25	1.2	46
4870	Carboxylate clamp tetratricopeptide repeat (TPR) domain containing Hsp90 cochaperones in Triticeace: An insight into structural and functional diversification. Environmental and Experimental Botany, 2018, 155, 31-44.	2.0	4
4871	The High-Quality Genome Sequence of the Oceanic Island Endemic Species Drosophila guanche Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. Genome Biology and Evolution, 2018, 10, 1956-1969.	1.1	14
4872	Coexpression network and phenotypic analysis identify metabolic pathways associated with the effect of warming on grain yield components in wheat. PLoS ONE, 2018, 13, e0199434.	1.1	18
4873	Transcriptomic and Network Analyses Reveal Mechanistic-Based Biomarkers of Endocrine Disruption in the Marine Mussel, <i>Mytilus edulis</i>. Environmental Science & Technology, 2018, 52, 9419-9430.	4.6	42
4874	Embryogenic Competence Acquisition in Sugar Cane Callus Is Associated with Differential H⁺-Pump Abundance and Activity. Journal of Proteome Research, 2018, 17, 2767-2779.	1.8	21

#	Article	IF	Citations
4875	Differentially expressed genes in response to amitraz treatment suggests a proposed model of resistance to amitraz in R. decoloratus ticks. International Journal for Parasitology: Drugs and Drug Resistance, 2018, 8, 361-371.	1.4	16
4876	Transcriptome analysis reveals heat tolerance of Tribolium castaneum (Herbst) (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.2	20
4877	Toxicology tailored low density oligonucleotide microarray for the thicklip grey mullets (Chelon) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 66 Environmental Research, 2018, 140, 265-277.	1.1	2
4878	Characterization of ladybird Henosepilachna vigintioctopunctata transcriptomes across various life stages. Scientific Data, 2018, 5, 180093.	2.4	30
4879	Guidelines for RNA-seq projects: applications and opportunities in non-model decapod crustacean species. Hydrobiologia, 2018, 825, 5-27.	1.0	13
4880	Whole Genome Sequencing of Greater Amberjack (<i>Seriola dumerili</i>) for SNP Identification on Aligned Scaffolds and Genome Structural Variation Analysis Using Parallel Resequencing. International Journal of Genomics, 2018, 2018, 1-12.	0.8	28
4881	Comparative analysis of the immune system of an invasive bark beetle, Dendroctonus valens, infected by an entomopathogenic fungus. Developmental and Comparative Immunology, 2018, 88, 65-69.	1.0	26
4882	RNA-Seq analysis revealed genes associated with drought stress response in kabuli chickpea (Cicer) Tj ETQq1 1 0.784314 rgBT /Overloc	1.1	86
4883	Resources for studies of iron walnut (Juglans sigillata) gene expression, genetic diversity, and evolution. Tree Genetics and Genomes, 2018, 14, 1.	0.6	12
4884	Evaluation of some potential target genes and methods for RNAi-mediated pest control of the corn earworm Helicoverpa zea. Pesticide Biochemistry and Physiology, 2018, 149, 67-72.	1.6	19
4885	De novo sequencing, assembly and characterisation of Aloe vera transcriptome and analysis of expression profiles of genes related to saponin and anthraquinone metabolism. BMC Genomics, 2018, 19, 427.	1.2	36
4886	Nutritional Quality and Antioxidant Activity of Wheatgrass (<i>Triticum aestivum</i>) Unwrap by Proteome Profiling and DPPH and FRAP assays. Journal of Food Science, 2018, 83, 2127-2139.	1.5	29
4887	Analysis of the Long-Lived Responses Induced by Immunostimulants and Their Effects on a Viral Infection in Zebrafish (Danio rerio). Frontiers in Immunology, 2018, 9, 1575.	2.2	28
4888	Genome-wide comparative analysis in Solanaceous species reveals evolution of microRNAs targeting defense genes in<i>Capsicum</i>spp.. DNA Research, 2018, 25, 561-575.	1.5	24
4889	Comparative transcriptome analysis of the swimbladder reveals expression signatures in response to low oxygen stress in channel catfish,<i>Ictalurus punctatus</i>. Physiological Genomics, 2018, 50, 636-647.	1.0	22
4890	The developmental transcriptomes of two sea biscuit species with differing larval types. BMC Genomics, 2018, 19, 368.	1.2	4
4891	Dietary aquaculture by-product hydrolysates: impact on the transcriptomic response of the intestinal mucosa of European seabass (Dicentrarchus labrax) fed low fish meal diets. BMC Genomics, 2018, 19, 396.	1.2	47
4892	Genome sequence and effectorome of Moniliophthora perniciosa and Moniliophthora roreri subpopulations. BMC Genomics, 2018, 19, 509.	1.2	18

#	ARTICLE	IF	CITATIONS
4893	Temporal transcriptome profiling of developing seeds reveals a concerted gene regulation in relation to oil accumulation in Pongamia (Millettia pinnata). BMC Plant Biology, 2018, 18, 140.	1.6	11
4894	RNA-Seq based transcriptome of whole blood from immunocompetent pigs (Sus scrofa) experimentally infected with Mycoplasma suis strain Illinois. Veterinary Research, 2018, 49, 49.	1.1	33
4895	Interactomics and tick vaccine development: new directions for the control of tick-borne diseases. Expert Review of Proteomics, 2018, 15, 627-635.	1.3	18
4896	Comparative studies of Toxoplasma gondii transcriptomes: insights into stage conversion based on gene expression profiling and alternative splicing. Parasites and Vectors, 2018, 11, 402.	1.0	21
4897	Identification of MicroRNAs and Their Target Genes Associated with Ovarian Development in Black Tiger Shrimp (Penaeus monodon) Using High-Throughput Sequencing. Scientific Reports, 2018, 8, 11602.	1.6	11
4898	Alternatively spliced variants in Atlantic cod (Gadus morhua) support response to variable salinity environment. Scientific Reports, 2018, 8, 11607.	1.6	11
4899	Prediction of miRNA and Identification of their Relationship Network Related to Late Blight Disease of Potato. MicroRNA (Shariqah, United Arab Emirates), 2018, 7, 11-19.	0.6	5
4900	Dynamic Changes in Chemosensory Gene Expression during the Dendrolimus punctatus Mating Process. Frontiers in Physiology, 2017, 8, 1127.	1.3	25
4901	Transcriptomic Analysis Reveal the Molecular Mechanisms of Wheat Higher-Temperature Seedling-Plant Resistance to Puccinia striiformis f. sp. tritici. Frontiers in Plant Science, 2018, 9, 240.	1.7	18
4902	An Updated Functional Annotation of Protein-Coding Genes in the Cucumber Genome. Frontiers in Plant Science, 2018, 9, 325.	1.7	2
4903	MorphDB: Prioritizing Genes for Specialized Metabolism Pathways and Gene Ontology Categories in Plants. Frontiers in Plant Science, 2018, 9, 352.	1.7	7
4904	Genome-Wide Gene Expression Disturbance by Single A1/C1 Chromosome Substitution in Brassica rapa Restituted From Natural B. napus. Frontiers in Plant Science, 2018, 9, 377.	1.7	13
4905	Hidden Effects of Seed Quality Breeding on Germination in Oilseed Rape (Brassica napus L.). Frontiers in Plant Science, 2018, 9, 419.	1.7	27
4906	The Pattern and Distribution of Induced Mutations in J. curcas Using Reduced Representation Sequencing. Frontiers in Plant Science, 2018, 9, 524.	1.7	9
4907	Identification of Putative Precursor Genes for the Biosynthesis of Cannabinoid-Like Compound in Radula marginata. Frontiers in Plant Science, 2018, 9, 537.	1.7	28
4908	Integration of the Pokeweed miRNA and mRNA Transcriptomes Reveals Targeting of Jasmonic Acid-Responsive Genes. Frontiers in Plant Science, 2018, 9, 589.	1.7	10
4909	Quantitative Trait Locus Mapping and Candidate Gene Analysis for Verticillium Wilt Resistance Using Gossypium barbadense Chromosomal Segment Introgressed Line. Frontiers in Plant Science, 2018, 9, 682.	1.7	18
4910	Stable QTLs for Plant Height on Chromosome A09 Identified From Two Mapping Populations in Peanut (Arachis hypogaea L.). Frontiers in Plant Science, 2018, 9, 684.	1.7	21

#	Article	IF	Citations
4911	Identification and Characterization of Genes Involved in Benzylisoquinoline Alkaloid Biosynthesis in Coptis Species. Frontiers in Plant Science, 2018, 9, 731.	1.7	52
4912	Identification and Phenotypic Characterization of ZEBRA LEAF16 Encoding a Î²-Hydroxyacyl-ACP Dehydratase in Rice. Frontiers in Plant Science, 2018, 9, 782.	1.7	12
4913	Endophytic Bacillus and Pseudomonas spp. Modulate Apple Shoot Growth, Cellular Redox Balance, and Protein Expression Under in Vitro Conditions. Frontiers in Plant Science, 2018, 9, 889.	1.7	49
4914	The involvement of long non-coding RNAs in the formation of high temperature-induced grain chalkiness in rice. Plant Growth Regulation, 2018, 86, 263-271.	1.8	4
4915	On the roles of landscape heterogeneity and environmental variation in determining population genomic structure in a dendritic system. Molecular Ecology, 2018, 27, 3484-3497.	2.0	52
4916	Asymmetric expression patterns reveal a strong maternal effect and dosage compensation in polyploid hybrid fish. BMC Genomics, 2018, 19, 517.	1.2	12
4917	Antennal transcriptome analysis of the chemosensory gene families in Carposina sasakii (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	28
4918	Integration of RNAi and RNA-seq Reveals the Immune Responses of Epinephelus coioides to sigX Gene of Pseudomonas plecoglossicida. Frontiers in Immunology, 2018, 9, 1624.	2.2	67
4919	Genome-wide identification and characterization of growth-regulating factors in mulberry (Morus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.9	6
4920	Comparative transcriptome analysis identifies genes involved in the regulation of the pollen cytoskeleton in a genic male sterile wheat line. Plant Growth Regulation, 2018, 86, 133-147.	1.8	13
4921	Complete Genome Sequence of Industrial Biocontrol Strain Paenibacillus polymyxa HY96-2 and Further Analysis of Its Biocontrol Mechanism. Frontiers in Microbiology, 2018, 9, 1520.	1.5	49
4922	Zn Stimulates the Phospholipids Biosynthesis via the Pathways of Oxidative and Endoplasmic Reticulum Stress in the Intestine of Freshwater Teleost Yellow Catfish. Environmental Science & Technology, 2018, 52, 9206-9214.	4.6	51
4923	Cotton rat lung transcriptome reveals host immune response to Respiratory Syncytial Virus infection. Scientific Reports, 2018, 8, 11318.	1.6	10
4924	Genetic variation associated with healthy traits and environmental conditions in Vaccinium vitis-idaea. BMC Genomics, 2018, 19, 4.	1.2	16
4925	Comparative transcriptome analysis of the invasive weed Mikania micrantha with its native congeners provides insights into genetic basis underlying successful invasion. BMC Genomics, 2018, 19, 392.	1.2	19
4926	Distinct sperm nucleus behaviors between genotypic and temperature-dependent sex determination males are associated with replication and expression-related pathways in a gynogenetic fish. BMC Genomics, 2018, 19, 437.	1.2	23
4927	Transcriptional and Translational Relationship in Environmental Stress: RNAseq and ITRAQ Proteomic Analysis Between Sexually Reproducing and Parthenogenetic Females in Moina micrura. Frontiers in Physiology, 2018, 9, 812.	1.3	24
4928	Toxicogenomic responses of low level anticancer drug exposures in Daphnia magna. Aquatic Toxicology, 2018, 203, 40-50.	1.9	24

#	Article	IF	Citations
4929	Comparative transcriptome analysis of field- and chamber-grown samples of Colobanthus quitensis (Kunth) Bartl, an Antarctic flowering plant. Scientific Reports, 2018, 8, 11049.	1.6	27
4930	Coordinated regulation of core and accessory genes in the multipartite genome of Sinorhizobium fredii. PLoS Genetics, 2018, 14, e1007428.	1.5	50
4931	Comparative transcriptomics reveals shared gene expression changes during independent evolutionary origins of stem and hypocotyl/root tubers in Brassica (Brassicaceae). PLoS ONE, 2018, 13, e0197166.	1.1	16
4932	Immune-Related Functional Differential Gene Expression in Koi Carp (Cyprinus carpio) after Challenge with Aeromonas sobria. International Journal of Molecular Sciences, 2018, 19, 2107.	1.8	19
4933	Comparative Transcriptome Analysis for Understanding Predator-Induced Polyphenism in the Water Flea Daphnia pulex. International Journal of Molecular Sciences, 2018, 19, 2110.	1.8	20
4934	A proteomics of gills approach to understanding salinity adaptation of Scylla paramamosain. Gene, 2018, 677, 119-131.	1.0	27
4935	Mining the effector repertoire of the biotrophic fungal pathogen <i>Ustilago hordei </i>during host and nonâ€host infection. Molecular Plant Pathology, 2018, 19, 2603-2622.	2.0	28
4936	Fungal attack and host defence pathways unveiled in nearâ€avirulent interactions of <i>Penicillium expansum creA </i>mutants on apples. Molecular Plant Pathology, 2018, 19, 2635-2650.	2.0	66
4937	Genomeâ€wide scans of selection highlight the impact of biotic and abiotic constraints in natural populations of the model grass <i>Brachypodium distachyon</i>. Plant Journal, 2018, 96, 438-451.	2.8	24
4938	The R2R3MYB Gene Family in Phyllostachys edulis: Genome-Wide Analysis and Identification of Stress or Development-Related R2R3MYBs. Frontiers in Plant Science, 2018, 9, 738.	1.7	45
4939	De novo transcriptome assembly based on RNA-seq and dynamic expression of key enzyme genes in loganin biosynthetic pathway of Cornus officinalis. Tree Genetics and Genomes, 2018, 14, 1.	0.6	6
4940	Identification of SNPs associated with residual feed intake from the muscle of Litopenaeus vannamei using bulk segregant RNA-seq. Aquaculture, 2018, 497, 56-63.	1.7	9
4941	The molecular genetic basis of herbivory between butterflies and their host plants. Nature Ecology and Evolution, 2018, 2, 1418-1427.	3.4	56
4942	De novo transcriptome assembly and positive selection analysis of an individual deep-sea fish. BMC Genomics, 2018, 19, 394.	1.2	49
4943	Transcriptome characterization of moso bamboo (Phyllostachys edulis) seedlings in response to exogenous gibberellin applications. BMC Plant Biology, 2018, 18, 125.	1.6	67
4944	Expression profiling of Trypanosoma congolense genes during development in the tsetse fly vector Glossina morsitans morsitans. Parasites and Vectors, 2018, 11, 380.	1.0	15
4945	Identification and Characterization of Blood and Neutrophil-Associated Microbiomes in Patients with Severe Acute Pancreatitis Using Next-Generation Sequencing. Frontiers in Cellular and Infection Microbiology, 2018, 8, 5.	1.8	73
4946	Genetic Separation of Listeria monocytogenes Causing Central Nervous System Infections in Animals. Frontiers in Cellular and Infection Microbiology, 2018, 8, 20.	1.8	22

#	ARTICLE	IF	CITATIONS
4947	Rhipicephalus bursa Sialotranscriptomic Response to Blood Feeding and Babesia ovis Infection: Identification of Candidate Protective Antigens. Frontiers in Cellular and Infection Microbiology, 2018, 8, 116.	1.8	30
4948	Genetic Characterization of the Fish Piaractus brachypomus by Microsatellites Derived from Transcriptome Sequencing. Frontiers in Genetics, 2018, 9, 46.	1.1	12
4949	Stress Tolerance-Related Genetic Traits of Fish Pathogen Flavobacterium psychrophilum in a Mature Biofilm. Frontiers in Microbiology, 2018, 9, 18.	1.5	13
4950	iTRAQ-Based Comparative Proteomic Analysis of Adult Schistosoma japonicum from Water Buffalo and Yellow Cattle. Frontiers in Microbiology, 2018, 9, 99.	1.5	14
4951	Genome-Based Characterization of Biological Processes That Differentiate Closely Related Bacteria. Frontiers in Microbiology, 2018, 9, 113.	1.5	14
4952	Genomic and Genotypic Characterization of Cylindrospermopsis raciborskii: Toward an Intraspecific Phylogenetic Evaluation by Comparative Genomics. Frontiers in Microbiology, 2018, 9, 306.	1.5	26
4953	Genome Sequence, Assembly and Characterization of Two Metschnikowia fructicola Strains Used as Biocontrol Agents of Postharvest Diseases. Frontiers in Microbiology, 2018, 9, 593.	1.5	58
4954	Exploring the Denitrification Proteome of Paracoccus denitrificans PD1222. Frontiers in Microbiology, 2018, 9, 1137.	1.5	41
4955	Arbuscular Mycorrhizal Symbiosis Leads to Differential Regulation of Drought-Responsive Genes in Tissue-Specific Root Cells of Common Bean. Frontiers in Microbiology, 2018, 9, 1339.	1.5	40
4956	The adaptation of Fusarium culmorum to DMI Fungicides Is Mediated by Major Transcriptome Modifications in Response to Azole Fungicide, Including the Overexpression of a PDR Transporter (FcABC1). Frontiers in Microbiology, 2018, 9, 1385.	1.5	50
4957	Genomic and proteomic analysis of lignin degrading and polyhydroxyalkanoate accumulating Î²-proteobacterium Pandoraea sp. ISTKB. Biotechnology for Biofuels, 2018, 11, 154.	6.2	88
4958	Identification and Analysis of Human Sex-biased MicroRNAs. Genomics, Proteomics and Bioinformatics, 2018, 16, 200-211.	3.0	88
4959	De Novo Sequencing and Assembly Analysis of Transcriptome in Pinus bungeana Zucc. ex Endl.. Forests, 2018, 9, 156.	0.9	7
4960	Head Kidney Transcriptome Analysis and Characterization for the Sub-Antarctic Notothenioid Fish Eleginops maclovinus. Fishes, 2018, 3, 8.	0.7	7
4961	De Novo Transcriptome Assembly and Characterization of the Synthesis Genes of Bioactive Constituents in Abelmoschus esculentus (L.) Moench. Genes, 2018, 9, 130.	1.0	15
4962	A Key Gene, PLIN1, Can Affect Porcine Intramuscular Fat Content Based on Transcriptome Analysis. Genes, 2018, 9, 194.	1.0	55
4963	Transcriptome Analysis of Two Rice Varieties Contrasting for Nitrogen Use Efficiency under Chronic N Starvation Reveals Differences in Chloroplast and Starch Metabolism-Related Genes. Genes, 2018, 9, 206.	1.0	65
4964	Genetic Evaluation of Natural Populations of the Endangered Conifer Thuja koraiensis Using Microsatellite Markers by Restriction-Associated DNA Sequencing. Genes, 2018, 9, 218.	1.0	10

#	ARTICLE	IF	CITATIONS
4965	Comparative Analysis of DNA Methylation Reveals Specific Regulations on Ethylene Pathway in Tomato Fruit. Genes, 2018, 9, 266.	1.0	18
4966	Transcriptome Analysis Reveals Potential Antioxidant Defense Mechanisms in <i>Antheraea pernyi</i> in Response to Zinc Stress. Journal of Agricultural and Food Chemistry, 2018, 66, 8132-8141.	2.4	33
4967	Transcriptome-Wide Analysis Reveals the Origin of Peloria in Chinese Cymbidium (Cymbidium sinense). Plant and Cell Physiology, 2018, 59, 2064-2074.	1.5	14
4968	A transcriptome study on Macrobrachium nipponense hepatopancreas experimentally challenged with white spot syndrome virus (WSSV). PLoS ONE, 2018, 13, e0200222.	1.1	24
4969	Recognition of candidate transcription factors related to bilberry fruit ripening by de novo transcriptome and qRT-PCR analyses. Scientific Reports, 2018, 8, 9943.	1.6	16
4970	Transcriptome-Wide Identification and Characterization of Potato Circular RNAs in Response to Pectobacterium carotovorum Subspecies brasiliense Infection. International Journal of Molecular Sciences, 2018, 19, 71.	1.8	47
4971	Proteomic Analysis and Identification of Possible Allergenic Proteins in Mature Pollen of Populus tomentosa. International Journal of Molecular Sciences, 2018, 19, 250.	1.8	11
4972	Transcriptome Analysis of Kiwifruit in Response to Pseudomonas syringae pv. actinidiae Infection. International Journal of Molecular Sciences, 2018, 19, 373.	1.8	30
4973	Comparative Transcriptome Analyses Uncover Key Candidate Genes Mediating Flight Capacity in Bactrocera dorsalis (Hendel) and Bactrocera correcta (Bezzi) (Diptera: Tephritidae). International Journal of Molecular Sciences, 2018, 19, 396.	1.8	14
4974	De Novo Assembly and Characterization of the Xenocatantops brachycerus Transcriptome. International Journal of Molecular Sciences, 2018, 19, 520.	1.8	17
4975	Transcriptome Analysis Identifies a 140 kb Region of Chromosome 3B Containing Genes Specific to Fusarium Head Blight Resistance in Wheat. International Journal of Molecular Sciences, 2018, 19, 852.	1.8	13
4976	Transcriptome Analysis Reveals Candidate Genes Associated with Leaf Etiolation of a Cytoplasmic Male Sterility Line in Chinese Cabbage (Brassica Rapa L. ssp. Pekinensis). International Journal of Molecular Sciences, 2018, 19, 922.	1.8	9
4977	Comparative Transcriptome Analysis of Waterlogging-Sensitive and Waterlogging-Tolerant Chrysanthemum morifolium Cultivars under Waterlogging Stress and Reoxygenation Conditions. International Journal of Molecular Sciences, 2018, 19, 1455.	1.8	44
4978	Fatty Acid Î²-Oxidation Is Essential in Leptin-Mediated Oocytes Maturation of Yellow Catfish Pelteobagrus fulvidraco. International Journal of Molecular Sciences, 2018, 19, 1457.	1.8	11
4979	Proteomic Analyses of the Unexplored Sea Anemone Bunodactis verrucosa. Marine Drugs, 2018, 16, 42.	2.2	23
4980	The Holo-Transcriptome of the Zoantharian Protopalythoa variabilis (Cnidaria: Anthozoa): A Plentiful Source of Enzymes for Potential Application in Green Chemistry, Industrial and Pharmaceutical Biotechnology. Marine Drugs, 2018, 16, 207.	2.2	10
4981	Mining and Development of Novel SSR Markers Using Next Generation Sequencing (NGS) Data in Plants. Molecules, 2018, 23, 399.	1.7	141
4982	Examination of S-Locus Regulated Differential Expression in Primula vulgaris Floral Development. Plants, 2018, 7, 38.	1.6	7

#	ARTICLE	IF	CITATIONS
4983	RNA-Seq as an Emerging Tool for Marine Dinoflagellate Transcriptome Analysis: Process and Challenges. Processes, 2018, 6, 5.	1.3	36
4984	Microbial Diversity and Toxin Risk in Tropical Freshwater Reservoirs of Cape Verde. Toxins, 2018, 10, 186.	1.5	8
4985	A Genomic and Proteomic Approach to Identify and Quantify the Expressed Bacillus thuringiensis Proteins in the Supernatant and Parasporal Crystal. Toxins, 2018, 10, 193.	1.5	8
4986	Time-Course Microarray Analysis Reveals Differences between Transcriptional Changes in Tomato Leaves Triggered by Mild and Severe Variants of Potato Spindle Tuber Viroid. Viruses, 2018, 10, 257.	1.5	26
4987	Integration of RNAi and RNA-seq uncovers the immune responses of Epinephelus coioides to L321_RS19110 gene of Pseudomonas plecoglossicida. Fish and Shellfish Immunology, 2018, 81, 121-129.	1.6	92
4988	Integration of proteomic and transcriptomic profiles reveals multiple levels of genetic regulation of salt tolerance in cotton. BMC Plant Biology, 2018, 18, 128.	1.6	42
4989	Preliminary RNA-Seq Analysis of Long Non-Coding RNAs Expressed in Human Term Placenta. International Journal of Molecular Sciences, 2018, 19, 1894.	1.8	24
4990	Differentially expressed genes in hemocytes of Litopenaeus vannamei challenged with Vibrio parahaemolyticus AHPND (VPAHPND) and VPAHPND toxin. Fish and Shellfish Immunology, 2018, 81, 284-296.	1.6	36
4991	Differential lncRNA expression profiles reveal the potential roles of lncRNAs in antiviral immune response of Crassostrea gigas. Fish and Shellfish Immunology, 2018, 81, 233-241.	1.6	47
4992	The mechanisms involved in ochratoxin A elimination by <i>Yarrowia lipolytica</i> Yâ€2. Annals of Applied Biology, 2018, 173, 164-174.	1.3	23
4993	Identifying genomic hotspots of differentiation and candidate genes involved in the adaptive divergence of pea aphid host races. Molecular Ecology, 2018, 27, 3287-3300.	2.0	34
4994	De novo transcriptome assembly of the eight major organs of Sacha Inchi (Plukenetia volubilis) and the identification of genes involved in Î±-linolenic acid metabolism. BMC Genomics, 2018, 19, 380.	1.2	14
4995	Transcriptomic analysis of adaptive mechanisms in response to sudden salinity drop in the mud crab, Scylla paramamosain. BMC Genomics, 2018, 19, 421.	1.2	51
4996	Validation of reference genes for quantitative real-time PCR in tiger beetles across sexes, body parts, sexual maturity and immune challenge. Scientific Reports, 2018, 8, 10743.	1.6	11
4997	Transcriptome characterization and differential expression analysis of disease-responsive genes in alfalfa leaves infected by Pseudopeziza medicaginis. Euphytica, 2018, 214, 1.	0.6	3
4998	Identification and expression profiling of genes governing lignin biosynthesis in Casuarina equisetifolia L.. Gene, 2018, 676, 37-46.	1.0	4
4999	The genome assembly of the fungal pathogen Pyrenochaeta lycopersici from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. PLoS ONE, 2018, 13, e0200217.	1.1	19
5000	Large-scale de novo transcriptome analysis reveals specific gene expression and novel simple sequence repeats markers in salinized roots of the euhalophyte Salicornia europaea. Acta Physiologiae Plantarum, 2018, 40, 1.	1.0	2

#	ARTICLE	IF	CITATIONS
5001	Molecular chaperoning helps safeguarding mitochondrial integrity and motor functions in the Sahara silver ant Cataglyphis bombycina. Scientific Reports, 2018, 8, 9220.	1.6	11
5002	Abies pinsapo Boiss. Transcriptome Sequencing and Molecular Marker Detection: A Novel Genetic Resources for a Relict Mediterranean Fir. Forest Science, 0, , .	0.5	3
5003	Comparative genomic and transcriptomic analysis of selected fatty acid biosynthesis genes and CNL disease resistance genes in oil palm. PLoS ONE, 2018, 13, e0194792.	1.1	16
5004	Coexpression network revealing the plasticity and robustness of population transcriptome during the initial stage of domesticating energy crop Miscanthus lutarioriparius. Plant Molecular Biology, 2018, 97, 489-506.	2.0	5
5005	Identification of Genes Related to Cell Wall Metabolism and Fruit Ripening in Ziziphus jujube Using RNA-seq and Expression Analysis. Russian Journal of Plant Physiology, 2018, 65, 604-610.	0.5	3
5006	Genome comparison of different Zymomonas mobilis strains provides insights on conservation of the evolution. PLoS ONE, 2018, 13, e0195994.	1.1	6
5007	The leaf transcriptome of fennel (Foeniculum vulgare Mill.) enables characterization of the t-anethole pathway and the discovery of microsatellites and single-nucleotide variants. Scientific Reports, 2018, 8, 10459.	1.6	14
5008	Transcriptomic, lipid, and histological profiles suggest changes in health in fish from a pesticide hot spot. Marine Environmental Research, 2018, 140, 299-321.	1.1	13
5009	De novo transcriptome assembly of Pueraria montana var. lobata and Neustanthus phaseoloides for the development of eSSR and SNP markers: narrowing the US origin(s) of the invasive kudzu. BMC Genomics, 2018, 19, 439.	1.2	11
5010	Computational identification and characterization of microRNAs and their targets in Penaeus monodon. Journal of Oceanology and Limnology, 2018, 36, 853-869.	0.6	1
5011	Transcriptome analysis of abscisic acid induced 20E regulation in suspension Ajuga lobata cells. 3 Biotech, 2018, 8, 320.	1.1	5
5012	The effect of entomopathogenic fungal culture filtrate on the immune response and haemolymph proteome of the large pine weevil, Hylobius abietis. Insect Biochemistry and Molecular Biology, 2018, 101, 1-13.	1.2	10
5013	Ceratocystis cacaofunesta genome analysis reveals a large expansion of extracellular phosphatidylinositol-specific phospholipase-C genes (PI-PLC). BMC Genomics, 2018, 19, 58.	1.2	19
5014	Comparative genomics of the miniature wasp and pest control agent Trichogramma pretiosum. BMC Biology, 2018, 16, 54.	1.7	57
5015	Comparative proteomics of two <i>Mycoplasma hyopneumoniae</i> strains and <i>Mycoplasma flocculare</i> identified potential porcine enzootic pneumonia determinants. Virulence, 2018, 9, 1230-1246.	1.8	20
5016	Genome-wide characterization of simple sequence repeats in Pyrus bretschneideri and their application in an analysis of genetic diversity in pear. BMC Genomics, 2018, 19, 473.	1.2	22
5017	An annotated CNS transcriptome of the medicinal leech, Hirudo verbana: De novo sequencing to characterize genes associated with nervous system activity. PLoS ONE, 2018, 13, e0201206.	1.1	15
5018	Whole-genome sequencing of Aspergillus tubingensis G131 and overview of its secondary metabolism potential. BMC Genomics, 2018, 19, 200.	1.2	25

#	Article	IF	Citations
5019	Functional characterization of the Hyles euphorbiae hawkmoth transcriptomeÂreveals strong expression of phorbol ester detoxification and seasonal cold hardiness genes. Frontiers in Zoology, 2018, 15, 20.	0.9	13
5020	Transcriptome analysis of a taxol-producing endophytic fungus Cladosporium cladosporioides MD2. AMB Express, 2018, 8, 41.	1.4	22
5021	Transcriptional analysis reveals the critical role of RNA polymerase-binding transcription factor, DksA, in regulating multi-drug resistance of Escherichia coli. International Journal of Antimicrobial Agents, 2018, 52, 63-69.	1.1	7
5022	The draft genome of the lichen-forming fungus<i>Lasallia hispanica</i>(Frey) Sancho & A. Crespo. Lichenologist, 2018, 50, 329-340.	0.5	24
5023	Exogenous ABA and endogenous ABA affects â€˜Kyohoâ€™ grape berry coloration in different pathway. Plant Gene, 2018, 14, 74-82.	1.4	6
5024	Dop1 enhances conspecific olfactory attraction by inhibiting miR-9a maturation in locusts. Nature Communications, 2018, 9, 1193.	5.8	48
5025	De novo transcriptome sequencing and analysis of male and female swimming crab (Portunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502	2.7	31
5026	Resistance to Plum Pox Virus (PPV) in apricot (Prunus armeniaca L.) is associated with down-regulation of two MATHd genes. BMC Plant Biology, 2018, 18, 25.	1.6	35
5027	Terzyme: a tool for identification and analysis of the plant terpenome. Plant Methods, 2018, 14, 4.	1.9	25
5028	Bisphenol A Induces a Distinct Transcriptome Profile in the Male Fish of the Marine Medaka Oryzias javanicus. Biochip Journal, 2018, 12, 25-37.	2.5	10
5029	Characterizing the transcriptome and microsatellite markers for almond (Amygdalus communis L.) using the Illumina sequencing platform. Hereditas, 2018, 155, 14.	0.5	10
5030	Comparative transcriptome analysis by RNA-Seq of the regulation of low temperature responses in Dendranthema morifolium. Horticulture Environment and Biotechnology, 2018, 59, 383-395.	0.7	17
5031	Transcriptome-based identification of genes related to resistance against Botrytis elliptica in Lilium regale. Canadian Journal of Plant Science, 2018, 98, 1058-1071.	0.3	17
5032	Transcriptome and metabolome analyses provide insights into root and root-released organic anion responses to phosphorus deficiency in oat. Journal of Experimental Botany, 2018, 69, 3759-3771.	2.4	42
5033	PANNZER2: a rapid functional annotation web server. Nucleic Acids Research, 2018, 46, W84-W88.	6.5	328
5034	Environmental history impacts gene expression during diapause development in the alfalfa leafcutting bee, <i>Megachile rotundata</i>. Journal of Experimental Biology, 2018, 221, .	0.8	17
5035	Ancient horizontally transferred genes in the genome of California two-spot octopus, Octopus bimaculoides. Gene, 2018, 667, 34-44.	1.0	1
5036	Molecular basis of autotrophic vs mixotrophic growth in Chlorella sorokiniana. Scientific Reports, 2018, 8, 6465.	1.6	90

#	Article	IF	Citations
5037	Identification and characterization of chemosensory genes in the antennal transcriptome of Spodoptera exigua. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 54-65.	0.4	39
5038	Response analysis of host Spodoptera exigua larvae to infection by Heliothis virescens ascovirus 3h (HvAV-3h) via transcriptome. Scientific Reports, 2018, 8, 5367.	1.6	26
5039	Identification of genes regulating ovary differentiation after pollination in hazel by comparative transcriptome analysis. BMC Plant Biology, 2018, 18, 84.	1.6	14
5040	Homoeolog-specific activation of genes for heat acclimation in the allopolyploid grass Brachypodium hybridum. GigaScience, 2018, 7, .	3.3	23
5041	A transcriptome resource for the Arctic Cod (Boreogadus saida). Marine Genomics, 2018, 41, 57-61.	0.4	3
5042	Plasticity and evolutionary divergence in gene expression associated with alternative habitat use in larvae of the European Fire Salamander. Molecular Ecology, 2018, 27, 2698-2713.	2.0	9
5043	Gene co-expression network analysis reveals coordinated regulation of three characteristic secondary biosynthetic pathways in tea plant (Camellia sinensis). BMC Genomics, 2018, 19, 616.	1.2	71
5044	MicroRNA Expression Analysis of Naked Silkworms. Journal of Economic Entomology, 2018, 111, 2876-2883.	0.8	4
5045	Regional differences in thermal adaptation of a cold-water fish Rhynchocypris oxycephalus revealed by thermal tolerance and transcriptomic responses. Scientific Reports, 2018, 8, 11703.	1.6	14
5046	De novo assembly and comparative transcriptome analysis of Monilinia fructicola, Monilinia laxa and Monilinia fructigena, the causal agents of brown rot on stone fruits. BMC Genomics, 2018, 19, 436.	1.2	32
5047	Gene Expression Response to Sea Lice in Atlantic Salmon Skin: RNA Sequencing Comparison Between Resistant and Susceptible Animals. Frontiers in Genetics, 2018, 9, 287.	1.1	50
5048	Excessive dietary lipid intake provokes an acquired form of lysosomal lipid storage disease in the kidney. Journal of Pathology, 2018, 246, 470-484.	2.1	32
5049	Genome Sequence of Oenococcus oeni UNQOe19, the First Fully Assembled Genome Sequence of a Patagonian Psychrotrophic Oenological Strain. Microbiology Resource Announcements, 2018, 7, .	0.3	8
5050	Evolutionary divergence of 3â€™ UTRs in cichlid fishes. BMC Genomics, 2018, 19, 433.	1.2	20
5051	Transcriptomic comparison of two barley genotypes differing in arsenic tolerance exposed to arsenate and phosphate treatments. Plant Physiology and Biochemistry, 2018, 130, 589-603.	2.8	14
5052	Transcriptome-seq provides insights into sex-preference pattern of gene expression between testis and ovary of the crucifix crab (<i>Charybdis feriatus</i>). Physiological Genomics, 2018, 50, 393-405.	1.0	24
5053	RNA-seq highlights parallel and contrasting patterns in the evolution of the nuclear genome of fully mycoheterotrophic plants. BMC Genomics, 2018, 19, 602.	1.2	16
5054	Detoxification- and Immune-Related Transcriptomic Analysis of Gills from Bay Scallops (Argopecten) Tj ETQq1 1 0.784314 rgBT /Overloc	1.5	32

#	Article	IF	Citations
5055	Transcriptome analysis of the effects of Cd and nanomaterial-loaded Cd on the liver in zebrafish. Ecotoxicology and Environmental Safety, 2018, 164, 530-539.	2.9	23
5056	Transcriptomic analyses of Chrysanthemum morifolium Ramat under UV-B radiation treatment reveal variations in the metabolisms associated with bioactive components. Industrial Crops and Products, 2018, 124, 475-486.	2.5	17
5057	Exploiting MEDLINE for gene molecular function prediction via NMF based multi-label classification. Journal of Biomedical Informatics, 2018, 86, 160-166.	2.5	15
5058	Monitoring sublethal changes in fish physiology following exposure to a light, unweathered crude oil. Aquatic Toxicology, 2018, 204, 27-45.	1.9	19
5059	Molecular and cellular characterization of apoptosis in flat oyster a key mechanisms at the heart of host-parasite interactions. Scientific Reports, 2018, 8, 12494.	1.6	23
5060	Gene Co-expression Network Analysis Suggests the Existence of Transcriptional Modules Containing a High Proportion of Transcriptionally Differentiated Homoeologs in Hexaploid Wheat. Frontiers in Plant Science, 2018, 9, 1163.	1.7	24
5061	Screening of Human Proteins for Fluoride and Aluminum Binding. Bioinformation, 2018, 14, 68-74.	0.2	4
5062	Mechanism of High-Level Daptomycin Resistance in <i>Corynebacterium striatum</i>. MSphere, 2018, 3, .	1.3	28
5063	The genome sequence of the commercially cultivated mushroom Agrocybe aegerita reveals a conserved repertoire of fruiting-related genes and a versatile suite of biopolymer-degrading enzymes. BMC Genomics, 2018, 19, 48.	1.2	39
5064	Differentially abundant proteins associated with heterosis in the primary roots of popcorn. PLoS ONE, 2018, 13, e0197114.	1.1	13
5065	De Novo Transcriptome Assembly and Population Genetic Analyses for an Endangered Chinese Endemic Acer miaotaiense (Aceraceae). Genes, 2018, 9, 378.	1.0	44
5066	De novo transcriptome sequencing reveals candidate genes involved in orange shell coloration of bay scallop Argopecten irradians. Journal of Oceanology and Limnology, 2018, 36, 1408-1416.	0.6	10
5067	The primary transcriptome of the fast-growing cyanobacterium Synechococcus elongatus UTEX 2973. Biotechnology for Biofuels, 2018, 11, 218.	6.2	50
5068	New tools to screen wild peanut species for aflatoxin accumulation and genetic fingerprinting. BMC Plant Biology, 2018, 18, 170.	1.6	13
5069	De novo transcriptomic assembly and mRNA expression patterns of Botryosphaeria dothidea infection with mycoviruses chrysovirus 1 (BdCV1) and partitivirus 1 (BdPV1). Virology Journal, 2018, 15, 126.	1.4	14
5070	The Genetics of a Behavioral Speciation Phenotype in an Island System. Genes, 2018, 9, 346.	1.0	16
5071	Identification of Antifungal Targets Based on Computer Modeling. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 Td	1.5	12
5072	A targeted in situ hybridization screen identifies putative seminal fluid proteins in a simultaneously hermaphroditic flatworm. BMC Evolutionary Biology, 2018, 18, 81.	3.2	20

#	ARTICLE	IF	CITATIONS
5073	Identifying genome-wide immune gene variation underlying infectious disease in wildlife populations â€“ a next generation sequencing approach in the gopher tortoise. BMC Genomics, 2018, 19, 64.	1.2	19
5074	Comparative transcriptome analysis of the interaction between Actinidia chinensis var. chinensis and Pseudomonas syringae pv. actinidiae in absence and presence of acibenzolar-S-methyl. BMC Genomics, 2018, 19, 585.	1.2	33
5075	SNP discovery of Korean short day onion inbred lines using double digest restriction site-associated DNA sequencing. PLoS ONE, 2018, 13, e0201229.	1.1	21
5076	Innate Immune Response and Off-Target Mis-splicing Are Common Morpholino-Induced Side Effects in Xenopus. Developmental Cell, 2018, 44, 597-610.e10.	3.1	43
5077	RNA-seq-based analysis of the hypertrophic scarring with and without pressure therapy in a Bama minipig model. Scientific Reports, 2018, 8, 11831.	1.6	7
5078	Biology and genome of a newly discovered sibling species of Caenorhabditis elegans. Nature Communications, 2018, 9, 3216.	5.8	102
5079	Oxytocinâ€like signaling in ants influences metabolic gene expression and locomotor activity. FASEB Journal, 2018, 32, 6808-6821.	0.2	17
5080	Homoeolog expression bias and expression level dominance in resynthesized allopolyploid Brassica napus. BMC Genomics, 2018, 19, 586.	1.2	100
5081	Effect of deletion of a trichothecene toxin regulatory gene on the secondary metabolism transcriptome of the saprotrophic fungus Trichoderma arundinaceum. Fungal Genetics and Biology, 2018, 119, 29-46.	0.9	27
5082	Comprehensive analysis of wintersweet flower reveals key structural genes involved in flavonoid biosynthetic pathway. Gene, 2018, 676, 279-289.	1.0	14
5083	The proteome map of the escamolera ant (Liometopum apiculatum Mayr) larvae reveals immunogenic proteins and several hexamerin proteoforms. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 107-121.	0.4	2
5084	Photosynthetic Accumulation of Lutein in Auxenochlorella protothecoides after Heterotrophic Growth. Marine Drugs, 2018, 16, 283.	2.2	32
5085	De novo assembly of English yew (Taxus baccata) transcriptome and its applications for intra- and inter-specific analyses. Plant Molecular Biology, 2018, 97, 337-345.	2.0	8
5086	Identification and expression analysis of long noncoding RNAs in embryogenesis and larval metamorphosis of Ciona savignyi. Marine Genomics, 2018, 40, 64-72.	0.4	3
5087	Proteogenomic Analyses Revealed Favorable Metabolism Pattern Alterations in Rotifer <i>Brachionus plicatilis</i> Fed with Selenium-rich <i>Chlorella</i>. Journal of Agricultural and Food Chemistry, 2018, 66, 6699-6707.	2.4	17
5088	Transcriptomic analysis of embryo development in the invasive snail Pomacea canaliculata. Journal of Molluscan Studies, 2018, 84, 233-239.	0.4	3
5089	Comparative transcriptome sequencing of the intestine reveals differentially expressed genes in <i>Pelteobagrus vachellii</i>. Aquaculture Research, 2018, 49, 2560-2571.	0.9	3
5090	RNA sequencing of leaf tissues from two contrasting chickpea genotypes reveals mechanisms for drought tolerance. Plant Physiology and Biochemistry, 2018, 129, 295-304.	2.8	26

#	Article	IF	Citations
5091	A reference genome of the European beech (Fagus sylvatica L.). GigaScience, 2018, 7, .	3.3	58
5092	<i>LITTLELEAF</i> (<i>LL</i>) encodes a WD40 repeat domainâ€containing protein associated with organ size variation in cucumber. Plant Journal, 2018, 95, 834-847.	2.8	58
5093	Rewired RNAi-mediated genome surveillance in house dust mites. PLoS Genetics, 2018, 14, e1007183.	1.5	32
5094	Comprehensive analysis of Verticillium nonalfalfae in silico secretome uncovers putative effector proteins expressed during hop invasion. PLoS ONE, 2018, 13, e0198971.	1.1	51
5095	A gene co-expression network model identifies yield-related vicinity networks in Jatropha curcas shoot system. Scientific Reports, 2018, 8, 9211.	1.6	5
5096	RNA-Seq reveals large quantitative differences between the transcriptomes of outbreak and non-outbreak locusts. Scientific Reports, 2018, 8, 9207.	1.6	10
5097	2,4-D and dicamba resistance mechanisms in wild radish: subtle, complex and population specific?. Annals of Botany, 2018, 122, 627-640.	1.4	22
5098	Identification of chemosensory genes from the antennal transcriptome of Indian meal moth Plodia interpunctella. PLoS ONE, 2018, 13, e0189889.	1.1	41
5099	Transcriptome profiling with focus on potential key genes for wing development and evolution in Megaloprepus caerulatus, the damselfly species with the world's largest wings. PLoS ONE, 2018, 13, e0189898.	1.1	4
5100	Quantitative proteome profile of water deficit stress responses in eastern cottonwood (Populus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	17
5101	De novo transcriptome analysis of Bagarius yarrelli (Siluriformes: Sisoridae) and the search for potential SSR markers using RNA-Seq. PLoS ONE, 2018, 13, e0190343.	1.1	14
5102	Midgut transcriptomal response of the rice leaffolder, Cnaphalocrocis medinalis (GuenÃ©e) to Cry1C toxin. PLoS ONE, 2018, 13, e0191686.	1.1	16
5103	Proteomic endorsed transcriptomic profiles of venom glands from Tityus obscurus and T. serrulatus scorpions. PLoS ONE, 2018, 13, e0193739.	1.1	55
5104	Comprehensive transcriptome analysis and flavonoid profiling of Ginkgo leaves reveals flavonoid content alterations in dayâ€"night cycles. PLoS ONE, 2018, 13, e0193897.	1.1	31
5105	Population genomics of Fusarium graminearum reveals signatures of divergent evolution within a major cereal pathogen. PLoS ONE, 2018, 13, e0194616.	1.1	75
5106	Digital gene-expression profiling analysis of the fatty liver of Landes geese fed different supplemental oils. Gene, 2018, 673, 32-45.	1.0	11
5107	Gene network of oil accumulation reveals expression profiles in developing embryos and fatty acid composition in Upland cotton. Journal of Plant Physiology, 2018, 228, 101-112.	1.6	46
5108	Genome survey sequencing of Dioscorea zingiberensis. Genome, 2018, 61, 567-574.	0.9	18

#	Article	IF	Citations
5109	Comparative transcriptome analysis reveals the regulatory networks of cytokinin in promoting the floral feminization in the oil plant Sapium sebiferum. BMC Plant Biology, 2018, 18, 96.	1.6	35
5110	Transcriptome analysis provides insights into the immunity function of venom glands in Pardosa pseudoannulata in responses to cadmium toxicity. Environmental Science and Pollution Research, 2018, 25, 23875-23882.	2.7	14
5111	Comparative transcriptome analysis of Sogatella furcifera (HorvÃ¡th) exposed to different insecticides. Scientific Reports, 2018, 8, 8773.	1.6	57
5112	Genomeâ€wide DNA methylation signatures of infection status in Trinidadian guppies (<i>Poecilia) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	34
5113	Comparative transcriptomics in three Passerida species provides insights into the evolution of avian mitochondrial complex I. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 27-36.	0.4	8
5114	Dietary niche partitioning between sympatric wood mouse species (Muridae: Apodemus) revealed by DNA meta-barcoding analysis. Journal of Mammalogy, 2018, 99, 952-964.	0.6	26
5115	NmEXT Extensin Gene: a Positive Regulator of Resistance Response Against the Oomycete Phytophthora nicotianae. Plant Molecular Biology Reporter, 2018, 36, 484-490.	1.0	2
5116	Long-read sequencing and de novo genome assembly of Ammopiptanthus nanus, a desert shrub. GigaScience, 2018, 7, .	3.3	22
5117	Examination of carbohydrate and lipid metabolic changes during Haematococcus pluvialis non-motile cell germination using transcriptome analysis. Journal of Applied Phycology, 2019, 31, 145-156.	1.5	9
5118	Effusion: prediction of protein function from sequence similarity networks. Bioinformatics, 2019, 35, 442-451.	1.8	12
5119	Review of applications of high-throughput sequencing in personalized medicine: barriers and facilitators of future progress in research and clinical application. Briefings in Bioinformatics, 2019, 20, 1795-1811.	3.2	112
5120	Complete Sequence of a Novel Multidrug-Resistant Pseudomonas putida Strain Carrying Two Copies of qnrVC6. Microbial Drug Resistance, 2019, 25, 1-7.	0.9	9
5121	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. Plant Biotechnology Journal, 2019, 17, 451-460.	4.1	89
5122	High throughput sequencing identifies chilling responsive genes in sweetpotato (Ipomoea batatas) Tj ETQq1 1 0.784314 rgBT /Overlock	1.3	24
5123	De novo transcriptomics analysis revealed a global reprogramming towards dehydration and hyposalinity in Bangia fuscopurpurea gametophytes (Rhodophyta). Journal of Applied Phycology, 2019, 31, 637-651.	1.5	8
5124	Characterization of milk protein composition of the Yangtze finless porpoise. Marine Mammal Science, 2019, 35, 252-260.	0.9	1
5125	Transcriptomic analysis of Aegilops tauschii during long-term salinity stress. Functional and Integrative Genomics, 2019, 19, 13-28.	1.4	30
5126	Global analysis of tissue-differential gene expression patterns and functional regulation of rapid antler growth. Mammal Research, 2019, 64, 235-248.	0.6	10

#	Article	IF	Citations
5127	Casteâ€specific microRNA expression in termites: insights into soldier differentiation. Insect Molecular Biology, 2019, 28, 86-98.	1.0	14
5128	Community composition of arbuscular mycorrhizal fungi associated with native plants growing in a petroleumâ€polluted soil of the Amazon region of Ecuador. MicrobiologyOpen, 2019, 8, e00703.	1.2	15
5129	Involvement of HPI-axis in anesthesia with Lippia alba essential oil citral and linalool chemotypes: gene expression in the secondary responses in silver catfish. Fish Physiology and Biochemistry, 2019, 45, 155-166.	0.9	21
5130	Gene expression analysis of bud burst process in European hazelnut (Corylus avellana L.) using RNA-Seq. Physiology and Molecular Biology of Plants, 2019, 25, 13-29.	1.4	10
5131	Comparative skin transcriptome of two Oujiang color common carp (Cyprinus carpio var. color) varieties. Fish Physiology and Biochemistry, 2019, 45, 177-185.	0.9	28
5132	Extension of Partial Gene Transcripts by Iterative Mapping of RNA-Seq Raw Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1036-1041.	1.9	3
5133	Genome-wide analysis of Excretory/Secretory proteins in Trypanosoma brucei brucei: Insights into functional characteristics and identification of potential targets by immunoinformatics approach. Genomics, 2019, 111, 1124-1133.	1.3	7
5134	Environmental drivers and genomic architecture of trait differentiation in fireâ€adapted <i>Banksia attenuata</i> ecotypes. Journal of Integrative Plant Biology, 2019, 61, 417-432.	4.1	10
5135	Landscape of ROD9 Island: Functional annotations and biological network of hypothetical proteins in Salmonella enterica. Computational Biology and Chemistry, 2019, 83, 107110.	1.1	1
5136	Genome-wide characterization of the AP2/ERF gene family in radish (Raphanus sativus L.): Unveiling evolution and patterns in response to abiotic stresses. Gene, 2019, 718, 144048.	1.0	39
5137	A unique life cycle transition in the red seaweed Pyropia yezoensis depends on apospory. Communications Biology, 2019, 2, 299.	2.0	27
5138	Comparative transcriptome analysis provides key insights into seedling development in switchgrass (Panicum virgatum L.). Biotechnology for Biofuels, 2019, 12, 193.	6.2	6
5139	A homolog of the ALOG family controls corolla tube differentiation in <i>Torenia fournieri</i>. Development (Cambridge), 2019, 146, .	1.2	7
5140	Joint RNA-Seq and miRNA Profiling Analyses to Reveal Molecular Mechanisms in Regulating Thickness of Pod Canopy in Brassica napus. Genes, 2019, 10, 591.	1.0	12
5141	Time-dependent effects of Pochonia chlamydosporia endophytism on gene expression profiles of colonized tomato roots. Applied Microbiology and Biotechnology, 2019, 103, 8511-8527.	1.7	14
5142	Involvement of sulfur assimilation in the low Î² subunit content of soybean seed storage protein revealed by comparative transcriptome analysis. Crop Journal, 2019, 7, 504-515.	2.3	7
5143	Transcriptome Analysis of Young Ovaries Reveals Candidate Genes Involved in Gamete Formation in Lantana camara. Plants, 2019, 8, 263.	1.6	5
5144	Elucidation of Galactomannan Biosynthesis Pathway Genes through Transcriptome Sequencing of Seeds Collected at Different Developmental Stages of Commercially Important Indian Varieties of Cluster Bean (Cyamopsis tetragonoloba L.). Scientific Reports, 2019, 9, 11539.	1.6	11

#	Article	IF	Citations
5145	The Queen Conch (Lobatus gigas) Proteome: A Valuable Tool for Biological Studies in Marine Gastropods. Protein Journal, 2019, 38, 628-639.	0.7	5
5146	Genome-wide Identification, Classification, Expression and Duplication Analysis of GRAS Family Genes in Juglans regia L.. Scientific Reports, 2019, 9, 11643.	1.6	25
5147	Transcriptome Analysis of Low-Temperature-Induced Breaking of Garlic Aerial Bulb Dormancy. International Journal of Genomics, 2019, 2019, 1-16.	0.8	6
5148	Generation of Virus- and dsRNA-Derived siRNAs with Species-Dependent Length in Insects. Viruses, 2019, 11, 738.	1.5	43
5149	Transcriptomic analysis reveals the mechanism of thermosensitive genic male sterility (TGMS) of Brassica napus under the high temperature inducement. BMC Genomics, 2019, 20, 644.	1.2	11
5150	Transcriptomic investigation into polyketide toxin synthesis in Ostreopsis (Dinophyceae) species. Environmental Microbiology, 2019, 21, 4196-4211.	1.8	12
5151	Transcriptome sequencing, de novo assembly, characterisation of wild accession of blackgram (Vigna) Tj ETQq0 0 0 rgBT /Overlock 10 T SNPs by high resolution melting (HRM) analysis. BMC Plant Biology, 2019, 19, 358.	1.6	22
5152	De novo transcriptome sequencing and analysis revealed the molecular basis of rapid fat accumulation by black soldier fly (Hermetia illucens, L.) for development of insectival biodiesel. Biotechnology for Biofuels, 2019, 12, 194.	6.2	31
5153	The conservation genomics of the endangered distylous gypsophile Oreocarya crassipes (Boraginaceae). Conservation Genetics, 2019, 20, 1315-1328.	0.8	4
5154	Integrated metabolomic and transcriptomic analyses suggest that high dietary lipid levels facilitate ovary development through the enhanced arachidonic acid metabolism, cholesterol biosynthesis and steroid hormone synthesis in Chinese sturgeon (<i>Acipenser sinensis</i>). British Journal of Nutrition, 2019, 122, 1230-1241.	1.2	27
5155	Transcriptional alterations reveal Bacillus amyloliquefaciens-rice cooperation under salt stress. Scientific Reports, 2019, 9, 11912.	1.6	84
5156	Immune Tolerance in Mytilus galloprovincialis Hemocytes After Repeated Contact With Vibrio splendidus. Frontiers in Immunology, 2019, 10, 1894.	2.2	32
5157	RNA-Seq Analysis Reveals Genes Related to Photoreception, Nutrient Uptake, and Toxicity in a Noxious Red-Tide Raphidophyte Chattonella antiqua. Frontiers in Microbiology, 2019, 10, 1764.	1.5	16
5158	<i>Chlorella vulgaris</i> genome assembly and annotation reveals the molecular basis for metabolic acclimation to high light conditions. Plant Journal, 2019, 100, 1289-1305.	2.8	39
5159	Efficient two-dimensional Haar$$^+$$ synopsis construction for the maximum absolute error measure. VLDB Journal, 2019, 28, 675-701.	2.7	1
5160	Transcriptome profile of Carrizo citrange roots in response to<i>Phytophthora parasitica</i>infection. Journal of Plant Interactions, 2019, 14, 187-204.	1.0	9
5161	Comparative Transcriptome Analysis of Unusual Localized Skin Laxity in Sika Deer (<i>Cervus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102	0.9	0
5162	Competing Endogenous RNA Networks Underlying Anatomical and Physiological Characteristics of Poplar Wood in Acclimation to Low Nitrogen Availability. Plant and Cell Physiology, 2019, 60, 2478-2495.	1.5	26

#	Article	IF	Citations
5163	Contrasting genomic shifts underlie parallel phenotypic evolution in response to fishing. Science, 2019, 365, 487-490.	6.0	123
5164	A Decoy-Receptor Approach Using Nicotinic Acetylcholine Receptor Mimics Reveals Their Potential as Novel Therapeutics Against Neurotoxic Snakebite. Frontiers in Pharmacology, 2019, 10, 848.	1.6	33
5165	RNA sequencing analysis of Cymbidium goeringii identifies floral scent biosynthesis related genes. BMC Plant Biology, 2019, 19, 337.	1.6	35
5166	LOS2 gene plays a potential role in barley (Hordeum vulgare L.) salinity tolerance as a hub gene. Molecular Breeding, 2019, 39, 1.	1.0	8
5167	Genome-wide transcriptomic analysis of a desert willow, Salix psammophila, reveals the function of hub genes SpMDP1 and SpWRKY33 in drought tolerance. BMC Plant Biology, 2019, 19, 356.	1.6	11
5168	MARPLE, a point-of-care, strain-level disease diagnostics and surveillance tool for complex fungal pathogens. BMC Biology, 2019, 17, 65.	1.7	56
5169	Transcriptome analysis of the effects of Hericium erinaceus polysaccharide on the lymphocyte homing in Muscovy duck reovirus-infected ducklings. International Journal of Biological Macromolecules, 2019, 140, 697-708.	3.6	10
5170	Morphological characterization and transcriptome analysis of pistillate flowering in pecan (Carya) Tj ETQq1 1 0.784314 rgBT /Overloc	1.7	15
5171	<i>VpSTS29/STS2</i> enhances fungal tolerance in grapevine through a positive feedback loop. Plant, Cell and Environment, 2019, 42, 2979-2998.	2.8	25
5172	Transcriptome analysis of virulence-differentiated Fusarium oxysporum f. sp. cucumerinum isolates during cucumber colonisation reveals pathogenicity profiles. BMC Genomics, 2019, 20, 570.	1.2	13
5173	Seasonal temperature, the lunar cycle and diurnal rhythms interact in a combinatorial manner to modulate genomic responses to the environment in a reefâ€building coral. Molecular Ecology, 2019, 28, 3629-3641.	2.0	14
5174	Identification of glutathione-S-transferase genes by transcriptome analysis in Meteorus pulchricornis (Hymenoptera: Braconidae) and their expression patterns under stress of phoxim and cypermethrin. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 31, 100607.	0.4	9
5175	How to build a fruit: Transcriptomics of a novel fruit type in the Brassiceae. PLoS ONE, 2019, 14, e0209535.	1.1	4
5176	De novo transcriptome sequencing and gene expression profiling of Magnolia wufengensis in response to cold stress. BMC Plant Biology, 2019, 19, 321.	1.6	42
5177	Comparative transcriptome analysis of translucent flesh disorder in mangosteen (Garcinia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182 Td	1.1	12
5178	Transcriptome analysis provides new insights into the growth superiority of a novel backcross variety, Megalobrama amblycephala â™€â€ Ã—â€ (M. amblycephala â™€â€ Ã—â€ Culter alburnus â™,) â™,. Aquaculture, 2019, 512, 734317.	1.7	14
5179	Transcriptomic analysis of differentially expressed genes in the oviduct of Rhacophorus omeimontis provides insights into foam nest construction. BMC Genomics, 2019, 20, 562.	1.2	4
5180	Comparative proteomics and gene expression analyses revealed responsive proteins and mechanisms for salt tolerance in chickpea genotypes. BMC Plant Biology, 2019, 19, 300.	1.6	48

#	ARTICLE	IF	CITATIONS
5181	Transcriptome analysis of Polygonatum cyrtonema Hua: identification of genes involved in polysaccharide biosynthesis. Plant Methods, 2019, 15, 65.	1.9	23
5182	P8 nuclear receptor responds to acaricides exposure and regulates transcription of P450 enzyme in the two-spotted spider mite, Tetranychus urticae. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2019, 224, 108561.	1.3	3
5183	Comparative proteomic analysis of sex-biased proteins in ovary and testis at different stages of Spodoptera litura. Journal of Proteomics, 2019, 206, 103439.	1.2	1
5184	Transcriptomics profile reveals the temporal molecular events triggered by cut-wounding in stem-ends of cut â€˜Tiberâ€™ lily flowers. Postharvest Biology and Technology, 2019, 156, 110950.	2.9	4
5185	Chromosomal-level assembly of the blood clam, Scapharca (Anadara) broughtonii, using long sequence reads and Hi-C. GigaScience, 2019, 8, .	3.3	63
5186	31Â° South: The physiology of adaptation to arid conditions in a passerine bird. Molecular Ecology, 2019, 28, 3709-3721.	2.0	11
5187	Systems-Level Understanding of Single-Cell Omics. , 2019, , 433-456.		0
5188	Pollination-Induced Transcriptome and Phylogenetic Analysis in Cymbidium tortisepalum (Orchidaceae). Russian Journal of Plant Physiology, 2019, 66, 618-627.	0.5	3
5189	Evolution of Phototransduction Genes in Lepidoptera. Genome Biology and Evolution, 2019, 11, 2107-2124.	1.1	32
5190	Unveiling the presence of biosynthetic pathways for bioactive compounds in the Thalassiosira rotula transcriptome. Scientific Reports, 2019, 9, 9893.	1.6	25
5191	Global distribution of mating types shows limited opportunities for mating across populations of fungi causing boxwood blight disease. Fungal Genetics and Biology, 2019, 131, 103246.	0.9	16
5192	Transcriptome analysis of the fish pathogen Flavobacterium columnare in biofilm suggests calcium role in pathogenesis. BMC Microbiology, 2019, 19, 151.	1.3	9
5193	Transcriptional comparison between pheromone gland-ovipositor and tarsi in the corn earworm moth Helicoverpa zea. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 31, 100604.	0.4	9
5194	Transcriptome analysis of ovary in relatively greater and lesser egg producing Jinghai Yellow Chicken. Animal Reproduction Science, 2019, 208, 106114.	0.5	50
5195	Differential expression of immune-related genes in head kidney and spleen of cobia (Rachycentron) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 842-850.	1.6	17
5196	Comparative genome analysis of Phyllosticta citricarpa and Phyllosticta capitalensis, two fungi species that share the same host. BMC Genomics, 2019, 20, 554.	1.2	20
5197	Identification of candidate genes involved in steroidal alkaloids biosynthesis in organ-specific transcriptomes of Veratrum nigrum L.. Gene, 2019, 712, 143962.	1.0	6
5198	The effects of the neonicotinoid imidacloprid on gene expression and DNA methylation in the buff-tailed bumblebee <i>Bombus terrestris</i>. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190718.	1.2	32

#	ARTICLE	IF	CITATIONS
5199	Helitron distribution in Brassicaceae and whole Genome Helitron density as a character for distinguishing plant species. BMC Bioinformatics, 2019, 20, 354.	1.2	30
5200	Comparative transcriptomics reveals the selection patterns of domesticated ramie. Ecology and Evolution, 2019, 9, 7057-7068.	0.8	3
5201	Genome sequence of Isaria javanica and comparative genome analysis insights into family S53 peptidase evolution in fungal entomopathogens. Applied Microbiology and Biotechnology, 2019, 103, 7111-7128.	1.7	14
5202	iTRAQ-based quantitative proteomic analysis of cotton (Gossypium hirsutum L.) leaves reveals pathways associated throughout the aging process. Acta Physiologiae Plantarum, 2019, 41, 1.	1.0	4
5203	Transcriptome sequencing, molecular markers, and transcription factor discovery of Platanus acerifolia in the presence of Corythucha ciliata. Scientific Data, 2019, 6, 128.	2.4	4
5204	Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau Agaricus bisporus. Frontiers in Microbiology, 2019, 10, 1786.	1.5	14
5205	Proteomic Data Integration Highlights Central Actors Involved in Einkorn (Triticum monococcum ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Science, 2019, 10, 832.	1.7	2
5206	Large Scale Profiling of Protein Isoforms Using Label-Free Quantitative Proteomics Revealed the Regulation of Nonsense-Mediated Decay in Moso Bamboo (Phyllostachys edulis). Cells, 2019, 8, 744.	1.8	13
5207	Monarch butterflies use an environmentally sensitive, internal timer to control overwintering dynamics. Molecular Ecology, 2019, 28, 3642-3655.	2.0	37
5208	Pheromone gland transcriptome of the pink bollworm moth, Pectinophora gossypiella: Comparison between a laboratory and field population. PLoS ONE, 2019, 14, e0220187.	1.1	8
5209	Genome-Wide Identification of Long Noncoding RNAs and Their Responses to Salt Stress in Two Closely Related Poplars. Frontiers in Genetics, 2019, 10, 777.	1.1	38
5210	Systematic identification of long noncoding <scp>RNA</scp>s expressed during lightâ€induced anthocyanin accumulation in apple fruit. Plant Journal, 2019, 100, 572-590.	2.8	91
5211	Comparative transcriptomics suggest unique molecular adaptations within tardigrade lineages. BMC Genomics, 2019, 20, 607.	1.2	68
5212	Transcriptomic Analysis of <i>Mucor irregularis</i> Containing a Negative Single-Stranded RNA Mycovirus. Microbiology Resource Announcements, 2019, 8, .	0.3	3
5213	GAAP: A Genome Assembly + Annotation Pipeline. BioMed Research International, 2019, 2019, 1-12.	0.9	8
5214	Viral Long-Term Evolutionary Strategies Favor Stability over Proliferation. Viruses, 2019, 11, 677.	1.5	4
5215	Molecular insights into ovary degeneration induced by environmental factors in female oriental river prawns Macrobrachium nipponense. Environmental Pollution, 2019, 253, 882-888.	3.7	5
5216	De Novo assembly and characterization of the transcriptome of susceptible and resistant rose species in response to powdery mildew. Scientia Horticulturae, 2019, 257, 108653.	1.7	9

#	ARTICLE	IF	CITATIONS
5217	Comparative Analysis of the Characteristics of Triterpenoid Transcriptome from Different Strains of Wolfiporia cocos. International Journal of Molecular Sciences, 2019, 20, 3703.	1.8	7
5218	Mechanistic insight into the roles of Pseudomonas plecoglossicida clpV gene in host-pathogen interactions with Larimichthys crocea by dual RNA-seq. Fish and Shellfish Immunology, 2019, 93, 344-353.	1.6	32
5219	Detoxification, Apoptosis, and Immune Transcriptomic Responses of the Gill Tissue of Bay Scallop Following Exposure to the Algicide Thiazolidinedione 49. Biomolecules, 2019, 9, 310.	1.8	7
5220	De novo transcriptome analysis of lettuce (Lactuca sativa L.) and the identification of structural genes involved in anthocyanin biosynthesis in response to UV-B radiation. Acta Physiologiae Plantarum, 2019, 41, 1.	1.0	7
5221	Transcriptome assembly and abiotic related gene expression analysis of date palm reveal candidate genes involved in response to cadmium stress. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2019, 225, 108569.	1.3	10
5222	Characterization of genes in guar gum biosynthesis based on quantitative RNA-sequencing in guar bean (Cyamopsis tetragonoloba). Scientific Reports, 2019, 9, 10991.	1.6	13
5223	Chance and predictability in evolution: The genomic basis of convergent dietary specializations in an adaptive radiation. Molecular Ecology, 2019, 28, 4028-4045.	2.0	21
5224	Transcriptome profiling of Gerbera hybrida reveals that stem bending is caused by water stress and regulation of abscisic acid. BMC Genomics, 2019, 20, 600.	1.2	14
5225	Genomic signatures of sympatric speciation with historical and contemporary gene flow in a tropical anthozoan (Hexacorallia: Actiniaria). Molecular Ecology, 2019, 28, 3572-3586.	2.0	18
5226	Whole genome sequencing of Asia II 1 species of whitefly reveals that genes involved in virus transmission and insecticide resistance have genetic variances between Asia II 1 and MEAM1 species. BMC Genomics, 2019, 20, 507.	1.2	25
5227	Disentangling Genetic Variation for Resistance and Endurance to Scuticociliatosis in Turbot Using Pedigree and Genomic Information. Frontiers in Genetics, 2019, 10, 539.	1.1	49
5228	Structure-Specific Regulation of Nutrient Transport and Metabolism in Arbuscular Mycorrhizal Fungi. Plant and Cell Physiology, 2019, 60, 2272-2281.	1.5	30
5229	Oxidative stress under low oxygen conditions triggers hyperflagellation and motility in the Antarctic bacterium Pseudomonas extremaustralis. Extremophiles, 2019, 23, 587-597.	0.9	10
5230	Small RNA profiling of Cavendish banana roots inoculated with Fusarium oxysporum f. sp. cubense race 1 and tropical race 4. Phytopathology Research, 2019, 1, .	0.9	10
5231	Development of EST-based SSR and SNP markers in Gastrodia elata (herbal medicine) by sequencing, de novo assembly and annotation of the transcriptome. 3 Biotech, 2019, 9, 292.	1.1	11
5232	Tandem mass tag-based quantitative proteomic analysis reveal the inhibition mechanism of thyme essential oil against flagellum of Listeria monocytogenes. Food Research International, 2019, 125, 108508.	2.9	21
5233	Morphological, Transcriptomic and Hormonal Characterization of Trimonoecious and Subandroecious Pumpkin (Cucurbita maxima) Suggests Important Roles of Ethylene in Sex Expression. International Journal of Molecular Sciences, 2019, 20, 3185.	1.8	12
5234	Genes functioned in kleptoplastids of Dinophysis are derived from haptophytes rather than from cryptophytes. Scientific Reports, 2019, 9, 9009.	1.6	15

#	Article	IF	Citations
5235	Characterization and analysis of the transcriptome in Gymnocypris selincuoensis on the Qinghai-Tibetan Plateau using single-molecule long-read sequencing and RNA-seq. DNA Research, 2019, 26, 353-363.	1.5	31
5236	Global Dynamics in Protein Disorder during Maize Seed Development. Genes, 2019, 10, 502.	1.0	4
5237	Chromosome-level genome assembly of golden pompano (Trachinotus ovatus) in the family Carangidae. Scientific Data, 2019, 6, 216.	2.4	42
5238	Genome-wide identification, expression profiles and regulatory network of MAPK cascade gene family in barley. BMC Genomics, 2019, 20, 750.	1.2	45
5239	Analysis of miRNAs in the Heads of Different Castes of the Bumblebee Bombus lantschouensis (Hymenoptera: Apidae). Insects, 2019, 10, 349.	1.0	7
5240	Little evidence of adaptation potential to ocean acidification in sea urchins living in â€œFuture Oceanâ€• conditions at a CO₂ vent. Ecology and Evolution, 2019, 9, 10004-10016.	0.8	16
5241	GABAa receptor subunits expression in silver catfish (Rhamdia quelen) brain and its modulation by Nectandra grandiflora Nees essential oil and isolated compounds. Behavioural Brain Research, 2019, 376, 112178.	1.2	4
5242	A high-quality Actinidia chinensis (kiwifruit) genome. Horticulture Research, 2019, 6, 117.	2.9	109
5243	Reference gene and small RNA data from multiple tissues of Davidia involucrata Baill. Scientific Data, 2019, 6, 181.	2.4	4
5244	A chromosomal-level genome assembly for the giant African snail Achatina fulica. GigaScience, 2019, 8, .	3.3	42
5245	Single-nucleotide polymorphism markers within MVA and MEP pathways among Hevea brasiliensis clones through transcriptomic analysis. 3 Biotech, 2019, 9, 388.	1.1	4
5246	Dynamic immune and metabolism response of clam Meretrix petechialis to Vibrio challenge revealed by a time series of transcriptome analysis. Fish and Shellfish Immunology, 2019, 94, 17-26.	1.6	20
5247	Functional and genomic characterization of a wound- and methyl jasmonate-inducible chalcone isomerase in Eremochloa ophiuroides [Munro] Hack. Plant Physiology and Biochemistry, 2019, 144, 355-364.	2.8	4
5248	Identification and Expression Analyses of Olfactory Gene Families in the Rice Grasshopper, Oxya chinensis, From Antennal Transcriptomes. Frontiers in Physiology, 2019, 10, 1223.	1.3	19
5249	Dataset of suppression subtractive hybridization libraries of banana-biostimulant-Pseudocercospora fijiensis molecular interaction. Data in Brief, 2019, 27, 104557.	0.5	3
5250	The mixed liver and heart transcriptome dataset of the New Zealand brushtail possum, Trichosurus vulpecula. Data in Brief, 2019, 27, 104577.	0.5	1
5251	Draft genome sequence of fastidious pathogen Ceratobasidium theobromae, which causes vascular-streak dieback in Theobroma cacao. Fungal Biology and Biotechnology, 2019, 6, 14.	2.5	10
5252	A Bioinformatics Guide to Plant Microbiome Analysis. Frontiers in Plant Science, 2019, 10, 1313.	1.7	54

#	Article	IF	Citations
5253	Analysis of gene co-expression networks of phosphate starvation and aluminium toxicity responses in Populus spp.. PLoS ONE, 2019, 14, e0223217.	1.1	7
5254	The Mediator subunit OsMED15a is a transcriptional co-regulator of seed size/weightâ€“modulating genes in rice. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 194432.	0.9	16
5255	An â€œomicâ€•approach to Pyrocystis lunula: New insights related with this bioluminescent dinoflagellate. Journal of Proteomics, 2019, 209, 103502.	1.2	11
5256	Cis-regulatory CYP6P9b P450Âvariants associated with loss of insecticide-treated bed net efficacy against Anopheles funestus. Nature Communications, 2019, 10, 4652.	5.8	72
5257	Changes of Gene Expression in Euglena gracilis Obtained During the 29th DLR Parabolic Flight Campaign. Scientific Reports, 2019, 9, 14260.	1.6	10
5258	Comparative genomics of Leishmania (Mundinia). BMC Genomics, 2019, 20, 726.	1.2	27
5259	Genome-Wide Identification and Transcriptomic Analysis of MicroRNAs Across Various Amphioxus Organs Using Deep Sequencing. Frontiers in Genetics, 2019, 10, 877.	1.1	1
5260	The Tsetse Fly Displays an Attenuated Immune Response to Its Secondary Symbiont, Sodalis glossinidius. Frontiers in Microbiology, 2019, 10, 1650.	1.5	16
5261	FIB-SEM 3D CLEM of Cultured Cells. Microscopy and Microanalysis, 2019, 25, 1044-1045.	0.2	0
5262	Host and geography together drive early adaptive radiation of Hawaiian planthoppers. Molecular Ecology, 2019, 28, 4513-4528.	2.0	6
5263	Edaphic and host plant factors are linked to the composition of arbuscular mycorrhizal fungal communities in the root zone of endangered <i>Ulmus chenmoui</i> Cheng in China. Ecology and Evolution, 2019, 9, 8900-8910.	0.8	16
5264	Hydroxyl-substituted double Schiff-base condensed 4-piperidone/cyclohexanones as potential anticancer agents with biological evaluation. Journal of Enzyme Inhibition and Medicinal Chemistry, 2019, 34, 264-271.	2.5	26
5265	Transcript-Level Analysis in Combination with Real-Time PCR Elucidates Heat Adaptation Mechanism of Tribolium castaneum (Herbst) (Coleoptera: Tenebrionidae) Larvae. Journal of Economic Entomology, 2019, 112, 2984-2992.	0.8	2
5266	Lysine acetylation contributes to development, aflatoxin biosynthesis and pathogenicity in <i>Aspergillus flavus</i>. Environmental Microbiology, 2019, 21, 4792-4807.	1.8	27
5267	Transcriptome analysis of two radiated Cycas species and the subsequent species delimitation of the Cycas taiwaniana complex. Applications in Plant Sciences, 2019, 7, e11292.	0.8	1
5268	Draft genome sequence data of Cercospora kikuchii, a causal agent of Cercospora leaf blight and purple seed stain of soybeans. Data in Brief, 2019, 27, 104693.	0.5	11
5269	Comparative transcriptomic analysis and endocuticular protein gene expression of alate adults, workers and soldiers of the termite Reticulitermes aculabialis. BMC Genomics, 2019, 20, 742.	1.2	8
5270	Auâ€“PbS coreâ€“shell nanorods for plasmon-enhanced near-infrared photodetection. Journal of Materials Science, 2019, 54, 14720-14727.	1.7	8

#	ARTICLE	IF	CITATIONS
5271	The Rhododendron Genome and Chromosomal Organization Provide Insight into Shared Whole-Genome Duplications across the Heath Family (Ericaceae). Genome Biology and Evolution, 2019, 11, 3353-3371.	1.1	47
5272	Integrated dual RNA-seq and dual iTRAQ of infected tissue reveals the functions of a diguanylate cyclase gene of Pseudomonas plecoglossicida in host-pathogen interactions with Epinephelus coioides. Fish and Shellfish Immunology, 2019, 95, 481-490.	1.6	37
5274	Identification of candidate chemosensory genes of Ophraella communa LeSage (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	1.6	18
5275	Integrated Metabolome and Transcriptome Analysis Uncovers the Role of Anthocyanin Metabolism in <i>Michelia maudiae</i>. International Journal of Genomics, 2019, 2019, 1-14.	0.8	21
5276	Chromosome genome assembly and annotation of the yellowbelly pufferfish with PacBio and Hi-C sequencing data. Scientific Data, 2019, 6, 267.	2.4	21
5277	Lignin degradation potential and draft genome sequence of Trametes trogii S0301. Biotechnology for Biofuels, 2019, 12, 256.	6.2	16
5278	Transcriptomic and metabolomic profiling provide novel insights into fruit development and flesh coloration in Prunus mira Koehne, a special wild peach species. BMC Plant Biology, 2019, 19, 463.	1.6	45
5279	Identification and analysis of full-length transcripts involved in the biosynthesis of insecticidal lignan (+)-haedoxan A in Phryma leptostachya. Industrial Crops and Products, 2019, 142, 111868.	2.5	7
5280	Root Transcriptomic Analysis Reveals Global Changes Induced by Systemic Infection of Solanum lycopersicum with Mild and Severe Variants of Potato Spindle Tuber Viroid. Viruses, 2019, 11, 992.	1.5	21
5281	Sex- and tissue-specific transcriptome analyses and expression profiling of olfactory-related genes in Ceracris nigricornis Walker (Orthoptera: Acrididae). BMC Genomics, 2019, 20, 808.	1.2	12
5282	Evolutionary basis of high-frequency hearing in the cochleae of echolocators revealed by comparative genomics. Genome Biology and Evolution, 2020, 12, 3740-3753.	1.1	10
5283	Identification of Bna.IAA7.C05 as allelic gene for dwarf mutant generated from tissue culture in oilseed rape. BMC Plant Biology, 2019, 19, 500.	1.6	11
5284	Simulating Bleaching: Long-Term Adaptation to the Dark Reveals Phenotypic Plasticity of the Mediterranean Sea Coral Oculina patagonica. Frontiers in Marine Science, 2019, 6, .	1.2	11
5285	Culm transcriptome sequencing of Badila (Saccharum officinarum L.) and analysis of major genes involved in sucrose accumulation. Plant Physiology and Biochemistry, 2019, 144, 455-465.	2.8	12
5286	Small RNA analysis provides new insights into cytoplasmic incompatibility in Drosophila melanogaster induced by Wolbachia. Journal of Insect Physiology, 2019, 118, 103938.	0.9	8
5287	Comparative analysis reveals changes in transcriptomes of sugarcane upon infection by <i>Leifsoniaxyli</i> subsp. <i>xyli</i>. Journal of Phytopathology, 2019, 167, 633-644.	0.5	7
5288	A transcriptional response of Clostridium beijerinckii NRRL B-598 to a butanol shock. Biotechnology for Biofuels, 2019, 12, 243.	6.2	18
5289	Novel Pituitary Actions of Epidermal Growth Factor: Receptor Specificity and Signal Transduction for UTS1, EGR1, and MMP13 Regulation by EGF. International Journal of Molecular Sciences, 2019, 20, 5172.	1.8	6

#	Article	IF	Citations
5290	Utility of PacBio Iso-Seq for transcript and gene discovery in Hevea latex. Journal of Rubber Research (Kuala Lumpur, Malaysia), 2019, 22, 169-186.	0.4	10
5291	De novo transcriptome sequencing of radish (Raphanus sativus L.) fleshy roots: analysis of major genes involved in the anthocyanin synthesis pathway. BMC Molecular and Cell Biology, 2019, 20, 45.	1.0	14
5292	Transcriptome changes reveal the genetic mechanisms of the reproductive plasticity of workers in lower termites. BMC Genomics, 2019, 20, 702.	1.2	17
5293	A Transcriptomics Approach Reveals Putative Interaction of Candidatus Liberibacter Solanacearum with the Endoplasmic Reticulum of Its Psyllid Vector. Insects, 2019, 10, 279.	1.0	18
5294	Transcriptional foliar profile of the C3-CAM bromeliad Guzmania monostachia. PLoS ONE, 2019, 14, e0224429.	1.1	7
5295	Transcriptomic Revelation of Phenolic Compounds Involved in Aluminum Toxicity Responses in Roots of Cunninghamia lanceolata (Lamb.) Hook. Genes, 2019, 10, 835.	1.0	11
5296	Comparative Proteomics on Deep-Sea Amphipods after in Situ Copper Exposure. Environmental Science & Technology, 2019, 53, 13981-13991.	4.6	9
5297	Transcriptional analysis of insect extreme freeze tolerance. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20192019.	1.2	16
5298	Microbial communities of the Mediterranean rocky shore: ecology and biotechnological potential of the seaâ€land transition. Microbial Biotechnology, 2019, 12, 1359-1370.	2.0	4
5299	Comparative transcriptome profiling uncovers a <i>Lilium regale</i> NAC transcription factor, <i>LrNAC35</i>, contributing to defence response against cucumber mosaic virus and tobacco mosaic virus. Molecular Plant Pathology, 2019, 20, 1662-1681.	2.0	47
5300	Fine mapping of a clubroot resistance gene from turnip using SNP markers identified from bulked segregant RNA-Seq. Molecular Breeding, 2019, 39, 1.	1.0	36
5301	Transcriptome analysis of gene expression in Chlorella vulgaris under salt stress. World Journal of Microbiology and Biotechnology, 2019, 35, 141.	1.7	17
5302	Comparative Identification of MicroRNAs in Apis cerana cerana Workersâ€™ Midguts in Responseto Nosema ceranae Invasion. Insects, 2019, 10, 258.	1.0	14
5303	The Single-molecule long-read sequencing of Scylla paramamosain. Scientific Reports, 2019, 9, 12401.	1.6	17
5304	Proteomic Comparison of Three Extraction Methods Reveals the Abundance of Protease Inhibitors in the Seeds of Grass Pea, a Unique Orphan Legume. Journal of Agricultural and Food Chemistry, 2019, 67, 10296-10305.	2.4	1
5305	Comparative transcriptome combined with physiological analyses revealed key factors for differential cadmium tolerance in two contrasting hemp (Cannabis sativa L.) cultivars. Industrial Crops and Products, 2019, 140, 111638.	2.5	23
5306	Coupling caging and proteomics on the European flounder (Platichthys flesus) to assess the estuarine water quality at micro scale. Science of the Total Environment, 2019, 695, 133760.	3.9	14
5307	Comparative transcriptome and metabolite profiling of four tissues from Alisma orientale (Sam.) Juzep reveals its inflorescence developmental and medicinal characteristics. Scientific Reports, 2019, 9, 12310.	1.6	7

#	Article	IF	Citations
5308	Dissecting molecular mechanisms underlying salt tolerance in rice: a comparative transcriptional profiling of the contrasting genotypes. Rice, 2019, 12, 13.	1.7	46
5309	Validation and delineation of a locus conferring Fusarium crown rot resistance on 1HL in barley by analysing transcriptomes from multiple pairs of near isogenic lines. BMC Genomics, 2019, 20, 650.	1.2	16
5310	Normal transcription of cellulolytic enzyme genes relies on the balance between the methylation of H3K36 and H3K4 in Penicillium oxalicum. Biotechnology for Biofuels, 2019, 12, 198.	6.2	28
5311	Comparative transcriptome analysis reveals potential fruiting body formation mechanisms in Morchella importuna. AMB Express, 2019, 9, 103.	1.4	29
5312	Evaluating responses to temperature during pre-metamorphosis and carry-over effects at post-metamorphosis in the wood tiger moth (<i>Arctia plantaginis</i>). Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190295.	1.8	21
5313	Genome-wide identification and characterization of long non-coding RNAs involved in fruit ripening and the climacteric in Cucumis melo. BMC Plant Biology, 2019, 19, 369.	1.6	36
5314	Gene expression during the germination of coffee seed. Journal of Seed Science, 2019, 41, 168-179.	0.7	6
5315	Universal stress protein in Malus sieversii confers enhanced drought tolerance. Journal of Plant Research, 2019, 132, 825-837.	1.2	12
5316	Regulation of the Larval Transcriptome of Diatraea saccharalis (Lepidoptera: Crambidae) by Maternal and Other Factors of the Parasitoid Cotesia flavipes (Hymenoptera: Braconidae). Frontiers in Physiology, 2019, 10, 1106.	1.3	8
5317	An Aromatic Aldehyde Synthase Controls the Synthesis of Hydroxytyrosol Derivatives Present in Virgin Olive Oil. Antioxidants, 2019, 8, 352.	2.2	10
5318	Natural resistance to Fasciola hepatica (Trematoda) in Pseudosuccinea columella snails: A review from literature and insights from comparative â€œomicâ€•analyses. Developmental and Comparative Immunology, 2019, 101, 103463.	1.0	10
5319	Comparative genomics of Aeromonas veronii: Identification of a pathotype impacting aquaculture globally. PLoS ONE, 2019, 14, e0221018.	1.1	50
5320	Transcriptome and gene expression analysis of three developmental stages of the coffee berry borer, Hypothenemus hampei. Scientific Reports, 2019, 9, 12804.	1.6	17
5321	An integrated approach to determine interactive genotoxic and global gene expression effects of multiwalled carbon nanotubes (MWCNTs) and benzo[a]pyrene (BaP) on marine mussels: evidence of reverse â€˜Trojan Horseâ€™ effects. Nanotoxicology, 2019, 13, 1324-1343.	1.6	9
5322	The Tannat genome: Unravelling its unique characteristics. BIO Web of Conferences, 2019, 12, 01016.	0.1	1
5323	Chemosensory Characteristics of Two Semanotus bifasciatus Populations. Forests, 2019, 10, 655.	0.9	4
5324	Carbohydrate, glutathione, and polyamine metabolism are central to Aspergillus flavus oxidative stress responses over time. BMC Microbiology, 2019, 19, 209.	1.3	18
5325	The population genetics of structural variants in grapevine domestication. Nature Plants, 2019, 5, 965-979.	4.7	229

#	ARTICLE	IF	CITATIONS
5326	Genome-wide mining of microsatellites in king cobra (Ophiophagus hannah) and cross-species development of tetranucleotide SSR markers in Chinese cobra (Naja atra). Molecular Biology Reports, 2019, 46, 6087-6098.	1.0	10
5327	De novo transcriptome profile of coccolithophorid alga Emiliania huxleyi CCMP371 at different calcium concentrations with proteome analysis. PLoS ONE, 2019, 14, e0221938.	1.1	11
5328	Whole-Genome Resequencing of Seven Eggplant (Solanum melongena) and One Wild Relative (S.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 in Plant Science, 2019, 10, 1220.	1.7	46
5329	Ethical and policy issues raised by uterus transplants. British Medical Bulletin, 2019, 131, 19-28.	2.7	21
5330	Spodoptera frugiperda transcriptional response to infestation by Steinernema carpocapsae. Scientific Reports, 2019, 9, 12879.	1.6	15
5331	Comparative study of excretoryâ€“secretory proteins released by Schistosoma mansoni-resistant, susceptible and naÃ¯ve Biomphalaria glabrata. Parasites and Vectors, 2019, 12, 452.	1.0	19
5332	Additive and heterozygous (dis)advantage GWAS models reveal candidate genes involved in the genotypic variation of maize hybrids to Azospirillum brasilense. PLoS ONE, 2019, 14, e0222788.	1.1	19
5333	Effects and transcriptional responses in the hepatopancreas of red claw crayfish Cherax quadricarinatus under cold stress. Journal of Thermal Biology, 2019, 85, 102404.	1.1	40
5334	Maternal pluripotency factors initiate extensive chromatin remodelling to predefine first response to inductive signals. Nature Communications, 2019, 10, 4269.	5.8	45
5335	Hibernation induces widespread transcriptional remodeling in metabolic tissues of the grizzly bear. Communications Biology, 2019, 2, 336.	2.0	61
5336	Storage time affects the germination and proteomic profile of seeds of Cariniana legalis (Mart.) O. Kuntze (Lecythidaceae), an endangered tree species native to the Brazilian Atlantic Forest. Revista Brasileira De Botanica, 2019, 42, 407-419.	0.5	8
5337	Transcriptome profiling reveals insights into the molecular mechanism of drought tolerance in sweetpotato. Journal of Integrative Agriculture, 2019, 18, 9-23.	1.7	33
5338	Unraveling vascular development-related genes in laticifer-containing tissue of rubber tree by high-throughput transcriptome sequencing. Current Plant Biology, 2019, 19, 100112.	2.3	9
5339	The dataset of de novo transcriptome assembly of Falcataria moluccana cambium from gall-rust (Uromycladium falcatarium) infected and non-infected tree. Data in Brief, 2019, 26, 104489.	0.5	2
5340	Proteome of resistant and susceptible Passiflora species in the interaction with cowpea aphid-borne mosaic virus reveals distinct responses to pathogenesis. Euphytica, 2019, 215, 1.	0.6	11
5341	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. BMC Genomics, 2019, 20, 712.	1.2	17
5342	Expression Analysis of the NAC Transcription Factor Family of Populus in Response to Salt Stress. Forests, 2019, 10, 688.	0.9	10
5343	Histone Methylation Participates in Gene Expression Control during the Early Development of the Pacific Oyster Crassostrea gigas. Genes, 2019, 10, 695.	1.0	27

#	Article	IF	Citations
5344	Transcription analysis of the response of the porcine adrenal cortex to a single subclinical dose of lipopolysaccharide from Salmonella Enteritidis. International Journal of Biological Macromolecules, 2019, 141, 1228-1245.	3.6	5
5345	Comparative Transcriptomics Reveals the Expression Differences Between Four Developmental Stages of American Cockroach (<i>Periplaneta americana</i>). DNA and Cell Biology, 2019, 38, 1078-1087.	0.9	4
5346	Physiological and molecular responses to drought stress in teak (Tectona grandis L.f.). PLoS ONE, 2019, 14, e0221571.	1.1	34
5347	Population genomics reveals possible genetic evidence for parallel evolution of <i>Sebastiscus marmoratus</i> in the northwestern Pacific Ocean. Open Biology, 2019, 9, 190028.	1.5	8
5348	Transcriptome analysis of Globodera pallida from the susceptible host Solanum tuberosum or the resistant plant Solanum sisymbriifolium. Scientific Reports, 2019, 9, 13256.	1.6	13
5349	Transcriptome analysis in the skin of Carassius auratus challenged with Aeromonas hydrophila. Fish and Shellfish Immunology, 2019, 94, 510-516.	1.6	27
5350	A retinal-binding protein mediates olfactory attraction in the migratory locusts. Insect Biochemistry and Molecular Biology, 2019, 114, 103214.	1.2	2
5351	Temporal changes in transcriptome profile provide insights of White Spot Syndrome Virus infection in Litopenaeus vannamei. Scientific Reports, 2019, 9, 13509.	1.6	32
5352	Effects of Essential Oil Citral on the Growth, Mycotoxin Biosynthesis and Transcriptomic Profile of Alternaria alternata. Toxins, 2019, 11, 553.	1.5	45
5353	A comparative morphological and transcriptomic study on autotetraploid Stevia rebaudiana (bertoni) and its diploid. Plant Physiology and Biochemistry, 2019, 143, 154-164.	2.8	18
5354	Transcriptome Profiles of Strawberry (Fragaria vesca) Fruit Interacting With Botrytis cinerea at Different Ripening Stages. Frontiers in Plant Science, 2019, 10, 1131.	1.7	54
5355	Horizontal and vertical integrative analysis methods for mental disorders omics data. Scientific Reports, 2019, 9, 13430.	1.6	5
5356	Comparative Transcriptomics Provides Insights into Reticulate and Adaptive Evolution of a Butterfly Radiation. Genome Biology and Evolution, 2019, 11, 2963-2975.	1.1	7
5357	Interaction of a Densovirus with Glycans of the Peritrophic Matrix Mediates Oral Infection of the Lepidopteran Pest Spodoptera frugiperda. Viruses, 2019, 11, 870.	1.5	3
5358	Genetic Characteristic and RNA-Seq Analysis in Transparent Mutant of Carpâ€"Goldfish Nucleocytoplasmic Hybrid. Genes, 2019, 10, 704.	1.0	4
5359	Gene expression during the early stages of host perception and attachment in adult female Rhipicephalus microplus ticks. Experimental and Applied Acarology, 2019, 79, 107-124.	0.7	0
5360	Comparative transcriptome analysis of the transcriptional heterogeneity in different IgM+ cell subsets from peripheral blood of Nile tilapia (Oreochromis niloticus). Fish and Shellfish Immunology, 2019, 93, 612-622.	1.6	10
5361	Analysis of the circadian transcriptome of the Antarctic krill Euphausia superba. Scientific Reports, 2019, 9, 13894.	1.6	19

#	Article	IF	Citations
5362	Functional annotation of mulberry (Morus spp.) transcriptome, differential expression of genes related to growth and identification of putative genic SSRs, SNPs and InDels. Molecular Biology Reports, 2019, 46, 6421-6434.	1.0	4
5363	A cornucopia of Shigella phages from the Cornhusker State. Virology, 2019, 538, 45-52.	1.1	8
5364	A Survey of Gene Prioritization Tools for Mendelian and Complex Human Diseases. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	25
5365	RNA-seq revealed the signatures of immunity and metabolism in the Litopenaeus vannamei intestine in response to dietary succinate. Fish and Shellfish Immunology, 2019, 95, 16-24.	1.6	9
5366	Transcriptomic analysis of postharvest toon buds and key enzymes involved in terpenoid biosynthesis during cold storage. Scientia Horticulturae, 2019, 257, 108747.	1.7	10
5367	Identification and characterization of jasmonic acid- and linolenic acid-mediated transcriptional regulation of secondary laticifer differentiation in Hevea brasiliensis. Scientific Reports, 2019, 9, 14296.	1.6	11
5368	Haplotype-resolved genomes of geminivirus-resistant and geminivirus-susceptible African cassava cultivars. BMC Biology, 2019, 17, 75.	1.7	42
5369	Comparative proteomic analysis of trypomastigotes from Trypanosoma cruzi strains with different pathogenicity. Infection, Genetics and Evolution, 2019, 76, 104041.	1.0	13
5370	Using de novo transcriptome assembly and analysis to study RNAi in Phenacoccus solenopsis Tinsley (Hemiptera: Pseudococcidae). Scientific Reports, 2019, 9, 13710.	1.6	17
5371	De novo transcriptome sequencing of Monodopsis subterranea CCALA 830 and identification of genes involved in the biosynthesis of eicosapentanoic acid and triacylglycerol. Vegetos, 2019, 32, 600-608.	0.8	2
5372	Time matters! Developmental shift in gene expression between the head and the trunk region of the cichlid fish Astatotilapia burtoni. BMC Genomics, 2019, 20, 39.	1.2	2
5373	MicroRNA profile of immune response in gills of zebrafish (Danio rerio) upon Staphylococcus aureus infection. Fish and Shellfish Immunology, 2019, 87, 307-314.	1.6	19
5374	Universality of the DNA methylation codes in Eucaryotes. Scientific Reports, 2019, 9, 173.	1.6	37
5375	Low-temperature-induced changes in the transcriptome reveal a major role of CgSVP genes in regulating flowering of Cymbidium goeringii. BMC Genomics, 2019, 20, 53.	1.2	33
5376	Transcriptome analysis of genes and metabolic pathways associated with nicotine degradation in Aspergillus oryzae 112822. BMC Genomics, 2019, 20, 86.	1.2	10
5377	Tissue-Specific Transcriptome Analysis Reveals Candidate Genes for Terpenoid and Phenylpropanoid Metabolism in the Medicinal Plant <i>Ferula assafoetida</i>. G3: Genes, Genomes, Genetics, 2019, 9, 807-816.	0.8	25
5379	In-depth analysis of the genome of Trypanosoma evansi, an etiologic agent of surra. Science China Life Sciences, 2019, 62, 406-419.	2.3	9
5380	Environmental and Evolutionary Drivers of the Modular Gene Regulatory Network Underlying Phenotypic Plasticity for Stress Resistance in the Nematode <i>Caenorhabditis remanei</i>. G3: Genes, Genomes, Genetics, 2019, 9, 969-982.	0.8	22

#	ARTICLE	IF	CITATIONS
5381	Transcriptional Basis of Copper-Induced Olfactory Impairment in the Sea Lamprey, a Primitive Invasive Fish. G3: Genes, Genomes, Genetics, 2019, 9, 933-941.	0.8	9
5382	NBS-Encoding Genes in Brassica napus Evolved Rapidly After Allopolyploidization and Co-localize With Known Disease Resistance Loci. Frontiers in Plant Science, 2019, 10, 26.	1.7	27
5383	Proteomic analysis of adult Galeruca daurica (Coleoptera: Chrysomelidae) at different stages during summer diapause. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 351-357.	0.4	6
5384	Identification of new regulators through transcriptome analysis that regulate anthocyanin biosynthesis in apple leaves at low temperatures. PLoS ONE, 2019, 14, e0210672.	1.1	34
5385	Complete Genome Sequence and Comparative Analysis of Synechococcus sp. CS-601 (SynAce01), a Cold-Adapted Cyanobacterium from an Oligotrophic Antarctic Habitat. International Journal of Molecular Sciences, 2019, 20, 152.	1.8	27
5386	Comparative transcriptome analysis of two selenium-accumulating genotypes of Aegilops tauschii Coss. in response to selenium. BMC Genetics, 2019, 20, 9.	2.7	10
5387	Comparative transcriptomes and development of expressed sequence tagâ€simple sequence repeat markers for two closely related oak species. Journal of Systematics and Evolution, 2019, 57, 440-450.	1.6	7
5388	Transcriptomic profiling reveals molecular regulation of seasonal reproduction in Tibetan highland fish, Gymnocypris przewalskii. BMC Genomics, 2019, 20, 2.	1.2	38
5389	Comparative transcriptome analysis reveals differential gene expression in resistant and susceptible tobacco cultivars in response to infection by cucumber mosaic virus. Crop Journal, 2019, 7, 307-321.	2.3	16
5390	RNA-seq analysis of the response of plant-pathogenic oomycete Phytophthora parasitica to the fungicide dimethomorph. Revista Argentina De Microbiologia, 2019, 51, 268-277.	0.4	5
5391	Comparative transcriptomic analysis provides insights into the response to the benzo(a)pyrene stress in aquatic firefly (Luciola leii). Science of the Total Environment, 2019, 661, 226-234.	3.9	21
5392	The interplay between microRNA and alternative splicing of linear and circular RNAs in eleven plant species. Bioinformatics, 2019, 35, 3119-3126.	1.8	18
5393	Algal Protein Kinase, Triacylglycerol Accumulation Regulator 1, Modulates Cell Viability and Gametogenesis in Carbon/Nitrogen-Imbalanced Conditions. Plant and Cell Physiology, 2019, 60, 916-930.	1.5	15
5394	Effects of adult temperature on gene expression in a butterfly: identifying pathways associated with thermal acclimation. BMC Evolutionary Biology, 2019, 19, 32.	3.2	8
5395	Integrative omics analysis in Pandanus odorifer (Forssk.) Kuntze reveals the role of Asparagine synthetase in salinity tolerance. Scientific Reports, 2019, 9, 932.	1.6	24
5396	Usability of reference-free transcriptome assemblies for detection of differential expression: a case study on Aethionema arabicum dimorphic seeds. BMC Genomics, 2019, 20, 95.	1.2	18
5397	Dual RNA-seq reveals the effect of the flgM gene of Pseudomonas plecoglossicida on the immune response of Epinephelus coioides. Fish and Shellfish Immunology, 2019, 87, 515-523.	1.6	39
5398	Interaction of roses with a biotrophic and a hemibiotrophic leaf pathogen leads to differences in defense transcriptome activation. Plant Molecular Biology, 2019, 99, 299-316.	2.0	29

#	ARTICLE	IF	CITATIONS
5399	Genetic Analysis of <i>Candida auris</i> Implicates Hsp90 in Morphogenesis and Azole Tolerance and Cdr1 in Azole Resistance. MBio, 2019, 10, .	1.8	77
5400	Metaproteomics reveals potential mechanisms by which dietary resistant starch supplementation attenuates chronic kidney disease progression in rats. PLoS ONE, 2019, 14, e0199274.	1.1	25
5401	The Gene Toolkit Implicated in Functional Sex in Sparidae Hermaphrodites: Inferences From Comparative Transcriptomics. Frontiers in Genetics, 2018, 9, 749.	1.1	20
5402	Genome-Wide Identification and Transcriptional Expression of the PAL Gene Family in Common Walnut (Juglans Regia L.). Genes, 2019, 10, 46.	1.0	31
5403	The transcriptional response of the Pacific oyster Crassostrea gigas under simultaneous bacterial and heat stresses. Developmental and Comparative Immunology, 2019, 94, 1-10.	1.0	28
5404	Analysis of the common bean (Phaseolus vulgaris L.) transcriptome regarding efficiency of phosphorus use. PLoS ONE, 2019, 14, e0210428.	1.1	16
5405	Investigating proteome and transcriptome response of Cryptococcus podzolicus Y3 to citrinin and the mechanisms involved in its degradation. Food Chemistry, 2019, 283, 345-352.	4.2	18
5406	SOX2 participates in spermatogenesis of Zhikong scallop Chlamys farreri. Scientific Reports, 2019, 9, 76.	1.6	27
5407	Participation of Wheat and Rye Genome in Drought Induced Senescence in Winter Triticale (X) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	1.3	10
5408	Genomic Characterization and Virulence Potential of Two<i>Fusarium oxysporum</i>Isolates Cultured from the International Space Station. MSystems, 2019, 4, .	1.7	26
5409	How fall dormancy benefits alfalfa winter-survival? Physiologic and transcriptomic analyses of dormancy process. BMC Plant Biology, 2019, 19, 205.	1.6	15
5410	Early Sex-Chromosome Evolution in the Diploid Dioecious Plant <i>Mercurialis annua</i>. Genetics, 2019, 212, 815-835.	1.2	53
5411	Transcriptomic analysis provides insight into the mechanism of salinity adjustment in swimming crab Portunus trituberculatus. Genes and Genomics, 2019, 41, 961-971.	0.5	11
5412	Transcriptomic analysis of interstock-induced dwarfism in Sweet Persimmon (Diospyros kaki Thunb.). Horticulture Research, 2019, 6, 51.	2.9	26
5413	Transcriptome Analysis Provides Novel Insights into the Capacity of the Ectomycorrhizal Fungus <i>Amanita pantherina</i> To Weather K-Containing Feldspar and Apatite. Applied and Environmental Microbiology, 2019, 85, .	1.4	16
5414	Genome-wide analysis of bHLH transcription factor family reveals their involvement in biotic and abiotic stress responses in wheat (Triticum aestivum L.). 3 Biotech, 2019, 9, 236.	1.1	41
5415	Hypothalamus-pituitary-gonad axis transcriptome profiling for sex differentiation in Acipenser sinensis. Scientific Data, 2019, 6, 87.	2.4	12
5416	Ovarian transcriptome analysis of Mactra chinensis provides insights into genes expressed during the intermediate and ripening stages. Animal Reproduction Science, 2019, 208, 106078.	0.5	0

#	ARTICLE	IF	CITATIONS
5417	Cell number explains the intraspecific spur-length variation in an Aquilegia species. Plant Diversity, 2019, 41, 307-314.	1.8	4
5418	Transcriptome changes in the phenylpropanoid pathway in senescing leaves of Toona sinensis. Acta Physiologiae Plantarum, 2019, 41, 126.	1.0	7
5419	Quantitative proteomic profiling of ochratoxin A repression in Penicillium nordicum by protective cultures. International Journal of Food Microbiology, 2019, 305, 108243.	2.1	30
5420	Transcriptomic investigation of immune responses of the Apis cerana cerana larval gut infected by Ascosphaera apis. Journal of Invertebrate Pathology, 2019, 166, 107210.	1.5	24
5421	Ancient introgression drives adaptation to cooler and drier mountain habitats in a cypress species complex. Communications Biology, 2019, 2, 213.	2.0	64
5422	A Reference Genome Sequence for the European Silver Fir (<i>Abies alba</i>Mill.): A Community-Generated Genomic Resource. G3: Genes, Genomes, Genetics, 2019, 9, 2039-2049.	0.8	53
5423	Transcriptome analysis reveals global gene expression changes of Chilo suppressalis in response to sublethal dose of chlorantraniliprole. Chemosphere, 2019, 234, 648-657.	4.2	39
5424	Signatures of selection for bonamiosis resistance in European flat oyster (Ostrea edulis): New genomic tools for breeding programs and management of natural resources. Evolutionary Applications, 2019, 12, 1781-1796.	1.5	35
5425	Time-based LC-MS/MS analysis provides insights into early responses to mechanical wounding, a major trigger to agarwood formation in Aquilaria malaccensis Lam. RSC Advances, 2019, 9, 18383-18393.	1.7	6
5426	Stimulation of asymbiotic sporulation in arbuscular mycorrhizal fungi by fatty acids. Nature Microbiology, 2019, 4, 1654-1660.	5.9	58
5427	Transcriptome sequence resource for the cucurbit powdery mildew pathogen Podosphaera xanthii. Scientific Data, 2019, 6, 95.	2.4	10
5428	Anaplasma phagocytophilum modifies tick cell microRNA expression and upregulates isc-mir-79 to facilitate infection by targeting the Roundabout protein 2 pathway. Scientific Reports, 2019, 9, 9073.	1.6	12
5429	Species-specific mechanisms of cytotoxicity toward immune cells determine the successful outcome ofVibrioinfections. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14238-14247.	3.3	62
5430	Serotype-specific evolutionary patterns of antimicrobial-resistant Salmonella enterica. BMC Evolutionary Biology, 2019, 19, 132.	3.2	20
5431	Survey of the Bradysia odoriphaga Transcriptome Using PacBio Single-Molecule Long-Read Sequencing. Genes, 2019, 10, 481.	1.0	8
5432	Distribution and Characteristics of Transposable Elements in the Mulberry Genome. Plant Genome, 2019, 12, 180094.	1.6	5
5433	Comparative Integrated Omics Analysis of the Hfq Regulon in Bordetella pertussis. International Journal of Molecular Sciences, 2019, 20, 3073.	1.8	11
5434	Emerging Sample Treatments in Proteomics. Advances in Experimental Medicine and Biology, 2019, , .	0.8	6

#	ARTICLE	IF	CITATIONS
5435	A Method for Comprehensive Proteomic Analysis of Human Faecal Samples to Investigate Gut Dysbiosis in Patients with Cystic Fibrosis. Advances in Experimental Medicine and Biology, 2019, 1073, 137-160.	0.8	5
5436	The Spatiotemporal Control of Zygotic Genome Activation. IScience, 2019, 16, 485-498.	1.9	20
5437	Transcriptome-guided identification and functional characterization of key terpene synthases involved in constitutive and methyl jasmonate-inducible volatile terpene formation in Eremochloa ophiuroides (Munro) Hack. Plant Physiology and Biochemistry, 2019, 141, 193-201.	2.8	4
5438	Draft Genome Sequence of Bacillus coagulans MA-13, a Thermophilic Lactic Acid Producer from Lignocellulose. Microbiology Resource Announcements, 2019, 8, .	0.3	10
5439	Population Genomic Signatures of Genetic Structure and Environmental Selection in the Catadromous Roughskin Sculpin Trachidermus fasciatus. Genome Biology and Evolution, 2019, 11, 1751-1764.	1.1	18
5440	Proteomic Basis of Symbiosis: A Heterologous Partner Fails to Duplicate Homologous Colonization in a Novel Cnidarianâ€“ Symbiodiniaceae Mutualism. Frontiers in Microbiology, 2019, 10, 1153.	1.5	22
5441	Comparative transcriptomic profiling of High- and Low- grain Zinc and Iron containing Indian wheat genotypes. Current Plant Biology, 2019, 18, 100105.	2.3	18
5442	Transcriptomics of host-specific interactions in natural populations of the parasitic plant purple witchweed (<i>Striga hermonthica</i>). Weed Science, 2019, 67, 397-411.	0.8	16
5443	De novo Assembly and Annotation of the Blood Transcriptome of the Southern Elephant Seal Mirounga leonina from the South Shetland Islands, Antarctica. Ocean Science Journal, 2019, 54, 307-315.	0.6	3
5444	Dual RNA-Seq uncovers the function of an ABC transporter gene in the host-pathogen interaction between Epinephelus coioides and Pseudomonas plecoglossicida. Fish and Shellfish Immunology, 2019, 92, 45-53.	1.6	27
5445	Latitudinal divergence in a widespread amphibian: Contrasting patterns of neutral and adaptive genomic variation. Molecular Ecology, 2019, 28, 2996-3011.	2.0	30
5446	Hybrid Assembly of the Genome of the Entomopathogenic Nematode <i>Steinernema carpocapsae</i> Identifies the X-Chromosome. G3: Genes, Genomes, Genetics, 2019, 9, 2687-2697.	0.8	18
5447	Transcriptome and differentially expressed genes of Busseola fusca (Lepidoptera: Noctuidae) larvae challenged with Cry1Ab toxin. Gene, 2019, 710, 387-398.	1.0	7
5448	Comparative transcriptome analysis reveals resistance-related genes and pathways in Musa acuminata banana 'Guijiao 9' in response to Fusarium wilt. Plant Physiology and Biochemistry, 2019, 141, 83-94.	2.8	44
5449	Differential expression of innate and adaptive immune genes in the survivors of three gibel carp gynogenetic clones after herpesvirus challenge. BMC Genomics, 2019, 20, 432.	1.2	27
5450	Genome description of Phlebia radiata 79 with comparative genomics analysis on lignocellulose decomposition machinery of phlebioid fungi. BMC Genomics, 2019, 20, 430.	1.2	16
5451	Genome-wide analysis of magnesium transporter genes in Solanum lycopersicum. Computational Biology and Chemistry, 2019, 80, 498-511.	1.1	18
5452	4-NBT, a specific inhibitor of Babesia microti thioredoxin reductase, affects parasite biochemistry and proteomic properties. Ticks and Tick-borne Diseases, 2019, 10, 1018-1027.	1.1	3

#	ARTICLE	IF	CITATIONS
5453	Transcriptional analysis of renal dopamine-mediated Na+ homeostasis response to environmental salinity stress in Scatophagus argus. BMC Genomics, 2019, 20, 418.	1.2	11
5454	Leaf Transcriptome Assembly of Protium copal (Burseraceae) and Annotation of Terpene Biosynthetic Genes. Genes, 2019, 10, 392.	1.0	6
5455	Proteomic Landscape of the Mature Roots in a Rubber-Producing Grass Taraxacum Kok-saghyz. International Journal of Molecular Sciences, 2019, 20, 2596.	1.8	13
5456	Sex-biased gene discovery from the gonadal transcriptomes of the large yellow croaker (Larimichthys) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	8
5457	Transcriptome Analysis of Clinopodium chinense (Benth.) O. Kuntze and Identification of Genes Involved in Triterpenoid Saponin Biosynthesis. International Journal of Molecular Sciences, 2019, 20, 2643.	1.8	9
5458	Title is missing!. Turkish Journal of Fisheries and Aquatic Sciences, 2019, 19, .	0.4	0
5459	AaMps1 protein inhibition regulates the protein profile, nitric oxide, carbohydrate and polyamine contents in embryogenic suspension cultures of Araucaria angustifolia (Bertol.) Kuntze (Araucariaceae). Plant Cell, Tissue and Organ Culture, 2019, 138, 273-286.	1.2	5
5460	Comparative transcriptomic analysis reveals genetic divergence and domestication genes in Diospyros. BMC Plant Biology, 2019, 19, 227.	1.6	16
5461	Clubroot resistance gene Rcr6 in Brassica nigra resides in a genomic region homologous to chromosome A08 in B. rapa. BMC Plant Biology, 2019, 19, 224.	1.6	32
5462	Physiological responses of the abalone Haliotis discus hannai to daily and seasonal temperature variations. Scientific Reports, 2019, 9, 8019.	1.6	14
5463	Honey Bee Parasitic Mite Contains the Sensilla-Rich Sensory Organ on the Foreleg Tarsus Expressing Ionotropic Receptors With Conserved Functions. Frontiers in Physiology, 2019, 10, 556.	1.3	8
5464	The important role of phagocytosis and interleukins for nile tilapia (Oreochromis niloticus) to defense infection of Aeromonas hydrophila based on transcriptome analysis. Fish and Shellfish Immunology, 2019, 92, 54-63.	1.6	33
5465	Kinetic evaluation for rapid degradation of dimethylamine enriched with Agromyces and Ochrobactrum sp.. Journal of Environmental Management, 2019, 245, 322-329.	3.8	8
5466	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
5467	In-depth proteomic characterization of Schistosoma haematobium: Towards the development of new tools for elimination. PLoS Neglected Tropical Diseases, 2019, 13, e0007362.	1.3	31
5468	Characterization of Cucurbita maxima 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
5469	Unravelling the molecular mechanisms of nickel in woodlice.. Environmental Research, 2019, 176, 108507.	3.7	3
5470	<i>De Novo</i> Genome Sequence Assembly of Dwarf Coconut (<i>Cocos nucifera</i> L. â€˜Catigan Green) Tj ETQq1 1 0.784314 rgBT Genes, Genomes, Genetics, 2019, 9, 2377-2393.	0.8	55

#	ARTICLE	IF	CITATIONS
5471	Loss of Wood Formation Genes in Monocot Genomes. Genome Biology and Evolution, 2019, 11, 1986-1996.	1.1	20
5472	Not Just a Pathogen? Description of a Plant-Beneficial Pseudomonas syringae Strain. Frontiers in Microbiology, 2019, 10, 1409.	1.5	55
5473	Ovule Gene Expression Analysis in Sexual and Aposporous Apomictic Hypericum perforatum L. (Hypericaceae) Accessions. Frontiers in Plant Science, 2019, 10, 654.	1.7	14
5474	Early transcriptional response of seedling roots to Ralstonia solanacearum in tobacco (Nicotiana) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.8	9
5475	Pluripotency and the origin of animal multicellularity. Nature, 2019, 570, 519-522.	13.7	106
5476	Transcriptomic analysis of pollen-pistil interactions in almond (Prunus dulcis) identifies candidate genes for components of gametophytic self-incompatibility. Tree Genetics and Genomes, 2019, 15, 1.	0.6	13
5477	The Genomic Landscape of Crossover Interference in the Desert Tree Populus euphratica. Frontiers in Genetics, 2019, 10, 440.	1.1	2
5478	Population structure, demographic history and local adaptation of the grass carp. BMC Genomics, 2019, 20, 467.	1.2	53
5479	Gill transcriptome alterations in Macrobrachium rosenbergii under copper exposure. Chemosphere, 2019, 233, 796-808.	4.2	21
5480	De novo transcriptome assembly and co-expression network analysis of Cynanchum thesioides: Identification of genes involved in resistance to drought stress. Gene, 2019, 710, 375-386.	1.0	11
5481	Potential Molecular Mechanisms of AURKB in the Oncogenesis and Progression of Osteosarcoma Cells: A Label-Free Quantitative Proteomics Analysis. Technology in Cancer Research and Treatment, 2019, 18, 153303381985326.	0.8	6
5482	Transcriptome analysis reveals immune-related gene expression changes with age in giant panda (Ailuropoda melanoleuca) blood. Aging, 2019, 11, 249-262.	1.4	17
5483	Evolution of Gene Expression during a Transition from Environmental to Genetic Sex Determination. Molecular Biology and Evolution, 2019, 36, 1551-1564.	3.5	5
5484	Transcriptomic responses of the clam Meretrix meretrix to the organophosphorus pesticide (dimethoate). Ecotoxicology, 2019, 28, 539-549.	1.1	10
5485	The Reference Genome Sequence of Scutellaria baicalensis Provides Insights into the Evolution of Wogonin Biosynthesis. Molecular Plant, 2019, 12, 935-950.	3.9	121
5486	Analysis of an improved Cyanophora paradoxa genome assembly. DNA Research, 2019, 26, 287-299.	1.5	35
5487	Transcriptomic Response to Feeding and Starvation in a Herbivorous Dinoflagellate. Frontiers in Marine Science, 2019, 6, .	1.2	7
5488	Molecular basis underlying the successful invasion of hexaploid cytotypes of <i>Solidago canadensis </i>L.: Insights from integrated gene and miRNA expression profiling. Ecology and Evolution, 2019, 9, 4820-4852.	0.8	14

#	Article	IF	Citations
5489	Genomic Characterization Provides New Insights for Detailed Phage- Resistant Mechanism for Brucella abortus. Frontiers in Microbiology, 2019, 10, 917.	1.5	4
5490	Comparative Genomics Reveals the High Copy Number Variation of a Retro Transposon in Different Magnaporthe Isolates. Frontiers in Microbiology, 2019, 10, 966.	1.5	9
5491	Transcriptomic Analysis of Orange Fruit Treated with Pomegranate Peel Extract (PGE). Plants, 2019, 8, 101.	1.6	19
5492	Superantigen SpeA attenuates the biofilm forming capacity of Streptococcus pyogenes. Journal of Microbiology, 2019, 57, 626-636.	1.3	10
5493	Updated annotation of the wild strawberry Fragaria vesca V4 genome. Horticulture Research, 2019, 6, 61.	2.9	102
5494	Switching on the light: using metagenomic shotgun sequencing to characterize the intestinal microbiome of Atlantic cod. Environmental Microbiology, 2019, 21, 2576-2594.	1.8	27
5495	Identification of putative key genes for coastal environments and cold adaptation in mangrove Kandelia obovata through transcriptome analysis. Science of the Total Environment, 2019, 681, 191-201.	3.9	33
5496	Genome and Ontogenetic-Based Transcriptomic Analyses of the Flesh Fly,<i>Sarcophaga bullata</i>. G3: Genes, Genomes, Genetics, 2019, 9, 1313-1320.	0.8	11
5497	Transcriptome analysis of gill from Lateolabrax maculatus and aqp3 gene expression. Aquaculture and Fisheries, 2019, 4, 247-254.	1.2	9
5498	Chloroplast Genome of the Soap Bark Tree Quillaja saponaria. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	3
5499	Dual RNA-Seq Unveils Pseudomonas plecoglossicida htpG Gene Functions During Host-Pathogen Interactions With Epinephelus coioides. Frontiers in Immunology, 2019, 10, 984.	2.2	25
5500	The transcriptome analysis of the bamboo grasshopper provides insights into hypothermic stress acclimation. International Journal of Biological Macromolecules, 2019, 134, 237-246.	3.6	6
5501	Genetic and phenotypic analyses indicate that resistance to flooding stress is uncoupled from performance in cultivated sunflower. New Phytologist, 2019, 223, 1657-1670.	3.5	14
5502	Dynamic profile of proteome revealed multiple levels of regulation under heat stress in Saccharina japonica. Journal of Applied Phycology, 2019, 31, 3077-3089.	1.5	9
5503	Genome of the African cassava whitefly Bemisia tabaci and distribution and genetic diversity of cassava-colonizing whiteflies in Africa. Insect Biochemistry and Molecular Biology, 2019, 110, 112-120.	1.2	47
5504	High-throughput identification of heavy metal binding proteins from the byssus of chinese green mussel (Perna viridis) by combination of transcriptome and proteome sequencing. PLoS ONE, 2019, 14, e0216605.	1.1	7
5505	IlluminaÂ® Sequencing Reveals Candidate Genes of Carotenoid Metabolism in Three Pummelo Cultivars (Citrus Maxima) with Different Pulp Color. International Journal of Molecular Sciences, 2019, 20, 2246.	1.8	26
5506	A core set of venom proteins is released by entomopathogenic nematodes in the genus Steinernema. PLoS Pathogens, 2019, 15, e1007626.	2.1	58

#	Article	IF	Citations
5507	Uptake, depuration and sublethal effects of the neonicotinoid, imidacloprid, exposure in Sydney rock oysters. Chemosphere, 2019, 230, 1-13.	4.2	29
5508	Genome-wide characterization of drought stress responsive long non-coding RNAs in Tibetan wild barley. Environmental and Experimental Botany, 2019, 164, 124-134.	2.0	31
5509	Discovery of sex-related genes from embryonic development stage based on transcriptome analysis in Eriocheir sinensis. Gene, 2019, 710, 1-8.	1.0	14
5510	Comparative analysis of differentially expressed genes between the ovaries from pregnant and nonpregnant goats using RNA-Seq. Journal of Biological Research, 2019, 26, 3.	2.2	13
5511	Comparative profile analysis reveals differentially expressed microRNAs regulate anther and pollen development in kenaf cytoplasmic male sterility line. Genome, 2019, 62, 455-466.	0.9	5
5512	Transcriptional regulation of Lonicera japonica Thunb. during flower development as revealed by comprehensive analysis of transcription factors. BMC Plant Biology, 2019, 19, 198.	1.6	26
5513	A comparative analysis of small RNAs between two Upland cotton backcross inbred lines with different fiber length: Expression and distribution. Crop Journal, 2019, 7, 198-208.	2.3	7
5514	Octopus maya white body show sex-specific transcriptomic profiles during the reproductive phase, with high differentiation in signaling pathways. PLoS ONE, 2019, 14, e0216982.	1.1	14
5515	De novo Characterization of the Platycladus orientalis Transcriptome and Analysis of Photosynthesis-Related Genes during Aging. Forests, 2019, 10, 393.	0.9	4
5516	Increases in Genistein in Medicago sativa Confer Resistance against the Pisum Host Race of Acyrthosiphon pisum. Insects, 2019, 10, 97.	1.0	9
5517	Stage-specific transcriptome of Bursaphelenchus xylophilus reveals temporal regulation of effector genes and roles of the dauer-like stages in the lifecycle. Scientific Reports, 2019, 9, 6080.	1.6	26
5518	A Perspective on Comparative and Functional Genomics. Computational Biology, 2019, , 361-372.	0.1	1
5519	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	3.8	81
5520	Transcriptomic analysis reveals differences in the regulation of amino acid metabolism in asexual and sexual planarians. Scientific Reports, 2019, 9, 6132.	1.6	12
5521	Genome sequencing and transcript analysis of Hemileia vastatrix reveal expression dynamics of candidate effectors dependent on host compatibility. PLoS ONE, 2019, 14, e0215598.	1.1	30
5522	ASYMMETRIC LEAVES1 and REVOLUTA are the key regulatory genes associated with pitcher development in Nepenthes khasiana. Scientific Reports, 2019, 9, 6318.	1.6	10
5523	CENTRORADIALIS Interacts with <i>FLOWERING LOCUS T</i>-Like Genes to Control Floret Development and Grain Number. Plant Physiology, 2019, 180, 1013-1030.	2.3	40
5524	Transcriptome analysis and annotation: SNPs identified from single copy annotated unigenes of three polyploid blueberry crops. PLoS ONE, 2019, 14, e0216299.	1.1	9

#	ARTICLE	IF	CITATIONS
5525	Transcriptome analysis of differentially expressed genes in the fore- and hind-intestine of ovate pompano Trachinotus ovatus. Aquaculture, 2019, 508, 76-82.	1.7	8
5526	Transcriptome profiling of Populus tomentosa under cold stress. Industrial Crops and Products, 2019, 135, 283-293.	2.5	53
5527	Transcriptional Responses of the <i>Trichoplusia ni</i> Midgut to Oral Infection by the Baculovirus Autographa californica Multiple Nucleopolyhedrovirus. Journal of Virology, 2019, 93, .	1.5	20
5528	High-throughput sequencing analysis of Eugenia uniflora: insights into repetitive DNA, gene content and potential biotechnological applications. 3 Biotech, 2019, 9, 200.	1.1	5
5529	Pan Proteome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> Isolates Contrasting in Virulence. Proteomics, 2019, 19, e1900082.	1.3	4
5530	Genome-Wide Identification and Transcriptional Expression Profiles of the F-box Gene Family in Common Walnut (Juglans regia L.). Forests, 2019, 10, 275.	0.9	8
5531	MicroRNA396-mediated alteration in plant development and salinity stress response in creeping bentgrass. Horticulture Research, 2019, 6, 48.	2.9	64
5532	Multi-species transcriptome analyses for the regulation of crocins biosynthesis in Crocus. BMC Genomics, 2019, 20, 320.	1.2	16
5533	Treatment of Common Sunflower (Helianthus annus L.) Seeds with Radio-frequency Electromagnetic Field and Cold Plasma Induces Changes in Seed Phytohormone Balance, Seedling Development and Leaf Protein Expression. Scientific Reports, 2019, 9, 6437.	1.6	93
5534	Development and validation of EST-SSR markers of Magnolia wufengensis using de novo transcriptome sequencing. Trees - Structure and Function, 2019, 33, 1213-1223.	0.9	9
5535	Transcriptome analysis and development of SSR markers of ethnobotanical plant Sterculia lanceolata. Tree Genetics and Genomes, 2019, 15, 1.	0.6	5
5536	Transcriptome data of the carrageenophyte Eucheuma denticulatum. Data in Brief, 2019, 24, 103824.	0.5	3
5537	Saprotrophic yeasts formerly classified as Pseudozyma have retained a large effector arsenal, including functional Pep1 orthologs. Mycological Progress, 2019, 18, 763-768.	0.5	19
5538	Proteomic analysis of Moringa oleifera Lam. leaf extract provides insights into milk-clotting proteases. LWT - Food Science and Technology, 2019, 109, 289-295.	2.5	19
5539	Transcriptome and Proteome Response of Rhipicephalus annulatus Tick Vector to Babesia bigemina Infection. Frontiers in Physiology, 2019, 10, 318.	1.3	24
5540	Phenotypic and molecular traits determine the tolerance of olive trees to drought stress. Plant Physiology and Biochemistry, 2019, 139, 521-527.	2.8	14
5541	Environmental interactions are regulated by temperature in Burkholderia seminalis TC3.4.2R3. Scientific Reports, 2019, 9, 5486.	1.6	3
5542	Comparative study of Cu uptake and early transcriptome responses in the green microalga Chlamydomonas reinhardtii and the macrophyte Elodea nuttallii. Environmental Pollution, 2019, 250, 331-337.	3.7	19

#	ARTICLE	IF	CITATIONS
5543	Transcriptome analyses of Paris polyphylla var. chinensis, Ypsilandra thibetica, and Polygonatum kingianum characterize their steroidal saponin biosynthesis pathway. FÃ¬toterapÃ¬Ã¢, 2019, 135, 52-63.	1.1	20
5544	Release from intralocus sexual conflict? Evolved loss of a male sexual trait demasculinizes female gene expression. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190497.	1.2	12
5545	Comparative Transcriptome Analysis of Developing Seeds and Silique Wall Reveals Dynamic Transcription Networks for Effective Oil Production in Brassica napus L.. International Journal of Molecular Sciences, 2019, 20, 1982.	1.8	45
5546	Transcriptome analysis reveals downregulation of virulence-associated genes expression in a low virulence Verticillium dahliae strain. Archives of Microbiology, 2019, 201, 927-941.	1.0	23
5547	Whole transcriptome analysis of an estuarine amphipod exposed to highway road dust. Science of the Total Environment, 2019, 675, 141-150.	3.9	4
5548	Genome of â€˜Charleston Grayâ€™, the principal American watermelon cultivar, and genetic characterization of 1,365 accessions in the U.S. National Plant Germplasm System watermelon collection. Plant Biotechnology Journal, 2019, 17, 2246-2258.	4.1	96
5549	Shedding Light on a Secretive Tertiary Urodelean Relict: Hynobiid Salamanders (Paradactylodon) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5 Genes, 2019, 10, 306.	1.0	4
5550	Shotgun proteomic analysis of quinoa seeds reveals novel lysine-rich seed storage globulins. Food Chemistry, 2019, 293, 299-306.	4.2	47
5551	The response to the DNA damaging agent methyl methanesulfonate in a fungal plant pathogen. Fungal Biology, 2019, 123, 408-422.	1.1	9
5552	Genome-informed Bradyrhizobium taxonomy: where to from here?. Systematic and Applied Microbiology, 2019, 42, 427-439.	1.2	62
5553	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i>. MBio, 2019, 10, .	1.8	50
5554	Differential gene expression in response to eCry3.1Ab ingestion in an unselected and eCry3.1Ab-selected western corn rootworm (Diabrotica virgifera virgifera LeConte) population. Scientific Reports, 2019, 9, 4896.	1.6	12
5555	Long-read based assembly and synteny analysis of a reference Drosophila subobscura genome reveals signatures of structural evolution driven by inversions recombination-suppression effects. BMC Genomics, 2019, 20, 223.	1.2	15
5556	Metabolic Peculiarities of Paracoccidioides brasiliensis Dimorphism as Demonstrated by iTRAQ Labeling Proteomics. Frontiers in Microbiology, 2019, 10, 555.	1.5	19
5557	Pinus massoniana Introgression Hybrids Display Differential Expression of Reproductive Genes. Forests, 2019, 10, 230.	0.9	5
5558	Transcriptome analysis of a powdery mildew pathogen (<i>Podosphaera pannosa</i>) infecting <i>Eucalyptus urophylla</i>: De novo assembly, expression profiling and secretome prediction. Forest Pathology, 2019, 49, e12508.	0.5	5
5559	A cytochrome P450 allele confers pyrethroid resistance on a major African malaria vector, reducing insecticide-treated bednet efficacy. Science Translational Medicine, 2019, 11, .	5.8	121
5560	The Patchy Distribution of Restrictionâ€“Modification System Genes and the Conservation of Orphan Methyltransferases in Halobacteria. Genes, 2019, 10, 233.	1.0	27

#	Article	IF	Citations
5561	Salinity-associated microRNAs and their potential roles in mediating salt tolerance in rice colonized by the endophytic root fungus Piriformospora indica. Functional and Integrative Genomics, 2019, 19, 659-672.	1.4	42
5562	Transcriptome profiling of the meristem tissue of Saccharina japonica (Phaeophyceae, Laminariales) under severe stress of copper. Marine Genomics, 2019, 47, 100671.	0.4	18
5563	Transcriptomic Mechanism of the Phytohormone 6-Benzylaminopurine (6-BAP) Stimulating Lipid and DHA Synthesis in <i>Aurantiochytrium</i> sp.. Journal of Agricultural and Food Chemistry, 2019, 67, 5560-5570.	2.4	23
5564	The genes expression difference between winged and wingless bird cherry-oat aphid Rhopalosiphum padi based on transcriptomic data. Scientific Reports, 2019, 9, 4754.	1.6	10
5565	A fruit firmness QTL identified on linkage group 4 in sweet cherry (Prunus avium L.) is associated with domesticated and bred germplasm. Scientific Reports, 2019, 9, 5008.	1.6	29
5566	Gossypium barbadense and Gossypium hirsutum genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics, 2019, 51, 739-748.	9.4	568
5567	Injury affects coelomic fluid proteome of the common starfish<i>Asterias rubens</i>. Journal of Experimental Biology, 2019, 222, .	0.8	11
5568	QTL mapping for maize starch content and candidate gene prediction combined with co-expression network analysis. Theoretical and Applied Genetics, 2019, 132, 1931-1941.	1.8	31
5569	Time-dependent transcriptomic responses of Daphnia magna exposed to metabolic disruptors that enhanced storage lipid accumulation.. Environmental Pollution, 2019, 249, 99-108.	3.7	17
5570	Hybrid sequencing reveals insight into heat sensing and signaling of bread wheat. Plant Journal, 2019, 98, 1015-1032.	2.8	73
5571	Genomic discovery of ion channel genes in the central nervous system of the lamprey Petromyzon marinus. Marine Genomics, 2019, 46, 29-40.	0.4	5
5572	Caffeine Content and Related Gene Expression: Novel Insight into Caffeine Metabolism in <i>Camellia</i> Plants Containing Low, Normal, and High Caffeine Concentrations. Journal of Agricultural and Food Chemistry, 2019, 67, 3400-3411.	2.4	61
5573	Early responses given distinct tactics to infection of Peronophythora litchii in susceptible and resistant litchi cultivar. Scientific Reports, 2019, 9, 2810.	1.6	12
5574	Genome-Wide Profiling of Circular RNAs in the Rapidly Growing Shoots of Moso Bamboo (Phyllostachys edulis). Plant and Cell Physiology, 2019, 60, 1354-1373.	1.5	56
5575	Transcriptomics analysis of propiconazole-treated Cochliobolus sativus reveals new putative azole targets in the plant pathogen. Functional and Integrative Genomics, 2019, 19, 453-465.	1.4	10
5576	New molecular insights on the response of the green alga Tetraselmis suecica to nitrogen starvation. Scientific Reports, 2019, 9, 3336.	1.6	47
5577	The Molecular Basis of Freshwater Adaptation in Prawns: Insights from Comparative Transcriptomics of Three <i>Macrobrachium</i> Species. Genome Biology and Evolution, 2019, 11, 1002-1018.	1.1	23
5578	Gonadal microRNA Expression Profiles and Their Potential Role in Sex Differentiation and Gonadal Maturation of Mud Crab Scylla paramamosain. Marine Biotechnology, 2019, 21, 320-334.	1.1	22

#	ARTICLE	IF	CITATIONS
5579	Unravelling paralogous gene expression dynamics during three-spined stickleback embryogenesis. Scientific Reports, 2019, 9, 3752.	1.6	8
5580	Analysis of genetic control and QTL mapping of essential wheat grain quality traits in a recombinant inbred population. PLoS ONE, 2019, 14, e0200669.	1.1	49
5581	Transcriptional Responses in Defense-Related Genes of <i>Sitobion avenae</i> (Hemiptera: Aphididae) Feeding on Wheat and Barley. Journal of Economic Entomology, 2019, 112, 382-395.	0.8	10
5582	Gene regulation of Sclerotinia sclerotiorum during infection of Glycine max: on the road to pathogenesis. BMC Genomics, 2019, 20, 157.	1.2	45
5583	Contrasting patterns of gene expression indicate differing pyrethroid resistance mechanisms across the range of the New World malaria vector Anopheles albimanus. PLoS ONE, 2019, 14, e0210586.	1.1	21
5584	Evidence for Highly Variable, Region-Specific Patterns of T-Cell Epitope Mutations Accumulating in Mycobacterium tuberculosis Strains. Frontiers in Immunology, 2019, 10, 195.	2.2	6
5585	Transcriptome driven characterization of curly- and smooth-leafed endives reveals molecular differences in the sesquiterpenoid pathway. Horticulture Research, 2019, 6, 1.	2.9	193
5586	Insights into the Draft Genome Sequence of the Kiwifruit-Associated Pathogenic Isolate Pseudomonas fluorescens AHK-1. Current Microbiology, 2019, 76, 552-557.	1.0	1
5587	De novo transcriptomic analysis of gonad of Strongylocentrotus nudus and gene discovery for biosynthesis of polyunsaturated fatty acids. Genes and Genomics, 2019, 41, 583-597.	0.5	9
5588	Gene expression patterns indicate that a high-fatâ€“high-carbohydrate diet causes mitochondrial dysfunction in fish. Genome, 2019, 62, 53-67.	0.9	5
5589	Transcriptomic responses of regenerating earthworms (Eisenia foetida) to retinoic acid reveals the role of pluripotency genes. Chemosphere, 2019, 226, 47-59.	4.2	3
5590	De novo whole transcriptome profiling of Edwardsiella tarda isolated from infected fish (Labeo) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	9
5591	De novo assembly and characterization of the transcriptome of the northern mauxia shrimp Acetes chinensis. Marine Genomics, 2019, 47, 100672.	0.4	4
5592	Insight into the genome and brackish water adaptation strategies of toxic and bloom-forming Baltic Sea Dolichospermum sp. UHCC 0315. Scientific Reports, 2019, 9, 4888.	1.6	14
5593	Mapping Gene Markers for Apple Fruit Ring Rot Disease Resistance Using a Multi-omics Approach. G3: Genes, Genomes, Genetics, 2019, 9, 1663-1678.	0.8	27
5594	Differential Alternative Splicing Genes in Response to Boron Deficiency in Brassica napus. Genes, 2019, 10, 224.	1.0	12
5595	Genome-wide identification and characterization of abiotic-stress responsive SOD (superoxide) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	1.2	94
5596	Proteomic profiling and integrated analysis with transcriptomic data bring new insights in the stress responses of Kluyveromyces marxianus after an arrest during high-temperature ethanol fermentation. Biotechnology for Biofuels, 2019, 12, 49.	6.2	24

#	Article	IF	Citations
5597	Gene coexpression analysis reveals dose-dependent and type-specific networks responding to ionizing radiation in the aquatic model plant Lemna minor using public data. Journal of Genetics, 2019, 98, 1.	0.4	5
5598	Comparative transcriptome analysis uncovers the regulatory functions of long noncoding RNAs in fruit development and color changes of Fragaria pentaphylla. Horticulture Research, 2019, 6, 42.	2.9	28
5599	Transcriptome profiling of coriander: a dual purpose crop unravels stem gall resistance genes. Journal of Genetics, 2019, 98, 1.	0.4	13
5600	Transcriptome analysis and discovery of genes involved in immune pathways in Solen strictus (Gould,) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	8
5601	Characterization of the Rosa roxburghii Tratt transcriptome and analysis of MYB genes. PLoS ONE, 2019, 14, e0203014.	1.1	20
5602	Allele-specific expression variation at different ploidy levels in Squalius alburnoides. Scientific Reports, 2019, 9, 3688.	1.6	5
5603	Draft Genome Sequences of Penicillium spp. from Deeply Buried Oligotrophic Marine Sediments. Microbiology Resource Announcements, 2019, 8, .	0.3	2
5604	Patterns of genomic differentiation between two Lake Victoria cichlid species, Haplochromis pyrrhocephalus and H. sp. â€˜maculaâ€™. BMC Evolutionary Biology, 2019, 19, 68.	3.2	4
5605	A precedented nuclear genetic code with all three termination codons reassigned as sense codons in the syndinean Amoebophrya sp. ex Karlodinium veneficum. PLoS ONE, 2019, 14, e0212912.	1.1	12
5606	Transcriptional Aneuploidy Responses of Brassica rapa-oleracea Monosomic Alien Addition Lines (MAALs) Derived From Natural Allopolyploid B. napus. Frontiers in Genetics, 2019, 10, 67.	1.1	6
5607	High individual variability in the transcriptomic response of Mediterranean mussels to Vibrio reveals the involvement of myticins in tissue injury. Scientific Reports, 2019, 9, 3569.	1.6	34
5608	Transposon mutagenesis and identification of mutated genes in growth-delayed Edwardsiella ictaluri. BMC Microbiology, 2019, 19, 55.	1.3	2
5609	Comparative analysis of the transcriptome of the Amazonian fish species Colossoma macropomum (tambaqui) and hybrid tambacu by next generation sequencing. PLoS ONE, 2019, 14, e0212755.	1.1	12
5610	Transcriptome analysis of the curry tree (Bergera koenigii L., Rutaceae) during leaf development. Scientific Reports, 2019, 9, 4230.	1.6	2
5611	Elymus nutans genes for seed shattering and candidate gene-derived EST-SSR markers for germplasm evaluation. BMC Plant Biology, 2019, 19, 102.	1.6	14
5612	Transcriptome response of roots to salt stress in a salinity-tolerant bread wheat cultivar. PLoS ONE, 2019, 14, e0213305.	1.1	70
5613	Circatidal gene expression in the mangrove cricket Apteronemobius asahinai. Scientific Reports, 2019, 9, 3719.	1.6	20
5614	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in Taxodium â€˜Zhongshanshanâ€™. International Journal of Molecular Sciences, 2019, 20, 1225.	1.8	32

#	ARTICLE	IF	CITATIONS
5615	Transcriptomes of Indian barnyard millet and barnyardgrass reveal putative genes involved in drought adaptation and micronutrient accumulation. Acta Physiologiae Plantarum, 2019, 41, 1.	1.0	22
5616	New Zealand Tree and Giant WÄ“tÄ•(Orthoptera) Transcriptomics Reveal Divergent Selection Patterns in Metabolic Loci. Genome Biology and Evolution, 2019, 11, 1293-1306.	1.1	6
5617	Aethionema arabicum: a novel model plant to study the light control of seed germination. Journal of Experimental Botany, 2019, 70, 3313-3328.	2.4	31
5618	Genome sequence of the corn leaf aphid (<i>Rhopalosiphum maidis</i>Fitch). GigaScience, 2019, 8, .	3.3	60
5619	Small nucleolar RNA Sf-15 regulates proliferation and apoptosis of Spodoptera frugiperda Sf9 cells. BMC Molecular Biology, 2019, 20, 12.	3.0	4
5620	Transcriptome profiling of faba bean (Vicia faba L.) drought-tolerant variety hassawi-2 under drought stress using RNA sequencing. Electronic Journal of Biotechnology, 2019, 39, 15-29.	1.2	19
5621	Transcriptome analysis of rare minnow (Gobiocypris rarus) infected by the grass carp reovirus. Fish and Shellfish Immunology, 2019, 89, 337-344.	1.6	27
5622	Advances in the technologies for studying consortia of bacteria and cyanobacteria/microalgae in wastewaters. Critical Reviews in Biotechnology, 2019, 39, 709-731.	5.1	55
5623	Population genomics of rapidly invading lionfish in the Caribbean reveals signals of range expansion in the absence of spatial population structure. Ecology and Evolution, 2019, 9, 3306-3320.	0.8	24
5624	Characterization of the transcriptional profiles in common buckwheat (Fagopyrum esculentum) under PEG-mediated drought stress. Electronic Journal of Biotechnology, 2019, 39, 42-51.	1.2	12
5625	BpAP1 directly regulates BpDEF to promote male inflorescence formation in Betula platyphylla Ã— B. pendula. Tree Physiology, 2019, 39, 1046-1060.	1.4	29
5626	Chromosomeâ€level genome assembly of <i>Triplophysa tibetana</i>, a fish adapted to the harsh highâ€altitude environment of the Tibetan Plateau. Molecular Ecology Resources, 2019, 19, 1027-1036.	2.2	39
5627	Developmental expression and evolution of hexamerin and haemocyanin from <i>Folsomia candida</i> (Collembola). Insect Molecular Biology, 2019, 28, 716-727.	1.0	5
5628	Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. BMC Genomics, 2019, 20, 278.	1.2	7
5629	Scavenging organic nitrogen and remodelling lipid metabolism are key survival strategies adopted by the endophytic fungi, <i>Serendipita vermifera</i> and <i>Serendipita bescii</i> to alleviate nitrogen and phosphorous starvation in vitro. Environmental Microbiology Reports, 2019, 11, 548-557.	1.0	18
5630	Identification and expression of microRNAs in european eels Anguilla anguilla from two natural sites with different pollution levels. Environmental Pollution, 2019, 250, 274-283.	3.7	4
5631	The effect of a LysR-type transcriptional regulator gene of Pseudomonas plecoglossicida on the immune responses of Epinephelus coioides. Fish and Shellfish Immunology, 2019, 89, 420-427.	1.6	26
5632	Transcriptome-wide gene expression alteration of sloe bug (Insecta: Hemiptera: Dolycoris baccarum) to divergent-altitude environments. AIP Conference Proceedings, 2019, , .	0.3	0

#	Article	IF	Citations
5633	Stock modelling of residential appliance energy considering technology and occupant behavior evolution: case study of television in urban China. IOP Conference Series: Earth and Environmental Science, 2019, 238, 012049.	0.2	0
5634	Transcriptome analysis reveals the activation of neuroendocrine-immune system in shrimp hemocytes at the early stage of WSSV infection. BMC Genomics, 2019, 20, 247.	1.2	32
5635	High-Throughput Identification and Analysis of Novel Conotoxins from Three Vermivorous Cone Snails by Transcriptome Sequencing. Marine Drugs, 2019, 17, 193.	2.2	18
5636	Transcriptomic analysis of the prothoracic gland from two lepidopteran insects, domesticated silkmoth Bombyx mori and wild silkmoth Antheraea pernyi. Scientific Reports, 2019, 9, 5313.	1.6	8
5637	Comparative genomics and transcriptomics analysis reveals evolution patterns of selection in the Salix phylogeny. BMC Genomics, 2019, 20, 253.	1.2	9
5638	Combining microfluidics and RNA-sequencing to assess the inducible defensome of a mushroom against nematodes. BMC Genomics, 2019, 20, 243.	1.2	19
5639	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	3.8	114
5640	Rapid Identification of a Genomic Region Conferring Dwarfism in Rapeseed (Brassica napus L.) YA2016-12. Agronomy, 2019, 9, 129.	1.3	5
5641	Transcriptomic Sequencing and Co-Expression Network Analysis on Key Genes and Pathways Regulating Nitrogen Use Efficiency in Myriophyllum aquaticum. International Journal of Molecular Sciences, 2019, 20, 1587.	1.8	10
5642	Heatâ€stress induced flowering can be a potential adaptive response to ocean warming for the iconic seagrass <i>Posidonia oceanica</i>. Molecular Ecology, 2019, 28, 2486-2501.	2.0	85
5643	The Transcriptome of Verticillium dahliae Responds Differentially Depending on the Disease Susceptibility Level of the Olive (Olea europaea L.) Cultivar. Genes, 2019, 10, 251.	1.0	34
5644	Comprehensive analysis of miRNA profiles reveals the role of Schistosoma japonicum miRNAs at different developmental stages. Veterinary Research, 2019, 50, 23.	1.1	11
5645	Comparative transcriptomic analysis provides insights into the development of a Salvia splendens Ker-Gawler mutant, SX919M. PLoS ONE, 2019, 14, e0213446.	1.1	0
5646	Transcriptome analysis reveals novel insights in air-breathing magur catfish (Clarias magur) in response to high environmental ammonia. Gene, 2019, 703, 35-49.	1.0	25
5647	Genomic analysis of the aggressive tree pathogen Ceratocystis albifundus. Fungal Biology, 2019, 123, 351-363.	1.1	11
5648	Transcriptomic response of durum wheat to cold stress at reproductive stage. Molecular Biology Reports, 2019, 46, 2427-2445.	1.0	29
5649	Transcriptomic insight into antimicrobial peptide factors involved in the prophylactic immunity of crowded Mythimna separata larvae. Developmental and Comparative Immunology, 2019, 98, 34-41.	1.0	11
5650	Transcriptional profiling of wheat (Triticum aestivum L.) during a compatible interaction with the cereal cyst nematode Heterodera avenae. Scientific Reports, 2019, 9, 2184.	1.6	11

#	Article	IF	Citations
5651	Comparative Transcriptome Analysis of the Pinewood Nematode Bursaphelenchus xylophilus Reveals the Molecular Mechanism Underlying Its Defense Response to Host-Derived Î±-pinene. International Journal of Molecular Sciences, 2019, 20, 911.	1.8	29
5652	De novo assembly and transcriptome dataset of liver, testis and head kidney from red drum (Sciaenops) Tj ETQq1 1 0.784314 rgBT /Ove	0.5	7
5653	Transcriptome sequencing analyses reveals mechanisms of eliminated russet by applying GA3 and CPPU on â€˜Shine Muscatâ€™ grape. Scientia Horticulturae, 2019, 250, 94-103.	1.7	17
5654	Functional annotation of putative QTL associated with black tea quality and drought tolerance traits. Scientific Reports, 2019, 9, 1465.	1.6	22
5655	Genome sequence of the barred knifejaw<i>Oplegnathus fasciatus</i>(Temminck & Schlegel, 1844): the first chromosome-level draft genome in the family Oplegnathidae. GigaScience, 2019, 8, .	3.3	32
5656	Genomic content of a novel yeast species Hanseniaspora gamundiae sp. nov. from fungal stromata (Cyttaria) associated with a unique fermented beverage in Andean Patagonia, Argentina. PLoS ONE, 2019, 14, e0210792.	1.1	37
5657	Delegating Sex: Differential Gene Expression in Stolonizing Syllids Uncovers the Hormonal Control of Reproduction. Genome Biology and Evolution, 2019, 11, 295-318.	1.1	13
5658	Limber pine (<i>Pinus flexilis</i> James) genetic map constructed by exomeâ€seq provides insight into the evolution of disease resistance and a genomic resource for genomicsâ€based breeding. Plant Journal, 2019, 98, 745-758.	2.8	33
5659	First RNA-seq approach to study fruit set and parthenocarpy in zucchini (Cucurbita pepo L.). BMC Plant Biology, 2019, 19, 61.	1.6	19
5660	Transcriptome, proteome and draft genome of Euglena gracilis. BMC Biology, 2019, 17, 11.	1.7	98
5661	Comparative de novo flower transcriptome analysis of polygamodioecious tree Garcinia indica. 3 Biotech, 2019, 9, 72.	1.1	6
5662	An experimental genetically attenuated live vaccine to prevent transmission of Toxoplasma gondii by cats. Scientific Reports, 2019, 9, 1474.	1.6	112
5663	Comparative transcriptome analysis reveals K+ transporter gene contributing to salt tolerance in eggplant. BMC Plant Biology, 2019, 19, 67.	1.6	25
5664	Comparative Study of Immune Reaction Against Bacterial Infection From Transcriptome Analysis. Frontiers in Immunology, 2019, 10, 153.	2.2	40
5665	Transcriptome and Proteome Alternation With Resistance to Bacillus thuringiensis Cry1Ah Toxin in Ostrinia furnacalis. Frontiers in Physiology, 2019, 10, 27.	1.3	16
5666	Complete Genome Sequence of <i>Halocella</i> sp. Strain SP3-1, an Extremely Halophilic, Glycoside Hydrolase- and Bacteriocin-Producing Bacterium Isolated from a Salt Evaporation Pond. Microbiology Resource Announcements, 2019, 8, .	0.3	8
5667	Identification of Early Salinity Stress-Responsive Proteins in Dunaliella salina by isobaric tags for relative and absolute quantitation (iTRAQ)-Based Quantitative Proteomic Analysis. International Journal of Molecular Sciences, 2019, 20, 599.	1.8	22
5668	Sex- and developmental-specific transcriptomic analyses of the Antarctic mite, Alaskozetes antarcticus, reveal transcriptional shifts underlying oribatid mite reproduction. Polar Biology, 2019, 42, 357-370.	0.5	8

#	ARTICLE	IF	CITATIONS
5669	Transcriptional differences provide insight into environmental acclimatization in wild amur ide (Leuciscus waleckii) during spawning migration from alkalized lake to freshwater river. Genomics, 2019, 111, 267-276.	1.3	15
5670	Toxins, 2019, 11, 97.	1.5	20
5671	Resistant and susceptible cacao genotypes exhibit defense gene polymorphism and unique early responses to Phytophthora megakarya inoculation. Plant Molecular Biology, 2019, 99, 499-516.	2.0	24
5672	Heterodera glycines utilizes promiscuous spliced leaders and demonstrates a unique preference for a species-specific spliced leader over C. elegans SL1. Scientific Reports, 2019, 9, 1356.	1.6	5
5673	Evolution and functional divergence of MADS-box genes in Pyrus. Scientific Reports, 2019, 9, 1266.	1.6	15
5674	Genomic and transcriptomic investigations of the evolutionary transition from oviparity to viviparity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3646-3655.	3.3	43
5675	The genome of the soybean cyst nematode (Heterodera glycines) reveals complex patterns of duplications involved in the evolution of parasitism genes. BMC Genomics, 2019, 20, 119.	1.2	55
5676	Transcriptomic analysis reveals adaptive strategies to chronic low nitrogen in Tibetan wild barley. BMC Plant Biology, 2019, 19, 68.	1.6	22
5677	How an ancient, salt-tolerant fruit crop, Ficus carica L., copes with salinity: a transcriptome analysis. Scientific Reports, 2019, 9, 2561.	1.6	26
5678	Genomic and Functional Characterization of Enterococcus mundtii QAUEM2808, Isolated From Artisanal Fermented Milk Product Dahi. Frontiers in Microbiology, 2019, 10, 434.	1.5	16
5679	Optimisation of protein extraction for in-depth profiling of the cereal grain proteome. Journal of Proteomics, 2019, 197, 23-33.	1.2	44
5680	Antarctic blackfin icefish genome reveals adaptations to extreme environments. Nature Ecology and Evolution, 2019, 3, 469-478.	3.4	115
5681	Changes in gene DNA methylation and expression networks accompany caste specialization and ageâ€•related physiological changes in a social insect. Molecular Ecology, 2019, 28, 1975-1993.	2.0	30
5682	Antennal transcriptome analysis of the maize weevil Sitophilus zeamais : Identification and tissue expression profiling of candidate odorantâ€•binding protein genes. Archives of Insect Biochemistry and Physiology, 2019, 101, e21542.	0.6	20
5683	Transcriptome analysis provides insights into the molecular mechanisms responsible for evisceration behavior in the sea cucumber Apostichopus japonicus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 143-157.	0.4	13
5684	Label-free quantification of protein expression in the rainbow trout (Oncorhynchus mykiss) in response to short-term exposure to heat stress. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 158-168.	0.4	10
5685	Genetic and expression differences between putative ecotypes of Sphagnum denticulatum Brid. (Sphagnaceae: Bryophyta) subjected to drought stress and rehydration. Perspectives in Plant Ecology, Evolution and Systematics, 2019, 37, 39-52.	1.1	4
5686	Genome analysis of the rice coral Montipora capitata. Scientific Reports, 2019, 9, 2571.	1.6	53

#	ARTICLE	IF	CITATIONS
5687	Mutational convergence acts as a major player in adaptive parallel evolution of Shigella spp.. Scientific Reports, 2019, 9, 3252.	1.6	6
5688	De novo assembly of transcriptomes, mining, and development of novel EST-SSR markers in Curcuma alismatifolia (Zingiberaceae family) through Illumina sequencing. Scientific Reports, 2019, 9, 3047.	1.6	61
5689	Design and Production of a Recombinant Hybrid Toxin to Raise Protective Antibodies against Loxosceles Spider Venom. Toxins, 2019, 11, 108.	1.5	13
5690	Analysis of novel immuneâ€"related genes and microsatellite markers in the transcriptome of Paphia undulata. Journal of Oceanology and Limnology, 2019, 37, 1301-1316.	0.6	2
5691	Activation of biochemical factors in CMV-infected tobacco by ningnanmycin. Pesticide Biochemistry and Physiology, 2019, 156, 116-122.	1.6	9
5692	De novo characterization of placental transcriptome in the Eurasian beaver (Castor fiber L.). Functional and Integrative Genomics, 2019, 19, 421-435.	1.4	4
5693	Exploring the influence of the surface proteins on probiotic effects performed by Lactobacillus pentosus HC-2 using transcriptome analysis in Litopenaeus vannamei midgut. Fish and Shellfish Immunology, 2019, 87, 853-870.	1.6	16
5694	Tree Response to Herbivory Is Affected by Endogenous Rhythmic Growth and Attenuated by Cotreatment With a Mycorrhizal Fungus. Molecular Plant-Microbe Interactions, 2019, 32, 770-781.	1.4	5
5695	Comparative Genome and Transcriptome Analysis Reveals Gene Selection Patterns Along with the Paleo-Climate Change in the Populus Phylogeny. Forests, 2019, 10, 163.	0.9	1
5696	Gene expression and metabolite profiling analyses of developing pomegranate fruit peel reveal interactions between anthocyanin and punicalagin production. Tree Genetics and Genomes, 2019, 15, 1.	0.6	12
5697	RNA sequencing, selection of reference genes and demonstration of feeding RNAi in Thrips tabaci (Lind.) (Thysanoptera: Thripidae). BMC Molecular Biology, 2019, 20, 6.	3.0	26
5698	Proteomic profile and polyamine contents are modulated by light source to promote in vitro shoot development in Cariniana legalis (Martius) O.Â Kuntze (Lecythidaceae). Plant Cell, Tissue and Organ Culture, 2019, 137, 329-342.	1.2	13
5699	Gene Identification and Characterization of Correlations for DEPs_DEGs Same Trend Responding to Salinity Adaptation in<i>Scylla paramamosain</i>. International Journal of Genomics, 2019, 2019, 1-12.	0.8	11
5700	Comprehensive analysis of the longan transcriptome reveals distinct regulatory programs during the floral transition. BMC Genomics, 2019, 20, 126.	1.2	21
5701	Genome-wide analysis of developmental stage-specific transcriptome in Bradysia odoriphaga. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 45-54.	0.4	4
5702	Transcriptome analysis of the spleen provides insight into the immunoregulation of Mastacembelus armatus under Aeromonas veronii infection. Fish and Shellfish Immunology, 2019, 88, 272-283.	1.6	22
5703	Transcriptome analysis and targeted metabolic profiling for pathway elucidation and identification of a geraniol synthase involved in iridoid biosynthesis from Gardenia jasminoides. Industrial Crops and Products, 2019, 132, 48-58.	2.5	24
5704	Proteome analysis of Mycoplasma fermentans cultured under aerobic and anaerobic conditions. Translational Medicine Communications, 2019, 4, .	0.5	4

#	Article	IF	Citations
5705	Transcriptome Atlas by Long-Read RNA Sequencing: Contribution to a Reference Transcriptome. , 2019, , .		0
5706	Transcriptomic analysis of genes involved in reproduction at different ages in Daphnia pulex (Branchiopoda, Cladocera). Crustaceana, 2019, 92, 1311-1335.	0.1	1
5707	Transcriptome Arofile of Brassica rapa L. Reveals the Involvement of Jasmonic Acid, Ethylene, and Brassinosteroid Signaling Pathways in Clubroot Resistance. Agronomy, 2019, 9, 589.	1.3	19
5708	Induction, identification and genetics analysis of tetraploid <i>Actinidia chinensis</i>. Royal Society Open Science, 2019, 6, 191052.	1.1	10
5709	Disease Resistance Genetics and Genomics in Octoploid Strawberry. G3: Genes, Genomes, Genetics, 2019, 9, 3315-3332.	0.8	26
5710	Parallel selection on ecologically relevant gene functions in the transcriptomes of highly diversifying salmonids. BMC Genomics, 2019, 20, 1010.	1.2	8
5711	Transcriptional Changes on Blight Fruiting Body of Flammulina velutipes Caused by Two New Bacterial Pathogens. Frontiers in Microbiology, 2019, 10, 2845.	1.5	12
5712	Greenlip Abalone (<i>Haliotis laevigata</i>) Genome and Protein Analysis Provides Insights into Maturation and Spawning. G3: Genes, Genomes, Genetics, 2019, 9, 3067-3078.	0.8	14
5713	Draft Genome Sequence of Clostridium estertheticum subsp. <i>laramiense</i> DSM 14864 ^T , Isolated from Spoiled Uncooked Beef. Microbiology Resource Announcements, 2019, 8, .	0.3	13
5714	Molecular evolution and expression of opsin genes in Hydra vulgaris. BMC Genomics, 2019, 20, 992.	1.2	18
5715	<i>De novo</i> transcriptome sequencing of genome analysis provides insights into <i>Solidago canadensis</i> invasive capability via photosynthesis. Journal of Plant Interactions, 2019, 14, 572-579.	1.0	6
5716	Integrated transcriptomic and functional immunological approach for assessing the invasiveness of bivalve alien species. Scientific Reports, 2019, 9, 19879.	1.6	5
5717	Species-specific transcriptional profiles of the gut and gut microbiome of Ceratitis quilicii and Ceratitis rosa sensu stricto. Scientific Reports, 2019, 9, 18355.	1.6	2
5718	Within species expressed genetic variability and gene expression response to different temperatures in the rotifer Brachionus calyciflorus sensu stricto. PLoS ONE, 2019, 14, e0223134.	1.1	10
5719	<i>De Novo</i> Assembly and Annotation from Parental and F1 Puma Genomes of the Florida Panther Genetic Restoration Program. G3: Genes, Genomes, Genetics, 2019, 9, 3531-3536.	0.8	12
5720	Structure Elucidation and Biochemical Characterization of Environmentally Relevant Novel Extradiol Dioxygenases Discovered by a Functional Metagenomics Approach. MSystems, 2019, 4, .	1.7	8
5721	Investigating the Influence of Glycerol on the Utilization of Glucose in <i>Yarrowia lipolytica</i> Using RNA-Seq-Based Transcriptomics. G3: Genes, Genomes, Genetics, 2019, 9, 4059-4071.	0.8	17
5722	A New Lineage of Cryptococcus gattii (VGV) Discovered in the Central Zambezian Miombo Woodlands. MBio, 2019, 10, .	1.8	66

#	ARTICLE	IF	CITATIONS
5723	Transcriptome Characterization of Reverse Development in <i>Turritopsis dohrnii</i> (Hydrozoa,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	15
5724	Differential gene expression in chronic wasting diseaseâ€positive whiteâ€tailed deer (<i>Odocoileus) Tj ETQq1 1 0.784314 rgBT /Overlo	0.8	4
5725	Comparative transcriptional analysis provides insights of possible molecular mechanisms of wing polyphenism induced by postnatal crowding in Aphis gossypii. Journal of Cotton Research, 2019, 2, .	1.0	4
5726	Resolution of deep divergence of club fungi (phylum Basidiomycota). Synthetic and Systems Biotechnology, 2019, 4, 225-231.	1.8	6
5727	The persimmon (Diospyros oleifera Cheng) genome provides new insights into the inheritance of astringency and ancestral evolution. Horticulture Research, 2019, 6, 138.	2.9	39
5728	Ecological genomics of adaptation to unpredictability in experimental rotifer populations. Scientific Reports, 2019, 9, 19646.	1.6	2
5729	The transcriptome analysis of males musk gland in <i>Moschus berezovskii</i> (Artiodactyla:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 502		4
5730	Transcriptome analysis reveals plasticity in gene regulation due to environmental cues in Primula sikkimensis, a high altitude plant species. BMC Genomics, 2019, 20, 989.	1.2	10
5731	Network Analyses and Data Integration of Proteomics and Metabolomics From Leaves of Two Contrasting Varieties of Sugarcane in Response to Drought. Frontiers in Plant Science, 2019, 10, 1524.	1.7	41
5732	Repeat-Induced Point Mutations Drive Divergence between Fusarium circinatum and Its Close Relatives. Pathogens, 2019, 8, 298.	1.2	11
5733	Transcriptome-based analysis of putative allergens of Chorioptes texanus. Parasites and Vectors, 2019, 12, 587.	1.0	2
5734	De novo transcriptome analysis and identification of genes associated with immunity, detoxification and energy metabolism from the fat body of the tephritid gall fly, Procecidochares utilis. PLoS ONE, 2019, 14, e0226039.	1.1	5
5735	Transcriptome landscape of Rafflesia cantleyi floral buds reveals insights into the roles of transcription factors and phytohormones in flower development. PLoS ONE, 2019, 14, e0226338.	1.1	13
5736	Proximal femoral head transcriptome reveals novel candidate genes related to epiphysiolysis in broiler chickens. BMC Genomics, 2019, 20, 1031.	1.2	11
5737	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (Brassica rapa L. ssp. pekinensis). BMC Plant Biology, 2019, 19, 517.	1.6	16
5738	Comparative Transcriptomics of Flammulina filiformis Suggests a High CO2 Concentration Inhibits Early Pileus Expansion by Decreasing Cell Division Control Pathways. International Journal of Molecular Sciences, 2019, 20, 5923.	1.8	10
5739	Nanopore sequencing improves the draft genome of the human pathogenic amoeba Naegleria fowleri. Scientific Reports, 2019, 9, 16040.	1.6	24
5740	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 2019, 8, .	3.3	106

#	ARTICLE	IF	CITATIONS
5741	Structural and functional insights into the Diabrotica virgifera virgifera ATP-binding cassette transporter gene family. BMC Genomics, 2019, 20, 899.	1.2	8
5742	Transcriptome profiling of posterior kidney of brown trout, Salmo trutta, during proliferative kidney disease. Parasites and Vectors, 2019, 12, 569.	1.0	20
5743	Antennal transcriptome analyses and olfactory protein identification in an important wood-boring moth pest, Streltzoviella insularis (Lepidoptera: Cossidae). Scientific Reports, 2019, 9, 17951.	1.6	17
5744	The Indispensable Role of Histone Methyltransferase PoDot1 in Extracellular Glycoside Hydrolase Biosynthesis of Penicillium oxalicum. Frontiers in Microbiology, 2019, 10, 2566.	1.5	16
5745	A chromosome-level genome assembly of the Chinese tupelo Nyssa sinensis. Scientific Data, 2019, 6, 282.	2.4	10
5746	Hostâ€"Symbiont Interactions in Deep-Sea Chemosymbiotic Vesicomyid Clams: Insights From Transcriptome Sequencing. Frontiers in Marine Science, 2019, 6, .	1.2	17
5747	Heat Shock Cognate 70 Functions as A Chaperone for the Stability of Kinetochore Protein CENP-N in Holocentric Insect Silkworms. International Journal of Molecular Sciences, 2019, 20, 5823.	1.8	3
5748	Transcriptome Profiling Unravels a Vital Role of Pectin and Pectinase in Anther Dehiscence in Chrysanthemum. International Journal of Molecular Sciences, 2019, 20, 5865.	1.8	6
5749	Comprehensive Stress-Based De Novo Transcriptome Assembly and Annotation of Guar (<i>Cyamopsis) Tj ETQq0 0 0 rgBT /Overlock 10 Genomics, 2019, 2019, 1-14.	0.8	23
5750	Organ transcriptomes of the lucinid clam Loripes orbiculatus (Poli, 1791) provide insights into their specialised roles in the biology of a chemosymbiotic bivalve. BMC Genomics, 2019, 20, 820.	1.2	13
5751	Identification of key genes and regulators associated with carotenoid metabolism in apricot (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.2	28
5752	The Principal Salivary Gland Is the Primary Source of Digestive Enzymes in the Saliva of the Brown Marmorated Stink Bug, Halyomorpha halys. Frontiers in Physiology, 2019, 10, 1255.	1.3	8
5753	A Method for the Structure-Based, Genome-Wide Analysis of Bacterial Intergenic Sequences Identifies Shared Compositional and Functional Features. Genes, 2019, 10, 834.	1.0	0
5754	Transcriptome Analysis and Identification of Insecticide Tolerance-Related Genes after Exposure to Insecticide in Sitobion avenae. Genes, 2019, 10, 951.	1.0	24
5755	Genome-wide association study of drought tolerance and biomass allocation in wheat. PLoS ONE, 2019, 14, e0225383.	1.1	46
5756	Rainbow Trout IgM+ B Cells Preferentially Respond to Thymus-Independent Antigens but Are Activated by CD40L. Frontiers in Immunology, 2019, 10, 2902.	2.2	16
5757	Investigating the Impact of Biostimulants on the Row Crops Corn and Soybean Using High-Efficiency Phenotyping and Next Generation Sequencing. Agronomy, 2019, 9, 761.	1.3	28
5758	Omics Potential in Herbicide-Resistant Weed Management. Plants, 2019, 8, 607.	1.6	17

#	ARTICLE	IF	CITATIONS
5759	Identification of lncRNA, MicroRNA, and mRNA-Associated CeRNA Network of Radiation-Induced Lung Injury in a Mice Model. Dose-Response, 2019, 17, 155932581989101.	0.7	14
5760	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo (Phyllostachys violascens). BMC Bioinformatics, 2019, 20, 687.	1.2	14
5761	Transcriptome analysis of the almond moth, Cadra cautella, female abdominal tissues and identification of reproduction control genes. BMC Genomics, 2019, 20, 883.	1.2	4
5762	JCDB: a comprehensive knowledge base for Jatropha curcas, an emerging model for woody energy plants. BMC Genomics, 2019, 20, 958.	1.2	7
5763	Transcriptome analysis of the fungal pathogen Rosellinia necatrix during infection of a susceptible avocado rootstock identifies potential mechanisms of pathogenesis. BMC Genomics, 2019, 20, 1016.	1.2	18
5764	Different transcriptional response between susceptible and resistant common carp (Cyprinus carpio) fish hints on the mechanism of CyHV-3 disease resistance. BMC Genomics, 2019, 20, 1019.	1.2	21
5765	Comparative iTRAQ proteomics revealed proteins associated with lobed fin regeneration in Bichirs. Proteome Science, 2019, 17, 6.	0.7	0
5766	Identification of Key Genes Involved in Embryo Development and Differential Oil Accumulation in Two Contrasting Maize Genotypes. Genes, 2019, 10, 993.	1.0	13
5767	Draft genome of Tanacetum cinerariifolium, the natural source of mosquito coil. Scientific Reports, 2019, 9, 18249.	1.6	21
5768	Direct conversion of carlactonoic acid to orobanchol by cytochrome P450 CYP722C in strigolactone biosynthesis. Science Advances, 2019, 5, eaax9067.	4.7	122
5769	Genome Survey of Male and Female Spotted Scat (Scatophagus argus). Animals, 2019, 9, 1117.	1.0	23
5770	GenFam: A web application and database for gene familyâ€based classification and functional enrichment analysis. Plant Direct, 2019, 3, e00191.	0.8	16
5771	The genetic diversity and population structure of Sophora alopecuroides (Faboideae) as determined by microsatellite markers developed from transcriptome. PLoS ONE, 2019, 14, e0226100.	1.1	12
5772	Differential gene expression among three sex types reveals a MALE STERILITY 1 (CpMS1) for sex differentiation in papaya. BMC Plant Biology, 2019, 19, 545.	1.6	12
5773	Transcriptomic Evidence of Adaptive Evolution of the Epiphytic Fern <i>Asplenium nidus</i>. International Journal of Genomics, 2019, 2019, 1-9.	0.8	15
5774	Transcriptome and microbiome of coconut rhinoceros beetle (Oryctes rhinoceros) larvae. BMC Genomics, 2019, 20, 957.	1.2	26
5775	Transcriptomic and proteomic analysis reveals mechanisms of low pollen-pistil compatibility during water lily cross breeding. BMC Plant Biology, 2019, 19, 542.	1.6	13
5776	Effect of growth rate on transcriptomic responses to immune stimulation in wild-type, domesticated, and GH-transgenic coho salmon. BMC Genomics, 2019, 20, 1024.	1.2	11

#	ARTICLE	IF	CITATIONS
5777	Characterization and proteomic profiling of pancreatic cancerâ€derived serum exosomes. Journal of Cellular Biochemistry, 2019, 120, 988-999.	1.2	36
5778	Dynamic genomic architecture of mutualistic cooperation in a wild population of <i>Mesorhizobium</i>. ISME Journal, 2019, 13, 301-315.	4.4	34
5779	Transcriptomic analysis of interactions between <scp><i>Hyphantria cunea</i></scp> larvae and nucleopolyhedrovirus. Pest Management Science, 2019, 75, 1024-1033.	1.7	21
5780	Comparative analysis of testis transcriptomes associated with male infertility in triploid cyprinid fish. Reproduction, Fertility and Development, 2019, 31, 248.	0.1	16
5781	Downregulation of mitochondrial alternative oxidase affects chloroplast function, redox status and stress response in a marine diatom. New Phytologist, 2019, 221, 1303-1316.	3.5	51
5782	A comparison of the transcriptomes between diploid and autotetraploid Paulownia fortunei under salt stress. Physiology and Molecular Biology of Plants, 2019, 25, 1-11.	1.4	16
5783	A pilot study of genetic structure of Porphyra umbilicalis KÃ¼tzing in the Gulf of Maine using SNP markers from RNA-Seq. Journal of Applied Phycology, 2019, 31, 1493-1503.	1.5	1
5784	Effects on tadpole snail gene expression after exposure to vinclozolin. Ecotoxicology and Environmental Safety, 2019, 170, 568-577.	2.9	10
5785	Insights into the intestine immune of Marsupenaeus japonicus under the white spot syndrome virus challenge using RNA sequencing. Veterinary Immunology and Immunopathology, 2019, 208, 25-33.	0.5	22
5786	Benzothiazole inhibits the growth of Phytophthora capsici through inducing apoptosis and suppressing stress responses and metabolic detoxification. Pesticide Biochemistry and Physiology, 2019, 154, 7-16.	1.6	24
5787	Rapid profiling of tropical marine cyanobacterial communities. Regional Studies in Marine Science, 2019, 25, 100485.	0.4	7
5788	Prevalence of a nematode castrator of the carrot weevil and impact on fecundity and survival. Parasitology, 2019, 146, 702-707.	0.7	1
5789	Transcriptome analysis and metabolic profiling reveal the key role of Î±-linolenic acid in dormancy regulation of European pear. Journal of Experimental Botany, 2019, 70, 1017-1031.	2.4	27
5790	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. Progress in Biophysics and Molecular Biology, 2019, 145, 19-39.	1.4	15
5791	Repurposing population genetics data to discern genomic architecture: A case study of linkage cohort detection in mountain pine beetle (Dendroctonus ponderosae). Ecology and Evolution, 2019, 9, 1147-1159.	0.8	6
5792	Transcriptome analysis of astringent â€˜Cheongdo-Bansiâ€™ persimmon fruit treated with ethylene for removal of astringency. Postharvest Biology and Technology, 2019, 150, 52-59.	2.9	12
5793	Annotating the â€˜hypotheticalâ€™ in hypothetical proteins: In-silico analysis of uncharacterised proteins for the Apicomplexan parasite, Neospora caninum. Veterinary Parasitology, 2019, 265, 29-37.	0.7	4
5794	De novo transcriptome assembly and preliminary analyses of two avian malaria parasites, Plasmodium delichoni and Plasmodium homocircumflexum. Genomics, 2019, 111, 1815-1823.	1.3	9

#	ARTICLE	IF	CITATIONS
5795	Nutritional value of potato (Solanum tuberosum) in hot climates: anthocyanins, carotenoids, and steroidal glycoalkaloids. Planta, 2019, 249, 1143-1155.	1.6	40
5796	Resolving population structure and genetic differentiation associated with RAD-SNP loci under selection in tossa jute (Corchorus olitorius L.). Molecular Genetics and Genomics, 2019, 294, 479-492.	1.0	20
5797	Transcriptome sequencing to reveal the genetic regulation of leaf margin variation at early stage in birch. Tree Genetics and Genomes, 2019, 15, 1.	0.6	5
5798	Identification of Salt Stress Response Genes in Rosa chinensis Leaves by Comparative RNA-seq Analysis of Transcriptome Dynamics. Russian Journal of Plant Physiology, 2019, 66, 119-127.	0.5	3
5799	Candidate olfactory genes identified in Heortia vitessoides (Lepidoptera: Crambidae) by antennal transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 117-130.	0.4	7
5800	Transcriptome-wide analysis of wild Asari (=Manila) clams affected by the Brown Muscle Disease: Etiology and impacts of the disease. Fish and Shellfish Immunology, 2019, 86, 179-185.	1.6	4
5801	Dimorphism of sex and gonad-development-related genes in male and female lined seahorse, Hippocampus erectus, based on transcriptome analyses. Genomics, 2019, 111, 260-266.	1.3	12
5802	Transcriptome-based mining and expression profiling of Pythium responsive transcription factors in Zingiber sp.. Functional and Integrative Genomics, 2019, 19, 249-264.	1.4	9
5803	A major QTL and candidate genes for capsaicinoid biosynthesis in the pericarp of Capsicum chinense revealed using QTL-seq and RNA-seq. Theoretical and Applied Genetics, 2019, 132, 515-529.	1.8	43
5804	Transcriptomic profiles of striped snakehead cells (SSN-1) infected with snakehead vesiculovirus (SHVV) identifying IFI35 as a positive factor for SHVV replication. Fish and Shellfish Immunology, 2019, 86, 46-52.	1.6	12
5805	Comparison of the Malpighian tubules and fat body transcriptional profiles of Zophobas morio larvae (Coleoptera: Tenebrionidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 95-105.	0.4	6
5806	Varroa chemosensory proteins: some are conserved across Arthropoda but others are arachnid specific. Insect Molecular Biology, 2019, 28, 321-341.	1.0	12
5807	De novo assembly and functional annotation of the emma field cricket (Teleogryllus emma) transcriptome. Journal of Asia-Pacific Entomology, 2019, 22, 1-5.	0.4	3
5808	Toward characterizing germination and early growth in the non-orthodox forest tree species Quercus ilex through complementary gel and gel-free proteomic analysis of embryo and seedlings. Journal of Proteomics, 2019, 197, 60-70.	1.2	18
5809	Integrated transcriptomic-metabolomic analysis reveals cellular responses of harvested strawberry fruit subjected to short-term exposure to high levels of carbon dioxide. Postharvest Biology and Technology, 2019, 148, 120-131.	2.9	44
5810	A highâ€quality chromosomeâ€level genome assembly of a generalist herbivore, <i>Trichoplusia ni</i>. Molecular Ecology Resources, 2019, 19, 485-496.	2.2	47
5811	Progressive behavioural, physiological and transcriptomic shifts over the course of prolonged starvation in ticks. Molecular Ecology, 2019, 28, 49-65.	2.0	39
5812	Retrotransposon methylation and activity in wild fish (A.Âanguilla): A matter of size. Environmental Pollution, 2019, 245, 494-503.	3.7	12

#	ARTICLE	IF	CITATIONS
5813	The transcriptome of the marine calanoid copepod Temora longicornis under heat stress and recovery. Marine Environmental Research, 2019, 143, 10-23.	1.1	29
5814	microRNA response in potato virus Y infected tobacco shows strain-specificity depending on host and symptom severity. Virus Research, 2019, 260, 20-32.	1.1	10
5815	<i>De novo</i> genome assembly of the stress tolerant forest species <i>Casuarina equisetifolia</i> provides insight into secondary growth. Plant Journal, 2019, 97, 779-794.	2.8	44
5816	A novel messenger RNA and long noncoding RNA signature associated with the progression of nonmuscle invasive bladder cancer. Journal of Cellular Biochemistry, 2019, 120, 8101-8109.	1.2	14
5817	Comparative transcriptome analysis highlights the hormone effects on somatic embryogenesis in Catalpa bungei. Plant Reproduction, 2019, 32, 141-151.	1.3	22
5818	Comparative Nuclear Proteomics Analysis Provides Insight into the Mechanism of Signaling and Immune Response to Blast Disease Caused by <i>Magnaporthe</i><i>oryzae</i> in Rice. Proteomics, 2019, 19, e1800188.	1.3	11
5819	Transcriptome analysis of Sclerotinia ginseng and comparative analysis with the genome of Sclerotinia sclerotiorum. Physiological and Molecular Plant Pathology, 2019, 106, 30-41.	1.3	8
5820	Comparative genomics inferred two distinct populations of piscine pathogenic Streptococcus agalactiae, serotype Ia ST7 and serotype III ST283, in Thailand and Vietnam. Genomics, 2019, 111, 1657-1667.	1.3	21
5821	<i>Rh6</i> gene modulates the visual mechanism of host utilization in fruit fly <scp><i>Bactrocera minax</i></scp>. Pest Management Science, 2019, 75, 1621-1629.	1.7	37
5822	Differential protein abundance during the first month of regeneration of the Caribbean star coral Montastraea cavernosa. Coral Reefs, 2019, 38, 45-61.	0.9	6
5823	Transcriptional responses to low-salinity stress in the gills of adult female Portunus trituberculatus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 86-94.	0.4	16
5824	The methionine biosynthesis regulator AaMetR contributes to oxidative stress tolerance and virulence in Alternaria alternata. Microbiological Research, 2019, 219, 94-109.	2.5	33
5825	Investigating the proteomic expression profile of tobacco (Nicotiana tabacum) leaves during four growth stages using the iTRAQ method. Analytical and Bioanalytical Chemistry, 2019, 411, 403-411.	1.9	3
5826	iTRAQ-based proteomic analysis of resistant Nicotiana tabacum in response to Bemisia tabaci infestation. Arthropod-Plant Interactions, 2019, 13, 505-516.	0.5	3
5827	Rapid Genomic and Genetic Changes in the First Generation of Autotetraploid Lineages Derived from Distant Hybridization of Carassius auratus Red Var. (â™€)â€‰Ã—â€‰Megalobrama amblycephala (â™,). Marine Biotechnology, 2019, 21, 139-149.	1.1	13
5828	Enriched networks â€˜nucleoside/nucleotide and ribonucleoside/ribonucleotide metabolic processesâ€™ and â€˜response to stimulusâ€™ potentially conferred to drought adaptation of the epiphytic orchid Dendrobium wangliangii. Physiology and Molecular Biology of Plants, 2019, 25, 31-45.	1.4	13
5829	Transcriptome analysis of differential expressed genes in hepatopancreas of Procambarus clarkii challenged with peptidoglycan. Fish and Shellfish Immunology, 2019, 86, 311-318.	1.6	11
5830	Comparative transcriptome analyses of venom glands from three scorpionfishes. Genomics, 2019, 111, 231-241.	1.3	6

#	Article	IF	Citations
5831	Genomic and transcriptomic insights into the survival of the subaerial cyanobacterium <i>Nostoc flagelliforme</i> in arid and exposed habitats. Environmental Microbiology, 2019, 21, 845-863.	1.8	32
5832	Site-specific regulation of transcriptional responses to cadmium stress in the hyperaccumulator, Sedum alfredii: based on stem parenchymal and vascular cells. Plant Molecular Biology, 2019, 99, 347-362.	2.0	12
5833	Transcript profiling reveals an important role of cell wall remodeling and hormone signaling under salt stress in garlic. Plant Physiology and Biochemistry, 2019, 135, 87-98.	2.8	32
5834	The miR164-dependent regulatory pathway in developing maize seed. Molecular Genetics and Genomics, 2019, 294, 501-517.	1.0	19
5835	Comparative Transcriptomics Reveals Patterns of Adaptive Evolution Associated with Depth and Age Within Marine Rockfishes (Sebastes). Journal of Heredity, 2019, 110, 340-350.	1.0	12
5836	Transcriptomic analysis related to the flowering of the citrus hybrid Microcitrangemonia. Current Plant Biology, 2019, 18, 100097.	2.3	1
5837	Expression of the GAF Sensor, Carbohydrate-Active Enzymes, Elicitins, and RXLRs Differs Markedly Between Two <i>Phytophthora cactorum</i> Isolates. Phytopathology, 2019, 109, 726-735.	1.1	7
5838	Transcriptomic signature reveals mechanism of flower bud distortion in witchesâ€™-broom disease of soybean (Glycine max). BMC Plant Biology, 2019, 19, 26.	1.6	15
5839	<i>Serendipita indica</i> E5â€² <scp>NT</scp> modulates extracellular nucleotide levels in the plant apoplast and affects fungal colonization. EMBO Reports, 2019, 20, .	2.0	59
5840	Investigation of graded levels of soybean meal diets for red drum, Sciaenops ocellatus, using quantitative PCR derived biomarkers. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 274-285.	0.4	8
5841	Genome-wide identification and comparative analysis of alternative splicing across four legume species. Planta, 2019, 249, 1133-1142.	1.6	16
5842	Discovery and profiling of small RNAs from Puccinia triticina by deep sequencing and identification of their potential targets in wheat. Functional and Integrative Genomics, 2019, 19, 391-407.	1.4	37
5843	Network Profiling of Brain-Expressed X-Chromosomal MicroRNA Genes Implicates Shared Key MicroRNAs in Intellectual Disability. Journal of Molecular Neuroscience, 2019, 67, 295-304.	1.1	12
5844	Transcriptomic analysis of the red and green light responses in Columba livia domestica. 3 Biotech, 2019, 9, 20.	1.1	5
5845	Gene expression profiling of Bothriochloa ischaemum leaves and roots under drought stress. Gene, 2019, 691, 77-86.	1.0	3
5846	De novo assembly of Vriesea carinata leaf transcriptome to identify candidate cysteine-proteases. Gene, 2019, 691, 96-105.	1.0	1
5847	Convergent evolution on the hypoxia-inducible factor (HIF) pathway genes EGLN1 and EPAS1 in high-altitude ducks. Heredity, 2019, 122, 819-832.	1.2	52
5848	Stout camphor tree genome fills gaps in understanding of flowering plant genome evolution. Nature Plants, 2019, 5, 63-73.	4.7	124

#	ARTICLE	IF	CITATIONS
5849	Genome-wide DNA methylation and transcriptomic profiles in the lifestyle strategies and asexual development of the forest fungal pathogen <i>Heterobasidion parviporum</i>. Epigenetics, 2019, 14, 16-40.	1.3	11
5850	Repeated Evolution Versus Common Ancestry: Sex Chromosome Evolution in the Haplochromine Cichlid<i>Pseudocrenilabrus philander</i>. Genome Biology and Evolution, 2019, 11, 439-458.	1.1	26
5851	De novo transcriptomic sequencing unraveled the molecular mechanisms of VvMybA1 underlying the alteration of Ficus lyrata leaf color. Acta Physiologiae Plantarum, 2019, 41, 1.	1.0	4
5852	Abnormal energy identification of variable refrigerant flow air-conditioning systems based on data mining techniques. Applied Thermal Engineering, 2019, 150, 398-411.	3.0	17
5853	Identification and characterization of differentially expressed genes in hepatopancreas of oriental river prawn Macrobrachium nipponense under nitrite stress. Fish and Shellfish Immunology, 2019, 87, 144-154.	1.6	27
5854	Molecular effects of a variable environment on Sydney rock oysters, Saccostrea glomerata: Thermal and low salinity stress, and their synergistic effect. Marine Genomics, 2019, 43, 19-32.	0.4	17
5855	Transcriptome-wide identification and characterization of resistant gene analogs (RGAs) of ginger (Zingiber officinale Rosc.) and mango ginger (Curcuma amada Roxb.) under stress induced by pathogen. Scientia Horticulturae, 2019, 248, 81-88.	1.7	5
5856	Recombination of ecologically and evolutionarily significant loci maintains genetic cohesion in the Pseudomonas syringae species complex. Genome Biology, 2019, 20, 3.	3.8	114
5857	Comparative Transcriptome Analysis Reveals an Efficient Mechanism of Î±-Linolenic Acid in Tree Peony Seeds. International Journal of Molecular Sciences, 2019, 20, 65.	1.8	25
5858	Proteomic profiling of the white shrimp Litopenaeus vannamei (Boone, 1931) hemocytes infected with white spot syndrome virus reveals the induction of allergy-related proteins. Developmental and Comparative Immunology, 2019, 91, 37-49.	1.0	27
5859	Seasonal variation in expression pattern of genes in irrigated and water stressed transcriptomes of Zea mays Z59. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 271-279.	0.9	1
5860	Multipath effects of berberine on peach Brown rot fungus Monilinia fructicola. Crop Protection, 2019, 116, 92-100.	1.0	23
5861	Characterization of the satellitome in lower vascular plants: the case of the endangered fern <i>Vandenboschia speciosa</i>. Annals of Botany, 2019, 123, 587-599.	1.4	20
5862	Identification of critical sex-biased genes in Andrias davidianus by de novo transcriptome. Molecular Genetics and Genomics, 2019, 294, 287-299.	1.0	17
5863	RNA-Seq analysis of the bioluminescent and non-bioluminescent species of Elateridae (Coleoptera): Comparison to others photogenic and non-photogenic tissues of Elateroidea species. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 154-165.	0.4	4
5864	Transcriptomic response of the Crassostrea virginica gonad after exposure to a water-accommodation fraction of hydrocarbons and the potential implications in reproduction. Marine Genomics, 2019, 43, 9-18.	0.4	7
5865	Differentially expressed genes during the transition from early to late development phases in somatic embryo of banana (Musa spp. AAB group, Silk subgroup) cv. Manzano. Plant Cell, Tissue and Organ Culture, 2019, 136, 289-302.	1.2	10
5866	Characterization and expression profiles of muscle transcriptome in Schizothoracine fish, Schizothorax prenanti. Gene, 2019, 685, 156-163.	1.0	17

#	Article	IF	Citations
5867	Deciphering key proteins of oil palm (<i>Elaeis guineensis</i> Jacq.) fruit mesocarp development by proteomics and chemometrics. Electrophoresis, 2019, 40, 254-265.	1.3	9
5868	Comparative transcriptome analysis identifies differentially expressed genes between normal and late-blooming Siberian apricot. Journal of Forestry Research, 2019, 30, 2277-2288.	1.7	6
5869	Transcriptome profiling suggests roles of innate immunity and digestion metabolism in purplish Washington clam. Genes and Genomics, 2019, 41, 183-191.	0.5	8
5870	RNA-seq coupled to proteomic analysis reveals high sperm proteome variation between two closely related marine mussel species. Journal of Proteomics, 2019, 192, 169-187.	1.2	14
5871	Transcriptome comparison between prenatal and postnatal Large White livers identifies differences in the expression level of genes related to metabolism and postnatal growth. Gene, 2019, 686, 92-103.	1.0	5
5872	SATrans: New Free Available Software for Annotation of Transcriptome and Functional Analysis of Differentially Expressed Genes. Journal of Computational Biology, 2019, 26, 117-123.	0.8	1
5873	Comparative proteomics of Tobacco mosaic virus-infected Nicotiana tabacum plants identified major host proteins involved in photosystems and plant defence. Journal of Proteomics, 2019, 194, 191-199.	1.2	30
5874	Draft Genome Sequence of Phoma arachidicola Wb2 Causing Peanut Web Blotch in China. Current Microbiology, 2019, 76, 200-206.	1.0	10
5875	Exposure to microplastics reduces attachment strength and alters the haemolymph proteome of blue mussels (Mytilus edulis). Environmental Pollution, 2019, 246, 423-434.	3.7	150
5876	Novel microRNAs are associated with population divergence in transcriptional response to thermal stress in an intertidal copepod. Molecular Ecology, 2019, 28, 584-599.	2.0	13
5877	GhNAC83 inhibits corm dormancy release by regulating ABA signaling and cytokinin biosynthesis in Gladiolus hybridus. Journal of Experimental Botany, 2019, 70, 1221-1237.	2.4	18
5878	Molecular characterization of anthocyanin and betulinic acid biosynthesis in red and white mulberry fruits using high-throughput sequencing. Food Chemistry, 2019, 279, 364-372.	4.2	28
5879	Computational analysis of the Plasmodiophora brassicae genome: mitochondrial sequence description and metabolic pathway database design. Genomics, 2019, 111, 1629-1640.	1.3	27
5880	Genome-wide gene expression analysis reveals novel insights into the response to nitrite stress in gills of Branchiostoma belcheri. Chemosphere, 2019, 218, 609-615.	4.2	3
5881	Defining the pathogenic threat of envenoming by South African shield-nosed and coral snakes (genus) Tj ETQq0 0 0 rgBT /Overlock 10 T 186-198.	1.2	29
5882	A full-length transcriptome of Sepia esculenta using a combination of single-molecule long-read (SMRT) and Illumina sequencing. Marine Genomics, 2019, 43, 54-57.	0.4	20
5883	Ecological Study on Biomineralization in Pinctada fucata. , 2019, , 661-694.		0
5884	Deciphering genome-wide WRKY gene family of Triticum aestivum L. and their functional role in response to Abiotic stress. Genes and Genomics, 2019, 41, 79-94.	0.5	31

#	Article	IF	Citations
5885	Identification of an anti-lipopolysaccharide factor AV-R isoform (LvALF AV-R) related to Vp_PirAB-like toxin resistance in Litopenaeus vannamei. Fish and Shellfish Immunology, 2019, 84, 178-188.	1.6	14
5886	Sexual dimorphism and rapid turnover in gene expression in pre-reproductive seedlings of a dioecious herb. Annals of Botany, 2019, 123, 1119-1131.	1.4	23
5887	Do the toll-like receptors and complement systems play equally important roles in freshwater adapted Dolly Varden char (Salvelinus malma)?. Fish and Shellfish Immunology, 2019, 86, 581-598.	1.6	4
5888	Liver transcriptome analysis of the Sparus macrocephlus in response to Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2019, 84, 825-833.	1.6	6
5889	<i>De novo</i> transcriptome combined with spectrophotometry and gas chromatography-mass spectrometer (GC-MS) reveals differentially expressed genes during accumulation of secondary metabolites in purple-leaf tea (<i>Camellia sinensis</i> cv Hongyafoshou). Journal of Horticultural Science and Biotechnology, 2019, 94, 349-367.	0.9	36
5890	<i>Cylindrospermopsis raciborskii</i> Virus and host: genomic characterization and ecological relevance. Environmental Microbiology, 2019, 21, 1942-1956.	1.8	16
5891	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. Bioinformatics, 2019, 35, 518-520.	1.8	22
5892	Genetic and Genome Analyses Reveal Genetically Distinct Populations of the Bee Pathogen Nosema ceranae from Thailand. Microbial Ecology, 2019, 77, 877-889.	1.4	8
5893	Identification of salt stress response genes using the Artemia transcriptome. Aquaculture, 2019, 500, 305-314.	1.7	31
5894	Critical assessment and performance improvement of plantâ€“pathogen proteinâ€“protein interaction prediction methods. Briefings in Bioinformatics, 2019, 20, 274-287.	3.2	47
5895	HTâ€SuperSAGE of the gut tissue of a Vip3Aaâ€resistantHeliothis virescens(Lepidoptera: Noctuidae) strain provides insights into the basis of resistance. Insect Science, 2019, 26, 479-498.	1.5	5
5896	Saturated or unsaturated fat supplemented maternal diets influence omental adipose tissue proteome of suckling goat-kids. Research in Veterinary Science, 2019, 125, 451-458.	0.9	4
5897	Whole genome sequence analysis of Geitlerinema sp. FC II unveils competitive edge of the strain in marine cultivation system for biofuel production. Genomics, 2019, 111, 465-472.	1.3	5
5898	Transcriptome analysis of <i>Oncidium</i> petals provides new insights into the initiation of petal senescence. Journal of Horticultural Science and Biotechnology, 2019, 94, 12-23.	0.9	5
5899	The genome-wide transcription response underlying the dorsal processes and dorsal setae of the body in Dasyaphis mirabilis (Aphididae: Calaphidinae). Oriental Insects, 2019, 53, 1-18.	0.1	1
5900	Screening of broad spectrum natural pesticides against conserved target arginine kinase in cotton pests by molecular modeling. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1022-1042.	2.0	6
5901	Response of Chinese fir seedlings to low phosphorus stress and analysis of gene expression differences. Journal of Forestry Research, 2019, 30, 183-192.	1.7	10
5902	Transcriptome sequencing of active buds from Populus deltoides CL. and Populusâ€Ã—â€zhaiguanheibaiyang reveals phytohormones involved in branching. Genomics, 2019, 111, 700-709.	1.3	8

#	Article	IF	Citations
5903	CRISPR disruption of TCTP gene impaired normal development in the silkworm <i>Bombyx mori</i>. Insect Science, 2019, 26, 973-982.	1.5	10
5904	When did the ancestor of true bugs become stinky? Disentangling the phylogenomics of Hemipteraâ€“Heteroptera. Cladistics, 2019, 35, 42-66.	1.5	53
5905	Molecular cloning and comparative analysis of transcripts encoding chemosensory proteins from two plant bugs, Lygus lineolaris and Lygus hesperus. Insect Science, 2020, 27, 404-424.	1.5	5
5906	Panaxadiol saponins treatment caused the subtle variations in the global transcriptional state of Asiatic corn borer, Ostrinia furnacalis. Journal of Ginseng Research, 2020, 44, 123-134.	3.0	1
5907	Transcriptome Characterization of Gene Profiling During Early Stage of Nitric Oxide-Induced Adventitious Rooting in Mung Bean Seedlings. Journal of Plant Growth Regulation, 2020, 39, 430-455.	2.8	6
5908	Transcriptome exploration to provide a resource for the study of Auricularia heimuer. Journal of Forestry Research, 2020, 31, 1881-1887.	1.7	4
5909	Proteomic profiles during adventitious rooting of Eucalyptus species relevant to the cellulose industry. New Forests, 2020, 51, 213-241.	0.7	6
5910	Strong temporal dynamics of QTL action on plant growth progression revealed through highâ€throughput phenotyping in canola. Plant Biotechnology Journal, 2020, 18, 68-82.	4.1	45
5911	Unravelling the Soil Microbiome. SpringerBriefs in Environmental Science, 2020, , .	0.3	9
5912	Gene silencing by RNAi <i>via</i> oral delivery of dsRNA by bacteria in the South American tomato pinworm, <i>Tuta absoluta</i>. Pest Management Science, 2020, 76, 287-295.	1.7	33
5913	Metatranscriptomics and Metaproteomics for Microbial Communities Profiling. SpringerBriefs in Environmental Science, 2020, , 51-60.	0.3	5
5914	Systematic identification and analysis of heatâ€stressâ€responsive lncRNAs, circRNAs and miRNAs with associated coâ€expression and ceRNA networks in cucumber (<i>Cucumis sativus</i> L.). Physiologia Plantarum, 2020, 168, 736-754.	2.6	90
5915	Muscle transcriptome signature and gene regulatory network analysis in two divergent lines of a hilly bovine species Mithun (Bos frontalis). Genomics, 2020, 112, 252-262.	1.3	12
5916	Berry transcriptome: insights into a novel resource to understand development dependent secondary metabolism in <i>Withania somnifera</i> (Ashwagandha). Physiologia Plantarum, 2020, 168, 148-173.	2.6	16
5917	Transcriptome analysis of maize reveals potential key genes involved in the response to belowground herbivore <i>Holotrichia parallela</i> larvae feeding. Genome, 2020, 63, 1-12.	0.9	12
5918	Transcriptome characterization and expression profiling in chestnut cultivars resistant or susceptible to the gall wasp Dryocosmus kuriphilus. Molecular Genetics and Genomics, 2020, 295, 107-120.	1.0	11
5919	Horizontal Gene Transfer. Methods in Molecular Biology, 2020, , .	0.4	8
5920	Transcriptome analysis of Idesia polycarpa Maxim. var vestita Diels flowers during sex differentiation. Journal of Forestry Research, 2020, 31, 2463-2478.	1.7	2

#	ARTICLE	IF	CITATIONS
5921	Natureâ€™s recyclers: anaerobic microbial communities drive crude biomass deconstruction. Current Opinion in Biotechnology, 2020, 62, 38-47.	3.3	35
5922	Proteogenomics of the house dust mite, Dermatophagoides farinae: Allergen repertoire, accurate allergen identification, isoforms, and sex-biased proteome differences. Journal of Proteomics, 2020, 210, 103535.	1.2	13
5923	Candidate Gene Networks for Acylsugar Metabolism and Plant Defense in Wild Tomato <i>Solanum pennellii</i>. Plant Cell, 2020, 32, 81-99.	3.1	25
5924	Identification of drought response genes by digital gene expression (DGE) analysis in Caragana korshinskii Kom.. Gene, 2020, 725, 144170.	1.0	14
5925	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. ISME Journal, 2020, 14, 135-150.	4.4	41
5926	YEASTRACT+: a portal for cross-species comparative genomics of transcription regulation in yeasts. Nucleic Acids Research, 2020, 48, D642-D649.	6.5	165
5927	Comparative Metabolomic and Transcriptome Analysis Reveal Distinct Flavonoid Biosynthesis Regulation Between Petals of White and Purple Phalaenopsis amabilis. Journal of Plant Growth Regulation, 2020, 39, 823-840.	2.8	42
5928	Aging peach palm (Bactris gasipaes Kunth) cultures lose embryogenic potential and metabolic cellular function due to continuous culture in hypoxic environments. Plant Cell, Tissue and Organ Culture, 2020, 140, 49-67.	1.2	13
5929	PcG Proteins MSI1 and BMI1 Function Upstream of miR156 to Regulate Aerial Tuber Formation in Potato. Plant Physiology, 2020, 182, 185-203.	2.3	14
5930	De novo and comparative transcriptome analysis of genetic male sterile and fertile lines in radish (Raphanus sativus). Journal of Horticultural Science and Biotechnology, 2020, 95, 32-43.	0.9	2
5931	Comparative de novo assembly and annotation of mantle tissue transcriptomes from the Mytilus edulis species complex (M. edulis, M. galloprovincialis, M. trossulus). Marine Genomics, 2020, 51, 100700.	0.4	11
5932	De novo genome assembly and comparative annotation reveals metabolic versatility in cellulolytic bacteria from cropland and forest soils. Functional and Integrative Genomics, 2020, 20, 89-101.	1.4	4
5933	In vitro and in vivo characterisation of Listeria monocytogenes outbreak isolates. Food Control, 2020, 107, 106784.	2.8	19
5934	<i>In silico</i> determination of transposon-derived miRNAs and targets in <i>Aegilops</i> species. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3098-3109.	2.0	1
5935	Transcriptome and proteome profiles of the diazotroph Nitrospirillum amazonense strain CBAmC in response to the sugarcane apoplast fluid. Plant and Soil, 2020, 451, 145-168.	1.8	15
5936	Intestinal responses of the oriental fruit fly <i>Bactrocera dorsalis</i> (Hendel) after ingestion of an entomopathogenic bacterium strain. Pest Management Science, 2020, 76, 653-664.	1.7	7
5937	Transcriptomic analysis to affirm the regulatory role of long non-coding RNA in horn cancer of Indian zebu cattle breed Kankrej (Bos indicus). Functional and Integrative Genomics, 2020, 20, 75-87.	1.4	5
5938	Transcriptomic responses of Artemia salina exposed to an environmentally relevant dose of Alexandrium minutum cells or Gonyautoxin2/3. Chemosphere, 2020, 238, 124661.	4.2	15

#	ARTICLE	IF	CITATIONS
5939	Ready for the journey: a comparative proteome profiling of porcine cauda epididymal fluid and spermatozoa. Cell and Tissue Research, 2020, 379, 389-405.	1.5	11
5940	Supplementation with an Inorganic Iron Source Modulates the Metalloproteomic Profile of the Royal Jelly Produced by Apis mellifera L.. Biological Trace Element Research, 2020, 195, 648-657.	1.9	2
5941	Genome-Wide Analysis of HSP70 Family Protein in Vigna radiata and Coexpression Analysis Under Abiotic and Biotic Stress. Journal of Computational Biology, 2020, 27, 738-754.	0.8	0
5942	WHITE STRIPE LEAF8, encoding a deoxyribonucleoside kinase, is involved in chloroplast development in rice. Plant Cell Reports, 2020, 39, 19-33.	2.8	8
5943	Epigenetic Regulator CoREST Controls Social Behavior in Ants. Molecular Cell, 2020, 77, 338-351.e6.	4.5	33
5944	Transcriptome analysis of Aconitum carmichaelii and exploration of the salsolinol biosynthetic pathway. FÃ¬toterapÃ¬Ã¢, 2020, 140, 104412.	1.1	7
5945	Analysis of terpenoid biosynthesis pathways in German chamomile (Matricaria recutita) and Roman chamomile (Chamaemelum nobile) based on co-expression networks. Genomics, 2020, 112, 1055-1064.	1.3	23
5946	Chromosomeâ€•level genome assembly of the predator <i>Propylea japonica</i> to understand its tolerance to insecticides and high temperatures. Molecular Ecology Resources, 2020, 20, 292-307.	2.2	43
5947	Resolving the genetic paradox of invasions: Preadapted genomes and postintroduction hybridization of bigheaded carps in the Mississippi River Basin. Evolutionary Applications, 2020, 13, 263-277.	1.5	20
5948	Retinoid X receptor modulates olfactory attraction through GÎ± signaling in the migratory locusts. Insect Biochemistry and Molecular Biology, 2020, 116, 103265.	1.2	1
5949	Vegetative desiccation tolerance in the resurrection plant <i>XerophytaÂ humilis</i> has not evolved through reactivation of the seed canonical LAFL regulatory network. Plant Journal, 2020, 101, 1349-1367.	2.8	19
5950	De novo transcriptomic analysis of light-induced flavonoid pathway, transcription factors in the flower buds of Lonicera japonica. Trees - Structure and Function, 2020, 34, 267-283.	0.9	14
5951	Identification and characterisation of heat shock protein gene (HSP70) family and its expression in <i>Agave sisalana</i> under heat stress. Journal of Horticultural Science and Biotechnology, 2020, 95, 470-482.	0.9	6
5952	Arabidopsis ZINC FINGER PROTEIN1 Acts Downstream of GL2 to Repress Root Hair Initiation and Elongation by Directly Suppressing bHLH Genes. Plant Cell, 2020, 32, 206-225.	3.1	67
5953	Identification of keratinases from <i>Fervidobacterium islandicum</i> AWâ€•1 using dynamic gene expression profiling. Microbial Biotechnology, 2020, 13, 442-457.	2.0	23
5954	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>EjAG</i>. Physiologia Plantarum, 2020, 168, 893-908.	2.6	16
5955	Genome and transcriptome analysis of the latent pathogen <i>Lasiodiplodia theobromae</i>, an emerging threat to the cacao industry. Genome, 2020, 63, 37-52.	0.9	26
5956	Integrated transcriptome and physiology analysis of Microcystis aeruginosa after exposure to copper sulfate. Journal of Oceanology and Limnology, 2020, 38, 102-113.	0.6	17

#	Article	IF	Citations
5957	Disease Severity Linked to Increase in Autoantibody Diversity in IgG4â€Related Disease. Arthritis and Rheumatology, 2020, 72, 687-693.	2.9	38
5958	The unique antimicrobial peptide repertoire of stick insects. Developmental and Comparative Immunology, 2020, 103, 103471.	1.0	20
5959	Identification and characterization of circular RNAs during wood formation of poplars in acclimation to low nitrogen availability. Planta, 2020, 251, 47.	1.6	14
5960	The complete genome sequence of the algicidal bacterium Bacillus subtilis strain JA and the use of quorum sensing to evaluate its antialgal ability. Biotechnology Reports (Amsterdam, Netherlands), 2020, 25, e00421.	2.1	14
5961	Insights into the strategy of micro-environmental adaptation: Transcriptomic analysis of two alvinocaridid shrimps at a hydrothermal vent. PLoS ONE, 2020, 15, e0227587.	1.1	8
5962	Structure and function analysis of various brain subregions and pituitary in grass carp (Ctenopharyngodon idellus). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100653.	0.4	7
5963	Transcriptome sequencing of the apricot (Prunus armeniaca L.) and identification of differentially expressed genes involved in drought stress. Phytochemistry, 2020, 171, 112226.	1.4	13
5964	Translocator protein mediates olfactory repulsion. FASEB Journal, 2020, 34, 513-524.	0.2	3
5965	Cloning and functional characterization of a floral repressor gene from Lavandula angustifolia. Planta, 2020, 251, 41.	1.6	7
5966	The genetic mechanism of selfishness and altruism in parent-offspring coadaptation. Science Advances, 2020, 6, eaaw0070.	4.7	8
5967	Comparative genomic and transcriptomic analyses reveal different pathogenicity-related genes among three eucalyptus fungal pathogens. Fungal Genetics and Biology, 2020, 137, 103332.	0.9	9
5968	Computational identification of conserved microRNAs and functional annotation of their target genes in Citrus limon. South African Journal of Botany, 2020, 130, 109-116.	1.2	4
5969	Extensive chromosomal rearrangements and rapid evolution of novel effector superfamilies contribute to host adaptation and speciation in the basal ascomycetous fungi. Molecular Plant Pathology, 2020, 21, 330-348.	2.0	22
5970	Malus niedzwetzkyana (Dieck) Langenf transcriptome comparison and phylogenetic analysis with Malus sieversii (Ledeb) Roem. Genetic Resources and Crop Evolution, 2020, 67, 313-323.	0.8	3
5971	Proteomic response of Euglena gracilis to heavy metal exposure â€" Identification of key proteins involved in heavy metal tolerance and accumulation. Algal Research, 2020, 45, 101764.	2.4	59
5972	Genome-wide identification and characterization of R2R3-MYB family in Hypericum perforatum under diverse abiotic stresses. International Journal of Biological Macromolecules, 2020, 145, 341-354.	3.6	35
5973	Identification of genes related to skeletal muscle growth and development by integrated analysis of transcriptome and proteome in myostatin-edited Meishan pigs. Journal of Proteomics, 2020, 213, 103628.	1.2	23
5974	Bioinformatics of excretory/secretory proteins of Toxoplasma gondii strain ME49. Microbial Pathogenesis, 2020, 140, 103951.	1.3	3

#	Article	IF	Citations
5975	Bioinformatics insights into microRNA mediated gene regulation in Triticum aestivum during multiple fungal diseases. Plant Gene, 2020, 21, 100219.	1.4	6
5976	Effects of terpinenâ€4â€ol fumigation on protein levels of detoxification enzymes in Tribolium confusum. Archives of Insect Biochemistry and Physiology, 2020, 103, e21653.	0.6	2
5977	Whole Genome Sequencing and Assembly of the Asian Honey Bee Apis dorsata. Genome Biology and Evolution, 2020, 12, 3677-3683.	1.1	21
5978	qOil-3, a major QTL identification for oil content in cottonseed across genomes and its candidate gene analysis. Industrial Crops and Products, 2020, 145, 112070.	2.5	11
5979	Transcriptional changes in the aphid species Myzus cerasi under different host and environmental conditions. Insect Molecular Biology, 2020, 29, 271-282.	1.0	10
5981	Genome-wide association study: Understanding the genetic basis of the gait type in Brazilian Mangalarga Marchador horses, a preliminary study. Livestock Science, 2020, 231, 103867.	0.6	4
5982	Complete genome sequence of Acinetobacter baumanni J1, a quorum sensing-producing algicidal bacterium, isolated from Eastern Pacific Ocean. Marine Genomics, 2020, 52, 100719.	0.4	7
5983	Evaluating the potential of direct RNA nanopore sequencing: Metatranscriptomics highlights possible seasonal differences in a marine pelagic crustacean zooplankton community. Marine Environmental Research, 2020, 153, 104836.	1.1	23
5984	Genomeâ€wide Transcriptional Analysis ofTetrahymena thermophilaResponse to Exogenous Cholesterol. Journal of Eukaryotic Microbiology, 2020, 67, 209-222.	0.8	4
5985	The fire ant social supergene is characterized by extensive gene and transposable element copy number variation. Molecular Ecology, 2020, 29, 105-120.	2.0	12
5986	Plant virus interaction mechanism and associated pathways in mosaic disease of small cardamom (Elettaria cardamomum Maton) by RNA-Seq approach. Genomics, 2020, 112, 2041-2051.	1.3	5
5987	Comparative Cytological and Gene Expression Analysis Reveals Potential Metabolic Pathways and Target Genes Responsive to Salt Stress in Kenaf (Hibiscus cannabinus L.). Journal of Plant Growth Regulation, 2020, 39, 1245-1260.	2.8	20
5988	Transcriptomic analyses of Pinus koraiensis under different cold stresses. BMC Genomics, 2020, 21, 10.	1.2	29
5989	Full-length transcriptome analysis of Coptis deltoidea and identification of putative genes involved in benzylisoquinoline alkaloids biosynthesis based on combined sequencing platforms. Plant Molecular Biology, 2020, 102, 477-499.	2.0	33
5990	pH Gradient Mitigation in the Leaf Cell Secretory Pathway Attenuates the Defense Response of <i>Nicotiana benthamiana</i> to Agroinfiltration. Journal of Proteome Research, 2020, 19, 106-118.	1.8	2
5991	A comparative synthesis of transcriptomic analyses reveals major differences between WSSV-susceptible Litopenaeus vannamei and WSSV-refractory Macrobrachium rosenbergii. Developmental and Comparative Immunology, 2020, 104, 103564.	1.0	23
5992	Morphological and stage-specific transcriptome analyses reveal distinct regulatory programs underlying yam (Dioscorea alata L.) bulbil growth. Journal of Experimental Botany, 2020, 71, 1899-1914.	2.4	15
5993	Discovery of differentially expressed genes in the intestines of Pelteobagrus vachellii within a light/dark cycle. Chronobiology International, 2020, 37, 339-352.	0.9	1

#	Article	IF	Citations
5994	Dual RNA-Seq analysis of Medicago truncatula and the pea powdery mildew Erysiphe pisi uncovers distinct host transcriptional signatures during incompatible and compatible interactions and pathogen effector candidates. Genomics, 2020, 112, 2130-2145.	1.3	13
5995	The impact of mercury on the genome-wide transcription profile of zebrafish intestine. Journal of Hazardous Materials, 2020, 389, 121842.	6.5	15
5996	Gain and loss of a transcription factor that regulates late trichothecene biosynthetic pathway genes in Fusarium. Fungal Genetics and Biology, 2020, 136, 103317.	0.9	13
5997	Development of the transcriptome for a sediment ecotoxicological model species, Chironomus dilutus. Chemosphere, 2020, 244, 125541.	4.2	13
5998	Genomic evidence of population genetic differentiation in deep-sea squat lobster Shinkaia crosnieri (crustacea: Decapoda: Anomura) from Northwestern Pacific hydrothermal vent and cold seep. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 156, 103188.	0.6	15
5999	Epigenetic patterns within the haplotype phased fig (<i>Ficus carica</i> L.) genome. Plant Journal, 2020, 102, 600-614.	2.8	43
6000	De novo assembly, transcriptome characterization, and simple sequence repeat marker development in duckweed Lemna gibba. Physiology and Molecular Biology of Plants, 2020, 26, 133-142.	1.4	6
6001	The developmental transcriptome for Lytechinus variegatus exhibits temporally punctuated gene expression changes. Developmental Biology, 2020, 460, 139-154.	0.9	16
6002	Comparative Proteomics Unravels the Differences in Salt Stress Response of Own-Rooted and 110R-Grafted Thompson Seedless Grapevines. Journal of Proteome Research, 2020, 19, 583-599.	1.8	8
6003	Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature Microbiology, 2020, 5, 166-180.	5.9	75
6004	Optimization of protein isolation by proteomic qualification from Cutaneotrichosporon oleaginosus. Analytical and Bioanalytical Chemistry, 2020, 412, 449-462.	1.9	11
6005	Transcriptional response of springtail (Folsomia candida) exposed to decabromodiphenyl ether-contaminated soil. Science of the Total Environment, 2020, 719, 134859.	3.9	5
6006	Identification and Evaluation of Long Noncoding RNAs in Response to Handling Stress in Red Cusk-Eel (Genypterus chilensis) via RNA-seq. Marine Biotechnology, 2020, 22, 94-108.	1.1	31
6007	Extracellular Vesicles From the Cotton Pathogen Fusarium oxysporum f. sp. vasinfectum Induce a Phytotoxic Response in Plants. Frontiers in Plant Science, 2019, 10, 1610.	1.7	92
6008	Metalloproteomic approach of mercury-binding proteins in liver and kidney tissues of Plagioscion squamosissimus (corvina) and Colossoma macropomum (tambaqui) from Amazon region: Possible identification of mercury contamination biomarkers. Science of the Total Environment, 2020, 711, 134547.	3.9	15
6009	Promotion of the Rapid Growth in Haematococcus pluvialis Under 0.16% CO2 Condition Revealed by Transcriptome and Metabolomic Analysis. Journal of Plant Growth Regulation, 2020, 39, 1177-1190.	2.8	2
6010	Transcriptomic analysis of root specific drought mediated response of G. arboreum and G. hirsutum. Biologia (Poland), 2020, 75, 627-636.	0.8	3
6011	The Coix Genome Provides Insights into Panicoideae Evolution and Papery Hull Domestication. Molecular Plant, 2020, 13, 309-320.	3.9	28

#	Article	IF	Citations
6012	Cold-inducible expression of an Arabidopsis thaliana AP2 transcription factor gene, AtCRAP2, promotes flowering under unsuitable low-temperatures in chrysanthemum. Plant Physiology and Biochemistry, 2020, 146, 220-230.	2.8	10
6013	Molecular insights into the sex-differential regulation of signal transduction in the cerebral ganglion and metabolism in the hepatopancreas of Eriocheir sinensis during reproduction. Genomics, 2020, 112, 71-81.	1.3	7
6014	Comparative transcriptomic analysis provides insights into immune responses of lamprey larvae under three pathogens infections. Molecular Immunology, 2020, 117, 147-154.	1.0	7
6015	Transcriptomic Changes of Piscirickettsia salmonis During Intracellular Growth in a Salmon Macrophage-Like Cell Line. Frontiers in Cellular and Infection Microbiology, 2019, 9, 426.	1.8	27
6016	Expression profiling of miRNAs indicates crosstalk between phytohormonal response and rhizobial infection in chickpea. Journal of Plant Biochemistry and Biotechnology, 2020, 29, 380-394.	0.9	12
6017	Characterization of a novel protein identified by proteomics analysis as a modulator of inflammatory networks in amphioxus. Fish and Shellfish Immunology, 2020, 96, 97-106.	1.6	2
6018	De novo transcriptome sequencing of the thecate colonial hydrozoan, Dynamena pumila. Marine Genomics, 2020, 51, 100726.	0.4	4
6019	Comprehensive transcriptome analysis of faba bean in response to vernalization. Planta, 2020, 251, 22.	1.6	10
6020	Profiling the transcriptome response of Atlantic salmon head kidney to formalin-killed Renibacterium salmoninarum. Fish and Shellfish Immunology, 2020, 98, 937-949.	1.6	33
6021	Comparative analysis of iTRAQ-based proteome profiles of Schistosoma japonicum female worms coming from single-sex infections and bisexual infections. Journal of Proteomics, 2020, 213, 103597.	1.2	16
6022	Acute hypoxia changes the mode of glucose and lipid utilization in the liver of the largemouth bass (Micropterus salmoides). Science of the Total Environment, 2020, 713, 135157.	3.9	81
6023	Chromosomalâ€level assembly of <i>Takifugu obscurus</i> (Abe, 1949) genome using thirdâ€generation DNA sequencing and Hiâ€C analysis. Molecular Ecology Resources, 2020, 20, 520-530.	2.2	46
6024	Transcriptomic Analysis Suggests Genes Expressed Stage-Independently and Stageâ€"Dependently Modulating the Wing Dimorphism of the Brown Planthopper. Genes, 2020, 11, 19.	1.0	3
6025	Comparative Proteomic Analysis of Nodulated and Non-Nodulated Casuarina glauca Sieb. ex Spreng. Grown under Salinity Conditions Using Sequential Window Acquisition of All Theoretical Mass Spectra (SWATH-MS). International Journal of Molecular Sciences, 2020, 21, 78.	1.8	13
6026	Evolutionary History of Major Chemosensory Gene Families across Panarthropoda. Molecular Biology and Evolution, 2020, 37, 3601-3615.	3.5	10
6027	Blue genome: chromosomeâ€scale genome reveals the evolutionary and molecular basis of indigo biosynthesis in <i>Strobilanthes cusia</i>. Plant Journal, 2020, 104, 864-879.	2.8	15
6028	Insights into the resistance of a synthetically-derived wheat to Septoria tritici blotch disease: less is more. BMC Plant Biology, 2020, 20, 407.	1.6	6
6029	Transcriptional responses in developing lesions of European common ash (Fraxinus excelsior) reveal genes responding to infection by Hymenoscyphus fraxineus. BMC Plant Biology, 2020, 20, 455.	1.6	1

#	Article	IF	Citations
6030	Genome- and Transcriptome-Wide Identification of C3Hs in Common Bean (Phaseolus vulgaris L.) and Structural and Expression-Based Analyses of Their Functions During the Sprout Stage Under Salt-Stress Conditions. Frontiers in Genetics, 2020, 11, 564607.	1.1	15
6031	Zebrafish Oxr1a Knockout Reveals Its Role in Regulating Antioxidant Defenses and Aging. Genes, 2020, 11, 1118.	1.0	14
6032	Conserved Patterns in Developmental Processes and Phases, Rather than Genes, Unite the Highly Divergent Bilateria. Life, 2020, 10, 182.	1.1	2
6033	Comprehensive Transcriptomic Analysis for Developing Seeds of a Synthetic Brassica Hexaploid. Plants, 2020, 9, 1141.	1.6	3
6034	Comparative transcriptomics reveals eyestalk ablation induced responses of the neuroendocrine-immune system in the Pacific white shrimp Litopenaeus vannamei. Fish and Shellfish Immunology, 2020, 106, 823-832.	1.6	16
6035	Genetic compensation rather than genetic assimilation drives the evolution of plasticity in response to mild warming across latitudes in a damselfly. Molecular Ecology, 2020, 29, 4823-4834.	2.0	17
6036	HybridMine: A Pipeline for Allele Inheritance and Gene Copy Number Prediction in Hybrid Genomes and Its Application to Industrial Yeasts. Microorganisms, 2020, 8, 1554.	1.6	8
6037	Correlation Analysis of Expression Profile and Quantitative iTRAQ-LC-MS/MS Proteomics Reveals Resistance Mechanism Against TuMV in Chinese Cabbage (Brassica rapa ssp. pekinensis). Frontiers in Genetics, 2020, 11, 963.	1.1	10
6038	Prodiamesa olivacea: de novo biomarker genes in a potential sentinel organism for ecotoxicity studies in natural scenarios. Aquatic Toxicology, 2020, 227, 105593.	1.9	3
6039	Transcriptomic Profiling of the Adaptive and Innate Immune Responses of Atlantic Salmon to Renibacterium salmoninarum Infection. Frontiers in Immunology, 2020, 11, 567838.	2.2	19
6040	Potential of Cell-Free Supernatant from Lactobacillus plantarum NIBR97, Including Novel Bacteriocins, as a Natural Alternative to Chemical Disinfectants. Pharmaceuticals, 2020, 13, 266.	1.7	24
6041	A comparative proteomics analysis of the egg secretions of three major schistosome species. Molecular and Biochemical Parasitology, 2020, 240, 111322.	0.5	21
6042	Differential expression of genes in olive leaves and buds of ON- versus OFF-crop trees. Scientific Reports, 2020, 10, 15762.	1.6	7
6043	The genomes of a monogenic fly: views of primitive sex chromosomes. Scientific Reports, 2020, 10, 15728.	1.6	6
6044	Comparative Transcriptomics Reveals the Molecular Genetic Basis of Cave Adaptability in Sinocyclocheilus Fish Species. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	3
6045	Pro-197-Ser Mutation in ALS and High-Level GST Activities: Multiple Resistance to ALS and ACCase Inhibitors in Beckmannia syzigachne. Frontiers in Plant Science, 2020, 11, 572610.	1.7	13
6046	The genome of Chinese flowering cherry (Cerasus serrulata) provides new insights into Cerasus species. Horticulture Research, 2020, 7, 165.	2.9	22
6047	Transcriptome analysis identifies key genes involved in carotenoid biosynthesis in the flesh of red pummelo (Citrus maxima). Biotechnology and Biotechnological Equipment, 2020, 34, 614-622.	0.5	2

#	Article	IF	Citations
6048	A Comparative Transcriptome Analysis, Conserved Regulatory Elements and Associated Transcription Factors Related to Accumulation of Fusariotoxins in Grain of Rye (Secale cereale L.) Hybrids. International Journal of Molecular Sciences, 2020, 21, 7418.	1.8	3
6049	Transcriptional profiling reveals molecular basis and the role of arginine in response to low-pH stress in Pichia kudriavzevii. Journal of Bioscience and Bioengineering, 2020, 130, 588-595.	1.1	6
6050	Resistant starch slows the progression of CKD in the 5/6 nephrectomy mouse model. Physiological Reports, 2020, 8, e14610.	0.7	15
6051	In silico identification and validation of miRNA and their DIR specific targets in Oryza sativa Indica under abiotic stress. Non-coding RNA Research, 2020, 5, 167-177.	2.4	21
6052	Transcriptomics of Chinese Sapium Sebiferum (L.) Roxb seed to reveal key enzymes involved in oil accumulation. Oil Crop Science, 2020, 5, 107-113.	0.9	0
6053	RNA-Seq and differential gene expression analysis in Temora stylifera copepod females with contrasting non-feeding nauplii survival rates: an environmental transcriptomics study. BMC Genomics, 2020, 21, 693.	1.2	14
6054	Comparative transcriptome analysis reveals heat stress-responsive genes and their signalling pathways in lilies (Lilium longiflorum vs. Lilium distichum). PLoS ONE, 2020, 15, e0239605.	1.1	6
6055	Reconstruction and functional annotation of Ascosphaera apis full-length transcriptome utilizing PacBio long reads combined with Illumina short reads. Journal of Invertebrate Pathology, 2020, 176, 107475.	1.5	6
6056	Penicillium oxalicum putative methyltransferase Mtr23B has similarities and differences with LaeA in regulating conidium development and glycoside hydrolase gene expression. Fungal Genetics and Biology, 2020, 143, 103445.	0.9	8
6057	Transcriptome analysis revealed key genes and pathways related to cadmium-stress tolerance in Kenaf (Hibiscus cannabinus L.). Industrial Crops and Products, 2020, 158, 112970.	2.5	45
6058	Identification and characterization of highly active promoters from the fall armyworm, Spodoptera frugiperda. Insect Biochemistry and Molecular Biology, 2020, 126, 103455.	1.2	16
6059	Comprehensive multiomics analysis reveals key roles of NACs in plant growth and development and its environmental adaption mechanism by regulating metabolite pathways. Genomics, 2020, 112, 4897-4911.	1.3	6
6060	Understanding salt tolerance mechanism using transcriptome profiling and de novo assembly of wild tomato Solanum chilense. Scientific Reports, 2020, 10, 15835.	1.6	35
6061	Combined transcriptome sequencing and prokaryotic expression to investigate the key enzyme in the 2-C-methylerythritol-4-phosphate pathway of Osmanthus fragrans. Functional Plant Biology, 2020, 47, 945.	1.1	6
6062	Convergent Evolution and Structural Adaptation to the Deep Ocean in the Protein-Folding Chaperonin CCTÎ±. Genome Biology and Evolution, 2020, 12, 1929-1942.	1.1	9
6063	Responses of Manila Grass (Zoysia matrella) to chilling stress: From transcriptomics to physiology. PLoS ONE, 2020, 15, e0235972.	1.1	8
6064	Transcriptome Analysis of Low- and High-Sucrose Pear Cultivars Identifies Key Regulators of Sucrose Biosynthesis in Fruits. Plant and Cell Physiology, 2020, 61, 1493-1506.	1.5	13
6065	Full-length sequencing of ginkgo transcriptomes for an in-depth understanding of flavonoid and terpenoid trilactone biosynthesis. Gene, 2020, 758, 144961.	1.0	22

#	Article	IF	Citations
6066	Searching large-scale scRNA-seq databases via unbiased cell embedding with Cell BLAST. Nature Communications, 2020, 11, 3458.	5.8	81
6067	Biological rhythms in the deep-sea hydrothermal mussel Bathymodiolus azoricus. Nature Communications, 2020, 11, 3454.	5.8	30
6068	Identification of genes expressed differentially in female and male gametes of Sipunculus nudus. Aquaculture Research, 2020, 51, 3780-3789.	0.9	0
6069	The highâ€quality genome of diploid strawberry (<i>Fragaria nilgerrensis</i>) provides new insights into anthocyanin accumulation. Plant Biotechnology Journal, 2020, 18, 1908-1924.	4.1	51
6070	Analysis of differential gene expression in Litopenaeus vannamei under High salinity stress. Aquaculture Reports, 2020, 18, 100423.	0.7	11
6071	IC4R-2.0: Rice Genome Reannotation Using Massive RNA-seq Data. Genomics, Proteomics and Bioinformatics, 2020, 18, 161-172.	3.0	18
6072	Genomic characterization of Parengyodontium americanum sp. nov. Fungal Genetics and Biology, 2020, 138, 103351.	0.9	4
6073	Transcriptome analysis of the medicinally significant plant Fontainea picrosperma (Euphorbiaceae) reveals conserved biosynthetic pathways. FÃ¬toterapÃ¬Ã¢, 2020, 146, 104680.	1.1	5
6074	Genome-wide discovery of DNA variants in cucumber somaclonal lines. Gene, 2020, 736, 144412.	1.0	10
6075	Expansion of Adhesion Genes Drives Pathogenic Adaptation of Nematode-Trapping Fungi. IScience, 2020, 23, 101057.	1.9	31
6076	Impact of high dietary plant protein with or without marine ingredients in gut mucosa proteome of gilthead seabream (Sparus aurata, L.). Journal of Proteomics, 2020, 216, 103672.	1.2	14
6077	Peroxisome proliferator-activated receptor alpha is involved in the temperature-induced sex differentiation of a vertebrate. Scientific Reports, 2020, 10, 11672.	1.6	13
6078	Transcriptomic analysis of polyaromatic hydrocarbon degradation by the halophilic fungus <i>Aspergillus sydowii</i> at hypersaline conditions. Environmental Microbiology, 2021, 23, 3435-3459.	1.8	41
6079	Transcriptome studies of the floodwater mosquito, <scp><i>Aedes vexans</i></scp> (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Research, 2020, 50, 563-574.	0.6	5
6080	Assessment of ethanol tolerance of Kluyveromyces marxianus CCT 7735 selected by adaptive laboratory evolution. Applied Microbiology and Biotechnology, 2020, 104, 7483-7494.	1.7	25
6081	Transcriptomic analysis of flower opening response to relatively low temperatures in Osmanthus fragrans. BMC Plant Biology, 2020, 20, 337.	1.6	8
6082	First Genome Sequences of Two Multidrug-Resistant Candida haemulonii var. vulnera Isolates From Pediatric Patients With Candidemia. Frontiers in Microbiology, 2020, 11, 1535.	1.5	8
6083	The conifer root rot pathogens Heterobasidion irregulare and Heterobasidion occidentale employ different strategies to infect Norway spruce. Scientific Reports, 2020, 10, 5884.	1.6	7

#	Article	IF	Citations
6084	Functional shell matrix proteins tentatively identified by asymmetric snail shell morphology. Scientific Reports, 2020, 10, 9768.	1.6	13
6085	Transcriptome analysis reveals key information on improving duck yolk lipid contents induced by dietary fish oil or flaxseed oil. Journal of Applied Animal Research, 2020, 48, 192-200.	0.4	0
6086	Comparative analysis of transcriptome and metabolome uncovers the metabolic differences between <i>Dendrobium officinale</i> protocorms and mature stems. International Journal of Transgender Health, 2020, 13, 346-359.	1.1	4
6087	Revealing Differentially Expressed Genes and Identifying Effector Proteins of Puccinia striiformis f. sp. <i>tritici</i> in Response to High-Temperature Seedling Plant Resistance of Wheat Based on Transcriptome Sequencing. MSphere, 2020, 5, .	1.3	8
6088	Differential protein abundance associated with delayed regeneration of the scleractinian coral Montastraea cavernosa. Coral Reefs, 2020, 39, 1175-1186.	0.9	4
6089	Genetic Architecture of Flowering Time and Sex Determination in Hemp (Cannabis sativa L.): A Genome-Wide Association Study. Frontiers in Plant Science, 2020, 11, 569958.	1.7	31
6090	Comparative Genomics Analysis Provides New Strategies for Bacteriostatic Ability of Bacillus velezensis HAB-2. Frontiers in Microbiology, 2020, 11, 594079.	1.5	12
6091	Transcriptome Analysis and Knockdown of the Juvenile Hormone Esterase Gene Reveal Abnormal Feeding Behavior in the Sugarcane Giant Borer. Frontiers in Physiology, 2020, 11, 588450.	1.3	5
6092	Transcriptomic Analysis Reveals Salt Tolerance Mechanisms Present in Date-Plum Persimmon Rootstock (Diospyros lotus L.). Agronomy, 2020, 10, 1703.	1.3	4
6093	Transcriptional Analysis of Metabolic Pathways and Regulatory Mechanisms of Essential Oil Biosynthesis in the Leaves of Cinnamomum camphora (L.) Presl. Frontiers in Genetics, 2020, 11, 598714.	1.1	19
6094	Transcriptome dataset from bark and latex tissues of three Hevea brasiliensis clones. Data in Brief, 2020, 32, 106188.	0.5	2
6095	Genomic and Transcriptomic Analysis for Identification of Genes and Interlinked Pathways Mediating Artemisinin Resistance in Leishmania donovani. Genes, 2020, 11, 1362.	1.0	6
6096	Dynamic and reversible DNA methylation changes induced by genome separation and merger of polyploid wheat. BMC Biology, 2020, 18, 171.	1.7	26
6097	Plasma activated water triggers plant defence responses. Scientific Reports, 2020, 10, 19211.	1.6	21
6098	Full-Length Transcriptome from <i>Camellia oleifera</i> Seed Provides Insight into the Transcript Variants Involved in Oil Biosynthesis. Journal of Agricultural and Food Chemistry, 2020, 68, 14670-14683.	2.4	33
6099	Temporal salt stress-induced transcriptome alterations and regulatory mechanisms revealed by PacBio long-reads RNA sequencing in Gossypium hirsutum. BMC Genomics, 2020, 21, 838.	1.2	19
6100	Transcriptomic analysis reveals growth-related genes in juvenile grass carp, Ctenopharyngodon idella. Aquaculture and Fisheries, 2020, , .	1.2	5
6101	Sequencing and analysis of gerbera daisy leaf transcriptomes reveal disease resistance and susceptibility genes differentially expressed and associated with powdery mildew resistance. BMC Plant Biology, 2020, 20, 539.	1.6	11

#	Article	IF	Citations
6102	Transcriptomics-Based Approach Identifies Spinosad-Associated Targets in the Colorado Potato Beetle, Leptinotarsa decemlineata. Insects, 2020, 11, 820.	1.0	12
6103	Wide-ranging transcriptomic analysis of Poncirus trifoliata, Citrus sunki, Citrus sinensis and contrasting hybrids reveals HLB tolerance mechanisms. Scientific Reports, 2020, 10, 20865.	1.6	22
6104	Liver and spleen transcriptome reveals that Oreochromis aureus under long-term salinity stress may cause excessive energy consumption and immune response. Fish and Shellfish Immunology, 2020, 107, 469-479.	1.6	8
6105	Transcriptional analysis reveals potential genes and regulatory networks involved in salicylic acid-induced flowering in duckweed (Lemna gibba). Plant Physiology and Biochemistry, 2020, 155, 512-522.	2.8	15
6106	Complementary Transcriptome and Proteome Analyses Provide Insight into the Floral Transition in Bamboo (Dendrocalamus latiflorus Munro). International Journal of Molecular Sciences, 2020, 21, 8430.	1.8	3
6107	Intricate genetic variation networks control the adventitious root growth angle in apple. BMC Genomics, 2020, 21, 852.	1.2	6
6108	Comparative transcriptome analysis of male and female flowers in Spinacia oleracea L. BMC Genomics, 2020, 21, 850.	1.2	15
6109	Salt-responsive transcriptome analysis of triticale reveals candidate genes involved in the key metabolic pathway in response to salt stress. Scientific Reports, 2020, 10, 20669.	1.6	16
6110	Optimized combination methods for exploring and verifying disease-resistant transcription factors in melon. Briefings in Bioinformatics, 2020, 22, .	3.2	0
6111	Multi-Omics Analysis Provides Novel Insight into Immuno-Physiological Pathways and Development of Thermal Resistance in Rainbow Trout Exposed to Acute Thermal Stress. International Journal of Molecular Sciences, 2020, 21, 9198.	1.8	24
6112	Comparative transcriptome analysis of lingonberry (<i>Vaccinium vitis-idaea</i>) provides insights into genes associated with flavonoids metabolism during fruit development. Biotechnology and Biotechnological Equipment, 2020, 34, 1252-1264.	0.5	8
6113	Transcriptome Profiling Provides Insights Into Potential Antagonistic Mechanisms Involved in Chaetomium globosum Against Bipolaris sorokiniana. Frontiers in Microbiology, 2020, 11, 578115.	1.5	19
6114	Comparative Transcriptome Analysis of Toxic and Non-Toxic Nassarius Communities and Identification of Genes Involved in TTX-Adaptation. Toxins, 2020, 12, 761.	1.5	6
6115	Ovarian transcriptomic analysis and follicular development of Leizhou black duck. Poultry Science, 2020, 99, 6173-6187.	1.5	14
6116	Comprehensive characterization of the ALMT and MATE families on Populus trichocarpa and gene co-expression network analysis of its members during aluminium toxicity and phosphate starvation stresses. 3 Biotech, 2020, 10, 525.	1.1	5
6117	Genome-wide analysis of PHD finger gene family and identification of potential miRNA and their PHD finger gene specific targets in Oryza sativa indica. Non-coding RNA Research, 2020, 5, 191-200.	2.4	2
6118	Functional identification of PsMYB57 involved in anthocyanin regulation of tree peony. BMC Genetics, 2020, 21, 124.	2.7	15
6119	Identification of Immune Response to Sacbrood Virus Infection in Apis cerana Under Natural Condition. Frontiers in Genetics, 2020, 11, 587509.	1.1	4

#	Article	IF	Citations
6120	Ocean Acidification and Warming Lead to Increased Growth and Altered Chloroplast Morphology in the Thermo-Tolerant Alga Symbiochlorum hainanensis. Frontiers in Plant Science, 2020, 11, 585202.	1.7	13
6121	Flavonoid accumulation and identification of flavonoid biosynthesis genes in Dimocarpus longan lour. by transcriptome sequencing. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 2020, 48, 636-655.	0.5	0
6122	Differential gene expression profile of male and female copepods in response to cadmium exposure. Ecotoxicology and Environmental Safety, 2020, 204, 111048.	2.9	18
6123	Bacillus amyloliquefaciens PDR1 from root of karst adaptive plant enhances Arabidopsis thaliana resistance to alkaline stress through modulation of plasma membrane H+-ATPase activity. Plant Physiology and Biochemistry, 2020, 155, 472-482.	2.8	7
6124	The basic helix-loop-helix transcription factor bHLH95 affects fruit ripening and multiple metabolisms in tomato. Journal of Experimental Botany, 2020, 71, 6311-6327.	2.4	27
6125	Genomewide analysis of microsatellite markers based on sequenced database in two anuran species. Journal of Genetics, 2020, 99, 1.	0.4	1
6126	Integration of RNA-seq and RNAi provides a novel insight into the effect of pvdE gene to the pathogenic of Pseudomonas plecoglossicida and on the immune responses of orange-spotted grouper (Epinephelus coioides). Aquaculture, 2020, 529, 735695.	1.7	22
6127	Multi-locus genome-wide association studies reveal novel genomic regions associated with vegetative stage salt tolerance in bread wheat (Triticum aestivum L.). Genomics, 2020, 112, 4608-4621.	1.3	32
6128	Comparative Transcriptome Analysis Reveals Candidate Genes Involved in Isoquinoline Alkaloid Biosynthesis in Stephania tetrandra. Planta Medica, 2020, 86, 1258-1268.	0.7	5
6129	Genome-wide association studies of callus differentiation for the desert tree,<i>Populus euphratica</i>. Tree Physiology, 2020, 40, 1762-1777.	1.4	18
6130	A tentacle for every occasion: comparing the hunting tentacles and sweeper tentacles, used for territorial competition, in the coral Galaxea fascicularis. BMC Genomics, 2020, 21, 548.	1.2	12
6131	Transcriptome analysis of the eggs of the silkworm pale red egg (rep-1) mutant at 36 hours after oviposition. PLoS ONE, 2020, 15, e0237242.	1.1	1
6132	JNK pathway restricts DENV2, ZIKV and CHIKV infection by activating complement and apoptosis in mosquito salivary glands. PLoS Pathogens, 2020, 16, e1008754.	2.1	44
6133	Pulse magnetization elicits differential gene expression in the central nervous system of the Caribbean spiny lobster, Panulirus argus. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology, 2020, 206, 725-742.	0.7	4
6134	Two-omics data revealed commonalities and differences between Rpv12- and Rpv3-mediated resistance in grapevine. Scientific Reports, 2020, 10, 12193.	1.6	24
6135	Sustained immune activation is associated with susceptibility to the amphibian chytrid fungus. Molecular Ecology, 2020, 29, 2889-2903.	2.0	24
6136	The Genome of Microthlaspi erraticum (Brassicaceae) Provides Insights Into the Adaptation to Highly Calcareous Soils. Frontiers in Plant Science, 2020, 11, 943.	1.7	4
6137	A transcriptomic, metabolomic and cellular approach to the physiological adaptation of tomato fruit to high temperature. Plant, Cell and Environment, 2021, 44, 2211-2229.	2.8	38

#	Article	IF	Citations
6138	Mountain stoneflies may tolerate warming streams: Evidence from organismal physiology and gene expression. Global Change Biology, 2020, 26, 5524-5538.	4.2	16
6139	Identification of Heat-Responsive Genes in Guar [<i>Cyamopsis tetragonoloba</i> (L.) Taub]. International Journal of Genomics, 2020, 2020, 1-17.	0.8	8
6140	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. BMC Biology, 2020, 18, 90.	1.7	40
6141	The Genome Sequence of the Octocoral <i>Paramuricea clavata</i> â€" A Key Resource To Study the Impact of Climate Change in the Mediterranean. G3: Genes, Genomes, Genetics, 2020, 10, 2941-2952.	0.8	6
6142	Response of Brassica napus to Plasmodiophora brassicae Involves Salicylic Acid-Mediated Immunity: An RNA-Seq-Based Study. Frontiers in Plant Science, 2020, 11, 1025.	1.7	42
6143	Organic Farming Sharpens Plant Defenses in the Field. Frontiers in Sustainable Food Systems, 2020, 4, .	1.8	11
6144	Tackling the Molecular Drug Sensitivity in the Sea Louse Caligus rogercresseyi Based on mRNA and lncRNA Interactions. Genes, 2020, 11, 857.	1.0	6
6145	Shotgun Proteomics of Ascidians Tunic Gives New Insights on Hostâ€"Microbe Interactions by Revealing Diverse Antimicrobial Peptides. Marine Drugs, 2020, 18, 362.	2.2	10
6146	Wheat Line â€œRYNO3936â€•Is Associated With Delayed Water Stress-Induced Leaf Senescence and Rapid Water-Deficit Stress Recovery. Frontiers in Plant Science, 2020, 11, 1053.	1.7	12
6147	A Genome-Wide View of Transcriptional Responses during Aphis glycines Infestation in Soybean. International Journal of Molecular Sciences, 2020, 21, 5191.	1.8	8
6148	Epigenetic Regulation of Verticillium dahliae Virulence: Does DNA Methylation Level Play A Role?. International Journal of Molecular Sciences, 2020, 21, 5197.	1.8	5
6149	Transcriptomic comparison reveals modifications in gene expression, photosynthesis, and cell wall in woody plant as responses to external pH changes. Ecotoxicology and Environmental Safety, 2020, 203, 111007.	2.9	9
6150	Draft Genome Sequence of Clostridium estertheticum-Like Strain FP3, Isolated from Spoiled Uncooked Lamb. Microbiology Resource Announcements, 2020, 9, .	0.3	3
6151	Integrated single-molecule long-read sequencing and Illumina sequencing reveal the resistance mechanism of Psathyrostachys huashanica in response to barley yellow dwarf virus-GAV. Phytopathology Research, 2020, 2, .	0.9	9
6152	Proteomic Responses to Ocean Acidification in the Brain of Juvenile Coral Reef Fish. Frontiers in Marine Science, 2020, 7, .	1.2	15
6153	Corticotropin-Releasing Hormone (CRH) Gene Family Duplications in Lampreys Correlate With Two Early Vertebrate Genome Doublings. Frontiers in Neuroscience, 2020, 14, 672.	1.4	18
6154	Potential Involvement of lncRNAs in the Modulation of the Transcriptome Response to Nodavirus Challenge in European Sea Bass (Dicentrarchus labrax L.). Biology, 2020, 9, 165.	1.3	13
6155	Proteomic and Bioinformatic Investigations of Heat-Treated Anisakis simplex Third-Stage Larvae. Biomolecules, 2020, 10, 1066.	1.8	8

#	ARTICLE	IF	CITATIONS
6156	Elucidation of metabolic responses in mud crab Scylla paramamosain challenged to WSSV infection by integration of metabolomics and transcriptomics. Developmental and Comparative Immunology, 2020, 113, 103799.	1.0	9
6157	A transcriptomic analysis of diploid and triploid Atlantic salmon lenses with and without cataracts. Experimental Eye Research, 2020, 199, 108150.	1.2	6
6158	Diversity and genome mapping assessment of disordered and functional domains in trypanosomatids. Journal of Proteomics, 2020, 227, 103919.	1.2	2
6159	Differential Expression of Fungal Genes Determines the Lifestyle of Plectosphaerella Strains During Arabidopsis thaliana Colonization. Molecular Plant-Microbe Interactions, 2020, 33, 1299-1314.	1.4	9
6160	Proteomic responses to progressive dehydration stress in leaves of chickpea seedlings. BMC Genomics, 2020, 21, 523.	1.2	28
6161	Early nodulin 93 protein gene: essential for induction of somatic embryogenesis in oil palm. Plant Cell Reports, 2020, 39, 1395-1413.	2.8	8
6162	Spatio-temporal patterns in the gene expression of the calanoid copepod Temora longicornis in the Belgian part of the North Sea. Marine Environmental Research, 2020, 160, 105037.	1.1	8
6163	Enjoying the warming Mediterranean: Transcriptomic responses to temperature changes of a thermophilous keystone species in benthic communities. Molecular Ecology, 2020, 29, 3299-3315.	2.0	11
6164	Wholeâ€genome <i>de novo</i> assemblies reveal extensive structural variations and dynamic organelleâ€toâ€nucleus DNA transfers in African and Asian rice. Plant Journal, 2020, 104, 596-612.	2.8	19
6165	De Novo Transcriptome Assembly and Gene Expression Profiling of the Copepod Calanus helgolandicus Feeding on the PUA-Producing Diatom Skeletonema marinoi. Marine Drugs, 2020, 18, 392.	2.2	23
6166	Illuminating the impact of diel vertical migration on visual gene expression in deepâ€sea shrimp. Molecular Ecology, 2020, 29, 3494-3510.	2.0	14
6167	Schistosoma haematobium Extracellular Vesicle Proteins Confer Protection in a Heterologous Model of Schistosomiasis. Vaccines, 2020, 8, 416.	2.1	27
6168	RNAâ€Seq analysis of the guppy immune response against <i>Gyrodactylus bullatarudis</i> infection. Parasite Immunology, 2020, 42, e12782.	0.7	10
6169	Investigation of essential cell cycle regulator genes as candidates for immortalized shrimp cell line establishment based on the effect of in vitro culturing on gene expression of shrimp primary cells. Aquaculture, 2020, 529, 735733.	1.7	4
6170	Identification and distribution of gene clusters required for synthesis of sphingolipid metabolism inhibitors in diverse species of the filamentous fungus Fusarium. BMC Genomics, 2020, 21, 510.	1.2	21
6171	Two Clubroot-Resistance Genes, Rcr3 and Rcr9wa, Mapped in Brassica rapa Using Bulk Segregant RNA Sequencing. International Journal of Molecular Sciences, 2020, 21, 5033.	1.8	32
6172	Structural and Functional Insights into a Lysine Deacylase in the Cyanobacterium <i>Synechococcus</i> sp. PCC 7002. Plant Physiology, 2020, 184, 762-776.	2.3	6
6173	Transcriptome profiling and gene expression analyses of eggplant (Solanum melongena L.) under heat stress. PLoS ONE, 2020, 15, e0236980.	1.1	9

#	ARTICLE	IF	CITATIONS
6174	Identification and expression analysis of some wheat F-box subfamilies during plant development and infection by Puccinia triticina. Plant Physiology and Biochemistry, 2020, 155, 535-548.	2.8	17
6175	Identification of novel microRNAs for cold deacclimation in barley. Plant Growth Regulation, 2020, 92, 389-400.	1.8	5
6176	Analysis on the virulomes and resistomes of multi-drug resistance clinical Escherichia coli isolates, as well as the interactome with gut microbiome. Microbial Pathogenesis, 2020, 148, 104423.	1.3	2
6177	Full-length transcriptome and long non-coding RNA profiling of whiteleg shrimp Penaeus vannamei hemocytes in response to Spiroplasma eriocheiris infection. Fish and Shellfish Immunology, 2020, 106, 876-886.	1.6	22
6178	Yellow-fruited phenotype is caused by 573 bp insertion at 5' UTR of YFT1 allele in yft1 mutant tomato. Plant Science, 2020, 300, 110637.	1.7	11
6179	Genome-guided insights of tropical Bacillus strains efficient in maize growth promotion. FEMS Microbiology Ecology, 2020, 96, .	1.3	8
6180	Genome-wide analysis of evolution and expression profiles of NAC transcription factor gene family in Juglans regia L.. Annals of Forest Science, 2020, 77, 1.	0.8	6
6181	Effect of the suppression of BpAP1 on the expression of lignin related genes in birch. Journal of Forestry Research, 2022, 33, 289-297.	1.7	0
6182	Characterization and Development of Microsatellite Markers in Pseudotaxus chienii (Taxaceae) Based on Transcriptome Sequencing. Frontiers in Genetics, 2020, 11, 574304.	1.1	11
6183	Phased diploid genome assemblies and pan-genomes provide insights into the genetic history of apple domestication. Nature Genetics, 2020, 52, 1423-1432.	9.4	168
6184	Identification of differentially expressed genes and pathways in isonuclear kenaf genotypes under salt stress. Physiologia Plantarum, 2021, 173, 1295-1308.	2.6	10
6185	Differential transcriptome and metabolome analysis of Plumbago zeylanica L. reveal putative genes involved in plumbagin biosynthesis. FÃ¬toterapÃ¬Ã¢, 2020, 147, 104761.	1.1	12
6186	Comparative morphological and transcriptomic analyses reveal chemosensory genes in the poultry red mite, Dermanyssus gallinae. Scientific Reports, 2020, 10, 17923.	1.6	7
6187	New insights into the evolution of the SBP-box family and expression analysis of genes in the growth and development of <i>Brassica juncea</i>. Biotechnology and Biotechnological Equipment, 2020, 34, 810-824.	0.5	4
6188	Combined Transcriptome and Metabolome analysis of Pitaya fruit unveiled the mechanisms underlying Peel and pulp color formation. BMC Genomics, 2020, 21, 734.	1.2	37
6189	Low-temperature effects on docosahexaenoic acid biosynthesis in Schizochytrium sp. TIO01 and its proposed underlying mechanism. Biotechnology for Biofuels, 2020, 13, 172.	6.2	25
6190	Characterization of Drought-Responsive Transcriptome During Seed Germination in Adzuki Bean (Vigna angularis L.) by PacBio SMRT and Illumina Sequencing. Frontiers in Genetics, 2020, 11, 996.	1.1	16
6191	Proteomic Analysis of UV-B-Induced Virulence-Mutant Strains of Puccinia striiformis f. sp. tritici Based on iTRAQ Technology. Frontiers in Microbiology, 2020, 11, 542961.	1.5	4

#	Article	IF	Citations
6192	Temperate Bacteriophages (Prophages) in Pseudomonas aeruginosa Isolates Belonging to the International Cystic Fibrosis Clone (CC274). Frontiers in Microbiology, 2020, 11, 556706.	1.5	18
6193	Changes in composition and levels of hemolymph proteins during metamorphosis of Manduca sexta. Insect Biochemistry and Molecular Biology, 2020, 127, 103489.	1.2	11
6194	A new esophageal gland transcriptome reveals signatures of large scale de novo effector birth in the root lesion nematode Pratylenchus penetrans. BMC Genomics, 2020, 21, 738.	1.2	15
6195	Î²-aminobutyric acid induces priming defence against Botrytis cinerea in grapefruit by reducing intercellular redox status that modifies posttranslation of VvNPR1 and its interaction with VvTGA1. Plant Physiology and Biochemistry, 2020, 156, 552-565.	2.8	15
6196	Screening of mungbean for drought tolerance and transcriptome profiling between drought-tolerant and susceptible genotype in response to drought stress. Plant Physiology and Biochemistry, 2020, 157, 229-238.	2.8	32
6197	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (Olea europaea L.). BMC Biology, 2020, 18, 148.	1.7	39
6198	Pollen development in cotton (<scp><i>Gossypium hirsutum</i></scp>) is highly sensitive to heat exposure during the tetrad stage. Plant, Cell and Environment, 2021, 44, 2150-2166.	2.8	29
6199	From Embryo to Adult: Low Temperatures Affect Phase Transitions of Allium sativum L. from Germination to Flowering. Agronomy, 2020, 10, 1651.	1.3	3
6200	Genomics and Proteomics Analyses Revealed Novel Candidate Pesticidal Proteins in a Lepidopteran-Toxic Bacillus thuringiensis Strain. Toxins, 2020, 12, 673.	1.5	7
6201	Changes in transcriptomic response to salinity stress induce the brackish water adaptation in a freshwater snail. Scientific Reports, 2020, 10, 16049.	1.6	5
6202	Evolutionary analysis of the Moringa oleifera genome reveals a recent burst of plastid to nucleus gene duplications. Scientific Reports, 2020, 10, 17646.	1.6	12
6203	Jasmonic acid and ERF family genes are involved in chilling sensitivity and seed browning of pepper fruit after harvest. Scientific Reports, 2020, 10, 17949.	1.6	10
6204	Unexpected mutual regulation underlies paralogue functional diversification and promotes epithelial tissue maturation in Tribolium. Communications Biology, 2020, 3, 552.	2.0	9
6205	Transcriptomic changes across vitellogenesis in the black tiger prawn (Penaeus monodon), neuropeptides and G protein-coupled receptors repertoire curation. General and Comparative Endocrinology, 2020, 298, 113585.	0.8	15
6206	Molecular insights into information processing and developmental and immune regulation of Eriocheir sinensis megalopa under hyposaline stress. Genomics, 2020, 112, 4647-4656.	1.3	3
6207	Comparative transcriptome analysis provides insight into regulation pathways and temporal and spatial expression characteristics of grapevine (Vitis vinifera) dormant buds in different nodes. BMC Plant Biology, 2020, 20, 390.	1.6	13
6208	An orphan protein of Fusarium graminearum modulates host immunity by mediating proteasomal degradation of TaSnRK1Î±. Nature Communications, 2020, 11, 4382.	5.8	92
6209	A 3K Axiom SNP array from a transcriptome-wide SNP resource sheds new light on the genetic diversity and structure of the iconic subtropical conifer tree Araucaria angustifolia (Bert.) Kuntze. PLoS ONE, 2020, 15, e0230404.	1.1	7

#	ARTICLE	IF	CITATIONS
6210	Proteomic and Transcriptomic Analyses Indicate Metabolic Changes and Reduced Defense Responses in Mycorrhizal Roots of Oeceoclades maculata (Orchidaceae) Collected in Nature. Journal of Fungi (Basel, Switzerland), 2020, 6, 148.	1.5	13
6211	Genome- wide structural and functional variant discovery of rice landraces using genotyping by sequencing. Molecular Biology Reports, 2020, 47, 7391-7402.	1.0	11
6212	Development of SSR markers and association studies of markers with phenology and yield-related traits in grass pea (Lathyrus sativus). Crop and Pasture Science, 2020, 71, 768.	0.7	6
6213	A Novel Mycovirus Evokes Transcriptional Rewiring in the Fungus <i>Malassezia</i> and Stimulates Beta Interferon Production in Macrophages. MBio, 2020, 11, .	1.8	30
6214	Skin transcriptome, tissue distribution of mucin genes and discovery of simple sequence repeats in crucian carp (<scp><i>Carassius auratus</i>)</scp>. Journal of Fish Biology, 2020, 97, 1542-1553.	0.7	8
6215	De novo transcriptome sequencing of Rhododendron molle and identification of genes involved in the biosynthesis of secondary metabolites. BMC Plant Biology, 2020, 20, 414.	1.6	9
6216	Legionella pneumophila Infection Rewires the Acanthamoeba castellanii Transcriptome, Highlighting a Class of Sirtuin Genes. Frontiers in Cellular and Infection Microbiology, 2020, 10, 428.	1.8	13
6217	Elucidating the Genetic Architecture of Fiber Quality in Hemp (Cannabis sativa L.) Using a Genome-Wide Association Study. Frontiers in Genetics, 2020, 11, 566314.	1.1	17
6218	The Molecular Machinery of Gametogenesis in<i>Geodia</i>Demosponges (Porifera): Evolutionary Origins of a Conserved Toolkit across Animals. Molecular Biology and Evolution, 2020, 37, 3485-3506.	3.5	19
6219	ABA-regulated ploidy-related genes and non-structural carbon accumulation may underlie cold tolerance in tetraploid Fragaria moupinensis. Environmental and Experimental Botany, 2020, 179, 104232.	2.0	12
6220	Genomeâ€•wide identification and characterization of long nonâ€•coding RNAs in <i>Tribolium castaneum</i>. Insect Science, 2021, 28, 1262-1276.	1.5	16
6221	SMRT- and Illumina-based RNA-seq analyses unveil the ginsinoside biosynthesis and transcriptomic complexity in Panax notoginseng. Scientific Reports, 2020, 10, 15310.	1.6	10
6222	Molecular study of drought response in the Mediterranean conifer <i>Pinus pinaster</i> Ait.: Differential transcriptomic profiling reveals constitutive water deficitâ€•independent drought tolerance mechanisms. Ecology and Evolution, 2020, 10, 9788-9807.	0.8	19
6223	Comparative de novo transcriptome analysis of barley varieties with different malting qualities. Functional and Integrative Genomics, 2020, 20, 801-812.	1.4	4
6224	Hepatopancreas immune response during molt cycle in the mud crab, Scylla paramamosain. Scientific Reports, 2020, 10, 13102.	1.6	23
6225	Twentieth-century emergence of antimicrobial resistant human- and bovine-associated Salmonella enterica serotype Typhimurium lineages in New York State. Scientific Reports, 2020, 10, 14428.	1.6	10
6226	A carotenoid-deficient mutant of the plant-associated microbe Pantoea sp. YR343 displays an altered membrane proteome. Scientific Reports, 2020, 10, 14985.	1.6	6
6227	PacBio Long-Read Sequencing Transcriptome Dataset of Adult Harmonia axyridis Under Diapause Inducing and Reproductive Inducing Photoperiod. Frontiers in Genetics, 2020, 11, 1010.	1.1	3

#	Article	IF	Citations
6228	Toxicological and molecular profiling of insecticide resistance in a Brazilian strain of fall armyworm resistant to Bt Cry1 proteins. Pest Management Science, 2021, 77, 3713-3726.	1.7	29
6229	Necrotrophic lifestyle of Rhizoctonia solani AG3-PT during interaction with its host plant potato as revealed by transcriptome analysis. Scientific Reports, 2020, 10, 12574.	1.6	21
6230	An outbreak of visceral white nodules disease caused by <i>Pseudomonas plecoglossicida</i> at a water temperature of 12Â°C in cultured large yellow croaker (<i>Larimichthys crocea</i>) in China. Journal of Fish Diseases, 2020, 43, 1353-1361.	0.9	52
6231	Transcriptome analysis and comparison reveal divergence between the Mediterranean and the greenhouse whiteflies. PLoS ONE, 2020, 15, e0237744.	1.1	2
6232	The Regulatory Network of CMPG1-V in Wheatâ€“Blumeria graminis f. sp. tritici Interaction Revealed by Temporal Profiling Using RNA-Seq. International Journal of Molecular Sciences, 2020, 21, 5967.	1.8	6
6233	Deep Sequencing of Small RNAs in the Whitefly Bemisia tabaci Reveals Novel MicroRNAs Potentially Associated with Begomovirus Acquisition and Transmission. Insects, 2020, 11, 562.	1.0	4
6234	Infectivity and genes differentially expressed between young and aging theront cells of the marine fish parasite Cryptocaryon irritans. PLoS ONE, 2020, 15, e0238167.	1.1	7
6235	A mini foxtail millet with an Arabidopsis-like life cycle as a C4 model system. Nature Plants, 2020, 6, 1167-1178.	4.7	111
6236	Characterization and analysis of full-length transcriptomes from two grasshoppers, Gomphocerus licenti and Mongolotettix japonicus. Scientific Reports, 2020, 10, 14228.	1.6	5
6237	Insecticidal and synergistic activity of dsRNAs targeting buprofezinâ€specific genes against the small brown planthopper, <i>Laodelphax striatellus</i>. Archives of Insect Biochemistry and Physiology, 2020, 105, e21739.	0.6	5
6238	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. MBio, 2020, 11, .	1.8	19
6239	Multiple Known Mechanisms and a Possible Role of an Enhanced Immune System in Bt-Resistance in a Field Population of the Bollworm, Helicoverpa zea: Differences in Gene Expression with RNAseq. International Journal of Molecular Sciences, 2020, 21, 6528.	1.8	14
6240	Multi-model seascape genomics identifies distinct environmental drivers of selection among sympatric marine species. BMC Evolutionary Biology, 2020, 20, 121.	3.2	11
6241	Transcriptomic Analysis of the Kuruma Prawn Marsupenaeus japonicus Reveals Possible Peripheral Regulation of the Ovary. Frontiers in Endocrinology, 2020, 11, 541.	1.5	13
6242	Characterization of the leaf rust responsive ARF genes in wheat (Triticum aestivum L.). Plant Cell Reports, 2020, 39, 1639-1654.	2.8	8
6243	The Use of Bioinformatic Tools in Symbiosis and Co-Evolution Studies. , 0, , .		1
6244	Combined Proteome and Transcriptome Analysis of Heat-Primed Azalea Reveals New Insights Into Plant Heat Acclimation Memory. Frontiers in Plant Science, 2020, 11, 1278.	1.7	18
6245	Cold Plasma Treatment of Sunflower Seeds Modulates Plant-Associated Microbiome and Stimulates Root and Lateral Organ Growth. Frontiers in Plant Science, 2020, 11, 568924.	1.7	20

#	Article	IF	Citations
6246	Identification and Expression Profile Analysis of Chemosensory Genes From the Antennal Transcriptome of Bamboo Locust (Ceracris kiangsu). Frontiers in Physiology, 2020, 11, 889.	1.3	5
6247	Time-series transcriptomic analysis reveals novel gene modules that control theanine biosynthesis in tea plant (Camellia sinensis). PLoS ONE, 2020, 15, e0238175.	1.1	2
6248	De novo sequencing, assembly and functional annotation of Armillaria borealis genome. BMC Genomics, 2020, 21, 534.	1.2	7
6249	Molecular Remodeling in Populus PdKOR RNAi Roots Profiled Using LCâ€MS/MS Proteomics. Proteomics, 2020, 20, 2000067.	1.3	0
6250	De novo assembly of transcriptome dataset from leaves of Dryobalanops aromatica (Syn.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 Td 2020, 13, 405.	0.6	3
6251	Transcriptome profiling revealed potentially important roles of defensive gene expression in the divergence of insect biotypes: a case study with the cereal aphid Sitobion avenae. BMC Genomics, 2020, 21, 546.	1.2	6
6252	Applications of Proteomic Tools to Study Insect Vectorâ€"Plant Virus Interactions. Life, 2020, 10, 143.	1.1	5
6253	Transcriptome sequencing of Coccinella septempunctata adults (Coleoptera: Coccinellidae) feeding on artificial diet and Aphis craccivora. PLoS ONE, 2020, 15, e0236249.	1.1	5
6254	2-Methoxy-1,4-naphthoquinone Induces Metabolic Shifts in <i>Penicillium Digitatum</i> Revealed by High-Dimensional Biological Data. Journal of Agricultural and Food Chemistry, 2020, 68, 9697-9706.	2.4	20
6255	Molecular insights into biochar-mediated plant growth promotion and systemic resistance in tomato against Fusarium crown and root rot disease. Scientific Reports, 2020, 10, 13934.	1.6	63
6256	De novo transcriptome assembly, functional annotation, and expression profiling of rye (Secale) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	1.6	16
6257	Genomic and transcriptomic insights into Raffaelea lauricola pathogenesis. BMC Genomics, 2020, 21, 570.	1.2	6
6258	The Teleost Thymus in Health and Disease: New Insights from Transcriptomic and Histopathological Analyses of Turbot, Scophthalmus maximus. Biology, 2020, 9, 221.	1.3	10
6259	Genes Modulating the Increase in Sexuality in the Facultative Diplosporous Grass Eragrostis curvula under Water Stress Conditions. Genes, 2020, 11, 969.	1.0	13
6260	Multi-level analysis of reproduction in an Antarctic midge identifies female and male accessory gland products that are altered by larval stress and impact progeny viability. Scientific Reports, 2020, 10, 19791.	1.6	18
6261	Transcriptome analysis identified the mechanism of synergy between sethoxydim herbicide and a mycoherbicide on green foxtail. Scientific Reports, 2020, 10, 21690.	1.6	3
6262	Evolutionary divergence of novel open reading frames in cichlids speciation. Scientific Reports, 2020, 10, 21570.	1.6	5
6263	Comparative Genome Analyses of 18 Verticillium dahliae Tomato Isolates Reveals Phylogenetic and Race Specific Signatures. Frontiers in Microbiology, 2020, 11, 573755.	1.5	13

#	ARTICLE	IF	CITATIONS
6264	Comparative transcriptomics indicates endogenous differences in detoxification capacity after formic acid treatment between honey bees and varroa mites. Scientific Reports, 2020, 10, 21943.	1.6	9
6265	Identification of Differentially Expressed Drought-Responsive Genes in Guar [Cyamopsis tetragonoloba (L.) Taub]. International Journal of Genomics, 2020, 2020, 1-16.	0.8	3
6266	Comparative transcriptome analysis of scaled and scaleless skins in Gymnocypris eckloni provides insights into the molecular mechanism of scale degeneration. BMC Genomics, 2020, 21, 835.	1.2	1
6267	First Draft Genome Assembly of the Malaysian Stingless Bee, Heterotrigona itama (Apidae, Meliponinae). Data, 2020, 5, 112.	1.2	0
6268	Identification and Analysis of MicroRNAs Associated with Wing Polyphenism in the Brown Planthopper, Nilaparvata lugens. International Journal of Molecular Sciences, 2020, 21, 9754.	1.8	8
6269	Transcriptomic analysis of the ark shell Scapharca kagoshimensis: De novo assembly and identification of genes and pathways involved growth. Aquaculture Reports, 2020, 18, 100522.	0.7	5
6270	Immunogenetic and tolerance strategies against a novel parasitoid of wild field crickets. Ecology and Evolution, 2020, 10, 13312-13326.	0.8	0
6271	Integrated transcriptome and proteome analysis provides insight into chilling-induced dormancy breaking in Chimonanthus praecox. Horticulture Research, 2020, 7, 198.	2.9	24
6272	A chromosome-scale reference genome of Lobularia maritima, an ornamental plant with high stress tolerance. Horticulture Research, 2020, 7, 197.	2.9	6
6273	Genome sequencing and phylogenetic analysis of allotetraploid Salix matsudana Koidz. Horticulture Research, 2020, 7, 201.	2.9	30
6274	An insight to flux-balance analysis for biochemical networks. Biotechnology and Genetic Engineering Reviews, 2020, 36, 32-55.	2.4	16
6275	Comparative transcriptomic analysis of antimony resistant and susceptible Leishmania infantum lines. Parasites and Vectors, 2020, 13, 600.	1.0	22
6276	Integrated Physiological and Transcriptomic Analyses Reveal a Regulatory Network of Anthocyanin Metabolism Contributing to the Ornamental Value in a Novel Hybrid Cultivar of Camellia japonica. Plants, 2020, 9, 1724.	1.6	8
6277	Melon short internode (CmSi) encodes an ERECTA-like receptor kinase regulating stem elongation through auxin signaling. Horticulture Research, 2020, 7, 202.	2.9	14
6278	Genome-Wide Identification of the Vacuolar H+-ATPase Gene Family in Five Rosaceae Species and Expression Analysis in Pear (Pyrus bretschneideri). Plants, 2020, 9, 1661.	1.6	3
6279	â€œIntegrative genomic analysis of the bioprospection of regulators and accessory enzymes associated with cellulose degradation in a filamentous fungus (Trichoderma harzianum)â€. BMC Genomics, 2020, 21, 757.	1.2	5
6280	Transcriptome Analysis Reveals Functional Diversity in Salivary Glands of Plant Virus Vector, Graminella nigrifrons. Genes, 2020, 11, 1289.	1.0	4
6281	Transcriptome analysis for molecular landscaping of genes controlling diterpene andrographolide biosynthesis in Andrographis paniculata (Burm. f.) Nees. 3 Biotech, 2020, 10, 512.	1.1	7

#	ARTICLE	IF	CITATIONS
6282	Short De-Etiolation Increases the Rooting of VC801 Avocado Rootstock. Plants, 2020, 9, 1481.	1.6	7
6283	Gene Sequences of Potential Targets of Insecticidal PF2 Lectin Identified from the Larval De Novo Transcriptome of the Mexican Bean Weevil (Zabrotes Subfasciatus; Boheman 1833). Insects, 2020, 11, 736.	1.0	3
6284	Contrasting Immunomodulatory Effects of Probiotic and Pathogenic Bacteria on Eastern Oyster, Crassostrea Virginica, Larvae. Vaccines, 2020, 8, 588.	2.1	20
6285	Interactions between the Parasite Philasterides dicentrarchi and the Immune System of the Turbot Scophthalmus maximus. A Transcriptomic Analysis. Biology, 2020, 9, 337.	1.3	9
6286	Genomic analysis of polycarpellary rice (Oryza sativa L.) through whole genome resequencing. Journal of Plant Biochemistry and Biotechnology, 2020, 30, 364.	0.9	2
6287	The genetic adaptations of fall armyworm <i>Spodoptera frugiperda</i> facilitated its rapid global dispersal and invasion. Molecular Ecology Resources, 2020, 20, 1050-1068.	2.2	88
6288	Draft Genome Sequence of Psychrotolerant <i>Clostridium</i> sp. Strain M14, Isolated from Spoiled Uncooked Venison. Microbiology Resource Announcements, 2020, 9, .	0.3	3
6289	Candidate resistance genes selection and transcriptome analysis for the early responses to Plasmopara viticola infection in grape cultivars. Journal of Plant Pathology, 2020, 102, 857-869.	0.6	6
6290	Stress-induced expression is enriched for evolutionarily young genes in diverse budding yeasts. Nature Communications, 2020, 11, 2144.	5.8	24
6291	Transcriptome profile analysis of two Vicia faba cultivars with contrasting salinity tolerance during seed germination. Scientific Reports, 2020, 10, 7250.	1.6	23
6292	Transcriptomic analysis of sea star development through metamorphosis to the highly derived pentameral body plan with a focus on neural transcription factors. DNA Research, 2020, 27, .	1.5	11
6293	Sequencing and Functional Annotation of the Whole Genome of Shiraia bambusicola. G3: Genes, Genomes, Genetics, 2020, 10, 23-35.	0.8	8
6294	Genetic Architecture of Early Vigor Traits in Wild Soybean. International Journal of Molecular Sciences, 2020, 21, 3105.	1.8	3
6295	Improving Gene Annotation of the Peanut Genome by Integrated Proteogenomics Workflow. Journal of Proteome Research, 2020, 19, 2226-2235.	1.8	7
6296	iTRAQ-based proteomic analysis reveals several key metabolic pathways associated with male sterility in <i>Salvia miltiorrhiza</i>. RSC Advances, 2020, 10, 16959-16970.	1.7	4
6297	Metabolic and transcriptomic analysis of two Cucurbita moschata germplasms throughout fruit development. BMC Genomics, 2020, 21, 365.	1.2	24
6298	Transcriptomic profiling of purple broccoli reveals light-induced anthocyanin biosynthetic signaling and structural genes. PeerJ, 2020, 8, e8870.	0.9	19
6299	Histopathological examination and transcriptome analyses to assess the acute toxic effects of arsenite exposure on rare minnows (Gobiocypris rarus). Ecotoxicology, 2020, 29, 613-624.	1.1	2

#	Article	IF	Citations
6300	Genome data of shrimp acute hepatopancreatic necrosis disease causative Vibrio parahaemolyticus strains isolated from South Korea aquaculture farms. Data in Brief, 2020, 31, 105697.	0.5	2
6301	High confidence copy number variants identified in Holstein dairy cattle from whole genome sequence and genotype array data. Scientific Reports, 2020, 10, 8044.	1.6	16
6302	Characterization of Gene Isoforms Related to Cellulose and Lignin Biosynthesis in Kenaf (Hibiscus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	3
6303	Variation among 532 genomes unveils the origin and evolutionary history of a global insect herbivore. Nature Communications, 2020, 11, 2321.	5.8	47
6304	Comparative transcriptome analysis reveals the responses of winter rye to cold stress. Acta Physiologiae Plantarum, 2020, 42, 1.	1.0	5
6305	Proteome Analysis of Hordein-Null Barley Lines Reveals Storage Protein Synthesis and Compensation Mechanisms. Journal of Agricultural and Food Chemistry, 2020, 68, 5763-5775.	2.4	13
6306	Structural venomics reveals evolution of a complex venom by duplication and diversification of an ancient peptide-encoding gene. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11399-11408.	3.3	59
6307	<p>Discovery of Potential Plasma Biomarkers for Tuberculosis in HIV-Infected Patients by Data-Independent Acquisition-Based Quantitative Proteomics</p>. Infection and Drug Resistance, 2020, Volume 13, 1185-1196.	1.1	4
6308	De novo Assembly and Genome-Wide SNP Discovery in Rohu Carp, Labeo rohita. Frontiers in Genetics, 2020, 11, 386.	1.1	17
6309	Morpho-Anatomical and Molecular Characterization of the Oversprouting Symptoms Caused by Fusarium decemcellulare in Guarana Plants (Paullinia cupana var. sorbilis). Tropical Plant Biology, 2020, 13, 274-286.	1.0	1
6310	Draft Genome of the Liver Fluke <i>Fasciola gigantica</i>. ACS Omega, 2020, 5, 11084-11091.	1.6	25
6311	Transcriptome profiling of spike provides expression features of genes related to terpene biosynthesis in lavender. Scientific Reports, 2020, 10, 6933.	1.6	9
6312	Chromosomeâ€level genome assembly of the greenfin horseâ€faced filefish (<i>Thamnaconus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 26 Ecology Resources, 2020, 20, 1069-1079.	2.2	27
6313	Analyses of chemosensory genes provide insight into the evolution of behavioral differences to phytochemicals in Bactrocera species. Molecular Phylogenetics and Evolution, 2020, 151, 106858.	1.2	12
6314	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. G3: Genes, Genomes, Genetics, 2020, 10, 2275-2296.	0.8	33
6315	Effect of Praziquantel on Schistosoma mekongi Proteome and Phosphoproteome. Pathogens, 2020, 9, 417.	1.2	7
6316	Proteomic studies of plant and bacteria interactions during benzene remediation. Journal of Environmental Sciences, 2020, 94, 161-170.	3.2	7
6317	Transcriptome characterization and gene expression analysis related to immune response in Gynaephora qinghaiensis pupae. Journal of Asia-Pacific Entomology, 2020, 23, 458-469.	0.4	5

#	ARTICLE	IF	CITATIONS
6318	Effects of dihydro-epi-deoxyarteannuin B on artemisinin biosynthesis, transcriptional profile and associated gene expression in suspension-cultured cells of Artemisia annua. Biochemical Engineering Journal, 2020, 160, 107633.	1.8	1
6319	Small RNA and Transcriptome Sequencing Reveals miRNA Regulation of Floral Thermogenesis in Nelumbo nucifera. International Journal of Molecular Sciences, 2020, 21, 3324.	1.8	9
6320	Changes in gene expression during female reproductive development in a color polymorphic insect. Evolution; International Journal of Organic Evolution, 2020, 74, 1063-1081.	1.1	13
6321	Genome-wide identification and analysis of long noncoding RNAs (lncRNAs) during seed development in peanut (Arachis hypogaea L.). BMC Plant Biology, 2020, 20, 192.	1.6	28
6322	Protein phosphorylation networks in spargana of Spirometra erinaceieuropaei revealed by phosphoproteomic analysis. Parasites and Vectors, 2020, 13, 248.	1.0	8
6323	De novo transcriptome sequence of Senna tora provides insights into anthraquinone biosynthesis. PLoS ONE, 2020, 15, e0225564.	1.1	14
6324	Systematic Identification and Analysis of Light-Responsive Circular RNA and Co-expression Networks in Lettuce (Lactuca sativa). G3: Genes, Genomes, Genetics, 2020, 10, 2397-2410.	0.8	6
6325	Transcriptome Sequencing and Differential Expression Analysis Reveal Molecular Mechanisms for Starch Accumulation in Chestnut. Forests, 2020, 11, 388.	0.9	5
6326	Endosulfan exposure alters transcription of genes involved in the detoxification and stress responses in Physella acuta. Scientific Reports, 2020, 10, 7847.	1.6	9
6327	Phylogenomic incongruence in Ceratocystis: a clue to speciation?. BMC Genomics, 2020, 21, 362.	1.2	11
6328	Integrated miRNAome and Transcriptome Analysis Reveals Argonaute 2-Mediated Defense Responses Against the Devastating Phytopathogen Sclerotinia sclerotiorum. Frontiers in Plant Science, 2020, 11, 500.	1.7	6
6329	Gene Expression Pattern in Olive Tree Organs (Olea europaea L.). Genes, 2020, 11, 544.	1.0	14
6330	Transcriptome analysis of grass carp (Ctenopharyngodon idella) between fast- and slow-growing fish. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 35, 100688.	0.4	27
6331	Peeling back the layers of crassulacean acid metabolism: functional differentiation between <i>KalanchoÃ« fedtschenkoi</i> epidermis and mesophyll proteomes. Plant Journal, 2020, 103, 869-888.	2.8	11
6332	Genome mining of the citrus pathogen ElsinoÃ« fawcettii; prediction and prioritisation of candidate effectors, cell wall degrading enzymes and secondary metabolite gene clusters. PLoS ONE, 2020, 15, e0227396.	1.1	9
6333	Transcriptome and metabolome integration analysis of mud crab Scylla paramamosain challenged to Vibrio parahaemolyticus infection. Fish and Shellfish Immunology, 2020, 103, 430-437.	1.6	13
6334	Comparative Transcriptome Analysis between Cytoplasmic Male-sterile Line and Its Maintainer During the Floral Bud Development of Pepper. Horticultural Plant Journal, 2020, 6, 89-98.	2.3	17
6335	Seasonal variation in physiology and shell condition of the pteropod Limacina retroversa in the Gulf of Maine relative to life cycle and carbonate chemistry. Progress in Oceanography, 2020, 186, 102371.	1.5	10

#	ARTICLE	IF	CITATIONS
6336	Genetic basis for virulence differences of various Cryptosporidium parvum carcinogenic isolates. Scientific Reports, 2020, 10, 7316.	1.6	10
6337	Transcriptomic evidence that insulin signalling pathway regulates the ageing of subterranean termite castes. Scientific Reports, 2020, 10, 8187.	1.6	14
6338	A Clone Resource of <i>Magnaporthe oryzae</i> Effectors That Share Sequence and Structural Similarities Across Host-Specific Lineages. Molecular Plant-Microbe Interactions, 2020, 33, 1032-1035.	1.4	20
6339	The N¹-Methyladenosine Methylome of Petunia mRNA. Plant Physiology, 2020, 183, 1710-1724.	2.3	31
6340	Comprehensive analysis of the secreted proteome of adult Necator americanusÂhookworms. PLoS Neglected Tropical Diseases, 2020, 14, e0008237.	1.3	25
6341	Aromatic Cytokinin Arabinosides Promote PAMP-like Responses and Positively Regulate Leaf Longevity. ACS Chemical Biology, 2020, 15, 1949-1963.	1.6	22
6342	Identification of putative olfactory genes in newly hatched larvae of a Coleopteran ectoparasitoid Dastarcus helophoroides (Fairmaire) (Coleoptera: Bothrideridae) by transcriptome analysis. Entomological Research, 2020, 50, 329-342.	0.6	5
6343	Historical demography and climate driven distributional changes in a widespread Neotropical freshwater species with high economic importance. Ecography, 2020, 43, 1291-1304.	2.1	10
6344	Physiological and genome-wide RNA-sequencing analyses identify candidate genes in a nitrogen-use efficient potato cv. Kufri Gaurav. Plant Physiology and Biochemistry, 2020, 154, 171-183.	2.8	23
6345	Insights of Bipolaris sorokiniana secretome - an in silico approach. Biologia (Poland), 2020, 75, 2367-2381.	0.8	4
6346	Gill Transcriptome Sequencing and De Novo Annotation of Acanthogobius ommaturus in Response to Salinity Stress. Genes, 2020, 11, 631.	1.0	16
6347	Genome scan detection of selective sweeps among biotypes of the soybean aphid, Aphis glycines, with differing virulence to resistance to A. glycines (Rag) traits in soybean, Glycine max. Insect Biochemistry and Molecular Biology, 2020, 124, 103364.	1.2	6
6348	Transcriptome Profiling of Haloxylon persicum (Bunge ex Boiss and Buhse) an Endangered Plant Species under PEG-Induced Drought Stress. Genes, 2020, 11, 640.	1.0	8
6349	NetMet: A Network-Based Tool for Predicting Metabolic Capacities of Microbial Species and their Interactions. Microorganisms, 2020, 8, 840.	1.6	13
6350	Identification of Functional SSR Markers in Freshwater Ornamental Shrimps Neocaridina denticulata Using Transcriptome Sequencing. Marine Biotechnology, 2020, 22, 772-785.	1.1	15
6351	Transcriptome profiling of the flowering transition in saffron (Crocus sativus L.). Scientific Reports, 2020, 10, 9680.	1.6	28
6352	Nonâ€homologyâ€based prediction of gene functions in maize (Zea mays ssp. mays). Plant Genome, 2020, 13, e20015.	1.6	7
6353	Novel Benedenia disease resistance QTLs in five F1 families of yellowtail (Seriola quinqueradiata). Aquaculture, 2020, 529, 735622.	1.7	5

#	Article	IF	Citations
6354	DNA Methylation and Demethylation Are Regulated by Functional DNA Methyltransferases and DnTET Enzymes in Diuraphis noxia. Frontiers in Genetics, 2020, 11, 452.	1.1	11
6355	Inducible aging in Hydra oligactis implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. GeroScience, 2020, 42, 1119-1132.	2.1	13
6356	HGT in the human and skin commensal <i>Malassezia</i> : A bacterially derived flavohemoglobin is required for NO resistance and host interaction. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15884-15894.	3.3	37
6357	Novel partiti-like viruses are conditional mutualistic symbionts in their normal lepidopteran host, African armyworm, but parasitic in a novel host, Fall armyworm. PLoS Pathogens, 2020, 16, e1008467.	2.1	34
6358	Wheat Encodes Small, Secreted Proteins That Contribute to Resistance to Septoria Tritici Blotch. Frontiers in Genetics, 2020, 11, 469.	1.1	11
6359	Monogalactosyldiacylglycerol and Sulfolipid Synthesis in Microalgae. Marine Drugs, 2020, 18, 237.	2.2	27
6360	Comparative transcriptome analysis of MeJA-responsive AP2/ERF transcription factors involved in notoginsenosides biosynthesis. 3 Biotech, 2020, 10, 290.	1.1	8
6361	Transcriptome Analysis by RNAâ€“Seq Reveals Genes Related to Plant Height in Two Sets of Parent-hybrid Combinations in Easter lily (Lilium longiflorum). Scientific Reports, 2020, 10, 9082.	1.6	19
6362	Revealing biomass heterosis in the allodiploid xBrassicoraphanus, a hybrid between Brassica rapa and Raphanus sativus, through integrated transcriptome and metabolites analysis. BMC Plant Biology, 2020, 20, 252.	1.6	13
6363	Transcriptome analysis of heat stress response genes in potato leaves. Molecular Biology Reports, 2020, 47, 4311-4321.	1.0	26
6364	Transcriptome Analysis Reveals Potential Genes Involved in Digestive Enzyme Function in a Mudflat Crab Helice tientsinensis. Thalassas, 2020, 36, 573-583.	0.1	1
6365	Molecular and Physiological Alterations in Chickpea under Elevated CO2 Concentrations. Plant and Cell Physiology, 2020, 61, 1449-1463.	1.5	15
6366	Transcriptome Analysis of Maternal Gene Transcripts in Unfertilized Eggs of Misgurnus anguillicaudatus and Identification of Immune-Related Maternal Genes. International Journal of Molecular Sciences, 2020, 21, 3872.	1.8	4
6367	Transcriptome sequencing reveals signatures of positive selection in the Spot-Tailed Earless Lizard. PLoS ONE, 2020, 15, e0234504.	1.1	5
6368	Acute and chronic effects of polystyrene microplastics on brine shrimp: First evidence highlighting the molecular mechanism through transcriptome analysis. Journal of Hazardous Materials, 2020, 400, 123220.	6.5	100
6369	Full-length transcript sequencing accelerates the transcriptome research of Gymnocypris namensis, an iconic fish of the Tibetan Plateau. Scientific Reports, 2020, 10, 9668.	1.6	12
6370	Increased density of endosymbiotic Buchnera related to pesticide resistance in yellow morph of melon aphid. Journal of Pest Science, 2020, 93, 1281-1294.	1.9	17
6371	Transcriptome analysis of crude oil degrading Pseudomonas aeruginosa strains for identification of potential genes involved in crude oil degradation. Gene, 2020, 755, 144909.	1.0	21

#	Article	IF	Citations
6372	A chromosomeâ€level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i>. Molecular Ecology Resources, 2020, 20, 1384-1402.	2.2	35
6373	Evolutionary Patterns of Sex-Biased Genes in Three Species of Haplodiploid Insects. Insects, 2020, 11, 326.	1.0	1
6374	Temporospatial modulation of <i>Lymantria dispar</i> immune system against an entomopathogenic fungal infection. Pest Management Science, 2020, 76, 3982-3989.	1.7	13
6375	Development of a Large Gene-Associated SSR Marker Set and in-Depth Genetic Characterization in Scarlet Sage. Frontiers in Genetics, 2020, 11, 504.	1.1	4
6376	Development of EST-SSR markers and their application in the analysis of the genetic diversity of Sophora japonica Linn. Trees - Structure and Function, 2020, 34, 1147-1156.	0.9	5
6377	RNA-seq analysis reveals divergent adaptive response to hyper- and hypo-salinity in cobia, Rachycentron canadum. Fish Physiology and Biochemistry, 2020, 46, 1713-1727.	0.9	16
6378	Comparative transcriptomics reveal insights into the drought response of the three Panicum species P. bisulcatum, P. laetum and P. turgidum. Plant Gene, 2020, 23, 100232.	1.4	1
6379	Comparative transcriptomic analysis of fireflies (Coleoptera: Lampyridae) to explore the molecular adaptations to fresh water. Molecular Ecology, 2020, 29, 2676-2691.	2.0	17
6380	iTRAQ-Based Comparative Proteomic Analysis of Larval Midgut From the Beet Armyworm, Spodoptera exigua (HÃ¼bner) (Lepidoptera: Noctuidae) Challenged With the Entomopathogenic Bacteria Serratia marcescens. Frontiers in Physiology, 2020, 11, 442.	1.3	13
6381	Profiling and Functional Analysis of Circular RNAs in Porcine Fast and Slow Muscles. Frontiers in Cell and Developmental Biology, 2020, 8, 322.	1.8	24
6382	iTRAQ-Based Proteomic Profile Analysis of the Hepatopancreas of Caribbean Spiny Lobsters Infected With Panulirus argus Virus 1: Metabolic and Physiological Implications. Frontiers in Microbiology, 2020, 11, 1084.	1.5	6
6383	Transcriptome analysis of the brain provides insights into the regulatory mechanism for Coilia nasus migration. BMC Genomics, 2020, 21, 410.	1.2	6
6384	Characterization and Analysis of the Full-Length Transcriptomes of Multiple Organs in Pseudotaxus chienii (W.C.Cheng) W.C.Cheng. International Journal of Molecular Sciences, 2020, 21, 4305.	1.8	4
6385	Transcriptomic analysis of resistant and susceptible cabbage lines reveals differential expressions and candidate genes involved in cabbage early responses to black rot. 3 Biotech, 2020, 10, 308.	1.1	7
6386	Draft genomic sequence of Armillaria gallica 012m: insights into its symbiotic relationship with Gastrodia elata. Brazilian Journal of Microbiology, 2020, 51, 1539-1552.	0.8	21
6387	Genomic signatures of domestication in Old World camels. Communications Biology, 2020, 3, 316.	2.0	32
6388	Representational Difference Analysis of Transcripts Involved in Jervine Biosynthesis. Life, 2020, 10, 88.	1.1	7
6389	Root transcriptome reveals efficient cell signaling and energy conservation key to aluminum toxicity tolerance in acidic soil adapted rice genotype. Scientific Reports, 2020, 10, 4580.	1.6	16

#	ARTICLE	IF	CITATIONS
6390	Genome-wide identification and expression analysis of WRKY transcription factors in pearl millet (Pennisetum glaucum) under dehydration and salinity stress. BMC Genomics, 2020, 21, 231.	1.2	56
6391	Identification and Sequence-Based Validation of the EST-SSR Markers from Calotropis procera. Plant Molecular Biology Reporter, 2020, 38, 430-440.	1.0	0
6392	The ankyrin repeat gene family in Capsicum spp: Genome-wide survey, characterization and gene expression profile. Scientific Reports, 2020, 10, 4044.	1.6	33
6393	Structural variation, functional differentiation and expression characteristics of the AP2/ERF gene family and its response to cold stress and methyl jasmonate in Panax ginsengÂC.A. Meyer. PLoS ONE, 2020, 15, e0226055.	1.1	30
6394	Distinct epigenomic and transcriptomic modifications associated with Wolbachia-mediated asexuality. PLoS Pathogens, 2020, 16, e1008397.	2.1	18
6395	Sexual-biased gene expression of olfactory-related genes in the antennae of Conogethes pinicolalis (Lepidoptera: Crambidae). BMC Genomics, 2020, 21, 244.	1.2	12
6396	On the Trail of Tetu1: Genome-Wide Discovery of CACTA Transposable Elements in Sunflower Genome. International Journal of Molecular Sciences, 2020, 21, 2021.	1.8	4
6397	Moniliophthora perniciosa development: key genes involved in stress-mediated cell wall organization and autophagy. International Journal of Biological Macromolecules, 2020, 154, 1022-1035.	3.6	8
6398	Toward a chimeric vaccine against multiple isolates of Mycobacteroides - An integrative approach. Life Sciences, 2020, 250, 117541.	2.0	11
6399	Gene expression in the smut fungus Ustilago esculenta governs swollen gall metamorphosis in Zizania latifolia. Microbial Pathogenesis, 2020, 143, 104107.	1.3	14
6400	Allopatric divergence and hybridization within <i>Cupressus chengiana</i> (Cupressaceae), a threatened conifer in the northern Hengduan Mountains of western China. Molecular Ecology, 2020, 29, 1250-1266.	2.0	46
6401	Phenotypic and Transcriptomic Response of the Grasshopper Oedaleus asiaticus (Orthoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.3	9
6402	Transcriptome-based identification of small RNA in plants: The need for robust prediction algorithms. , 2020, , 65-97.		0
6403	Transcriptome Analysis Identifies Two Ethylene Response Factors That Regulate Proanthocyanidin Biosynthesis During Malus Crabapple Fruit Development. Frontiers in Plant Science, 2020, 11, 76.	1.7	14
6404	De novo transcriptome of the diatom Cylindrotheca closterium identifies genes involved in the metabolism of anti-inflammatory compounds. Scientific Reports, 2020, 10, 4138.	1.6	22
6405	Î²â€Glucan is a major growth substrate for human gut bacteria related to <scp><i>Coprococcus eutactus</i></scp>. Environmental Microbiology, 2020, 22, 2150-2164.	1.8	22
6406	The draft genome of a new Verminephrobacter eiseniae strain: a nephridial symbiont of earthworms. Annals of Microbiology, 2020, 70, .	1.1	3
6407	The ghost of temperature past: interactive effects of previous and current thermal conditions on gene expression in Manduca sexta. Journal of Experimental Biology, 2020, 223, .	0.8	7

#	ARTICLE	IF	CITATIONS
6408	Evaluation of Whole-Genome Sequence, Genetic Diversity, and Agronomic Traits of Basmati Rice (Oryza) Tj ETQq0 0 0 rgBT /Overlock 10	1.1	14
6409	Quantitative Proteomics Identifies Metabolic Pathways Affected by Babesia Infection and Blood Feeding in the Sialoproteome of the Vector Rhipicephalus bursa. Vaccines, 2020, 8, 91.	2.1	7
6410	IPA-1 a Putative Chromatin Remodeler/Helicase-Related Protein of <i>Trichoderma virens</i> Plays Important Roles in Antibiosis Against <i>Rhizoctonia solani</i> and Induction of <i>Arabidopsis</i> Systemic Disease Resistance. Molecular Plant-Microbe Interactions, 2020, 33, 808-824.	1.4	10
6411	Exosomes Transmit Viral Genetic Information and Immune Signals may cause Immunosuppression and Immune Tolerance in ALV-J Infected HD11 cells. International Journal of Biological Sciences, 2020, 16, 904-920.	2.6	7
6413	Proteomic profiling of yellow catfish (Pelteobagrus fulvidraco) skin mucus identifies differentially-expressed proteins in response to Edwardsiella ictaluri infection. Fish and Shellfish Immunology, 2020, 100, 98-108.	1.6	26
6414	In silico mining and functional analysis of AP2/ERF gene in Withania somnifera. Scientific Reports, 2020, 10, 4877.	1.6	13
6415	Genome-Scale Identification, in Silico Characterization and Interaction Study Between Wheat SNARE and NPSN Gene Families Involved in Vesicular Transport. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2492-2501.	1.9	8
6416	Gene Expression Profiling Indicated Diverse Functions and Characteristics of Core Genes in Pea Aphid. Insects, 2020, 11, 186.	1.0	1
6417	FXR-mediated inhibition of autophagy contributes to FA-induced TG accumulation and accordingly reduces FA-induced lipotoxicity. Cell Communication and Signaling, 2020, 18, 47.	2.7	35
6418	Drosophila-associated bacteria differentially shape the nutritional requirements of their host during juvenile growth. PLoS Biology, 2020, 18, e3000681.	2.6	79
6419	Deep phosphoproteome analysis of Schistosoma mansoni leads development of a kinomic array that highlights sex-biased differences in adult worm protein phosphorylation. PLoS Neglected Tropical Diseases, 2020, 14, e0008115.	1.3	11
6420	Metaproteomics characterizes human gut microbiome function in colorectal cancer. Npj Biofilms and Microbiomes, 2020, 6, 14.	2.9	79
6421	Transcriptome Analysis of the Cytokinin Response in Medicago truncatula. Journal of Plant Biology, 2020, 63, 189-202.	0.9	2
6422	A Chromosome-Scale Assembly of the Asian Honeybee Apis cerana Genome. Frontiers in Genetics, 2020, 11, 279.	1.1	13
6423	New proposal of nitrogen metabolism regulation by small RNAs in the extreme halophilic archaeon Haloferax mediterranei. Molecular Genetics and Genomics, 2020, 295, 775-785.	1.0	7
6424	Comparative transcriptomics of toxin synthesis genes between the non-toxin producing dinoflagellate Cochlodinium polykrikoides and toxigenic Alexandrium pacificum. Harmful Algae, 2020, 93, 101777.	2.2	24
6425	Genome-wide identification of miRNAs and their targets during early somatic embryogenesis in Dimocarpus longan Lour.. Scientific Reports, 2020, 10, 4626.	1.6	26
6426	A single polyploidization event at the origin of the tetraploid genome of Coffea arabica is responsible for the extremely low genetic variation in wild and cultivated germplasm. Scientific Reports, 2020, 10, 4642.	1.6	86

#	Article	IF	Citations
6427	De novo transcriptome sequencing and analysis of the cuttlefish (<i>Sepiella japonica</i>) with different embryonic developmental stages. Animal Biotechnology, 2021, 32, 602-609.	0.7	3
6428	TeaMiD: a comprehensive database of simple sequence repeat markers of tea. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	19
6429	Hepatic transcriptome of the freeze-tolerant Copeâ€™s gray treefrog, Dryophytes chrysoscelis: responses to cold acclimation and freezing. BMC Genomics, 2020, 21, 226.	1.2	17
6430	Identification and Functional Study of Chitin Metabolism and Detoxification-Related Genes in Glyphodes pyloalis Walker (Lepidoptera: Pyralidae) Based on Transcriptome Analysis. International Journal of Molecular Sciences, 2020, 21, 1904.	1.8	14
6431	Loci associated with variation in gene expression and growth in juvenile salmon are influenced by the presence of a growth hormone transgene. BMC Genomics, 2020, 21, 185.	1.2	5
6432	Identification and characterization of circRNAs in the skin during wool follicle development in Aohan fine wool sheep. BMC Genomics, 2020, 21, 187.	1.2	30
6433	In silico evolution of Aspergillus niger organic acid production suggests strategies for switching acid output. Biotechnology for Biofuels, 2020, 13, 27.	6.2	14
6434	Genome-Wide Analysis of the DREB Subfamily in Saccharum spontaneum Reveals Their Functional Divergence During Cold and Drought Stresses. Frontiers in Genetics, 2019, 10, 1326.	1.1	28
6435	Constitutive and Cold Acclimation-Regulated Protein Expression Profiles of Scots Pine Seedlings Reveal Potential for Adaptive Capacity of Geographically Distant Populations. Forests, 2020, 11, 89.	0.9	4
6436	Novel Aspects on The Interaction Between Grapevine and Plasmopara viticola: Dual-RNA-Seq Analysis Highlights Gene Expression Dynamics in The Pathogen and The Plant During The Battle For Infection. Genes, 2020, 11, 261.	1.0	37
6437	The Estrogen-Responsive Transcriptome of Female Secondary Sexual Traits in the Gulf Pipefish. Journal of Heredity, 2020, 111, 294-306.	1.0	11
6438	Comparative Transcriptomics Analysis of the Responses of the Filamentous Fungus Glarea lozoyensis to Different Carbon Sources. Frontiers in Microbiology, 2020, 11, 190.	1.5	5
6439	A comprehensive non-redundant reference transcriptome for the Atlantic silverside Menidia menidia. Marine Genomics, 2020, 53, 100738.	0.4	6
6440	Genome-wide transcriptome and physiological analyses provide new insights into peanut drought response mechanisms. Scientific Reports, 2020, 10, 4071.	1.6	20
6441	Salivary proteins of Phloeomyzus passerinii, a plant-manipulating aphid, and their impact on early gene responses of susceptible and resistant poplar genotypes. Plant Science, 2020, 294, 110468.	1.7	5
6442	Analysis of the genes controlling three quantitative traits in three diverse plant species reveals the molecular basis of quantitative traits. Scientific Reports, 2020, 10, 10074.	1.6	37
6443	Genomic variation between PRSV resistant transgenic SunUp and its progenitor cultivar Sunset. BMC Genomics, 2020, 21, 398.	1.2	3
6444	Environmental Enrichment Improved Learning and Memory, Increased Telencephalic Cell Proliferation, and Induced Differential Gene Expression in Colossoma macropomum. Frontiers in Pharmacology, 2020, 11, 840.	1.6	11

#	Article	IF	Citations
6445	Comparative transcriptomics revealed differential regulation of defense related genes in Brassica juncea leading to successful and unsuccessful infestation by aphid species. Scientific Reports, 2020, 10, 10583.	1.6	14
6446	Characterization of the phenotypic and genotypic tolerance to abiotic stresses of natural populations of Heterorhabditis bacteriophora. Scientific Reports, 2020, 10, 10500.	1.6	16
6447	Comparative transcriptome analysis of a taxol-producing endophytic fungus, Aspergillus aculeatinus Tax-6, and its mutant strain. Scientific Reports, 2020, 10, 10558.	1.6	18
6448	Insecticidal Activity of Artemisia vulgaris Essential Oil and Transcriptome Analysis of Tribolium castaneum in Response to Oil Exposure. Frontiers in Genetics, 2020, 11, 589.	1.1	50
6449	Transcriptomic Analysis Reveals the Involvement of lncRNAâ€"miRNAâ€"mRNA Networks in Hair Follicle Induction in Aohan Fine Wool Sheep Skin. Frontiers in Genetics, 2020, 11, 590.	1.1	16
6450	Fulvic acid increases forage legume growth inducing preferential up-regulation of nodulation and signalling-related genes. Journal of Experimental Botany, 2020, 71, 5689-5704.	2.4	19
6451	Influence of genetic diversity of seventeen Beauveria bassiana isolates from different hosts on virulence by comparative genomics. BMC Genomics, 2020, 21, 451.	1.2	15
6452	Genomic analysis of the domestication and post-Spanish conquest evolution of the llama and alpaca. Genome Biology, 2020, 21, 159.	3.8	46
6453	Fineâ€scale structure among mesophotic populations of the great star coral <i>Montastraea cavernosa</i> revealed by SNP genotyping. Ecology and Evolution, 2020, 10, 6009-6019.	0.8	10
6454	Differences in gene expression profiles at the early stage of Solanum lycopersicum infection with mild and severe variants of potato spindle tuber viroid. Virus Research, 2020, 286, 198090.	1.1	8
6455	No evidence for accumulation of deleterious mutations and fitness degradation in clonal fish hybrids: Abandoning sex without regrets. Molecular Ecology, 2020, 29, 3038-3055.	2.0	18
6456	Proteomics Reveals the Mechanism Underlying the Inhibition of <i>Phytophthora sojae</i> by Propyl Gallate. Journal of Agricultural and Food Chemistry, 2020, 68, 8151-8162.	2.4	11
6457	Potential of Bacteriocins from Lactobacillus taiwanensis for Producing Bacterial Ghosts as a Next Generation Vaccine. Toxins, 2020, 12, 432.	1.5	13
6458	Regional differences in gene regulation may underlie patterns of sensitivity to novel insecticides in <i>Leptinotarsa decemlineata</i>. Pest Management Science, 2020, 76, 4278-4285.	1.7	18
6459	SAGER: a database of Symbiodiniaceae and Algal Genomic Resource. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	19
6460	Phenylalanine increases chrysanthemum flower immunity against <i>Botrytis cinerea</i> attack. Plant Journal, 2020, 104, 226-240.	2.8	30
6461	Combined transcriptomics and proteomics to identify differential proteins involved in the immune response to the parasite schistosoma japonicum in snail hosts pre-infected with exorchis sp. Acta Tropica, 2020, 211, 105623.	0.9	3
6462	Transcriptome analysis of Clarias magur brain and gonads suggests neuro-endocrine inhibition of milt release from captive GnRH-induced males. Genomics, 2020, 112, 4041-4052.	1.3	9

#	ARTICLE	IF	CITATIONS
6463	Genome sequencing and transcriptome analysis of Geotrichum citri-aurantii on citrus reveal the potential pathogenic- and guazatine-resistance related genes. Genomics, 2020, 112, 4063-4071.	1.3	15
6464	A new brilliantly blue-emitting luciferin-luciferase system from Orfelia fultoni and Keroplatinae (Diptera). Scientific Reports, 2020, 10, 9608.	1.6	17
6465	A Genomic and Transcriptomic Overview of MATE, ABC, and MFS Transporters in Citrus sinensis Interaction with Xanthomonas citri subsp. citri. Plants, 2020, 9, 794.	1.6	9
6466	Candida auris Phenotypic Heterogeneity Determines Pathogenicity <i>In Vitro</i>. MSphere, 2020, 5, .	1.3	46
6467	Understanding the early cold response mechanism in IR64 indica rice variety through comparative transcriptome analysis. BMC Genomics, 2020, 21, 425.	1.2	21
6468	Transcription analysis of Ganoderma lucidum reveals candidate genes and pathways in response to excess exogenous indoleacetic acid (IAA). Mycoscience, 2020, 61, 226-234.	0.3	2
6469	Transcriptome analysis of Cryptococcus humicola under aluminum stress revealed the potential role of the cell wall in aluminum tolerance. Metallomics, 2020, 12, 1370-1379.	1.0	0
6470	Cooperation between passive and active silicon transporters clarifies the ecophysiology and evolution of biosilicification in sponges. Science Advances, 2020, 6, eaba9322.	4.7	22
6471	Single Nucleotide Polymorphisms as Practical Molecular Tools to Support European Chestnut Agrobiodiversity Management. International Journal of Molecular Sciences, 2020, 21, 4805.	1.8	11
6472	Transcriptome Sequencing and Chemical Analysis Reveal the Formation Mechanism of White Florets in Carthamus tinctorius L.. Plants, 2020, 9, 847.	1.6	7
6473	The auxin response factor gene family in wheat (Triticum aestivum L.): Genome-wide identification, characterization and expression analyses in response to leaf rust. South African Journal of Botany, 2021, 140, 312-325.	1.2	13
6474	Identification and characterization of differentially expressed genes in the rice root following exogenous application of spermidine during salt stress. Genomics, 2020, 112, 4125-4136.	1.3	2
6475	Flufenacet activity is affected by GST inhibitors in blackgrass (<i>Alopecurus myosuroides</i>) populations with reduced flufenacet sensitivity and higher expression levels of GSTs. Weed Science, 2020, 68, 451-459.	0.8	22
6476	Phyloâ€biogeographical distribution of whitefly Bemisia tabaci (Insecta: Aleyrodidae) mitotypes in Ecuador. Ecosphere, 2020, 11, e03154.	1.0	13
6477	Mining lycodine-type alkaloid biosynthetic genes and genetic markers from transcriptome of Lycopodiastrum casuarinoides. Chinese Herbal Medicines, 2020, 12, 133-141.	1.2	2
6478	A Methionine Sulfoxide Reductase B Is Required for the Establishment of Astragalus sinicusâ€“Mesorhizobium Symbiosis. Plant and Cell Physiology, 2020, 61, 1631-1645.	1.5	6
6479	Signatures of adaptation to a monocot host in the plantâ€parasitic cyst nematode Heterodera sacchari. Plant Journal, 2020, 103, 1263-1274.	2.8	9
6480	De Novo Assembly and Annotation of the Juvenile Tuber Transcriptome of a Gastrodia elata Hybrid by RNA Sequencing: Detection of SSR Markers. Biochemical Genetics, 2020, 58, 914-934.	0.8	6

#	ARTICLE	IF	CITATIONS
6481	Comparative Transcriptome Analyses of Drugâ€sensitive and Drugâ€resistant Strains of <i>Eimeria tenella</i> by <scp>RNA</scp>â€sequencing. Journal of Eukaryotic Microbiology, 2020, 67, 406-416.	0.8	19
6482	The Genome Assembly and Annotation of the Southern Elephant Seal Mirounga leonina. Genes, 2020, 11, 160.	1.0	3
6483	Transcriptome Profiling Revealed Potentially Critical Roles for Digestion and Defense-Related Genes in Insectsâ€™ Use of Resistant Host Plants: A Case Study with Sitobion Avenae. Insects, 2020, 11, 90.	1.0	6
6484	Complete transcriptome assembly and annotation of a critically important amphipod species in freshwater ecotoxicological risk assessment: Gammarus fossarum. Environment International, 2020, 137, 105319.	4.8	8
6485	Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp Cotesia vestalis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 34, 100657.	0.4	18
6486	Sex-specific variation in the antennal proteome of the migratory locust. Journal of Proteomics, 2020, 216, 103681.	1.2	6
6487	Transcriptome of tambaqui Colossoma macropomum during gonad differentiation: Different molecular signals leading to sex identity. Genomics, 2020, 112, 2478-2488.	1.3	29
6488	Improved genome assembly provides new insights into genome evolution in a desert poplar (<i>Populus euphratica</i>). Molecular Ecology Resources, 2020, 20, 781-794.	2.2	45
6489	Transcriptomic profiles of Dunaliella salina in response to hypersaline stress. BMC Genomics, 2020, 21, 115.	1.2	23
6490	Comparative transcriptome profiling provides insights into plant salt tolerance in seashore paspalum (Paspalum vaginatum). BMC Genomics, 2020, 21, 131.	1.2	26
6491	Exposure to the Florida red tide dinoflagellate, Karenia brevis, and its associated brevetoxins induces ecophysiological and proteomic alterations in Porites astreoides. PLoS ONE, 2020, 15, e0228414.	1.1	9
6492	Comprehensive Transcriptomic Analysis of Auxin Responses in Submerged Rice Coleoptile Growth. International Journal of Molecular Sciences, 2020, 21, 1292.	1.8	19
6493	Differential gene regulation in selected lines for high and low sperm production in male guppies. Molecular Reproduction and Development, 2020, 87, 430-441.	1.0	2
6494	De novo transcriptome assembly and sex-biased gene expression in the gonads of Amur catfish (Silurus) Tj ETQq1 1 0.784314 rgBT /Ov	1.3	17
6495	Comparative Transcriptome Analysis Reveals Stem Secondary Growth of Grafted Rosa rugosa â€˜Roseaâ€™ Scion and R. multiflora â€˜Innermisâ€™ Rootstock. Genes, 2020, 11, 228.	1.0	6
6496	Transcriptome Analysis Reveals Differences in Key Genes and Pathways Regulating Carbon and Nitrogen Metabolism in Cotton Genotypes under N Starvation and Resupply. International Journal of Molecular Sciences, 2020, 21, 1500.	1.8	30
6497	Comparative Transcriptome Analysis of the Gills from the Chinese Mitten Crab (Eriocheir japonica) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 20, .	0.4	3
6498	Genome-Wide Association Study Uncovers Novel Genomic Regions Associated With Coleoptile Length in Hard Winter Wheat. Frontiers in Genetics, 2019, 10, 1345.	1.1	26

#	Article	IF	Citations
6499	Proteomic analysis of <i>Aspergillus niger</i> 3.316 under heat stress. MicrobiologyOpen, 2020, 9, e1012.	1.2	11
6500	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer Sabina chinensis. Journal of Biosciences, 2020, 45, 1.	0.5	2
6501	Soybean aphid biotype 1 genome: Insights into the invasive biology and adaptive evolution of a major agricultural pest. Insect Biochemistry and Molecular Biology, 2020, 120, 103334.	1.2	15
6502	Identification of a molecular marker associated with lignotuber in Eucalyptus ssp. Scientific Reports, 2020, 10, 3608.	1.6	4
6503	Functional microRNA screening for dietary vitamin E regulation of abdominal fat deposition in broilers. British Poultry Science, 2020, 61, 344-349.	0.8	8
6504	Transcriptomic analysis reveals root metabolic alteration and induction of huanglongbing resistance by sulphonamide antibiotics in huanglongbingâ€affected citrus plants. Plant Pathology, 2020, 69, 733-743.	1.2	9
6505	Cellular alteration and differential protein profile explain effects of GA₃ and ABA and their inhibitor on <i>Trichocline catharinensis</i> (Asteraceae) seed germination. Physiologia Plantarum, 2020, 169, 258-275.	2.6	5
6506	Comparative iTRAQ proteomic profiling of sweet orange fruit on sensitive and tolerant rootstocks infected by â€˜CandidatusÂLiberibacter asiaticusâ€™. PLoS ONE, 2020, 15, e0228876.	1.1	8
6507	Immune transcriptome analysis in predatory beetles reveals two cecropin genes overexpressed in mandibles. Journal of Invertebrate Pathology, 2020, 171, 107346.	1.5	1
6508	Phytochemical and comparative transcriptome analyses reveal different regulatory mechanisms in the terpenoid biosynthesis pathways between Matricaria recutita L. and Chamaemelum nobile L.. BMC Genomics, 2020, 21, 169.	1.2	11
6509	Crosstalk in the darkness: bulb vernalization activates meristem transition via circadian rhythm and photoperiodic pathway. BMC Plant Biology, 2020, 20, 77.	1.6	14
6510	Resequencing 93 accessions of coffee unveils independent and parallel selection during Coffea species divergence. Plant Molecular Biology, 2020, 103, 51-61.	2.0	10
6511	Physiological and transcriptomic analysis provide novel insight into cobalt stress responses in willow. Scientific Reports, 2020, 10, 2308.	1.6	15
6512	Transcriptional profiling of human macrophages during infection with<i>Bordetella pertussis</i>. RNA Biology, 2020, 17, 731-742.	1.5	15
6513	De novo Transcriptome Reveals Gene Changes in the Development of the Endosperm Chalazal Haustorium in Taxillus chinensis (DC.) Danser. BioMed Research International, 2020, 2020, 1-12.	0.9	8
6514	Proteome interrogation using gold nanoprobes to identify targets of arctigenin in fish parasites. Journal of Nanobiotechnology, 2020, 18, 32.	4.2	10
6515	Dual Transcriptome and Metabolic Analysis of Vitis vinifera cv. Pinot Noir Berry and Botrytis cinerea During Quiescence and Egressed Infection. Frontiers in Plant Science, 2019, 10, 1704.	1.7	26
6516	Identification and expression of main genes involved in nonâ€target site resistance mechanisms to fenoxapropâ€pâ€ethyl in <i>Beckmannia syzigachne</i>. Pest Management Science, 2020, 76, 2619-2626.	1.7	34

#	ARTICLE	IF	CITATIONS
6517	Identification and characterization of mRNAs and lncRNAs of a barley shrunken endosperm mutant using RNA-seq. Genetica, 2020, 148, 55-68.	0.5	5
6518	Venomics of the asp viper Vipera aspis aspis from France. Journal of Proteomics, 2020, 218, 103707.	1.2	10
6519	Genome-wide gene expression profiling of the melon fly, Zeugodacus cucurbitae, during thirteen life stages. Scientific Data, 2020, 7, 45.	2.4	18
6520	The Genetics of Differential Gene Expression Related to Fruit Traits in Strawberry (Fragaria) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.1	20
6521	Plant regeneration in leaf culture of Centaurium erythraea Rafn. Part 3: de novo transcriptome assembly and validation of housekeeping genes for studies of in vitro morphogenesis. Plant Cell, Tissue and Organ Culture, 2020, 141, 417-433.	1.2	9
6522	Metabolome and Transcriptome Analyses Reveal Tissue-Specific Variations in Gene Expression and Metabolites of Olive. Journal of Plant Biology, 2020, 63, 73-82.	0.9	8
6523	New insights into the Manila clam â€“ Perkinsus olseni interaction based on gene expression analysis of clam hemocytes and parasite trophozoites through in vitro challenges. International Journal for Parasitology, 2020, 50, 195-208.	1.3	3
6524	Genome-wide inference of the Camponotus floridanus protein-protein interaction network using homologous mapping and interacting domain profile pairs. Scientific Reports, 2020, 10, 2334.	1.6	9
6525	Population genetic structure and predominance of cyclical parthenogenesis in the bird cherryâ€•oat aphid <i>Rhopalosiphum padi</i> in England. Evolutionary Applications, 2020, 13, 1009-1025.	1.5	16
6526	Aryl hydrocarbon receptor nuclear translocators (ARNT1, ARNT2, and ARNT3) of white sturgeon (Acipenser transmontanus): Sequences, tissue-specific expressions, and response to Î²-naphthoflavone. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2020, 231, 108726.	1.3	2
6527	Inducement and cultivation of novel red Cyclocarya paliurus callus and its unique morphological and metabolic characteristics. Industrial Crops and Products, 2020, 147, 112266.	2.5	12
6528	Transcriptome analysis of terpenoid biosynthetic genes and simple sequence repeat marker screening in Eucommia ulmoides. Molecular Biology Reports, 2020, 47, 1979-1990.	1.0	13
6529	De novo transcriptome analysis of halotolerant bacterium Staphylococcus sp. strain P-TSB-70 isolated from East coast of India: In search of salt stress tolerant genes. PLoS ONE, 2020, 15, e0228199.	1.1	10
6530	The Genome-Wide Analysis of RALF-Like Genes in Strawberry (Wild and Cultivated) and Five Other Plant Species (Rosaceae). Genes, 2020, 11, 174.	1.0	6
6531	Genetic Differentiation in Hatchery and Stocked Populations of Sea Trout in the Southern Baltic: Selection Evidence at SNP Loci. Genes, 2020, 11, 184.	1.0	7
6532	Metabolome and Transcriptome Analysis of Hexaploid Solidago canadensis Roots Reveals its Invasive Capacity Related to Polyploidy. Genes, 2020, 11, 187.	1.0	15
6533	A chromosome-level reference genome of the hornbeam, Carpinus fangiana. Scientific Data, 2020, 7, 24.	2.4	8
6534	Transcriptome profiling of differentially expressed genes in cytoplasmic male-sterile line and its fertility restorer line in pigeon pea (Cajanus cajan L.). BMC Plant Biology, 2020, 20, 74.	1.6	13

#	ARTICLE	IF	CITATIONS
6535	Liver Transcriptome Profiling Reveals That Dietary DHA and EPA Levels Influence Suites of Genes Involved in Metabolism, Redox Homeostasis, and Immune Function in Atlantic Salmon (Salmo salar). Marine Biotechnology, 2020, 22, 263-284.	1.1	17
6536	A time-resolved dual transcriptome analysis reveals the molecular regulating network underlying the compatible/incompatible interactions between cabbage (Brassica oleracea) and Fusarium oxysporum f. sp. conglutinans. Plant and Soil, 2020, 448, 455-478.	1.8	7
6537	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. Phytopathology, 2020, 110, 1161-1173.	1.1	16
6538	The genome sequence of celery (Apium graveolens L.), an important leaf vegetable crop rich in apigenin in the Apiaceae family. Horticulture Research, 2020, 7, 9.	2.9	61
6539	Recent trends and advances in identification and functional characterization of plant miRNAs. Acta Physiologiae Plantarum, 2020, 42, 1.	1.0	22
6540	Mechanistic insights into bacterial metabolic reprogramming from omics-integrated genome-scale models. Npj Systems Biology and Applications, 2020, 6, 1.	1.4	62
6541	Genome- and transcriptome-derived microsatellite loci in lumpfish Cyclopterus lumpus: molecular tools for aquaculture, conservation and fisheries management. Scientific Reports, 2020, 10, 559.	1.6	8
6542	Evolutionary dynamics of recent selection on cognitive abilities. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 3045-3052.	3.3	34
6543	Transcriptome analysis of Clinopodium gracile (Benth.) Matsum and identification of genes related to Triterpenoid Saponin biosynthesis. BMC Genomics, 2020, 21, 49.	1.2	12
6544	Gene regulatory response to hyposalinity in the brown seaweed Fucus vesiculosus. BMC Genomics, 2020, 21, 42.	1.2	10
6545	Transcriptomic Analysis Reveals the Wound Healing Activity of Mussel Myticin C. Biomolecules, 2020, 10, 133.	1.8	15
6546	Water Deficit Transcriptomic Responses Differ in the Invasive Tamarix chinensis and T. ramosissima Established in the Southern and Northern United States. Plants, 2020, 9, 86.	1.6	10
6547	Transcriptome profiles of a native rice variety Hongyou-4 responding to infections of hypervirulent and hypovirulent Xanthomonas oryzae pv. oryzicola strains. Physiological and Molecular Plant Pathology, 2020, 110, 101462.	1.3	3
6548	Phylogeny and highland adaptation of Chinese species in Allium section Daghestanica (Amaryllidaceae) revealed by transcriptome sequencing. Molecular Phylogenetics and Evolution, 2020, 146, 106737.	1.2	10
6549	The ability to manipulate ROS metabolism in pepper may affect aphid virulence. Horticulture Research, 2020, 7, 6.	2.9	10
6550	Top-Down and Bottom-Up Controls on Microeukaryotic Diversity (i.e., Amplicon Analyses of SAR) Tj ETQq1 1 0.784314 rgBT /Overlock Frontiers in Marine Science, 2020, 6, .	1.2	5
6551	Transcriptome analyses provide insights into development of the Zingiber zerumbet flower, revealing potential genes related to floral organ formation and patterning. Plant Growth Regulation, 2020, 90, 331-345.	1.8	10
6552	Genomic regions associated with principal components for growth, visual score and reproductive traits in Nellore cattle. Livestock Science, 2020, 233, 103936.	0.6	4

#	ARTICLE	IF	CITATIONS
6553	Identification of putative Type-I sex pheromone biosynthesis-related genes expressed in the female pheromone gland of Streltzoviella insularis. PLoS ONE, 2020, 15, e0227666.	1.1	4
6554	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of Morchella crassipes. International Journal of Molecular Sciences, 2020, 21, 483.	1.8	27
6555	Host and symbiont genetic determinants of nutritional phenotype in a natural population of the pea aphid. Molecular Ecology, 2020, 29, 848-858.	2.0	15
6556	Transcriptome-wide-scale-predicted dsRNAs potentially involved in RNA homoeostasis are remarkably excluded from genes with no/very low expression in all developmental stages. RNA Biology, 2020, 17, 554-570.	1.5	2
6557	Genomic analyses of a â€œliving fossilâ€ The endangered doveâ€tree. Molecular Ecology Resources, 2020, 20, 756-769.	2.2	26
6558	Transcriptome-based screening of intracellular pathways and angiogenesis related genes at different stages of thiram induced tibial lesions in broiler chickens. BMC Genomics, 2020, 21, 50.	1.2	22
6559	Host Transcriptional Response of Sclerotinia sclerotiorum Induced by the Mycoparasite Coniothyrium minitans. Frontiers in Microbiology, 2020, 11, 183.	1.5	4
6560	A long nonâ€coding apple RNA, MSTRG.85814.11, acts as a transcriptional enhancer of <i>SAUR32</i> and contributes to the Feâ€deficiency response. Plant Journal, 2020, 103, 53-67.	2.8	42
6561	The complete mitochondrial genome of Taxus cuspidata (Taxaceae): eight protein-coding genes have transferred to the nuclear genome. BMC Evolutionary Biology, 2020, 20, 10.	3.2	39
6562	Concomitant phytonutrient and transcriptome analysis of mature fruit and leaf tissues of tomato (Solanum lycopersicum L. cv. Oregon Spring) grown using organic and conventional fertilizer. PLoS ONE, 2020, 15, e0227429.	1.1	14
6563	Plateau Grass and Greenhouse Flower? Distinct Genetic Basis of Closely Related Toad Tadpoles Respectively Adapted to High Altitude and Karst Caves. Genes, 2020, 11, 123.	1.0	4
6564	RNA-seq analysis of the peduncle development of Rht12 dwarf plants and primary mapping of Rht12 in common wheat. Cereal Research Communications, 2020, 48, 139-147.	0.8	3
6565	Transcriptomic profiles reveal that inactivated iridovirus and rhabdovirus bivalent vaccine elicits robust adaptive immune responses against lethal challenge in marbled sleepy goby. Fish and Shellfish Immunology, 2020, 98, 429-437.	1.6	6
6566	Leaf Transcriptome Analysis and Development of EST-SSR Markers in Arrowhead (Sagittaria trifolia L.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	6
6567	Comparing control options for timeâ€series RNA sequencing experiments in nonmodel organisms: An example from grasses. Molecular Ecology Resources, 2020, 20, 681-691.	2.2	2
6568	Identification and characterization of differentially expressed lncRNA in 2,3,7,8-tetrachlorodibenzo-<i>p</i>-dioxin-induced cleft palate. Human and Experimental Toxicology, 2020, 39, 748-761.	1.1	9
6569	Transcriptome Analysis Identifies <i>Plasmodiophora brassicae</i> Secondary Infection Effector Candidates. Journal of Eukaryotic Microbiology, 2020, 67, 337-351.	0.8	38
6570	Dissection of Dynamic Transcriptome Landscape of Leaf, Bract, and Lupulin Gland in Hop (Humulus) Tj ETQq1 1 0.784314 rgBT /Overloc	1.8	19

#	ARTICLE	IF	CITATIONS
6571	Transcriptome analysis of maize inbred lines differing in drought tolerance provides novel insights into the molecular mechanisms of drought responses in roots. Plant Physiology and Biochemistry, 2020, 149, 11-26.	2.8	30
6572	Transcriptome sequencing and identification of key callus browning-related genes from petiole callus of tree peony (Paeonia suffruticosa cv. Kao) cultured on media with three browning inhibitors. Plant Physiology and Biochemistry, 2020, 149, 36-49.	2.8	25
6573	Whole-genome and time-course dual RNA-Seq analyses reveal chronic pathogenicity-related gene dynamics in the ginseng rusty root rot pathogen Ilyonectria robusta. Scientific Reports, 2020, 10, 1586.	1.6	18
6574	Molecular and expression characterization of Toll-like receptor family genes from the Anadara sativa (Bivalvia, Arcidae) transcriptome. Developmental and Comparative Immunology, 2020, 106, 103630.	1.0	7
6575	Proteomic analysis of two populations of Schistosoma mansoni-derived extracellular vesicles: 15k pellet and 120k pellet vesicles. Molecular and Biochemical Parasitology, 2020, 236, 111264.	0.5	42
6576	Set up of an in vitro model to study early host-parasite interactions between newly excysted juveniles of Fasciola hepatica and host intestinal cells using a quantitative proteomics approach. Veterinary Parasitology, 2020, 278, 109028.	0.7	10
6577	Urbanization without isolation: the absence of genetic structure among cities and forests in the tiny acorn ant <i>Temnothorax nylanderi</i>. Biology Letters, 2020, 16, 20190741.	1.0	21
6578	Population Genomics in Rhamdia quelen (Heptapteridae, Siluriformes) Reveals Deep Divergence and Adaptation in the Neotropical Region. Genes, 2020, 11, 109.	1.0	4
6579	De Novo Transcriptome Identifies Olfactory Genes in Diachasmimorpha longicaudata (Ashmead). Genes, 2020, 11, 144.	1.0	8
6580	Methoprene-Induced Genes in Workers of Formosan Subterranean Termites (Coptotermes formosanus) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	7
6581	Comparative transcriptome analysis of wing discs from Bombyx mori and Bombyx mandarina. Journal of Asia-Pacific Entomology, 2020, 23, 327-335.	0.4	1
6582	Differential basal expression of immune genes confers Crassostrea gigas resistance to Pacific oyster mortality syndrome. BMC Genomics, 2020, 21, 63.	1.2	42
6583	Draft Genome of the Asian Buffalo Leech Hirudinaria manillensis. Frontiers in Genetics, 2019, 10, 1321.	1.1	11
6584	Differential Gene Profiling of the Heartwood Formation Process in Taiwania cryptomerioides Hayata Xylem Tissues. International Journal of Molecular Sciences, 2020, 21, 960.	1.8	11
6585	Comparative analysis of transcriptomes from different coloration of Chinese mitten crab Eriocheir sinensis. Fish and Shellfish Immunology, 2020, 98, 515-521.	1.6	2
6586	Distinct Expression and Methylation Patterns for Genes with Different Fates following a Single Whole-Genome Duplication in Flowering Plants. Molecular Biology and Evolution, 2020, 37, 2394-2413.	3.5	75
6587	De novo transcriptomic analysis predicts the effects of phenolic compounds in Ba River on the liver of female sharpbelly (Hemiculter lucidus). Environmental Pollution, 2020, 264, 114642.	3.7	8
6588	A putative transcription factor LFC1 negatively regulates development and yield of winter mushroom. Applied Microbiology and Biotechnology, 2020, 104, 5827-5844.	1.7	12

#	ARTICLE	IF	CITATIONS
6589	Transcriptome analysis and immune-related genes expression reveals the immune responses of Macrobrachium rosenbergii infected by Enterobacter cloacae. Fish and Shellfish Immunology, 2020, 101, 66-77.	1.6	28
6590	Characterization of a specific odorant receptor for linalool in the Chinese citrus fly Bactrocera minax (Diptera: Tephritidae). Insect Biochemistry and Molecular Biology, 2020, 122, 103389.	1.2	19
6591	Phytoplankton pangenome reveals extensive prokaryotic horizontal gene transfer of diverse functions. Science Advances, 2020, 6, eaba0111.	4.7	36
6592	Molecular Response to High Hydrostatic Pressure: Time-Series Transcriptomic Analysis of Shallow-Water Sea Cucumber Apostichopus japonicus. Frontiers in Genetics, 2020, 11, 355.	1.1	2
6593	Rocket Science: The Effect of Spaceflight on Germination Physiology, Ageing, and Transcriptome of Eruca sativa Seeds. Life, 2020, 10, 49.	1.1	19
6594	Species-specific molecular responses of wild coral reef fishes during a marine heatwave. Science Advances, 2020, 6, eaay3423.	4.7	52
6595	Draft genome sequences of Hirudo medicinalis and salivary transcriptome of three closely related medicinal leeches. BMC Genomics, 2020, 21, 331.	1.2	21
6596	Transcriptome analysis of the response provided by Lasiopodomys mandarinus to severe hypoxia includes enhancing DNA repair and damage prevention. Frontiers in Zoology, 2020, 17, 9.	0.9	11
6597	Effect of Transgenesis on mRNA and miRNA Profiles in Cucumber Fruits Expressing Thaumatin II. Genes, 2020, 11, 334.	1.0	7
6598	Comparative Transcriptome Analysis Reveals the Potential Mechanism of Abortion in Tobacco sua-Cytoplasmic Male Sterility. International Journal of Molecular Sciences, 2020, 21, 2445.	1.8	7
6599	The First Genome Survey of the Antarctic Krill (Euphausia superba) Provides a Valuable Genetic Resource for Polar Biomedical Research. Marine Drugs, 2020, 18, 185.	2.2	9
6600	Genome-wide analysis of LATERAL ORGAN BOUNDARIES DOMAIN-in Physcomitrella patens and stress responses. Genes and Genomics, 2020, 42, 651-662.	0.5	11
6601	Intervention of triethylamine on Dunaliella tertiolecta reveals metabolic insights into triacylglycerol accumulation. Algal Research, 2020, 47, 101876.	2.4	2
6602	Gene expression profiling identifies pathways involved in seed maturation of Jatropha curcas. BMC Genomics, 2020, 21, 290.	1.2	2
6603	Plant hormonal changes and differential expression profiling reveal seed dormancy removal process in double dormant plant-herbaceous peony. PLoS ONE, 2020, 15, e0231117.	1.1	7
6604	The bHLH gene family and its response to saline stress in Jilin ginseng, Panax ginseng C.A. Meyer. Molecular Genetics and Genomics, 2020, 295, 877-890.	1.0	17
6605	Transcriptome analysis of metabolisms related to fruit cracking during ripening of a cracking-susceptible grape berry cv. Xiangfei (Vitis vinifera L.). Genes and Genomics, 2020, 42, 639-650.	0.5	15
6606	Histologic examination and transcriptome analysis uncovered liver damage in largemouth bass from formulated diets. Aquaculture, 2020, 526, 735329.	1.7	15

#	Article	IF	Citations
6607	The effects of chronic cadmium exposure on Bufo gargarizans larvae: Histopathological impairment, gene expression alteration and fatty acid metabolism disorder in the liver. Aquatic Toxicology, 2020, 222, 105470.	1.9	15
6608	Partner-specific induction of Spodoptera frugiperda immune genes in response to the entomopathogenic nematobacterial complex Steinernema carpocapsae-Xenorhabdus nematophila. Developmental and Comparative Immunology, 2020, 108, 103676.	1.0	0
6609	Transcriptome survey and toxin measurements reveal evolutionary modification and loss of saxitoxin biosynthesis genes in the dinoflagellates Amphidinium carterae and Prorocentrum micans. Ecotoxicology and Environmental Safety, 2020, 195, 110474.	2.9	19
6610	Acute toxic effects of lead (Pb2+) exposure to rare minnow (Gobiocypris rarus) revealed by histopathological examination and transcriptome analysis. Environmental Toxicology and Pharmacology, 2020, 78, 103385.	2.0	20
6611	Comparative transcriptomic analysis of rhizomes, stems, and leaves of Polygonatum odoratum (Mill.) Druce reveals candidate genes associated with polysaccharide synthesis. Gene, 2020, 744, 144626.	1.0	15
6612	Study on the virulome and resistome of a vancomycin intermediate-resistance Staphylococcus aureus. Microbial Pathogenesis, 2020, 145, 104187.	1.3	5
6613	Precise promoter integration improves cellulose bioconversion and thermotolerance in Clostridium cellulolyticum. Metabolic Engineering, 2020, 60, 110-118.	3.6	18
6614	Transcriptome profiles reveal that gibberellin-related genes regulate weeping traits in crape myrtle. Horticulture Research, 2020, 7, 54.	2.9	17
6615	Assessment of unconventional antimicrobial compounds for the control of â€˜Candidatus Liberibacter asiaticusâ€™, the causative agent of citrus greening disease. Scientific Reports, 2020, 10, 5395.	1.6	17
6616	Genetic and genomic analysis for cocoon yield traits in silkworm. Scientific Reports, 2020, 10, 5682.	1.6	11
6617	Experimental Parasite Infection Causes Genome-Wide Changes in DNA Methylation. Molecular Biology and Evolution, 2020, 37, 2287-2299.	3.5	16
6618	Phylotranscriptomics of the Pentapetalae Reveals Frequent Regulatory Variation in Plant Local Responses to the Fungal Pathogen <i>Sclerotinia sclerotiorum</i>. Plant Cell, 2020, 32, 1820-1844.	3.1	21
6619	Development of Genetic Novel SSR Markers by Transcriptome Sequencing in Ophicephalus argus Cantor. Russian Journal of Genetics, 2020, 56, 253-260.	0.2	0
6620	Gearing Up for Warmer Times: Transcriptomic Response of Spongia officinalis to Elevated Temperatures Reveals Recruited Mechanisms and Potential for Resilience. Frontiers in Marine Science, 2020, 6, .	1.2	15
6621	Insights into the Synthesis, Secretion and Curing of Barnacle Cyprid Adhesive via Transcriptomic and Proteomic Analyses of the Cement Gland. Marine Drugs, 2020, 18, 186.	2.2	10
6622	The Spread and Transmission of Sweet Potato Virus Disease (SPVD) and Its Effect on the Gene Expression Profile in Sweet Potato. Plants, 2020, 9, 492.	1.6	17
6623	Temporal transcriptome change of Oncomelania hupensis revealed by Schistosoma japonicum invasion. Cell and Bioscience, 2020, 10, 58.	2.1	14
6624	Transcriptome Profiling of Ornithogalum dubium Leaves and Flowers to Identify Key Carotenoid Genes for CRISPR Gene Editing. Plants, 2020, 9, 540.	1.6	10

#	ARTICLE	IF	CITATIONS
6625	Metabolic engineering of Cupriavidus necator H16 for improved chemoautotrophic growth and PHB production under oxygen-limiting conditions. Metabolic Engineering, 2020, 61, 11-23.	3.6	40
6626	Improved lipid productivity in Nannochloropsis gaditana in nitrogen-replete conditions by selection of pale green mutants. Biotechnology for Biofuels, 2020, 13, 78.	6.2	27
6627	Comparison of Transcriptome Profiles of the Fungus Botrytis cinerea and Insect Pest Bradysia odoriphaga in Response to Benzothiazole. Frontiers in Microbiology, 2020, 11, 1043.	1.5	9
6628	Analysis of differentially expressed genes and pathways associated with male sterility lines in watermelon via bulked segregant RNA-seq. 3 Biotech, 2020, 10, 222.	1.1	9
6629	Transcribed microsatellite allele lengths are often correlated with gene expression in natural sunflower populations. Molecular Ecology, 2020, 29, 1704-1716.	2.0	12
6630	Differential Transcriptome Analysis of Cervus elaphus songaricus and Cervus elaphus yarkandensis Reveals Candidate Genes for Antler Regeneration. Russian Journal of Genetics, 2020, 56, 324-332.	0.2	1
6631	Time-series expression profiling of sugarcane leaves infected with Puccinia kuehnii reveals an ineffective defense system leading to susceptibility. Plant Cell Reports, 2020, 39, 873-889.	2.8	25
6632	The completed macronuclear genome of a model ciliate Tetrahymena thermophila and its application in genome scrambling and copy number analyses. Science China Life Sciences, 2020, 63, 1534-1542.	2.3	67
6633	Molecular cloning and expression analysis of the transcription factor CobHLH40 from Cornus officinalis on the basis of de novo transcriptome sequencing. Plant Biotechnology Reports, 2020, 14, 419-428.	0.9	1
6634	Dataset of dual RNA-sequencing of Phytophthora palmivora infecting coconut (Cocos nucifera L.). Data in Brief, 2020, 30, 105455.	0.5	10
6635	Snakehead vesiculovirus (SHVV) infection alters striped snakehead (Ophicephalus striatus) cells (SSN-1) glutamine metabolism and apoptosis pathways. Fish and Shellfish Immunology, 2020, 102, 36-46.	1.6	3
6636	Alternative splicing (AS) mechanism plays important roles in response to different salinity environments in spotted sea bass. International Journal of Biological Macromolecules, 2020, 155, 50-60.	3.6	18
6637	Transcriptome Analysis Reveals Clues into leaf-like flower mutant in Chinese orchid Cymbidium ensifolium. Plant Diversity, 2020, 42, 92-101.	1.8	6
6638	Transcriptome Analysis Reveals Candidate Genes for Petroselinic Acid Biosynthesis in Fruits of <i>Coriandrum sativum</i> L.. Journal of Agricultural and Food Chemistry, 2020, 68, 5507-5520.	2.4	12
6639	Transcriptional regulation of amino acid metabolism in response to nitrogen deficiency and nitrogen forms in tea plant root (Camellia sinensis L.). Scientific Reports, 2020, 10, 6868.	1.6	50
6640	<i>Camellia</i> Plant Resistance and Susceptibility to Petal Blight Disease Are Defined by the Timing of Defense Responses. Molecular Plant-Microbe Interactions, 2020, 33, 982-995.	1.4	2
6641	Sugarâ€regulated susceptibility of tomato fruit to <i>Colletotrichum</i> and <i>Penicillium</i> requires differential mechanisms of pathogenicity and fruit responses. Environmental Microbiology, 2020, 22, 2870-2891.	1.8	5
6642	Relationships between genome methylation, levels of nonâ€coding RNAs, mRNAs and metabolites in ripening tomato fruit. Plant Journal, 2020, 103, 980-994.	2.8	46

#	Article	IF	Citations
6643	De novo assembly of the olive fruit fly (Bactrocera oleae) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. BMC Genomics, 2020, 21, 259.	1.2	21
6644	Transcriptomic analysis of sea cucumber (Holothuria leucospilota) coelomocytes revealed the echinoderm cytokine response during immune challenge. BMC Genomics, 2020, 21, 306.	1.2	10
6645	High post-anthesis temperature effects on bread wheat (Triticum aestivum L.) grain transcriptome during early grain-filling. BMC Plant Biology, 2020, 20, 170.	1.6	11
6646	Immune Suppressive Extracellular Vesicle Proteins of<i>Leptopilina heterotoma</i>Are Encoded in the Wasp Genome. G3: Genes, Genomes, Genetics, 2020, 10, 1-12.	0.8	12
6647	<i>De Novo</i> Genome Assembly of <i>Populus simonii</i> Further Supports That <i>Populus simonii</i> and <i>Populus trichocarpa</i> Belong to Different Sections. G3: Genes, Genomes, Genetics, 2020, 10, 455-466.	0.8	21
6648	Comprehensive Transcriptome Analysis Reveals Insights into Phylogeny and Positively Selected Genes of Sillago Species. Animals, 2020, 10, 633.	1.0	5
6649	Analysis of Long Noncoding RNA and mRNA Expression Profiles of Testes with High and Low Sperm Motility in Domestic Pigeons (Columba livia). Genes, 2020, 11, 349.	1.0	9
6650	Characterization of Nuclear and Mitochondrial Genomes of Two Tobacco Endophytic Fungi Leptosphaerulina chartarum and Curvularia trifolii and Their Contributions to Phylogenetic Implications in the Pleosporales. International Journal of Molecular Sciences, 2020, 21, 2461.	1.8	7
6651	Transcriptome analysis reveals <i>wingless</i> regulates neural development and signaling genes in the region of wing pigmentation of a polkaâ€dotted fruit fly. FEBS Journal, 2021, 288, 115-126.	2.2	15
6652	A Comparative Genomics Approach for Shortlisting Broad-Spectrum Drug Targets in Nontuberculous Mycobacteria. Microbial Drug Resistance, 2021, 27, 212-226.	0.9	4
6653	De novo transcriptome assembly for Pachygrapsus marmoratus, an intertidal brachyuran crab. Marine Genomics, 2021, 55, 100792.	0.4	4
6654	Wide crossâ€species RNAâ€Seq comparison reveals convergent molecular mechanisms involved in nickel hyperaccumulation across dicotyledons. New Phytologist, 2021, 229, 994-1006.	3.5	21
6655	Exposure to benzo[a]pyrene triggers distinct patterns of microRNA transcriptional profiles in aquatic firefly Aquatica wuhana (Coleoptera: Lampyridae). Journal of Hazardous Materials, 2021, 401, 123409.	6.5	8
6656	MiRNAs regulate iron homeostasis in Paracoccidioides brasiliensis. Microbes and Infection, 2021, 23, 104772.	1.0	1
6657	The chromosomeâ€level genome sequence and karyotypic evolution of Megadenia pygmaea (Brassicaceae). Molecular Ecology Resources, 2021, 21, 871-879.	2.2	7
6658	Sugar accumulation and characterization of metabolizing enzyme genes in leafy head of Chinese cabbage (Brassica campestris L. ssp. pekinensis). Horticulture Environment and Biotechnology, 2021, 62, 17-29.	0.7	8
6659	Chromosomalâ€level genomes of three rice planthoppers provide new insights into sex chromosome evolution. Molecular Ecology Resources, 2021, 21, 226-237.	2.2	44
6660	The banana (<i>Musa acuminata</i>) <i>MYB</i> gene family and <i>MaMYB14</i>, <i>MaMYB63</i> and <i>MaMYB110</i> expression in response to salinity-stress in cv. Berangan. Plant Biosystems, 2021, 155, 856-870.	0.8	3

#	Article	IF	Citations
6661	A king and vassals' tale: Molecular signatures of clonal integration in <i>Posidonia oceanica</i> under chronic light shortage. Journal of Ecology, 2021, 109, 294-312.	1.9	28
6662	Transcriptome analysis reveals pathways responsible for the promoting effect of sucrose on astaxanthin accumulation in Haematococcus pluvialis under high light condition. Aquaculture, 2021, 530, 735757.	1.7	28
6663	Transcriptomic analysis of a nearâ€isogenic line of melon with high fruit flesh firmness during ripening. Journal of the Science of Food and Agriculture, 2021, 101, 754-777.	1.7	9
6664	Microbial community and transcriptional responses to increased temperatures in coral <scp><i>Pocillopora damicornis</i></scp> holobiont. Environmental Microbiology, 2021, 23, 826-843.	1.8	38
6665	Comparative transcriptomic analysis reveals key genes and pathways in two different cadmium tolerance kenaf (Hibiscus cannabinus L.) cultivars. Chemosphere, 2021, 263, 128211.	4.2	53
6666	An insight into the role of silicon on retaliation to osmotic stress in finger millet (Eleusine coracana) Tj ETQq1 1 0.784314 rgBT /Overlo	6.5	20
6667	Small-scale population divergence is driven by local larval environment in a temperate amphibian. Heredity, 2021, 126, 279-292.	1.2	3
6668	A chromosomeâ€level genome assembly of the woolly apple aphid, <i>Eriosoma lanigerum</i> Hausmann (Hemiptera: Aphididae). Molecular Ecology Resources, 2021, 21, 316-326.	2.2	28
6669	Comparative proteomics of Mesembryanthemum crystallinum guard cells and mesophyll cells in transition from C3 to CAM. Journal of Proteomics, 2021, 231, 104019.	1.2	10
6670	Transcriptome analysis reveals the effects of sand substrate removal and body colour change of kuruma shrimp, <i>Marsupenaeus japonicus</i>. Aquaculture Research, 2021, 52, 577-588.	0.9	6
6671	Proteomics reveals sex-specific heat shock response of Baikal amphipod Eulimnogammarus cyaneus. Science of the Total Environment, 2021, 763, 143008.	3.9	4
6672	Recycling resources: silica of diatom frustules as a source for spicule building in Antarctic siliceous demosponges. Zoological Journal of the Linnean Society, 2021, 192, 259-276.	1.0	2
6673	Climate change facilitates a parasiteâ€™s host exploitation via temperatureâ€mediated immunometabolic processes. Global Change Biology, 2021, 27, 94-107.	4.2	13
6674	Novel pituitary actions of NKB for anorectic peptides regulation in grass carp. Aquaculture, 2021, 531, 735857.	1.7	4
6675	Genome-wide analysis of intermuscular bone development reveals changes of key genes expression and signaling pathways in blunt snout bream (Megalobrama amblycephala). Genomics, 2021, 113, 654-663.	1.3	8
6676	The transcription factors of tall fescue in response to temperature stress. Plant Biology, 2021, 23, 89-99.	1.8	7
6677	Genome-wide identification and expression pattern analysis of the KCS gene family in barley. Plant Growth Regulation, 2021, 93, 89-103.	1.8	35
6678	The genome of <i>Draba nivalis</i> shows signatures of adaptation to the extreme environmental stresses of the Arctic. Molecular Ecology Resources, 2021, 21, 661-676.	2.2	14

#	Article	IF	Citations
6679	The elephant grass (<i>Cenchrus purpureus</i>) genome provides insights into anthocyanidin accumulation and fast growth. Molecular Ecology Resources, 2021, 21, 526-542.	2.2	33
6680	Comparative Analysis of Root Transcriptome Profiles of Sesame (Sesamum indicum L.) in Response to Osmotic Stress. Journal of Plant Growth Regulation, 2021, 40, 1787-1801.	2.8	8
6681	The Polycomb group methyltransferase StE(z)2 and deposition of H3K27me3 and H3K4me3 regulate the expression of tuberization genes in potato. Journal of Experimental Botany, 2021, 72, 426-444.	2.4	7
6682	Complete Genome Sequence of Zearalenone Degrading Bacteria Bacillus velezensis A2. Current Microbiology, 2021, 78, 347-350.	1.0	3
6683	Proteome responses of Rhizobium tropici CIAT 899 upon apigenin and salt stress induction. Applied Soil Ecology, 2021, 159, 103815.	2.1	6
6684	High-resolution temporal transcriptome sequencing unravels ERF and WRKY as the master players in the regulatory networks underlying sesame responses to waterlogging and recovery. Genomics, 2021, 113, 276-290.	1.3	21
6685	A multilayered cross-species analysis of GRAS transcription factors uncovered their functional networks in plant adaptation to the environment. Journal of Advanced Research, 2021, 29, 191-205.	4.4	10
6686	Development of a dense genetic map and QTL analysis for pod borer Helicoverpa armigera (HÃ¼bner) resistance component traits in chickpea (Cicer arietinum L .). Plant Genome, 2021, 14, e20071.	1.6	16
6687	Behavioral and molecular response of the insect parasitic nematode Steinernema carpocapsae to cues emitted by a host, the red palm weevil, Rhynchophorus ferrugineus. Molecular and Biochemical Parasitology, 2021, 241, 111345.	0.5	4
6688	Proteomic changes in Trypanosoma cruzi epimastigotes treated with the proapoptotic compound PAC-1. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140582.	1.1	3
6689	Novel components of Tityus serrulatus venom: A transcriptomic approach. Toxicon, 2021, 189, 91-104.	0.8	15
6690	Gene expression remodelling and immune response during adaptive divergence in an African cichlid fish. Molecular Ecology, 2021, 30, 274-296.	2.0	5
6691	Differential responses of the antennal proteome of male and female migratory locusts to infection by a fungal pathogen. Journal of Proteomics, 2021, 232, 104050.	1.2	7
6692	SCAP knockout in SM22Î±-Cre mice induces defective angiogenesis in the placental labyrinth. Biomedicine and Pharmacotherapy, 2021, 133, 111011.	2.5	6
6693	Identification of early and late flowering time candidate genes in endodormant and ecodormant almond flower buds. Tree Physiology, 2021, 41, 589-605.	1.4	29
6694	Effects of dietary icariin supplementation on the ovary development-related transcriptome of Chinese mitten crab (Eriocheir sinensis). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 37, 100756.	0.4	6
6695	Genome-Wide Analysis of Heat Shock Transcription Factors in Ziziphus jujuba Identifies Potential Candidates for Crop Improvement Under Abiotic Stress. Applied Biochemistry and Biotechnology, 2021, 193, 1023-1041.	1.4	6
6696	Diversity and species composition of arbuscular mycorrhizal fungi across maize fields in the southern part of Belgium. Mycorrhiza, 2021, 31, 265-272.	1.3	6

#	Article	IF	Citations
6697	Transcriptomic analysis of tea plant (Camellia sinensis) revealed the co-expression network of 4111 paralogous genes and biosynthesis of quality-related key metabolites under multiple stresses. Genomics, 2021, 113, 908-918.	1.3	6
6698	The transcriptome of anterior regeneration in earthworm Eudrilus eugeniae. Molecular Biology Reports, 2021, 48, 259-283.	1.0	14
6699	Large-scale advances in SSR markers with high-throughput sequencing in Euphorbia fischeriana Steud. Electronic Journal of Biotechnology, 2021, 49, 50-55.	1.2	5
6700	Comparative genomics of Clostridium species associated with vacuum-packed meat spoilage. Food Microbiology, 2021, 95, 103687.	2.1	25
6701	In planta transcriptome analysis reveals tissue-specific expression of pathogenicity genes and microRNAs during rice-Magnaporthe interactions. Genomics, 2021, 113, 265-275.	1.3	5
6702	Analysis of N6-methyladenosine reveals a new important mechanism regulating the salt tolerance of sweet sorghum. Plant Science, 2021, 304, 110801.	1.7	52
6703	Identification of miRNA responsive to early flowering in tree peony (<i>Paeonia ostii</i>) by high-throughput sequencing. Journal of Horticultural Science and Biotechnology, 2021, 96, 297-310.	0.9	6
6704	Drought responsiveness in black pepper (<scp><i>Piper nigrum</i></scp> L.): Genes associated and development of a webâ€genomic resource. Physiologia Plantarum, 2021, 172, 669-683.	2.6	7
6705	Bisphenol A promotes breast cancer cell proliferation by driving miR-381-3p-PTTG1-dependent cell cycle progression. Chemosphere, 2021, 268, 129221.	4.2	25
6706	Elite allele mining for growth rate traits in common carp (Cyprinus carpio) by association analysis. Aquaculture Research, 2021, 52, 1192-1200.	0.9	2
6707	Comprehensive analysis of the <scp>isomiRome</scp> in the vegetative organs of the conifer <scp><i>Pinus pinaster</i></scp> under contrasting water availability. Plant, Cell and Environment, 2021, 44, 706-728.	2.8	9
6708	Transcriptome analysis of the pheromone glands in Noorda blitealis reveals a novel AOX group of the superfamily Pyraloidea. Journal of Asia-Pacific Entomology, 2021, 24, 110-119.	0.4	2
6709	Transcriptome analysis of <i>Macrobrachium rosenbergii</i> hepatopancreas in response to <i>Vibrio harveyi</i> infection. Aquaculture Research, 2021, 52, 1855-1875.	0.9	3
6710	Deciphering the molecular regulatory mechanism orchestrating ovary development of the Pacific whiteleg shrimp Litopenaeus vannamei through integrated transcriptomic analysis of reproduction-related organs. Aquaculture, 2021, 533, 736160.	1.7	10
6711	Penicillium oxalicum S-adenosylmethionine synthetase is essential for the viability of fungal cells and the expression of genes encoding cellulolytic enzymes. Fungal Biology, 2021, 125, 1-11.	1.1	5
6712	Adaptive roots of mangrove Avicennia marina: Structure and gene expressions analyses of pneumatophores. Science of the Total Environment, 2021, 757, 143994.	3.9	9
6713	Affinityâ€based proteomics reveals novel targets of inositol pyrophosphate (5â€IP 7)â€dependent phosphorylation and binding in Trypanosoma cruzi replicative stages. Molecular Microbiology, 2021, 115, 986-1004.	1.2	5
6714	A new genome allows the identification of genes associated with natural variation in aluminium tolerance in<i>Brachiaria</i>grasses. Journal of Experimental Botany, 2021, 72, 302-319.	2.4	23

#	ARTICLE	IF	CITATIONS
6715	Phosphate availability and ectomycorrhizal symbiosis with Pinus sylvestris have independent effects on the Paxillus involutus transcriptome. Mycorrhiza, 2021, 31, 69-83.	1.3	7
6716	Expression of miRNAs and their target genes in roots of â€˜Sanhuâ€™ tangerine (Citrus reticulata blanco) Tj ETQq1 1 0.784314 rgBT /O Protection, 2021, 128, 407-420.	1.6	2
6717	Transcriptional flexibility during thermal challenge corresponds with expanded thermal tolerance in an invasive compared to native fish. Evolutionary Applications, 2021, 14, 931-949.	1.5	14
6718	Transcriptome expression profiles between diploid and triploid Pacific abalone (Haliotis discus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 100820.	0.4	7
6719	RNA-Seq transcriptome analysis to identify candidate genes involved in non-target site-based mesosulfuron-methyl resistance in Beckmannia syzigachne. Pesticide Biochemistry and Physiology, 2021, 171, 104738.	1.6	16
6720	Proteomic screening for the identification of proteins involved in resistance to Xanthomonas campestris pv. malvacearum in cotton. Physiological and Molecular Plant Pathology, 2021, 113, 101562.	1.3	2
6721	TMT-based quantitative proteomics analyses of sterile/fertile anthers from a genic male-sterile line and its maintainer in cotton (Gossypium hirsutum L.). Journal of Proteomics, 2021, 232, 104026.	1.2	8
6722	Transcriptome characteristics and the expression profiles of resistance-related genes in healthy and <i>Mycocentrospora acerina</i>-infected <i>Asarum</i> sp. leaves treated with <i>Penicillium janthinellum</i> F1-6. Biocontrol Science and Technology, 2021, 31, 171-189.	0.5	0
6723	Using historical genomeâ€wide DNA to unravel the confused taxonomy in a songbird lineage that is extinct in the wild. Evolutionary Applications, 2021, 14, 698-709.	1.5	10
6724	A comprehensive integrated transcriptome and metabolome analyses to reveal key genes and essential metabolic pathways involved in CMS in kenaf. Plant Cell Reports, 2021, 40, 223-236.	2.8	5
6725	Putative Effector Genes Distinguish Two Pathogenicity Groups of<i>Fusarium oxysporum</i>f. sp.<i>spinaciae</i>. Molecular Plant-Microbe Interactions, 2021, 34, 141-156.	1.4	14
6726	Expression and functional analysis of cytochrome P450 genes in the integument of the oriental armyworm, <i>Mythimna separata</i> (<scp>Walker</scp>). Pest Management Science, 2021, 77, 577-587.	1.7	11
6727	Proteomic analysis and optimized production of Alkalihalobacillus patagoniensis PAT 05T extracellular proteases. Bioprocess and Biosystems Engineering, 2021, 44, 225-234.	1.7	2
6728	Colocality to Cofunctionality: Eukaryotic Gene Neighborhoods as a Resource for Function Discovery. Molecular Biology and Evolution, 2021, 38, 650-662.	3.5	14
6729	An apoplastic fluid extraction method for the characterization of grapevine leaves proteome and metabolome from a single sample. Physiologia Plantarum, 2021, 171, 343-357.	2.6	18
6730	Genome Analysis and Genomic Comparison of the Novel Species Arthrobacter ipsi Reveal Its Potential Protective Role in Its Bark Beetle Host. Microbial Ecology, 2021, 81, 471-482.	1.4	9
6731	Genotyping-by-sequencing to determine the genetic structure of a Tibetan medicinal plant Swertia mussotii Franch.. Genetic Resources and Crop Evolution, 2021, 68, 469-484.	0.8	3
6732	Transcriptome Analysis of Gluconobacter oxydans WSH-003 Exposed to Elevated 2-Keto-L-Gulonic Acid Reveals the Responses to Osmotic and Oxidative Stress. Applied Biochemistry and Biotechnology, 2021, 193, 128-141.	1.4	9

#	Article	IF	Citations
6733	Weighted gene co-expression analysis for identification of key genes regulating heat stress in wheat. Cereal Research Communications, 2021, 49, 73-81.	0.8	7
6734	Next Generation Sequencing: Transcriptomics. , 2021, , 1-11.		0
6735	Whole-genome sequencing reveals sex determination and liver high-fat storage mechanisms of yellowstripe goby (Mugilogobius chulae). Communications Biology, 2021, 4, 15.	2.0	11
6736	Fine Mapping of a Locus Underlying the Ectopic Blade-Like Outgrowths on Leaf and Screening Its Candidate Genes in Rapeseed (Brassica napus L.). Frontiers in Plant Science, 2020, 11, 616844.	1.7	6
6737	Transcriptome profiling analysis of two contrasting barley genotypes in general combining ability for yield traits. Revista Brasileira De Botanica, 2021, 44, 117-123.	0.5	0
6739	Tropical Endophytic Bacillus Species Enhance Plant Growth and Nutrient Uptake in Cereals. Sustainable Development and Biodiversity, 2021, , 157-180.	1.4	2
6740	Genome wide identification and expression pattern analysis of the GRAS family in quinoa. Functional Plant Biology, 2021, 48, 948-962.	1.1	9
6741	Advances in Biotechnological Tools and Techniques for Metatranscriptomics. , 2021, , 567-579.		0
6742	Genome-wide analysis of growth-regulating factors (GRFs) in<i>Triticum aestivum</i>. PeerJ, 2021, 9, e10701.	0.9	22
6743	Whole-transcriptome analysis of differentially expressed genes in the mutant and normal capitula of Chrysanthemum morifolium. BMC Genomic Data, 2021, 22, 2.	0.7	15
6745	Development of EST-Molecular Markers from RNA Sequencing for Genetic Management and Identification of Growth Traits in Potato Grouper (Epinephelus tukula). Biology, 2021, 10, 36.	1.3	5
6746	Transcriptional responses to water stress and recovery in a drought-tolerant fescue wild grass (Festuca ovina; Poaceae). Genome, 2021, 64, 15-27.	0.9	1
6747	Genome-wide signatures of mammalian skin covering evolution. Science China Life Sciences, 2021, 64, 1765-1780.	2.3	5
6748	Design and Analysis of RNA Sequencing Data. Learning Materials in Biosciences, 2021, , 143-175.	0.2	0
6749	Proteomics of exhaled breath condensate in lung cancer and controls using data-independent acquisition (DIA): a pilot study. Journal of Breath Research, 2021, 15, 026002.	1.5	10
6750	Computational Genomics. , 2021, , 213-241.		0
6751	New insights on key genes involved in drought stress response of barley: gene networks reconstruction, hub, and promoter analysis. Journal of Genetic Engineering and Biotechnology, 2021, 19, 2.	1.5	12
6752	Next Generation Sequencing. , 2021, , 277-302.		0

#	Article	IF	Citations
6753	Comparative Proteomic Analysis of Rhipicephalus sanguineus sensu lato (Acari: Ixodidae) Tropical and Temperate Lineages: Uncovering Differences During Ehrlichia canis Infection. Frontiers in Cellular and Infection Microbiology, 2020, 10, 611113.	1.8	6
6754	Coordinated Gene Expression and Chromatin Regulation during <i>Hydra</i> Head Regeneration. Genome Biology and Evolution, 2021, 13, .	1.1	12
6755	Chromosomal assembly of the Antarctic toothfish (<i>Dissostichus mawsoni</i>) genome using third-generation DNA sequencing and Hi-C technology. Zoological Research, 2021, 42, 124-129.	0.9	17
6757	Bruchid beetle ovipositioning mediated defense responses in black gram pods. BMC Plant Biology, 2021, 21, 38.	1.6	4
6758	Genome-Wide Analysis and the Expression Pattern of the ERF Gene Family in Hypericum perforatum. Plants, 2021, 10, 133.	1.6	3
6759	Full-Length Transcriptome Analysis of Four Different Tissues of Cephalotaxus oliveri. International Journal of Molecular Sciences, 2021, 22, 787.	1.8	16
6760	<i>Bodo saltans</i> (Kinetoplastida) is dependent on a novel <i>Paracaedibacter</i>-like endosymbiont that possesses multiple putative toxin-antitoxin systems. ISME Journal, 2021, 15, 1680-1694.	4.4	11
6761	Genomic adaptation of Pseudomonas strains to acidity and antibiotics in hydrothermal vents at Kolumbo submarine volcano, Greece. Scientific Reports, 2021, 11, 1336.	1.6	9
6762	Complete genome sequence of Lactococcus lactis strain K_LL005, a xylose-utilizing bacterium isolated from grasshopper (Oxya chinensis sinuosa). Journal of Animal Science and Technology, 2021, 63, 191-193.	0.8	1
6763	InSexBase: an annotated genomic resource of sex chromosomes and sex-biased genes in insects. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	3
6764	Convergent evolution of pain-inducing defensive venom components in spitting cobras. Science, 2021, 371, 386-390.	6.0	96
6765	Prediction of neuropeptide precursors and differential expression of adipokinetic hormone/corazonin-related peptide, hugin and corazonin in the brain of malaria vector Nyssorhynchus albimanus during a Plasmodium berghei infection. Current Research in Insect Science, 2021, 1, 100014.	0.8	0
6766	Integrated miRNA-mRNA analysis reveals the roles of miRNAs in the replanting benefit of Achyranthes bidentata roots. Scientific Reports, 2021, 11, 1628.	1.6	8
6767	Common bean as a potential crop for future food security: an overview of past, current and future contributions in genomics, transcriptomics, transgenics and proteomics. Biotechnology and Biotechnological Equipment, 2021, 35, 759-787.	0.5	39
6768	Relevance of Metatranscriptomics in Symbiotic Associations Between Plants and Rhizosphere Microorganisms. , 2021, , 59-90.		2
6769	Pretreatment free of 2,4-dichlorophenoxyacetic acid improves the differentiation of sugarcane somatic embryos by affecting the hormonal balance and the accumulation of reserves. Plant Cell, Tissue and Organ Culture, 2021, 145, 101-115.	1.2	26
6770	Interspecific Variation in the Unsaturation Level of Seed Oils Were Associated With the Expression Pattern Shifts of Duplicated Desaturase Genes and the Potential Role of Other Regulatory Genes. Frontiers in Plant Science, 2020, 11, 616338.	1.7	3
6771	Genome sequence analysis provides insights on genomic variation and late blight resistance genes in potato somatic hybrid (parents and progeny). Molecular Biology Reports, 2021, 48, 623-635.	1.0	23

#	Article	IF	Citations
6772	An Ebola, Neisseria and Trypanosoma human protein interaction census reveals a conserved human protein cluster targeted by various human pathogens. Computational and Structural Biotechnology Journal, 2021, 19, 5292-5308.	1.9	4
6774	Hormonal and transcriptional analyses provides new insights into the molecular mechanisms underlying root thickening and isoflavonoid biosynthesis in Callerya speciosa (Champ. ex) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.6	12
6775	Identification of proteins and metabolic networks associated with sucrose accumulation in sugarcane (<i>Saccharum</i> spp. interspecific hybrids). Journal of Plant Interactions, 2021, 16, 166-178.	1.0	9
6776	RNA-Seq-based high-resolution linkage map reveals the genetic architecture of fruiting body development in shiitake mushroom, Lentinula edodes. Computational and Structural Biotechnology Journal, 2021, 19, 1641-1653.	1.9	12
6777	Elevation of vitellogenin expression in Sunn pest is associated with preâ€migration and migration phases of the life cycle. Physiological Entomology, 2021, 46, 94-104.	0.6	1
6778	Chemoreceptor Diversity in Apoid Wasps and Its Reduction during the Evolution of the Pollen-Collecting Lifestyle of Bees (Hymenoptera: Apoidea). Genome Biology and Evolution, 2021, 13, .	1.1	11
6779	Critical Role of MetR/MetB/MetC/MetX in Cysteine and Methionine Metabolism, Fungal Development, and Virulence of Alternaria alternata. Applied and Environmental Microbiology, 2021, 87, .	1.4	14
6780	Induced defense response in red mango fruit against Colletotrichum gloeosporioides. Horticulture Research, 2021, 8, 17.	2.9	26
6781	Orf165 is associated with cytoplasmic male sterility in pepper. Genetics and Molecular Biology, 2021, 44, e20210030.	0.6	2
6782	Enhanced Biosynthesis of Chlorogenic Acid and Its Derivatives in Methyl-Jasmonate-Treated Gardenia jasminoides Cells: A Study on Metabolic and Transcriptional Responses of Cells. Frontiers in Bioengineering and Biotechnology, 2020, 8, 604957.	2.0	8
6783	Investigation of the Molecular Mechanisms of Antioxidant Damage and Immune Response Downregulation in Liver of Coilia nasus Under Starvation Stress. Frontiers in Endocrinology, 2021, 12, 622315.	1.5	11
6784	First insight into the whole genome shotgun sequence of the endangered noble pen shell <i>Pinna nobilis</i>: a giant bivalve undergoing a mass mortality event. Journal of Molluscan Studies, 2021, 87, .	0.4	4
6785	De novo assembly of the Mylia taylorii transcriptome and identification of sesquiterpene synthases. Archives of Biochemistry and Biophysics, 2021, 698, 108742.	1.4	2
6786	Characterizing the Leaf Transcriptome of Chrysanthemum rhombifolium (Ling et C. Shih), a Drought Resistant, Endemic Plant From China. Frontiers in Genetics, 2021, 12, 625985.	1.1	11
6787	The <i>Mastigamoeba balamuthi</i> Genome and the Nature of the Free-Living Ancestor of <i>Entamoeba</i>. Molecular Biology and Evolution, 2021, 38, 2240-2259.	3.5	14
6789	Overexpression of the Transcription Factor AtLEC1 Significantly Improved the Lipid Content of Chlorella ellipsoidea. Frontiers in Bioengineering and Biotechnology, 2021, 9, 626162.	2.0	8
6790	Identification of genes associated with the biosynthesis of unsaturated fatty acid and oil accumulation in herbaceous peony â€˜Hangshaoâ€™ (Paeonia lactiflora â€˜Hangshaoâ€™) seeds based on transcriptome analysis. BMC Genomics, 2021, 22, 94.	1.2	17
6791	Transcriptome analysis reveals the mechanism of improving erect-plant-type peanut yield by single-seeding precision sowing. PeerJ, 2021, 9, e10616.	0.9	1

#	Article	IF	Citations
6792	A transcriptomic view to wounding response in young Scots pine stems. Scientific Reports, 2021, 11, 3778.	1.6	9
6793	Isolation and Functional Analysis of Genes Involved in Polyacylated Anthocyanin Biosynthesis in Blue Senecio cruentus. Frontiers in Plant Science, 2021, 12, 640746.	1.7	11
6794	Comparative transcriptome and tolerance mechanism analysis in the two contrasting wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 T 101-114.	1.8	28
6795	Quantitative Proteomics Analysis of Sugarcane Ratoon Crop Chlorosis. Sugar Tech, 2021, 23, 673-681.	0.9	6
6796	Integrative analysis of chloroplast DNA methylation in a marine algaâ€"Saccharina japonica. Plant Molecular Biology, 2021, 105, 611-623.	2.0	5
6797	Deciphering the dynamic gene expression patterns of pollen abortion in a male sterile line of Avena sativa through transcriptome analysis at different developmental stages. BMC Plant Biology, 2021, 21, 101.	1.6	2
6798	CoExp: A Web Tool for the Exploitation of Co-expression Networks. Frontiers in Genetics, 2021, 12, 630187.	1.1	16
6799	Transcriptome analysis and molecular mechanism of linseed (Linum usitatissimum L.) drought tolerance under repeated drought using single-molecule long-read sequencing. BMC Genomics, 2021, 22, 109.	1.2	22
6800	Comparative transcriptomic analysis of the liver of <i>Centropristis</i> <i>striata</i> in response to <i>Edwardsiella</i> <i>piscicida</i> infection. Aquaculture Research, 2021, 52, 2672-2684.	0.9	1
6801	Comparative Analysis, Characterization and Evolutionary Study of Dirigent Gene Family in Cucurbitaceae and Expression of Novel Dirigent Peptide against Powdery Mildew Stress. Genes, 2021, 12, 326.	1.0	16
6802	Transcriptome analysis of genes involved in starch biosynthesis in developing Chinese chestnut (Castanea mollissima Blume) seed kernels. Scientific Reports, 2021, 11, 3570.	1.6	10
6803	Identification of miRNA targets in eggplant in response to Verticillium dahliae by degradome sequencing. European Journal of Plant Pathology, 2021, 160, 97-111.	0.8	2
6804	RNA sequencing-based exploration of the effects of far-red light on lncRNAs involved in the shade-avoidance response of <i>D. officinale</i>. PeerJ, 2021, 9, e10769.	0.9	10
6805	iTRAQ-Based Quantitative Proteomics Reveals <i>ChAcb1</i> as a Novel Virulence Factor in <i>Colletotrichum higginsianum</i>. Phytopathology, 2021, 111, 1571-1582.	1.1	2
6806	Wing plasticity and associated gene expression varies across the pea aphid biotype complex. Evolution; International Journal of Organic Evolution, 2021, 75, 1143-1149.	1.1	9
6807	Molecular insight into somaclonal variation phenomena from transcriptome profiling of cucumber (Cucumis sativus L.) lines. Plant Cell, Tissue and Organ Culture, 2021, 145, 239-259.	1.2	14
6808	First annotated draft genomes of nonmarine ostracods (Ostracoda, Crustacea) with different reproductive modes. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	9
6809	Genome-wide identification and characterization of long non-coding RNAs involved in flag leaf senescence of rice. Plant Molecular Biology, 2021, 105, 655-684.	2.0	24

#	Article	IF	Citations
6810	Genome annotation of disease-causing microorganisms. Briefings in Bioinformatics, 2021, 22, 845-854.	3.2	13
6811	An RNA-seq Analysis Reveals Differential Transcriptional Responses to Different Light Qualities in Leaf Color of Camellia sinensis cv. Huangjinya. Journal of Plant Growth Regulation, 0, , 1.	2.8	9
6813	Comparing transcriptional responses to Fusarium crown rot in wheat and barley identified an important relationship between disease resistance and drought tolerance. BMC Plant Biology, 2021, 21, 73.	1.6	7
6814	Integrated Full-Length Transcriptome and RNA-Seq to Identify Immune System Genes from the Skin of Sperm Whale (Physeter macrocephalus). Genes, 2021, 12, 233.	1.0	4
6815	Integrated metabolic profiling and transcriptome analysis of pigment accumulation in Lonicera japonica flower petals during colour-transition. BMC Plant Biology, 2021, 21, 98.	1.6	36
6816	New validated Eucalyptus SSR markers located in candidate genes involved in growth and plant development. Forest Systems, 2021, 29, eSC08.	0.1	0
6817	Azadirachta indica MicroRNAs: Genome-Wide Identification, Target Transcript Prediction, and Expression Analyses. Applied Biochemistry and Biotechnology, 2021, 193, 1924-1944.	1.4	1
6819	A tale of two fish: Comparative transcriptomics of resistant and susceptible steelhead following exposure to Ceratonova shasta highlights differences in parasite recognition. PLoS ONE, 2021, 16, e0234837.	1.1	16
6820	Bacillus spp. metabolites are effective in eradicating Aedes aegypti (Diptera: Culicidae) larvae with low toxicity to non-target species. Journal of Invertebrate Pathology, 2021, 179, 107525.	1.5	15
6821	A large genome with chromosomeâ€scale assembly sheds light on the evolutionary success of a true toad (<i>Bufo gargarizans</i>). Molecular Ecology Resources, 2021, 21, 1256-1273.	2.2	32
6822	Transcriptome Analysis of the Fruit of Two Strawberry Cultivars â€œSunnyberryâ€• and â€œKingsberryâ€• That Show Different Susceptibility to Botrytis cinerea after Harvest. International Journal of Molecular Sciences, 2021, 22, 1518.	1.8	10
6824	Genome Sequencing of Kocuria varians Strain 80, Isolated from Starter Culture for Dry Sausage. Microbiology Resource Announcements, 2021, 10, .	0.3	0
6825	A chromosomeâ€level genome of the mud crab (<i>Scylla paramamosain</i> estampador) provides insights into the evolution of chemical and light perception in this crustacean. Molecular Ecology Resources, 2021, 21, 1299-1317.	2.2	17
6826	RNAi activation with homologous and heterologous sequences that induce resistance against the begomovirus Pepper golden mosaic virus (PepGMV). 3 Biotech, 2021, 11, 114.	1.1	3
6828	Wholeâ€genome characterization of chronological ageâ€associated changes in methylome and circular RNAs in moso bamboo (<i>Phyllostachys edulis</i>) from vegetative to floral growth. Plant Journal, 2021, 106, 435-453.	2.8	27
6829	Detection of horizontal gene transfer in the genome of the choanoflagellate Salpingoeca rosetta. Scientific Reports, 2021, 11, 5993.	1.6	14
6831	De novo transcriptome reveals blood coagulation/antithrombin factors and infection mechanisms in Angiostrongylus cantonensis adult worms. Parasitology, 2021, 148, 857-870.	0.7	0
6832	Molecular Analysis Associated with Early Flowering Mutant in Brassica napus. Journal of Plant Biology, 2021, 64, 227-241.	0.9	1

#	Article	IF	Citations
6833	Phylogenomics of Ichneumonoidea (Hymenoptera) and implications for evolution of mode of parasitism and viral endogenization. Molecular Phylogenetics and Evolution, 2021, 156, 107023.	1.2	30
6834	Identification of Genes Involved in Digestion from Transcriptome of Parasesarma pictum and Parasesarma affine Hepatopancreas. Thalassas, 2022, 38, 93-101.	0.1	2
6835	Environmentally Driven Color Variation in the Pearl Oyster Pinctada margaritifera var. cumingii (Linnaeus, 1758) Is Associated With Differential Methylation of CpGs in Pigment- and Biomineralization-Related Genes. Frontiers in Genetics, 2021, 12, 630290.	1.1	7
6836	Transcriptome sequencing and microsatellite marker discovery in Ailanthus altissima (Mill.) Swingle (Simaroubaceae). Molecular Biology Reports, 2021, 48, 2007-2023.	1.0	7
6837	Combined Transcriptome Analysis Reveals the Ovule Abortion Regulatory Mechanisms in the Female Sterile Line of Pinus tabuliformis Carr.. International Journal of Molecular Sciences, 2021, 22, 3138.	1.8	0
6838	Thuricin17 Production and Proteome Differences in Bacillus thuringiensis NEB17 Cell-Free Supernatant Under NaCl Stress. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	6
6839	Proteomic profile and protease activity in the skin mucus of greater amberjack (Seriola dumerili) infected with the ectoparasite Neobenedenia girellae â€" An immunological approach. Fish and Shellfish Immunology, 2021, 110, 100-115.	1.6	17
6840	Long-term persistence of supernumerary B chromosomes in multiple species of Astyanax fish. BMC Biology, 2021, 19, 52.	1.7	8
6841	Planarians (Platyhelminthes)â€"An Emerging Model Organism for Investigating Innate Immune Mechanisms. Frontiers in Cellular and Infection Microbiology, 2021, 11, 619081.	1.8	8
6842	Physiological and transcriptional response to drought stress among bioenergy grass Miscanthus species. Biotechnology for Biofuels, 2021, 14, 60.	6.2	13
6843	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i>. GigaScience, 2021, 10, .	3.3	88
6844	Draft genome sequencing of the foxglove aphid (Aulacorthum solani Kaltenbach), a vector of potato viruses, provides insights on virulence genes. Journal of Asia-Pacific Entomology, 2021, 24, 93-93.	0.4	3
6845	Physiological and gene expression profiles of leg muscle provide insights into molting-dependent growth of Chinese mitten crab (Eriocheir sinensis). Reproduction and Breeding, 2021, 1, 32-38.	0.8	1
6846	Antennal transcriptome analysis of olfactory genes and characterizations of odorant binding proteins in two woodwasps, Sirex noctilio and Sirex nitobei (Hymenoptera: Siricidae). BMC Genomics, 2021, 22, 172.	1.2	18
6847	Transcriptional identification of differentially expressed genes during the prepupalâ€"pupal transition in the oriental armyworm, Mythimna separata (Walker) (Lepidoptera: Noctuidae). Bulletin of Entomological Research, 2021, 111, 485-498.	0.5	2
6848	Epigenetic Variability Among Saffron Crocus (Crocus sativus L.) Accessions Characterized by Different Phenotypes. Frontiers in Plant Science, 2021, 12, 642631.	1.7	15
6849	A Comparison of the Transcriptomes of Cowpeas in Response to Two Different Ionizing Radiations. Plants, 2021, 10, 567.	1.6	9
6850	Innate Resistance and Phosphite Treatment Affect Both the Pathogenâ€™s and Hostâ€™s Transcriptomes in the Tanoak-Phytophthora ramorum Pathosystem. Journal of Fungi (Basel, Switzerland), 2021, 7, 198.	1.5	11

#	ARTICLE	IF	CITATIONS
6851	Genome-wide differential expression analysis explores antibacterial molecular mechanisms of zebrafish intestine upon pathogenic Streptococcus agalactiae challenge. Aquaculture Reports, 2021, 19, 100639.	0.7	2
6852	Expression analysis of genes related to cold tolerance in<i> Dendroctonus valens</i>. PeerJ, 2021, 9, e10864.	0.9	9
6853	Microcracks on the Rat Root Surface Induced by Orthodontic Force, Crack Extension Simulation, and Proteomics Study. Annals of Biomedical Engineering, 2021, 49, 2228-2242.	1.3	3
6854	Genomic Signature for Stem Swollen of Kohlrabi Morphotype in <i>Brassica oleracea</i>. Plant Breeding and Biotechnology, 2021, 9, 45-54.	0.3	0
6855	Draft Genome Resource of a Novel Virulent <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> Race 1 Strain (VCG 0124) Infecting Cavendish (AAA) Group of Banana in India. Plant Disease, 2021, 105, 2708-2710.	0.7	5
6857	Transcriptome sequencing and analysis for the pigmentation of scale and skin in common carp (Cyprinus carpio). Molecular Biology Reports, 2021, 48, 2399-2410.	1.0	1
6859	Absence of 4-Formylaminooxyvinylglycine Production by Pseudomonas fluorescens WH6 Results in Resource Reallocation from Secondary Metabolite Production to Rhizocompetence. Microorganisms, 2021, 9, 717.	1.6	2
6860	Comparative transcriptome and metabolome analysis of Ostrinia furnacalis female adults under UV-A exposure. Scientific Reports, 2021, 11, 6797.	1.6	8
6861	A first insight into the genome of Prototheca wickerhamii, a major causative agent of human protothecosis. BMC Genomics, 2021, 22, 168.	1.2	9
6862	Comparative analysis of extracellular proteomes reveals putative effectors of the boxwood blight pathogens, Calonectria henricotiae and C. pseudonaviculata. Bioscience Reports, 2021, 41, .	1.1	3
6863	Comparative genome analyses suggest a hemibiotrophic lifestyle and virulence differences for the beech bark disease fungal pathogens Neonectria faginata and Neonectria coccinea. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
6864	Organic zinc supplementation modifies the metalloproteome of royal jelly produced by <i>Apis mellifera</i>. Journal of Apicultural Research, 2023, 62, 590-597.	0.7	3
6865	Transcriptome analysis revealed that multiple genes were related to the cyflumetofen resistance of Tetranychus cinnabarinus (Boisduval). Pesticide Biochemistry and Physiology, 2021, 173, 104799.	1.6	9
6866	Comparative Transcriptome Profiling of mRNA and lncRNA of Ovaries in High and Low Egg Production Performance in Domestic Pigeons (Columba livia). Frontiers in Genetics, 2021, 12, 571325.	1.1	4
6867	Toward Systematic Understanding of Flower Bud Induction in Apple: A Multi-Omics Approach. Frontiers in Plant Science, 2021, 12, 604810.	1.7	12
6868	Metabolic and immunological effects of gut microbiota in leaf beetles at the local and systemic levels. Integrative Zoology, 2021, 16, 313-323.	1.3	41
6869	Molecular control of the floral transition in the mast seeding plant Celmisia lyallii (Asteraceae). Molecular Ecology, 2021, 30, 1846-1863.	2.0	9
6870	Study of the olive <i>Î²</i>â€glucosidase gene family putatively involved in the synthesis of phenolic compounds of virgin olive oil. Journal of the Science of Food and Agriculture, 2021, 101, 5409-5418.	1.7	7

#	Article	IF	Citations
6871	Full-Length Transcriptome Analyses of Genes Involved in Triterpenoid Saponin Biosynthesis of Psammosilene tunicoides Hairy Root Cultures With Exogenous Salicylic Acid. Frontiers in Genetics, 2021, 12, 657060.	1.1	13
6872	Phylogenomics of Plant-Associated Botryosphaeriaceae Species. Frontiers in Microbiology, 2021, 12, 652802.	1.5	28
6873	Molecular Pathways and Pigments Underlying the Colors of the Pearl Oyster Pinctada margaritifera var. cumingii (Linnaeus 1758). Genes, 2021, 12, 421.	1.0	9
6874	Priming by High Temperature Stress Induces MicroRNA Regulated Heat Shock Modules Indicating Their Involvement in Thermopriming Response in Rice. Life, 2021, 11, 291.	1.1	14
6875	Transcriptional Analyses of Acute Exposure to Methylmercury on Erythrocytes of Loggerhead Sea Turtle. Toxics, 2021, 9, 70.	1.6	2
6877	Identification of putative ingestion-related olfactory receptor genes in the Chinese mitten crab (Eriocheir japonica sinensis). Genes and Genomics, 2021, 43, 479-490.	0.5	1
6878	Transcriptome analyses and weighted gene coexpression network analysis reveal key pathways and genes involved in the rapid cold resistance of the Chinese white wax scale insect. Archives of Insect Biochemistry and Physiology, 2021, 107, e21781.	0.6	11
6879	Transcriptional profiling of MED Bemisia tabaci exposed to thermal stress and verification of HSP70 expression. Entomological Research, 2021, 51, 251-262.	0.6	3
6880	Gene expression for secondary metabolite biosynthesis in hop (Humulus lupulus L.) leaf lupulin glands exposed to heat and low-water stress. Scientific Reports, 2021, 11, 5138.	1.6	16
6881	Comparative Analysis of Adelphocoris suturalis Jakovlev (Hemiptera: Miridae) Immune Responses to Fungal and Bacterial Pathogens. Frontiers in Physiology, 2021, 12, 646721.	1.3	5
6884	Comparative transcriptome profiling of Chinese wild grapes provides insights into powdery mildew resistance. Phytopathology, 2021, , PHYTO01210006R.	1.1	7
6885	The draft genome of the specialist flea beetle Altica viridicyanea (Coleoptera: Chrysomelidae). BMC Genomics, 2021, 22, 243.	1.2	6
6887	Preliminary investigations on the pathogenesis-related protein expression profile of the medicinal herb Macleaya cordata and anti-bacterial properties of recombinant proteins. Phytochemistry, 2021, 184, 112667.	1.4	2
6888	The molecular mechanisms of Chlorella sp. responding to high CO2: A study based on comparative transcriptome analysis between strains with high- and low-CO2 tolerance. Science of the Total Environment, 2021, 763, 144185.	3.9	27
6889	Transcriptome-Wide Analyses Provide Insights into Development of the Hedychium coronarium Flower, Revealing Potential Roles of PTL. Journal of Plant Biology, 2021, 64, 431-445.	0.9	2
6890	Differential expression of microRNAs and tRNA fragments mediate the adaptation of the liver fluke Fasciola gigantica to its intermediate snail and definitive mammalian hosts. International Journal for Parasitology, 2021, 51, 405-414.	1.3	15
6891	Transcriptome analysis of immune- and iron-related genes after Francisella noatunensis subsp. orientalis infection in Nile tilapia (Oreochromis niloticus). Fish and Shellfish Immunology, 2021, 111, 36-48.	1.6	13
6892	A Chromosomeâ€"Level Genome Assembly of the Spotted Scat (<i>Scatophagus argus</i>). Genome Biology and Evolution, 2021, 13, .	1.1	17

#	Article	IF	Citations
6893	Unraveling the polypharmacology of a natural antifungal product, eugenol, against <i>Rhizoctonia solani</i>. Pest Management Science, 2021, 77, 3469-3483.	1.7	30
6894	Toxicity of silver nanoparticles (AgNPs) in the model ciliate Paramecium multimicronucleatum: Molecular mechanisms of activation are dose- and particle size-dependent. European Journal of Protistology, 2021, 81, 125792.	0.5	2
6895	SNP markers associated with resistance to frosty pod and black pod rot diseases in an F1 population of Theobroma cacao L.. Tree Genetics and Genomes, 2021, 17, 1.	0.6	11
6896	Understanding the Transcriptional Changes During Infection of Meloidogyne incognita Eggs by the Egg-Parasitic Fungus Purpureocillium lilacinum. Frontiers in Microbiology, 2021, 12, 617710.	1.5	5
6897	The Regulation of Adaptation to Cold and Drought Stresses in Poa crymophila Keng Revealed by Integrative Transcriptomics and Metabolomics Analysis. Frontiers in Plant Science, 2021, 12, 631117.	1.7	8
6898	Transcriptomic analysis of Î±-linolenic acid content and biosynthesis in Paeonia ostii fruits and seeds. BMC Genomics, 2021, 22, 297.	1.2	9
6899	Identification of Novel Toxin Genes from the Stinging Nettle Caterpillar Parasa lepida (Cramer, 1799): Insights into the Evolution of Lepidoptera Toxins. Insects, 2021, 12, 396.	1.0	2
6900	Genome-wide identification and analysis of long non-coding RNAs involved in fatty acid biosynthesis in young soybean pods. Scientific Reports, 2021, 11, 7603.	1.6	11
6902	Genomic and transcriptomic insights into the habitat adaptation of the diazotrophic paddyâ€field cyanobacterium <i>Nostoc sphaeroides</i>. Environmental Microbiology, 2021, 23, 5802-5822.	1.8	5
6903	Comparative transcriptome profiling reveals the basis of differential sheath blight disease response in tolerant and susceptible rice genotypes. Protoplasma, 2022, 259, 61-73.	1.0	9
6905	Verticillium dahliae reduces plant growth, constitutively induces antioxidant metabolism and gene expression in eggplant (Solanum melongena L.). Physiological and Molecular Plant Pathology, 2021, 114, 101641.	1.3	5
6906	Biosyntheses characterization of alkaloids and flavonoids in Sophora flavescens by combining metabolome and transcriptome. Scientific Reports, 2021, 11, 7388.	1.6	11
6907	Transcriptome Profile Reveals Drought-Induced Genes Preferentially Expressed in Response to Water Deficit in Cultivated Peanut (Arachis hypogaea L.). Frontiers in Plant Science, 2021, 12, 645291.	1.7	7
6908	Deep Insight Into Long Non-coding RNA and mRNA Transcriptome Profiling in HepG2 Cells Expressing Genotype IV Swine Hepatitis E Virus ORF3. Frontiers in Veterinary Science, 2021, 8, 625609.	0.9	1
6909	Genome of the destructive oomycete Phytophthora cinnamomi provides insights into its pathogenicity and adaptive potential. BMC Genomics, 2021, 22, 302.	1.2	24
6910	Combination of RNA-Seq transcriptomics and iTRAQ proteomics reveal the mechanism involved in fresh-cut yam yellowing. Scientific Reports, 2021, 11, 7755.	1.6	6
6911	Transcriptome analysis of the liver of <i>Eospalax fontanierii</i> under hypoxia. PeerJ, 2021, 9, e11166.	0.9	3
6912	Comparison of Gonadal Transcriptomes Uncovers Reproduction-Related Genes with Sexually Dimorphic Expression Patterns in Diodon hystrix. Animals, 2021, 11, 1042.	1.0	9

#	ARTICLE	IF	CITATIONS
6913	Chromosomeâ€level genome assembly of burbot (<i>Lota lota</i>) provides insights into the evolutionary adaptations in freshwater. Molecular Ecology Resources, 2021, 21, 2022-2033.	2.2	8
6914	miRNA-Based Drought Regulation in the Important Medicinal Plant Dendrobium huoshanense. Journal of Plant Growth Regulation, 0, , 1.	2.8	11
6915	Physiological and Transcriptomic Analysis Provide Insight into Low Temperature Enhancing Hypericin Biosynthesis in Hypericum perforatum. Molecules, 2021, 26, 2294.	1.7	5
6916	Comparative transcriptome analyses revealed different heat stress responses in pigeonpea (Cajanus) Tj ETQq1 1 0.784314 rgBT /Over	2.8	6
6918	An Introduction to Next Generation Sequencing Bioinformatic Analysis in Gut Microbiome Studies. Biomolecules, 2021, 11, 530.	1.8	62
6919	Crowdsourced Identification of Potential Target Genes for CTV Induced Gene Silencing for Controlling the Citrus Greening Vector Diaphorina citri. Frontiers in Physiology, 2021, 12, 571826.	1.3	3
6922	Physical map of lncRNAs and lincRNAs linked with stress responsive miRs and genes network of pigeonpea (Cajanus cajan L.). Journal of Plant Biochemistry and Biotechnology, 2022, 31, 271-292.	0.9	4
6923	Differential expression of starch and sucrose metabolic genes linked to varying biomass yield in Miscanthus hybrids. Biotechnology for Biofuels, 2021, 14, 98.	6.2	8
6924	Transcriptome of weeping pinyon pine, Pinus pinceana, shows differences across heterogeneous habitats. Trees - Structure and Function, 2021, 35, 1351-1365.	0.9	4
6925	FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks. NAR Genomics and Bioinformatics, 2021, 3, lqab057.	1.5	3
6926	Data of de novo transcriptome assembly of the myxozoan parasite Tetracapsuloides bryosalmonae. Data in Brief, 2021, 35, 106831.	0.5	5
6927	Transcriptional Profiling of Three<i>Pseudomonas syringae</i>pv.<i>actinidiae</i>Biovars Reveals Different Responses to Apoplast-Like Conditions Related to Strain Virulence on the Host. Molecular Plant-Microbe Interactions, 2021, 34, 376-396.	1.4	15
6928	High-quality, haplotype-phased de novo assembly of the highly heterozygous fig genome, a major genetic resource for fig breeding. Acta Horticulturae, 2021, , 21-28.	0.1	1
6929	Integrated transcriptomics and metabolites at different growth stages reveals the regulation mechanism of bolting and flowering of <i>Angelica</i><i>sinensis</i>. Plant Biology, 2021, 23, 574-582.	1.8	13
6930	Integration of early disease-resistance phenotyping, histological characterization, and transcriptome sequencing reveals insights into downy mildew resistance in impatiens. Horticulture Research, 2021, 8, 108.	2.9	5
6931	Global Changes in Asexual EpichloÃ« Transcriptomes during the Early Stages, from Seed to Seedling, of Symbiotum Establishment. Microorganisms, 2021, 9, 991.	1.6	6
6932	Integrated Analysis of Long Noncoding RNA Expression Profiles in Acute-on-Chronic Liver Failure. BioMed Research International, 2021, 2021, 1-13.	0.9	2
6933	Chromosomal-Level Reference Genome of the Neotropical Tree Jacaranda mimosifolia D. Don. Genome Biology and Evolution, 2021, 13, .	1.1	7

#	ARTICLE	IF	CITATIONS
6934	Three putative DNA methyltransferases of Verticillium dahliae differentially contribute to DNA methylation that is dispensable for growth, development and virulence. Epigenetics and Chromatin, 2021, 14, 21.	1.8	8
6935	Genome-wide identification and phylogenetic relationships of the Hsp70 gene family of Aegilops tauschii, wild emmer wheat (Triticum dicoccoides) and bread wheat (Triticum aestivum). 3 Biotech, 2021, 11, 301.	1.1	6
6936	Population transcriptomic sequencing reveals allopatric divergence and local adaptation in Pseudotaxus chienii (Taxaceae). BMC Genomics, 2021, 22, 388.	1.2	11
6937	Genome wide analysis of Mycobacterium leprae for identification of putative microRNAs and their possible targets in human. Biologia (Poland), 2021, 76, 2437-2454.	0.8	0
6938	Comparative transcriptomics of albino and warninglyâ€coloured caterpillars. Ecology and Evolution, 2021, 11, 7507-7517.	0.8	6
6939	The transcriptome analysis on urea response mechanism in the process of ergosterol synthesis by Cordyceps cicadae. Scientific Reports, 2021, 11, 10927.	1.6	4
6940	Metabolic Plasticity of Gilthead Seabream Under Different Stressors: Analysis of the Stress Responsive Hepatic Proteome and Gene Expression. Frontiers in Marine Science, 2021, 8, .	1.2	10
6941	Vasopressin Promoter Transgenic and Vasopressin Gene-Edited Ascidian, Ciona intestinalis Type A (Ciona robusta): Innervation, Gene Expression Profiles, and Phenotypes. Frontiers in Endocrinology, 2021, 12, 668564.	1.5	9
6942	Characterization of the differential expressed genes and transcriptomic pathway analysis in the liver of sub-adult red drum (Sciaenops ocellatus) exposed to Deepwater Horizon chemically dispersed oil. Ecotoxicology and Environmental Safety, 2021, 214, 112098.	2.9	2
6944	Basidiomycetes Are Particularly Sensitive to Bacterial Volatile Compounds: Mechanistic Insight Into the Case Study of Pseudomonas protegens Volatilome Against Heterobasidion abietinum. Frontiers in Microbiology, 2021, 12, 684664.	1.5	14
6946	Pan-Genome Analysis Reveals Host-Specific Functional Divergences in Burkholderia gladioli. Microorganisms, 2021, 9, 1123.	1.6	13
6948	Sensory gene identification in the transcriptome of the ectoparasitoid Quadrastichus mendeli. Scientific Reports, 2021, 11, 9726.	1.6	4
6949	A candidate gene identified in converting platycoside E to platycodin D from Platycodon grandiflorus by transcriptome and main metabolites analysis. Scientific Reports, 2021, 11, 9810.	1.6	13
6950	Combining targeted metabolite analyses and transcriptomics to reveal the specific chemical composition and associated genes in the incompatible soybean variety PI437654 infected with soybean cyst nematode HG1.2.3.5.7. BMC Plant Biology, 2021, 21, 217.	1.6	14
6951	Global Transcriptome Profiling Identified Transcription Factors, Biological Process, and Associated Pathways for Pre-Harvest Aflatoxin Contamination in Groundnut. Journal of Fungi (Basel,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 177 Td (	1.5	10
6952	Cionin, a vertebrate cholecystokinin/gastrin homolog, induces ovulation in the ascidian Ciona intestinalis type A. Scientific Reports, 2021, 11, 10911.	1.6	9
6953	The macronuclear genome of anaerobic ciliate Entodinium caudatum reveals its biological features adapted to the distinct rumen environment. Genomics, 2021, 113, 1416-1427.	1.3	20
6954	Species and population specific gene expression in blood transcriptomes of marine turtles. BMC Genomics, 2021, 22, 346.	1.2	9

#	ARTICLE	IF	CITATIONS
6955	De novo full length transcriptome analysis of Arachis glabrata provides insights into gene expression dynamics in response to biotic and abiotic stresses. Genomics, 2021, 113, 1579-1588.	1.3	11
6956	Transcriptome and morpho-physiological analyses reveal factors regulating cone bud differentiation in Qinghai spruce (Picea crassifolia Kom.). Trees - Structure and Function, 2021, 35, 1151-1166.	0.9	5
6957	Detection of alternative splicing in western corn rootworm (<scp><i>Diabrotica virgifera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 Td (<scp>RNA</scp>â€seq and <scp>PacBio Isoâ€Seq</scp>. Insect Molecular Biology, 2021, 30, 436-445.	1.0	6
6958	The membrane-localized protein kinase MAP4K4/TOT3 regulates thermomorphogenesis. Nature Communications, 2021, 12, 2842.	5.8	30
6959	The Zinc Nutritional Immunity of Epinephelus coioides Contributes to the Importance of znuC During Pseudomonas plecoglossicida Infection. Frontiers in Immunology, 2021, 12, 678699.	2.2	13
6960	The genome of Nautilus pompilius illuminates eye evolution and biomineralization. Nature Ecology and Evolution, 2021, 5, 927-938.	3.4	40
6962	Comparative Analysis of the Intermolt and Postmolt Hepatopancreas Transcriptomes Provides Insight into the Mechanisms of Procambarus clarkii Molting Process. Life, 2021, 11, 480.	1.1	4
6963	Transcriptomic and metabolomic analyses provide insights into the biosynthesis of chlorogenic acids in Lonicera macranthoides Hand.-Mazz. PLoS ONE, 2021, 16, e0251390.	1.1	2
6964	From simple and specific zymographic detections to the annotation of a fungus Daldinia caldariorum D263 that encodes a wide range of highly bioactive cellulolytic enzymes. Biotechnology for Biofuels, 2021, 14, 120.	6.2	2
6965	LTR-retrotransposon dynamics in common fig (Ficus carica L.) genome. BMC Plant Biology, 2021, 21, 221.	1.6	5
6966	A promiscuous fatty acid Ï‰â€hydroxylase CYP94A90 is likely to be involved in biosynthesis of a floral nitro compound in loquat (<i>Eriobotrya japonica</i>). New Phytologist, 2021, 231, 1157-1170.	3.5	9
6967	Transcriptional Response in the Digestive Gland of the King Scallop (Pecten maximus) After the Injection of Domoic Acid. Toxins, 2021, 13, 339.	1.5	9
6968	A Chromosome-Level Assembly of Blunt Snout Bream (<i>Megalobrama amblycephala</i>) Genome Reveals an Expansion of Olfactory Receptor Genes in Freshwater Fish. Molecular Biology and Evolution, 2021, 38, 4238-4251.	3.5	32
6969	Molecular mechanisms of mutualistic and antagonistic interactions in a plantâ€“pollinator association. Nature Ecology and Evolution, 2021, 5, 974-986.	3.4	30
6970	Herbaspirillum seropedicae strain HRC54 expression profile in response to sugarcane apoplastic fluid. 3 Biotech, 2021, 11, 292.	1.1	2
6971	Genic introgression from an invasive exotic fungal forest pathogen increases the establishment potential of a sibling native pathogen. NeoBiota, 0, 65, 109-136.	1.0	6
6972	Oryzias curvinotus in Sanya Does Not Contain the Male Sex-Determining Gene dmy. Animals, 2021, 11, 1327.	1.0	7
6973	Identification of miRNAs and Their Targets Involved in Flower and Fruit Development across Domesticated and Wild Capsicum Species. International Journal of Molecular Sciences, 2021, 22, 4866.	1.8	13

#	Article	IF	Citations
6974	Bibliometric Analysis on Bibliometric-based Ontology Research. Science and Technology Libraries, 0, , 1-19.	0.8	3
6975	Sequencing and functional analysis of mRNAs and lncRNAs from tea (Camellia sinensis) leaves during infection by the fungal pathogen, Lasiodiplodia theobromae. PhytoFrontiers, 0, , .	0.8	4
6976	Comprehensive phylogeny of Konosirus punctatus (Clupeiformes: Clupeidae) based on transcriptomic data. Bioscience Reports, 2021, 41, .	1.1	2
6977	No pre-zygotic isolation mechanisms between Schistosoma haematobium and Schistosoma bovis parasites: From mating interactions to differential gene expression. PLoS Neglected Tropical Diseases, 2021, 15, e0009363.	1.3	9
6978	RNA-seq derived identification of coronatine-regulated genes putatively involved in terpenoid biosynthetic pathway in the rubber tree Hevea brasiliensis. IOP Conference Series: Earth and Environmental Science, 2021, 749, 012033.	0.2	1
6979	iTRAQ-based quantitative glutelin proteomic analysis reveals differentially expressed proteins in the physiological metabolism process during endosperm development and their impacts on yield and quality in autotetraploid rice. Plant Science, 2021, 306, 110859.	1.7	5
6980	Transcriptomic responses of saline-adapted Nile tilapia (Oreochromis niloticus) to rearing in both saline and freshwater. Marine Genomics, 2021, 60, 100879.	0.4	6
6981	Genome-wide Identification and Analysis of Late Embryogenesis Abundant (LEA) Genes in Musa acuminata. Tropical Plant Biology, 2021, 14, 295-312.	1.0	3
6983	Evaluation of the differences between biofilm and planktonic Brucella abortus via metabolomics and proteomics. Functional and Integrative Genomics, 2021, 21, 421-433.	1.4	10
6984	Not just shades of grey: life is full of colour for the ocellate river stingray (Potamotrygon motoro). Journal of Experimental Biology, 2021, 224, .	0.8	8
6985	Polyploidy underlies co-option and diversification of biosynthetic triterpene pathways in the apple tribe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37
6986	Monoterpenoid signals and their transcriptional responses to feeding and juvenile hormone regulation in bark beetle <i>Ips hauser</i> <i>i</i>. Journal of Experimental Biology, 2021, 224, .	0.8	4
6987	A prescient evolutionary model for genesis, duplication and differentiation of MIR160 homologs in Brassicaceae. Molecular Genetics and Genomics, 2021, 296, 985-1003.	1.0	6
6988	Characterization of a gene co-expression network associated with MGST, the pollen modifier gene of gametophytic self-incompatibility in sweet cherry (Prunus avium L.). Acta Horticulturae, 2021, , 9-16.	0.1	1
6989	MiR8181 is involved in the cell growth regulation of Saccharina japonica. Journal of Plant Physiology, 2021, 260, 153394.	1.6	3
6990	De novo transcriptome analysis and identification of reproduction control genes from the red palm weevil Rhynchophorus ferrugineus. PLoS ONE, 2021, 16, e0251278.	1.1	6
6991	Genomics and transcriptomics analyses provide insights into the cold adaptation strategies of an Antarctic bacterium, Cryobacterium sp. SO1. Polar Biology, 2021, 44, 1305-1319.	0.5	7
6992	Characterization of the detrimental effects of type IV glandular trichomes on the aphid Macrosiphum euphorbiae in tomato. Pest Management Science, 2021, 77, 4117-4127.	1.7	10

#	ARTICLE	IF	CITATIONS
6993	Genome and transcriptome sequencing of a newly isolated 2,4-dinitrophenol-degrading strain Rhodococcus imtechensis XM24D. Genes and Genomics, 2021, 43, 829-835.	0.5	0
6994	Transcriptome Analysis of the Japanese Pine Sawyer Beetle, Monochamus alternatus, Infected with the Entomopathogenic Fungus Metarhizium anisopliae JEF-197. Journal of Fungi (Basel, Switzerland), 2021, 7, 373.	1.5	6
6995	An improved direct metamobilome approach increases the detection of larger-sized circular elements across kingdoms. Plasmid, 2021, 115, 102576.	0.4	6
6996	EMS Derived Wheat Mutant BIG8-1 (Triticum aestivum L.)â€"A New Drought Tolerant Mutant Wheat Line. International Journal of Molecular Sciences, 2021, 22, 5314.	1.8	9
6997	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. PLoS Genetics, 2021, 17, e1009530.	1.5	26
6998	De Novo Sporophyte Transcriptome Assembly and Functional Annotation in the Endangered Fern Species Vandenboschia speciosa (Willd.) G. Kunkel. Genes, 2021, 12, 1017.	1.0	3
6999	A New Look at the Genus Solobacterium: A Retrospective Analysis of Twenty-Seven Cases of Infection Involving S. moorei and a Review of Sequence Databases and the Literature. Microorganisms, 2021, 9, 1229.	1.6	13
7000	Transcriptome analysis unravels RNAi pathways genes and putative expansion of CYP450 gene family in cotton leafhopper Amrasca biguttula (Ishida). Molecular Biology Reports, 2021, 48, 4383-4396.	1.0	3
7001	Comparative Transcriptome Profiling of Kappaphycus alvarezii (Rhodophyta, Solieriaceae) in Response to Light of Different Wavelengths and Carbon Dioxide Enrichment. Plants, 2021, 10, 1236.	1.6	6
7002	Full-length transcriptome sequences by a combination of sequencing platforms applied to isoflavonoid and triterpenoid saponin biosynthesis of Astragalus mongholicus Bunge. Plant Methods, 2021, 17, 61.	1.9	6
7003	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. Plant Genome, 2022, 15, e20109.	1.6	53
7004	Postâ€mating gene expression of <scp>Mexican</scp> fruit fly females: disentangling the effects of the male accessory glands. Insect Molecular Biology, 2021, 30, 480-496.	1.0	10
7005	Revealing the Characteristics of the Antarctic Snow Alga Chlorominima collina gen. et sp. nov. Through Taxonomy, Physiology, and Transcriptomics. Frontiers in Plant Science, 2021, 12, 662298.	1.7	9
7006	Rootstock effects on scion gene expression in maritime pine. Scientific Reports, 2021, 11, 11582.	1.6	12
7007	To hum or not to hum: Neural transcriptome signature of male courtship vocalization in a teleost fish. Genes, Brain and Behavior, 2021, 20, e12740.	1.1	2
7008	A chromosome-level Camptotheca acuminata genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. Nature Communications, 2021, 12, 3531.	5.8	66
7009	A Combined Morphological and Molecular Evolutionary Analysis of Karst-Environment Adaptation for the Genus Urophysa (Ranunculaceae). Frontiers in Plant Science, 2021, 12, 667988.	1.7	2
7010	Exploring the biosynthetic pathway of lignin in <i>Acorus tatarinowii</i> Schott using <i>de novo</i> leaf and rhizome transcriptome analysis. Bioscience Reports, 2021, 41, .	1.1	5

#	Article	IF	Citations
7011	Global transcriptome landscape of the rabbit protozoan parasite Eimeria stiedae. Parasites and Vectors, 2021, 14, 308.	1.0	9
7012	Whole Transcriptome Analysis Reveals a Potential Regulatory Mechanism of LncRNA-FNIP2/miR-24-3p/FNIP2 Axis in Chicken Adipogenesis. Frontiers in Cell and Developmental Biology, 2021, 9, 653798.	1.8	14
7013	Wolfberry genomes and the evolution of LyciumÂ(Solanaceae). Communications Biology, 2021, 4, 671.	2.0	40
7014	Whole genome data from Curtobacterium flaccumfaciens pv. flaccumfaciens strains associated with tan spot of mungbean and soybean reveal diverse plasmid profiles. Molecular Plant-Microbe Interactions, 2021, 34, 1216-1222.	1.4	7
7015	Genetic Divergence and Population Structure in Weedy and Cultivated Broomcorn Millets (Panicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Science, 2021, 12, 688444.	1.7	13
7016	De novo Transcriptome Assembly and Comparative Analysis Highlight the Primary Mechanism Regulating the Response to Selenium Stimuli in Oats (Avena sativa L.). Frontiers in Plant Science, 2021, 12, 625520.	1.7	2
7017	Response to selection for parasitism of a suboptimal, lowâ€preference host in an aphid parasitoid. Evolutionary Applications, 2021, 14, 2012-2024.	1.5	8
7018	Identification of differentially expressed microRNAs under imidacloprid exposure in Sitobion miscanthi. Pesticide Biochemistry and Physiology, 2021, 177, 104885.	1.6	13
7019	Molecular mechanisms of zooplanktonic toxicity in the okadaic acid-producing dinoflagellate Prorocentrum lima. Environmental Pollution, 2021, 279, 116942.	3.7	10
7020	Functional prediction of de novo uni-genes from chicken transcriptomic data following infectious bursal disease virus at 3-days post-infection. BMC Genomics, 2021, 22, 461.	1.2	1
7021	The synergistic actions of hydrolytic genes reveal the mechanism of Trichoderma harzianum for cellulose degradation. Journal of Biotechnology, 2021, 334, 1-10.	1.9	14
7022	Cellular Reprogramming and Immortality: Expression Profiling Reveals Putative Genes Involved in <i>Turritopsis dohrniiâ€™s</i> Life Cycle Reversal. Genome Biology and Evolution, 2021, 13, .	1.1	3
7023	Silencing lung cancer genes using miRNAs identified by 7mer-seed matching. Computational Biology and Chemistry, 2021, 92, 107483.	1.1	3
7024	Identification and Functional Characterization of Genes Encoding Phenylacetaldehyde Reductases That Catalyze the Last Step in the Biosynthesis of Hydroxytyrosol in Olive. Plants, 2021, 10, 1268.	1.6	2
7025	Transcriptome analysis of Cinnamomum migao seed germination in medicinal plants of Southwest China. BMC Plant Biology, 2021, 21, 270.	1.6	11
7026	Heat-killed endophytic bacterium induces robust plant defense responses against important pathogens. Scientific Reports, 2021, 11, 12182.	1.6	14
7027	The role of auxin during early berry development in grapevine as revealed by transcript profiling from pollination to fruit set. Horticulture Research, 2021, 8, 140.	2.9	15
7028	Evidence of Transcriptional Shutoff by Pathogenic Viral Haemorrhagic Septicaemia Virus in Rainbow Trout. Viruses, 2021, 13, 1129.	1.5	4

#	ARTICLE	IF	CITATIONS
7029	Global mRNA and miRNA Analysis Reveal Key Processes in the Initial Response to Infection with WSSV in the Pacific Whiteleg Shrimp. Viruses, 2021, 13, 1140.	1.5	11
7030	Chromosome anchoring in Senegalese sole (Solea senegalensis) reveals sex-associated markers and genome rearrangements in flatfish. Scientific Reports, 2021, 11, 13460.	1.6	14
7031	Insights into mesophilic virulence, antibiotic resistant and human pathogenicity: A genomics study on the Aeromonas salmonicida SRW-OG1 newly isolated from the Asian fish Epinephelus coioides. Aquaculture, 2021, 539, 736630.	1.7	13
7032	Gene Expression Profiling Reveals New Pathways and Genes Associated with Visna/Maedi Viral Disease. Animals, 2021, 11, 1785.	1.0	4
7033	Characterization of APX and APX-R gene family in Brassica juncea and B. rapa for tolerance against abiotic stresses. Plant Cell Reports, 2022, 41, 571-592.	2.8	18
7035	The chromosome-level Stevia genome provides insights into steviol glycoside biosynthesis. Horticulture Research, 2021, 8, 129.	2.9	35
7036	Comparative transcriptome analysis of Salix cupularis under drought stress. Global Ecology and Conservation, 2021, 27, e01532.	1.0	3
7037	Transcriptomic responses to heat stress in gill and liver of endangered Brachymystax lenok tsinlingensis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 38, 100791.	0.4	11
7038	Secretome Analysis of Arabidopsisâ€"Trichoderma atroviride Interaction Unveils New Roles for the Plant Glutamate:Glyoxylate Aminotransferase GGAT1 in Plant Growth Induced by the Fungus and Resistance against Botrytis cinerea. International Journal of Molecular Sciences, 2021, 22, 6804.	1.8	12
7039	Comparative Physiological and Transcriptomic Profiling Offers Insight into the Sexual Dimorphism of Hepatic Metabolism in Size-Dimorphic Spotted Scat (Scatophagus argus). Life, 2021, 11, 589.	1.1	7
7041	Comparative analysis of phenotypic plasticity sheds light on the evolution and molecular underpinnings of locust phase polyphenism. Scientific Reports, 2021, 11, 11925.	1.6	14
7042	Cross-tolerance and transcriptional shifts underlying abiotic stress in the seabird tick, Ixodes uriae. Polar Biology, 2021, 44, 1379-1389.	0.5	3
7043	Survival and transcriptomic response of Salmonella enterica on fresh-cut fruits. International Journal of Food Microbiology, 2021, 348, 109201.	2.1	6
7044	Protein extraction protocols for optimal proteome measurement and arginine kinase quantitation from cricket Acheta domesticus for food safety assessment. Food Chemistry, 2021, 348, 129110.	4.2	29
7045	Transcriptome-wide identification and characterization of microRNAs in diverse phases of wood formation in <i>Populus trichocarpa</i>. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	9
7046	Comparative Transcriptome Analysis Provides Insights into Response of <i>Ulva compressa</i> to Fluctuating Salinity Conditions. Journal of Phycology, 2021, 57, 1295-1308.	1.0	9
7047	Revealing the stability of aerobic granular sludge in a membrane bioreactor under different DO values by proteomics analysis. Bioresource Technology Reports, 2021, 14, 100673.	1.5	4
7048	Construction of a Full-Length Transcriptome Resource for the Chinese Sucker (Myxocyprinus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2021, 8, .	1.2	4

#	ARTICLE	IF	CITATIONS
7049	Transplanting experiment and transcriptome sequencing reveal the potential ecological adaptation to plateau environments in the allopolyploid Isoetes sinensis. Aquatic Botany, 2021, 172, 103394.	0.8	5
7050	Transcriptome survey, molecular identification, and expression analysis of stress-responsive genes in the toxic dinoflagellate Alexandrium pacificum under algicidal agents and metal stresses. Journal of Applied Phycology, 2021, 33, 3139-3151.	1.5	12
7051	Transcriptomic exploration of a high sucrose mutant in comparison with the low sucrose mother genotype in sugarcane during sugar accumulating stage. GCB Bioenergy, 2021, 13, 1448-1465.	2.5	11
7052	Cytosolic geraniol and citronellol biosynthesis require a Nudix hydrolase in roseâ€scented geranium (<i>Pelargonium graveolens</i>). Plant Journal, 2021, 107, 493-510.	2.8	12
7053	Computational Identification of miRNAs and Temperature-Responsive lncRNAs From Mango (Mangifera) Tj ETQq0 0 0 rgBT /Overlock 10	1.1	7
7054	Insights into enhanced biodegradation of sulfadimethoxine by catalyst: Transcriptomic responses and free radical interactions. Science of the Total Environment, 2021, 774, 145641.	3.9	9
7056	Okadaic Acid Exposure Induced Neural Tube Defects in Chicken (Gallus gallus) Embryos. Marine Drugs, 2021, 19, 322.	2.2	8
7057	Quantitative proteomic analyses reveal that energy metabolism and protein biosynthesis reinitiation are responsible for the initiation of bolting induced by high temperature in lettuce (Lactuca sativa L.). BMC Genomics, 2021, 22, 427.	1.2	8
7058	Exposure to dexamethasone modifies transcriptomic responses of free-living stages of Strongyloides stercoralis. PLoS ONE, 2021, 16, e0253701.	1.1	4
7059	Endophytic Bacillus altitudinis Strain Uses Different Novelty Molecular Pathways to Enhance Plant Growth. Frontiers in Microbiology, 2021, 12, 692313.	1.5	20
7060	Quantitative proteomic analyses on the mechanisms of cold tolerance in two peach cultivars (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.3	5
7061	Transcriptional Responses of Sclerotinia sclerotiorum to the Infection by SsHADV-1. Journal of Fungi (Basel, Switzerland), 2021, 7, 493.	1.5	20
7062	StuA-Regulated Processes in the Dermatophyte Trichophyton rubrum: Transcription Profile, Cell-Cell Adhesion, and Immunomodulation. Frontiers in Cellular and Infection Microbiology, 2021, 11, 643659.	1.8	7
7063	Development and Interrogation of a Transcriptomic Resource for the Giant Triton Snail (Charonia) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	6
7064	Genome-scale comparative analysis for host resistance against sea lice between Atlantic salmon and rainbow trout. Scientific Reports, 2021, 11, 13231.	1.6	9
7065	Capsaicinoid biosynthesis in the pericarp of chili pepper fruits is associated with a placental septum-like transcriptome profile and tissue structure. Plant Cell Reports, 2021, 40, 1859-1874.	2.8	7
7066	The pangenome of banana highlights differences between genera and genomes. Plant Genome, 2022, 15, e20100.	1.6	37
7067	Analysis of lncRNA and mRNA expression profiles in peripheral blood leukocytes of the half-smooth tongue sole (Cynoglossus semilaevis) treated with chitosan oligosaccharide. Developmental and Comparative Immunology, 2021, 120, 104043.	1.0	10

#	ARTICLE	IF	CITATIONS
7068	Dissecting the chromosome-level genome of the Asian Clam (Corbicula fluminea). Scientific Reports, 2021, 11, 15021.	1.6	5
7069	Transcriptome analysis reveals key defense-related genes upon SA induction in Cocos nucifera L.. Genes and Genomics, 2022, 44, 197-210.	0.5	2
7070	Constitutive expression of Ribosomal Protein L6 modulates salt tolerance in rice transgenic plants. Gene, 2021, 789, 145670.	1.0	20
7071	Selection of functional EPHB2 genotypes from ENU mutated grass carp treated with GCRV. BMC Genomics, 2021, 22, 516.	1.2	1
7072	Dual-Organ Transcriptomic Analysis of Rainbow Trout Infected With Ichthyophthirius multifiliis Through Co-Expression and Machine Learning. Frontiers in Immunology, 2021, 12, 677730.	2.2	10
7073	Metabolic responses of two pioneer wood decay fungi to diurnally cycling temperature. Journal of Ecology, 2022, 110, 68-79.	1.9	4
7074	Transcriptome Analysis and miRNA Target Profiling at Various Stages of Root-Knot Nematode Meloidogyne incognita Development for Identification of Potential Regulatory Networks. International Journal of Molecular Sciences, 2021, 22, 7442.	1.8	5
7075	Combined transcriptomic and metabolic analyses reveal potential mechanism for fruit development and quality control of Chinese raspberry (Rubus chingii Hu). Plant Cell Reports, 2021, 40, 1923-1946.	2.8	10
7076	The effects of genetic drift and genomic selection on differentiation and local adaptation of the introduced populations of <i>Aedes albopictus</i> in southern Russia. PeerJ, 2021, 9, e11776.	0.9	6
7077	Genome and transcriptome analysis of the mealybug Maconellicoccus hirsutus: Correlation with its unique phenotypes. Genomics, 2021, 113, 2483-2494.	1.3	8
7078	Chromosomeâ€level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. Molecular Ecology Resources, 2021, 21, 2533-2545.	2.2	30
7079	Comparative Transcriptome and Endophytic Bacterial Community Analysis of Morchella conica SH. Frontiers in Microbiology, 2021, 12, 682356.	1.5	3
7080	Comparative transcriptome analysis reveals regulatory network and regulators associated with proanthocyanidin accumulation in persimmon. BMC Plant Biology, 2021, 21, 356.	1.6	13
7081	Insights from the first genome assembly of Onion (<i>Allium cepa</i>). G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	32
7083	Different Immune Responses of the Lymphoid Organ in Shrimp at Early Challenge Stage of Vibrio parahaemolyticus and WSSV. Animals, 2021, 11, 2160.	1.0	13
7084	Long-Read Sequencing Reveals the Repertoire of Long-Chain Polyunsaturated Fatty Acid Biosynthetic Genes in the Purple Land Crab, Gecarcoidea lalandii (H. Milne Edwards, 1837). Frontiers in Marine Science, 2021, 8, .	1.2	2
7085	Decoding the molecular mechanism of parthenocarpy in Musa spp. through proteinâ€“protein interaction network. Scientific Reports, 2021, 11, 14592.	1.6	10
7086	The Chicken Pan-Genome Reveals Gene Content Variation and a Promoter Region Deletion in <i>IGF2BP1</i> Affecting Body Size. Molecular Biology and Evolution, 2021, 38, 5066-5081.	3.5	70

#	ARTICLE	IF	CITATIONS
7087	Cross-species Exon Capture and Whole Exome Sequencing: Application, Utility and Challenges for Genomic Resource Development in Non-model Species. Marine Biotechnology, 2021, 23, 560-575.	1.1	3
7088	DIA-Based Quantitative Proteomics Reveals the Protein Regulatory Networks of Floral Thermogenesis in Nelumbo nucifera. International Journal of Molecular Sciences, 2021, 22, 8251.	1.8	6
7089	The transcriptional dynamics during <i>de novo</i> shoot organogenesis of Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro): implication of the contributions of the abiotic stress response in this process. Plant Journal, 2021, 107, 1513-1532.	2.8	10
7090	Defense-Related Gene Expression Following an Orthotospovirus Infection Is Influenced by Host Resistance in Arachis hypogaea. Viruses, 2021, 13, 1303.	1.5	5
7091	Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. Journal of Dairy Science, 2021, 104, 8050-8061.	1.4	15
7092	Characterization of the whole transcriptome of spleens from Chinese indigenous breed Ningxiang pig reveals diverse coding and non-coding RNAs for immunity regulation. Genomics, 2021, 113, 2468-2482.	1.3	14
7093	A chromosome-level genome assembly of the yellowfin seabream (Acanthopagrus latus; Hottuyn, 1782) provides insights into its osmoregulation and sex reversal. Genomics, 2021, 113, 1617-1627.	1.3	13
7094	Genome of the pincer wasp Gonatopus flavifemur reveals unique venom evolution and a dual adaptation to parasitism and predation. BMC Biology, 2021, 19, 145.	1.7	15
7095	Common response of dominant plants in typical grassland of Inner Mongolia to longâ€term overgrazing revealed by transcriptome analysis. Grassland Science, 2021, 67, 352.	0.6	1
7096	Transcriptomic analysis to reveal the differentially expressed miRNA targets and their miRNAs in response to Ralstonia solanacearum in ginger species. BMC Plant Biology, 2021, 21, 355.	1.6	11
7097	Genome of the Southern Giant Petrel Assembled Using Third-Generation DNA Sequencing and Linked Reads Reveals Evolutionary Traits of Southern Avian. Animals, 2021, 11, 2046.	1.0	1
7098	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. Frontiers in Plant Science, 2021, 12, 668623.	1.7	18
7099	Transcriptomic Analysis of Salt-Stress-Responsive Genes in Barley Roots and Leaves. International Journal of Molecular Sciences, 2021, 22, 8155.	1.8	23
7100	Characterization of the blood and neutrophilâ€specific microbiomes and exploration of potential bacterial biomarkers for sepsis in surgical patients. Immunity, Inflammation and Disease, 2021, 9, 1343-1357.	1.3	17
7101	Genomic Signatures Supporting the Symbiosis and Formation of Chitinous Tube in the Deep-Sea Tubeworm <i>Paraescarpia echinospica</i>. Molecular Biology and Evolution, 2021, 38, 4116-4134.	3.5	37
7102	Gene Ontology Terms Visualization with Dynamic Distance-Graph and Similarity Measures. , 2021, 2021, 33-42.		1
7103	Combined transcriptomic, proteomic and genomic analysis identifies reproductive-related proteins and potential modulators of female behaviors in Spodoptera litura. Genomics, 2021, 113, 1876-1894.	1.3	14
7104	De novo transcriptome assembly data for sengon (Falcataria moluccana) trees displaying resistance and susceptibility to boktor stem borers (Xystrocera festiva Pascoe). BMC Research Notes, 2021, 14, 261.	0.6	3

#	Article	IF	Citations
7105	Genome-wide analysis of MYB transcription factors of Vaccinium corymbosum and their positive responses to drought stress. BMC Genomics, 2021, 22, 565.	1.2	10
7106	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. Molecular Plant-Microbe Interactions, 2021, 34, 1128-1142.	1.4	6
7107	The Single-Molecule Long-Read Sequencing of Intestine After Soy Meal-Induced Enteritis in Juvenile Pearl Gentian Grouper, Epinephelus fuscoguttatusâ™€ Ã— Epinephelus lanceolatusâ™‚. Frontiers in Marine Science, 2021, 8, .	1.2	3
7108	Transcriptome Profiling of Micromelalopha troglodyta (Lepidoptera: Notodontidae) Larvae under Tannin Stress Using Solexa Sequencing Technology. Journal of Entomological Science, 2021, 56, 321-342.	0.2	1
7109	Full-Length Transcriptome of Thalassiosira weissflogii as a Reference Resource and Mining of Chitin-Related Genes. Marine Drugs, 2021, 19, 392.	2.2	9
7110	Identification, through transcriptome analysis, of transcription factors that regulate anthocyanin biosynthesis in different parts of red-fleshed apple â€˜Mayâ€™ fruit. Horticultural Plant Journal, 2022, 8, 11-21.	2.3	6
7111	QTL Mapping and Diurnal Transcriptome Analysis Identify Candidate Genes Regulating Brassica napus Flowering Time. International Journal of Molecular Sciences, 2021, 22, 7559.	1.8	18
7112	The effects of climate and demographic history in shaping genomic variation across populations of the Desert Horned Lizard (<i>Phrynosoma platyrhinos</i>). Molecular Ecology, 2021, 30, 4481-4496.	2.0	8
7113	The transcription regulator ACTR controls ACT-toxin biosynthesis and pathogenicity in the tangerine pathotype of Alternaria alternata. Microbiological Research, 2021, 248, 126747.	2.5	9
7114	RNA-Seq reveals divergent gene expression between larvae with contrasting trophic modes in the poecilogonous polychaete Boccardia wellingtonensis. Scientific Reports, 2021, 11, 14997.	1.6	2
7115	Investigation Into Different Wood Formation Mechanisms Between Angiosperm and Gymnosperm Tree Species at the Transcriptional and Post-transcriptional Level. Frontiers in Plant Science, 2021, 12, 698602.	1.7	3
7116	The Enhanced Immune Protection in Small Abalone Haliotis diversicolor Against a Secondary Infection With Vibrio harveyi. Frontiers in Immunology, 2021, 12, 685896.	2.2	12
7117	Transcriptome and proteome of the corm, leaf and flower of Hypoxis hemerocallidea (African potato). PLoS ONE, 2021, 16, e0253741.	1.1	0
7118	Identification and characterization of long non-coding RNA and their response against citrus bark cracking viroid infection in Humulus lupulus. Genomics, 2021, 113, 2350-2364.	1.3	6
7119	Transcriptome analysis of the spleen provides insight into the immunoregulation of Cyprinus carpio koi under Aeromonas veronii infection. Aquaculture, 2021, 540, 736650.	1.7	7
7120	Probing the Energetic Metabolism of Resting Cysts under Different Conditions from Molecular and Physiological Perspectives in the Harmful Algal Blooms-Forming Dinoflagellate Scrippsiella trochoidea. International Journal of Molecular Sciences, 2021, 22, 7325.	1.8	3
7121	De novo transcriptome assembly of Angelica dahurica and characterization of coumarin biosynthesis pathway genes. Gene, 2021, 791, 145713.	1.0	15
7122	Transcriptional profiling analysis of susceptible and resistant strains of Anticarsia gemmatalis and their response to Bacillus thuringiensis. Genomics, 2021, 113, 2264-2275.	1.3	8

#	Article	IF	Citations
7123	TRAPID 2.0: a web application for taxonomic and functional analysis of<i>de novo</i>transcriptomes. Nucleic Acids Research, 2021, 49, e101-e101.	6.5	21
7124	Quantitative Proteomics Reveals the Protein Regulatory Network of <i>Anabaena</i> sp. PCC 7120 under Nitrogen Deficiency. Journal of Proteome Research, 2021, 20, 3963-3976.	1.8	6
7125	A reference-grade genome identifies salt-tolerance genes from the salt-secreting mangrove species Avicennia marina. Communications Biology, 2021, 4, 851.	2.0	32
7126	Transcriptome Analysis Identified Candidate Genes Involved in Fruit Body Development under Blue Light in Lentinula edodes. Applied Sciences (Switzerland), 2021, 11, 6997.	1.3	3
7127	Putative genes in alkaloid biosynthesis identified in Dendrobium officinale by correlating the contents of major bioactive metabolites with genes expression between Protocorm-like bodies and leaves. BMC Genomics, 2021, 22, 579.	1.2	26
7128	Transcriptome Analysis Reveals Key Genes Involved in Weevil Resistance in the Hexaploid Sweetpotato. Plants, 2021, 10, 1535.	1.6	5
7129	Characterization of <scp>glucoseâ€binding</scp> proteins isolated from health volunteers and human type 2 diabetes mellitus patients. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1413-1424.	1.5	1
7131	Genetic Dissection of Seedling Root System Architectural Traits in a Diverse Panel of Hexaploid Wheat through Multi-Locus Genome-Wide Association Mapping for Improving Drought Tolerance. International Journal of Molecular Sciences, 2021, 22, 7188.	1.8	20
7132	Identification of microRNA-like RNAs from Trichoderma asperellum DQ-1 during its interaction with tomato roots using bioinformatic analysis and high-throughput sequencing. PLoS ONE, 2021, 16, e0254808.	1.1	3
7133	Dual species dynamic transcripts reveal the interaction mechanisms between Chrysanthemum morifolium and Alternaria alternata. BMC Genomics, 2021, 22, 523.	1.2	8
7134	Bioinformatics analysis of PAE family in Populus trichocarpa and responsiveness to carbon and nitrogen treatment. 3 Biotech, 2021, 11, 370.	1.1	2
7135	Genome assembly, sex-biased gene expression and dosage compensation in the damselfly Ischnura elegans. Genomics, 2021, 113, 1828-1837.	1.3	17
7136	Genomeâ€wide profiling and identification of insulin signaling pathway genes of subterranean termite castes. Entomological Research, 2021, 51, 462-476.	0.6	2
7137	Genome assembly of Scorias spongiosa and comparative genomics provide insights into ecological adaptation of honeydew-dependent sooty mould fungi. Genomics, 2021, 113, 2189-2198.	1.3	2
7138	Major QTLs and Potential Candidate Genes for Heat Stress Tolerance Identified in Chickpea (Cicer) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	38
7139	Large-scale whole-genome resequencing unravels the domestication history of <i>Cannabis sativa</i>. Science Advances, 2021, 7, .	4.7	79
7140	Transcriptome analysis identifies putative genes involved in triterpenoidÂbiosynthesis in Platycodon grandiflorus. Planta, 2021, 254, 34.	1.6	18
7141	Dual Transcriptomic Analyses Unveil Hostâ€"Pathogen Interactions Between Salmonella enterica Serovar Enteritidis and Laying Ducks (Anas platyrhynchos). Frontiers in Microbiology, 2021, 12, 705712.	1.5	1

#	ARTICLE	IF	CITATIONS
7142	Identification of neural progenitor cells and their progeny reveals long distance migration in the developing octopus brain. ELife, 2021, 10, .	2.8	29
7143	Integration of RNAâ€seq and RNAi reveals the contribution of <i>znuA</i> gene to the pathogenicity of <i>Pseudomonas plecoglossicida</i> and to the immune response of <i>Epinephelus coioides</i>. Journal of Fish Diseases, 2021, 44, 1831-1841.	0.9	15
7144	Effects of nonylphenol exposure on histological changes, apoptosis and time-course transcriptome in gills of white shrimp Litopenaeus vannamei. Science of the Total Environment, 2021, 781, 146731.	3.9	18
7145	Gonadal transcriptomes associated with sex phenotypes provide potential male and female candidate genes of sex determination or early differentiation in Crassostrea gigas, a sequential hermaphrodite mollusc. BMC Genomics, 2021, 22, 609.	1.2	14
7146	Comparative physiology and transcriptome analysis reveals the regulatory mechanism of genome duplication enhancing cold resistance in Fragaria nilgerrensis. Environmental and Experimental Botany, 2021, 188, 104509.	2.0	8
7147	The distinctive flagellar proteome of <i>Euglena gracilis</i> illuminates the complexities of protistan flagella adaptation. New Phytologist, 2021, 232, 1323-1336.	3.5	14
7148	The Perception of Rhizosphere Bacterial Communication Signals Leads to Transcriptome Reprogramming in Lysobacter capsici AZ78, a Plant Beneficial Bacterium. Frontiers in Microbiology, 2021, 12, 725403.	1.5	3
7149	Phylogenomics Based on Transcriptome Data Provides Evidence for the Internal Phylogenetic Relationships and Potential Terrestrial Evolutionary Genes of Lungfish. Frontiers in Marine Science, 2021, 8, .	1.2	5
7150	The Effect of tonB Gene on the Virulence of Pseudomonas plecoglossicida and the Immune Response of Epinephelus coioides. Frontiers in Microbiology, 2021, 12, 720967.	1.5	8
7151	Seadragon genome analysis provides insights into its phenotype and sex determination locus. Science Advances, 2021, 7, .	4.7	32
7153	Diel <i>p</i>CO₂ fluctuations alter the molecular response of coral reef fishes to ocean acidification conditions. Molecular Ecology, 2021, 30, 5105-5118.	2.0	21
7154	Prevotella copri increases fat accumulation in pigs fed with formula diets. Microbiome, 2021, 9, 175.	4.9	100
7155	Approaching In Vivo Models of Pneumococcusâ€"Host Interaction: Insights into Surface Proteins, Capsule Production, and Extracellular Vesicles. Pathogens, 2021, 10, 1098.	1.2	4
7156	Effect of pH on the denitrification proteome of the soil bacterium Paracoccus denitrificans PD1222. Scientific Reports, 2021, 11, 17276.	1.6	18
7157	Genetic diversity and population structure of Leptosphaeria maculans isolates in Western Canada. Journal of Genetics and Genomics, 2021, 48, 994-1006.	1.7	0
7158	Comparative transcriptomics provides a strategy for phylogenetic analysis and SSR marker development in Chaenomeles. Scientific Reports, 2021, 11, 16441.	1.6	2
7159	Deep sequencing unravels methyl jasmonate responsive novel miRNAs in Podophyllum hexandrum. Journal of Plant Biochemistry and Biotechnology, 0, , 1.	0.9	4
7160	Identification and expression pattern of lentilâ€™s HSPs under different abiotic stresses. Plant Biotechnology Reports, 2021, 15, 609-625.	0.9	4

#	ARTICLE	IF	CITATIONS
7161	Data-Independent-Acquisition-Based Proteomic Approach towards Understanding the Acclimation Strategy of Oleaginous Microalga <i>Microchloropsis gaditana</i> CCMP526 in Hypersaline Conditions. ACS Omega, 2021, 6, 22151-22164.	1.6	2
7162	The genome of a thorny species: comparative genomic analysis among South and North American Cactaceae. Planta, 2021, 254, 44.	1.6	8
7164	Brain transcriptome analysis reveals genes involved in parental care behaviour in discus fish (Symphysodon haraldi). General and Comparative Endocrinology, 2021, 309, 113793.	0.8	4
7165	Transcriptome Analysis of Two Near-Isogenic Lines with Different NUE under Normal Nitrogen Conditions in Wheat. Biology, 2021, 10, 787.	1.3	9
7166	Stage- and sex-specific transcriptome analyses reveal distinctive sensory gene expression patterns in a butterfly. BMC Genomics, 2021, 22, 584.	1.2	9
7167	Transcriptomes of Saussurea (Asteraceae) Provide Insights into High-Altitude Adaptation. Plants, 2021, 10, 1715.	1.6	11
7168	Genetic response to nitrogen starvation in the aggressive Eucalyptus foliar pathogen Teratosphaeria destructans. Current Genetics, 2021, 67, 981-990.	0.8	2
7169	The Cardamine enshiensis genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. Cell Discovery, 2021, 7, 62.	3.1	15
7170	Full-length transcriptome analysis of <i>Spodoptera frugiperda</i> larval brain reveals detoxification genes. PeerJ, 2021, 9, e12069.	0.9	6
7171	De Novo Transcriptomic Characterization Enables Novel Microsatellite Identification and Marker Development in Betta splendens. Life, 2021, 11, 803.	1.1	3
7172	Transcriptome Profile Analysis Reveals the Regulation Mechanism of Stamen Abortion in Handeliodendron bodinieri. Forests, 2021, 12, 1071.	0.9	2
7174	Transcriptome and Metabolome Analyses of the Flowers and Leaves of Chrysanthemum dichrum. Frontiers in Genetics, 2021, 12, 716163.	1.1	6
7175	The Tomato ddm1b Mutant Shows Decreased Sensitivity to Heat Stress Accompanied by Transcriptional Alterations. Genes, 2021, 12, 1337.	1.0	5
7176	clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. Innovation(China), 2021, 2, 100141.	5.2	2,743
7177	Genome Analysis of Phytophthora nicotianae JM01 Provides Insights into Its Pathogenicity Mechanisms. Plants, 2021, 10, 1620.	1.6	4
7178	Transcriptome Analysis Provides New Insights into Host Response to Hepatopancreatic Necrosis Disease in the Black Tiger Shrimp Penaeus monodon. Journal of Ocean University of China, 2021, 20, 1183-1194.	0.6	2
7179	Overdominance at the Gene Expression Level Plays a Critical Role in the Hybrid Root Growth of Brassica napus. International Journal of Molecular Sciences, 2021, 22, 9246.	1.8	9
7180	Transcriptome profiling reveals potential genes involved in browning of fresh-cut eggplant (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlo	1.6	7

#	ARTICLE	IF	CITATIONS
7181	Insights into Alexandrium minutum Nutrient Acquisition, Metabolism and Saxitoxin Biosynthesis through Comprehensive Transcriptome Survey. Biology, 2021, 10, 826.	1.3	4
7182	Insights into the Host Specificity of a New Oomycete Root Pathogen, Pythium brassicum P1: Whole Genome Sequencing and Comparative Analysis Reveals Contracted Regulation of Metabolism, Protein Families, and Distinct Pathogenicity Repertoire. International Journal of Molecular Sciences, 2021, 22, 9002.	1.8	3
7183	Transcriptomic analysis of a wild and a cultivated varieties of Capsicum annuum over fruit development and ripening. PLoS ONE, 2021, 16, e0256319.	1.1	7
7184	5â€²-Nucleotidase Plays a Key Role in Uric Acid Metabolism of Bombyx mori. Cells, 2021, 10, 2243.	1.8	11
7185	High-Quality Genome Sequence Resource for Fusarium andiyazi Causing Pokkah Boeng Disease of Sugarcane in China. Molecular Plant-Microbe Interactions, 2021, 34, MPMI-11-20-0331.	1.4	2
7186	Iso-seq analysis and functional annotation of the Santa Fe cave crayfish (Procambarus erythrops) transcriptome. Marine Genomics, 2021, 58, 100842.	0.4	2
7187	Morphological, Physiological, and Molecular Responses of Sweetly Fragrant Luculia gratissima During the Floral Transition Stage Induced by Short-Day Photoperiod. Frontiers in Plant Science, 2021, 12, 715683.	1.7	0
7188	Identification and expression profile of the soil moisture and <i>Ralstonia solanacearum</i> response CYPome in ginger (<i>Zingiber officinale</i>). PeerJ, 2021, 9, e11755.	0.9	3
7189	Interspecies Evolution and Networks Investigation of the Auxin Response Protein (AUX/IAA) Family Reveals the Adaptation Mechanisms of Halophytes Crops in Nitrogen Starvation Agroecological Environments. Agriculture (Switzerland), 2021, 11, 780.	1.4	5
7190	Population Genomics Reveals Gene Flow and Adaptive Signature in Invasive Weed Mikania micrantha. Genes, 2021, 12, 1279.	1.0	2
7192	Alterations in Sucrose and Phenylpropanoid Metabolism Affected by BABA-Primed Defense in Postharvest Grapes and the Associated Transcriptional Mechanism. Molecular Plant-Microbe Interactions, 2021, 34, 1250-1266.	1.4	11
7193	Transcriptome analysis of sesame-Macrophomina phaseolina interactions revealing the distinct genetic components for early defense responses. Physiology and Molecular Biology of Plants, 2021, 27, 1675-1693.	1.4	6
7194	Pan-genome of Raphanus highlights genetic variation and introgression among domesticated, wild, and weedy radishes. Molecular Plant, 2021, 14, 2032-2055.	3.9	56
7195	Herbivory-Induced Emission of Volatile Terpenes in <i>Chrysanthemum morifolium</i> Functions as an Indirect Defense against <i>Spodoptera litura</i> Larvae by Attracting Natural Enemies. Journal of Agricultural and Food Chemistry, 2021, 69, 9743-9753.	2.4	16
7196	Brugia malayi Glycoproteins Detected by the Filariasis Test Strip Antibody AD12.1. Frontiers in Tropical Diseases, 2021, 2, .	0.5	1
7197	The potential for using shell proteins in gastropod systematics, assessed in patellogastropod limpets. Zoological Journal of the Linnean Society, 2022, 194, 1177-1193.	1.0	0
7198	Genome-wide association mapping reveals key genomic regions for physiological and yield-related traits under salinity stress in wheat (Triticum aestivum L.). Genomics, 2021, 113, 3198-3215.	1.3	22
7199	Identification of putative key genes for thermal adaptation in the Japanese mantis shrimp (Oratosquilla) Tj ETQq1 1 0.784314 rgBT /Ove Genomics and Proteomics, 2021, 39, 100828.	0.4	1

#	ARTICLE	IF	CITATIONS
7200	Activation of Cryptic Antibiotic Biosynthetic Gene Clusters Guided by RNA-seq Data from Both Streptomyces ansochromogenes and Î”wblA. Antibiotics, 2021, 10, 1097.	1.5	4
7201	Chromosomeâ€scale assembly and wholeâ€genome sequencing of 266 giant panda roundworms provide insights into their evolution, adaptation and potential drug targets. Molecular Ecology Resources, 2022, 22, 768-785.	2.2	6
7202	Transcriptome Adaptation of the Ovine Mammary Gland to Dietary Supplementation of Extruded Linseed. Animals, 2021, 11, 2707.	1.0	2
7203	Insight Into Whole Genome of Aeromonas veronii Isolated From Freshwater Fish by Resistome Analysis Reveal Extensively Antibiotic Resistant Traits. Frontiers in Microbiology, 2021, 12, 733668.	1.5	13
7204	Gene expression profiling by cDNAâ€AFLP reveals potential candidate genes for imazapyrâ€induced male sterility in sunflower. Crop Science, 0, , .	0.8	0
7205	Genome-Wide Transcriptional Changes of Rhodosporidium kratochvilovae at Low Temperature. Frontiers in Microbiology, 2021, 12, 727105.	1.5	5
7206	Intestinal Transcriptomic and Histologic Profiling Reveals Tissue Repair Mechanisms Underlying Resistance to the Parasite Ceratonova shasta. Pathogens, 2021, 10, 1179.	1.2	8
7207	Transcriptome Analysis Reveals Differential Gene Expression in Garlic Aerial Bulbs in Response to Gibberellin Application. Journal of Plant Growth Regulation, 2022, 41, 2967-2979.	2.8	1
7209	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus Lentinula edodes. Journal of Advanced Research, 2022, 38, 91-106.	4.4	16
7210	Whole-Genome and Transcriptome Sequencing of Phlebopus portentosus Reveals Its Associated Ectomycorrhizal Niche and Conserved Pathways Involved in Fruiting Body Development. Frontiers in Microbiology, 2021, 12, 732458.	1.5	8
7211	Introgression among North American wild grapes (Vitis) fuels biotic and abiotic adaptation. Genome Biology, 2021, 22, 254.	3.8	25
7212	Transcriptome characterization and expression profile of Coix lacryma-jobi L. in response to drought. PLoS ONE, 2021, 16, e0256875.	1.1	10
7213	Transcriptome Analysis of Cambium Tissue of Paulownia Collected during Winter and Spring. Diversity, 2021, 13, 423.	0.7	1
7214	PrbP modulates biofilm formation in Liberibacter crescens. Environmental Microbiology, 2021, 23, 7121-7138.	1.8	1
7215	Deciphering variation of 239 elite japonica rice genomes for whole genome sequences-enabled breeding. Genomics, 2021, 113, 3083-3091.	1.3	3
7217	Whole-genome assembly of<i>Ganoderma leucocontextum</i>(Ganodermataceae, Fungi) discovered from the Tibetan Plateau of China. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	11
7219	Description, Taxonomy, and Comparative Genomics of a Novel species, Thermoleptolyngbya sichuanensis sp. nov., Isolated From Hot Springs of Ganzi, Sichuan, China. Frontiers in Microbiology, 2021, 12, 696102.	1.5	14
7220	Transcriptional Controls for Early Bolting and Flowering in Angelica sinensis. Plants, 2021, 10, 1931.	1.6	13

#	Article	IF	Citations
7222	Key role of juvenile hormone in controlling reproductive diapause in females of the <scp>Asian</scp> lady beetle <scp><i>Harmonia axyridis</i></scp>. Pest Management Science, 2022, 78, 193-204.	1.7	10
7223	Comparative Genomics Sheds Light on the Convergent Evolution of Miniaturized Wasps. Molecular Biology and Evolution, 2021, 38, 5539-5554.	3.5	11
7224	Transcriptomic assessment of dietary fishmeal partial replacement by soybean meal and prebiotics inclusion in the liver of juvenile Pacific yellowtail (Seriola lalandi). Molecular Biology Reports, 2021, 48, 7127-7140.	1.0	4
7225	Tissueâ€specific gene expression shows a cynipid wasp repurposes oak host gene networks to create a complex and novel parasiteâ€specific organ. Molecular Ecology, 2022, 31, 3228-3240.	2.0	20
7226	Tramtrack acts during late pupal development to direct ant caste identity. PLoS Genetics, 2021, 17, e1009801.	1.5	8
7227	Arabidopsis LSH8 Positively Regulates ABA Signaling by Changing the Expression Pattern of ABA-Responsive Proteins. International Journal of Molecular Sciences, 2021, 22, 10314.	1.8	7
7228	Haplotype divergence supports long-term asexuality in the oribatid mite<i>Oppiella nova</i>. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	23
7229	Overexpression of DEFECTIVE IN ANTHER DEHISCENCE 1 increases rapeseed silique length through crosstalk between JA and auxin signaling. Industrial Crops and Products, 2021, 168, 113576.	2.5	8
7230	Dynamic neurogenomic responses to social interactions and dominance outcomes in female paper wasps. PLoS Genetics, 2021, 17, e1009474.	1.5	15
7231	Susceptibility of the Non-Targeted Crustacean Eurytemora affinis to the Endocrine Disruptor Tebufenozide: A Transcriptomic Approach. Genes, 2021, 12, 1484.	1.0	3
7232	Transcriptome analysis of differentially expressed genes in the red swamp crayfish Procambarus clarkii challenged with Aeromonas hydrophila. Fish and Shellfish Immunology, 2021, 119, 280-288.	1.6	12
7233	Transcriptome analysis provides genome annotation and expression profiles in the central nervous system of Lymnaea stagnalis at different ages. BMC Genomics, 2021, 22, 637.	1.2	5
7234	<i>Zanthoxylum-</i>specific whole genome duplication and recent activity of transposable elements in the highly repetitive paleotetraploid <i>Z. bungeanum</i> genome. Horticulture Research, 2021, 8, 205.	2.9	19
7235	The chromosome-scale genome of Magnolia officinalis provides insight into the evolutionary position of magnoliids. IScience, 2021, 24, 102997.	1.9	14
7236	Analysis of weighted gene co-expression network of triterpenoid-related transcriptome characteristics from different strains of Wolfiporia cocos. Scientific Reports, 2021, 11, 18207.	1.6	2
7237	Comparative transcriptome analysis at the onset of speciation in a mimetic butterflyâ€"The Ithomiini <i>Melinaea marsaeus</i>. Journal of Evolutionary Biology, 2021, 34, 1704-1721.	0.8	2
7238	Global Transcriptome Characterization and Assembly of the Thermophilic Ascomycete Chaetomium thermophilum. Genes, 2021, 12, 1549.	1.0	3
7239	Phylogenomic approach reveals strong signatures of introgression in the rapid diversification of neotropical true fruit flies (Anastrepha: Tephritidae). Molecular Phylogenetics and Evolution, 2021, 162, 107200.	1.2	8

#	ARTICLE	IF	CITATIONS
7240	Transcriptome analysis to elucidate the toxicity mechanisms of fenvalerate, sulfide gatifloxacin, and ridomil on the hepatopancreas of Procambarus clarkii. Fish and Shellfish Immunology, 2021, 116, 140-149.	1.6	8
7241	Transcriptional responses to Fusarium oxysporum f. sp. lycopersici (Sacc.) Snyder & Hansen infection in three Colombian tomato cultivars. BMC Plant Biology, 2021, 21, 412.	1.6	6
7242	Genomic Analyses of Penicillium Species Have Revealed Patulin and Citrinin Gene Clusters and Novel Loci Involved in Oxylipin Production. Journal of Fungi (Basel, Switzerland), 2021, 7, 743.	1.5	6
7243	Differential Expression of Long Non-Coding RNA (lncRNA) in Mediterranean Mussel (Mytilus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.0	9
7244	Quantitative Proteomic Analysis for High- and Low-Aflatoxin-Yield Aspergillus flavus Strains Isolated From Natural Environments. Frontiers in Microbiology, 2021, 12, 741875.	1.5	4
7245	Transmission of mushroom virus X and the impact of virus infection on the transcriptomes and proteomes of different strains of Agaricus bisporus. Fungal Biology, 2021, 125, 704-717.	1.1	11
7246	Functional Annotation of circRNAs of Tea Leaves During Infection by the Tea Leaf Spot Pathogen <i>Didymella segeticola</i>. PhytoFrontiers, 2022, 2, 80-83.	0.8	3
7247	Impact of pmrA on Cronobacter sakazakii planktonic and biofilm cells: A comprehensive transcriptomic study. Food Microbiology, 2021, 98, 103785.	2.1	10
7248	Transcriptome sequencing and functional characterization of new sesquiterpene synthases from Curcuma wenyujin. Archives of Biochemistry and Biophysics, 2021, 709, 108986.	1.4	9
7249	Role of Dicer-Dependent RNA Interference in Regulating Mycoparasitic Interactions. Microbiology Spectrum, 2021, 9, e0109921.	1.2	12
7250	The secreted proteome of necrotrophic Ciborinia camelliae causes nonâ€hostâ€specific virulence. Plant Pathology, 0, , .	1.2	1
7251	Sex-Biased Gene Expression and Isoform Profile of Brine Shrimp Artemia franciscana by Transcriptome Analysis. Animals, 2021, 11, 2630.	1.0	4
7252	Transcriptome Analysis of Effects of Folic Acid Supplement on Gene Expression in Liver of Broiler Chickens. Frontiers in Veterinary Science, 2021, 8, 686609.	0.9	3
7253	Wholeâ€genome sequencing of brownâ€marbled grouper (<i>Epinephelus fuscoguttatus</i>) provides insights into adaptive evolution and growth differences. Molecular Ecology Resources, 2022, 22, 711-723.	2.2	16
7254	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. Microbiology Spectrum, 2021, 9, e0050921.	1.2	6
7255	Comparative analysis of draft genome assemblies developed from whole genome sequences of two Hyaloperonospora brassicae isolate samples differing in field virulence on Brassica napus. Biotechnology Reports (Amsterdam, Netherlands), 2021, 31, e00653.	2.1	3
7256	Insights into angiosperm evolution, floral development and chemical biosynthesis from the Aristolochia fimbriata genome. Nature Plants, 2021, 7, 1239-1253.	4.7	51
7257	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. Plant Biotechnology Journal, 2022, 20, 116-128.	4.1	18

#	ARTICLE	IF	CITATIONS
7258	An Escherichia coli FdrA Variant Derived from Syntrophic Coculture with a Methanogen Increases Succinate Production Due to Changes in Allantoin Degradation. MSphere, 2021, 6, e0065421.	1.3	3
7259	A Global Analysis of Photoreceptor-Mediated Transcriptional Changes Reveals the Intricate Relationship Between Central Metabolism and DNA Repair in the Filamentous Fungus Trichoderma atroviride. Frontiers in Microbiology, 2021, 12, 724676.	1.5	8
7260	Joint effects of carbon nanotubes and copper oxide nanoparticles on fermentation metabolism towards Saccharofermentans acetigenes: Enhancing environmental adaptability and transcriptional expression. Bioresource Technology, 2021, 336, 125318.	4.8	19
7261	Full-Length Transcriptome Sequencing From the Longest-Lived Freshwater Bony Fish of the World: Bigmouth Buffalo (Ictiobus Cyprinellus). Frontiers in Marine Science, 2021, 8, .	1.2	2
7262	Comparative analysis of spleen transcriptome of immune response in <i>Sebastes schlegeli</i> against <i>Photobacterium damselae</i> subsp. <i>damselae</i> infection. Aquaculture Research, 2022, 53, 232-242.	0.9	2
7263	New perspective on the genetic structure and habitat adaptation of Pampus minor off the coast of China based on RAD-seq. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 39, 100865.	0.4	2
7264	Revelation of candidate genes and molecular mechanism of reproductive seasonality in female rohu (Labeo rohita Ham.) by RNA sequencing. BMC Genomics, 2021, 22, 685.	1.2	3
7265	Development of molecular markers based on LTR retrotransposon in the Cleistogenes songorica genome. Journal of Applied Genetics, 2022, 63, 61-72.	1.0	4
7266	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (Psidium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	1.7	8
7267	Transcriptome Reprogramming of Tomato Orchestrate the Hormone Signaling Network of Systemic Resistance Induced by Chaetomium globosum. Frontiers in Plant Science, 2021, 12, 721193.	1.7	11
7268	Proteomics Reveals an Increase in the Abundance of Glycolytic and Ethanolic Fermentation Enzymes in Developing Sugarcane Culms During Sucrose Accumulation. Frontiers in Plant Science, 2021, 12, 716964.	1.7	4
7269	Parallel subgenome structure and divergent expression evolution of allo-tetraploid common carp and goldfish. Nature Genetics, 2021, 53, 1493-1503.	9.4	52
7271	RNA-Seq analysis of the blue light-emitting Orfelia fultoni (Diptera: Keroplatidae) suggest photoecological adaptations at the molecular level. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 39, 100840.	0.4	0
7272	Exploring the Symbiotic Mechanism of a Virus-Mediated Endophytic Fungus in Its Host by Dual Unique Molecular Identifierâ€"RNA Sequencing. MSystems, 2021, 6, e0081421.	1.7	9
7273	Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538.	13.7	159
7274	Large-scale prospection of genes on caffeine-free Coffea arabica plants â€" Discovery of novel markers associated with development and secondary metabolism. Plant Gene, 2021, 27, 100314.	1.4	3
7275	The macronuclear genome of the Antarctic psychrophilic marine ciliate Euplotes focardii reveals new insights on molecular cold adaptation. Scientific Reports, 2021, 11, 18782.	1.6	15
7276	Development of the petaloid bracts of a paleoherb species, Saururus chinensis. PLoS ONE, 2021, 16, e0255679.	1.1	1

#	ARTICLE	IF	CITATIONS
7277	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cuelure by altering expression of chemoreceptor genes. Scientific Reports, 2021, 11, 17632.	1.6	2
7278	Proteogenomic Analysis Provides Novel Insight into Genome Annotation and Nitrogen Metabolism in <i>Nostoc</i> sp. PCC 7120. Microbiology Spectrum, 2021, 9, e0049021.	1.2	5
7279	Proteome and Nutritional Shifts Observed in Hordein Double-Mutant Barley Lines. Frontiers in Plant Science, 2021, 12, 718504.	1.7	4
7280	The molecular interplay of the establishment of an infection â€“ gene expression of Diaphorina citri gut and Candidatus Liberibacter asiaticus. BMC Genomics, 2021, 22, 677.	1.2	5
7281	Revealing the coexistence of differentiation and communication in an endemic hare, Lepus yarkandensis (Mammalia, Leporidae) using specific-length amplified fragment sequencing. Frontiers in Zoology, 2021, 18, 50.	0.9	2
7282	Overexpression of <scp>ATP</scp>â€‘binding cassette transporter <scp><i>Mdr49â€‘like</i></scp> confers resistance to imidacloprid in the field populations of brown planthopper, <scp><i>Nilaparvata lugens</i></scp>. Pest Management Science, 2022, 78, 579-590.	1.7	11
7283	De novo transcriptome sequencing of triton shell Charonia lampas sauliae: Identification of genes related to neurotoxins and discovery of genetic markers. Marine Genomics, 2021, 59, 100862.	0.4	5
7284	Shape-function of a novel metapyrocatechase, RW4-MPC: Metagenomics to SAXS data based insight into deciphering regulators of function. International Journal of Biological Macromolecules, 2021, 188, 1012-1024.	3.6	0
7285	Transcriptome and morphological analysis in Caligus rogercresseyi uncover the effects of Atlantic salmon vaccination with IPathÂ®. Fish and Shellfish Immunology, 2021, 117, 169-178.	1.6	5
7286	Comprehensive transcriptome-based characterization of differentially expressed genes involved in carotenoid biosynthesis of different ripening stages of Capsicum. Scientia Horticulturae, 2021, 288, 110311.	1.7	11
7287	A novel model construction of lithocholic acid-induced cholestasis and transcriptome analysis in snakehead fish (Channa argus). Aquaculture, 2021, 543, 737014.	1.7	11
7288	A metatranscriptomic analysis of changing dynamics in the plankton communities adjacent to aquaculture leases in southern Tasmania, Australia. Marine Genomics, 2021, 59, 100858.	0.4	1
7289	Comparative transcriptome profiling of horseshoe crab Tachypleus gigas hemocytes in response to lipopolysaccharides. Fish and Shellfish Immunology, 2021, 117, 148-156.	1.6	10
7290	Full-length sequencing of Ginkgo biloba L. reveals the synthesis of terpenoids during seed development. Industrial Crops and Products, 2021, 170, 113714.	2.5	10
7291	Integrated Analysis of MicroRNA and Target Genes in Brachypodium distachyon Infected by Magnaporthe oryzae by Small RNA and Degradome Sequencing. Frontiers in Plant Science, 2021, 12, 742347.	1.7	7
7292	A proteomic analysis of the effect of ocean acidification on the haemocyte proteome of the South African abalone Haliotis midae. Fish and Shellfish Immunology, 2021, 117, 274-290.	1.6	6
7293	Transcriptome analysis and response of three important detoxifying enzymes to Serratia marcescens Bizio (SM1) in Hyphantria cunea (Drury) (Lepidoptera: Noctuidae). Pesticide Biochemistry and Physiology, 2021, 178, 104922.	1.6	7
7294	Comparative transcriptome analysis reveals the molecular mechanism of salt tolerance in Apocynum venetum. Plant Physiology and Biochemistry, 2021, 167, 816-830.	2.8	12

#	ARTICLE	IF	CITATIONS
7295	Description of four Millepora spp. transcriptomes and their potential to delimit the Caribbean fire coral species. Marine Genomics, 2021, 59, 100863.	0.4	0
7296	Use Chou's 5-steps rule to identify protein post-translational modification and its linkage to secondary metabolism during the floral development of Lonicera japonica Thunb. Plant Physiology and Biochemistry, 2021, 167, 1035-1048.	2.8	4
7297	iTRAQ-based quantitative proteomic analysis reveals the toxic mechanism of diclofenac sodium on the kidney of broiler chicken. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2021, 249, 109129.	1.3	7
7298	Characterization of PyMAPK2, a D group mitogen-activated protein kinase gene from Pyropia yezoensis responding to various abiotic stress. Algal Research, 2021, 59, 102445.	2.4	3
7299	Analysis of secretome and N-glycosylation of Chlorella species. Algal Research, 2021, 59, 102466.	2.4	3
7300	RNA-Seq based global transcriptome analysis of rice unravels the key players associated with brown planthopper resistance. International Journal of Biological Macromolecules, 2021, 191, 118-128.	3.6	2
7301	Transcriptome-wide study in the green microalga Messastrum gracile SE-MC4 identifies prominent roles of photosynthetic integral membrane protein genes during exponential growth stage. Phytochemistry, 2021, 192, 112936.	1.4	4
7302	Prediction of adverse effects of effluents containing phenolic compounds in the Ba River on the ovary of fish (Hemiculter leucisculus) using transcriptomic and metabolomic analyses. Science of the Total Environment, 2021, 801, 149554.	3.9	12
7303	Transcriptome analysis provides the first insight into the molecular basis of temperature plasticity in Banggai cardinalfish, Pterapogon kauderni. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100909.	0.4	4
7304	Transcriptome analysis reveals molecular strategies of Bactrocera dorsalis (Hendel) larvae in response to anoxia. Journal of Asia-Pacific Entomology, 2021, 24, 975-982.	0.4	0
7305	Molecular and biochemical mechanisms underlying boron-induced alleviation of cadmium toxicity in rice seedlings. Ecotoxicology and Environmental Safety, 2021, 225, 112776.	2.9	8
7306	Transcriptional response to cold and fasting acclimation in Onychostoma macrolepis during the overwintering stage. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100901.	0.4	3
7307	Identification of Genes Involved in Celastrol Biosynthesis by Comparative Transcriptome Analysis in Tripterygium wilfordii. Phyton, 2022, 91, 279-291.	0.4	0
7308	Genomics, Genetics, and Breeding in Aquaculture. , 2022, , 3-43.		1
7309	Multi-omic approach to evaluate the response of gilt-head sea bream (Sparus aurata) exposed to the UV filter sulisobenzone. Science of the Total Environment, 2022, 803, 150080.	3.9	16
7310	Long-term effect of plastic feeding on growth and transcriptomic response of mealworms (Tenebrio) Tj ETQq1 1 0.784314 rgBT /Overlo	4.2	23
7311	Identification of key genes and molecular mechanisms associated with temperature stress in lentil. Gene, 2022, 807, 145952.	1.0	12
7312	Integrated volatile metabolome, multi-flux full-length sequencing, and transcriptome analyses provide insights into the aroma formation of postharvest jasmine (Jasminum sambac) during flowering. Postharvest Biology and Technology, 2022, 183, 111726.	2.9	19

#	Article	IF	Citations
7313	Freshwater mussels (Unionidae) brought into captivity exhibit up-regulation of genes involved in stress and energy metabolism. Scientific Reports, 2021, 11, 2241.	1.6	8
7314	De novo RNA sequencing and analysis reveal the putative genes involved in diterpenoid biosynthesis in Aconitum vilmorinianum roots. 3 Biotech, 2021, 11, 96.	1.1	7
7315	Draft genome assembly of the biofuel grass crop Miscanthus sacchariflorus. F1000Research, 2021, 10, 29.	0.8	4
7316	Transcriptome skimming of lentil (Lens culinaris Medikus) cultivars with contrast reaction to salt stress. Functional and Integrative Genomics, 2021, 21, 139-156.	1.4	12
7317	Transcriptomics Integrated with Free and Bound Terpenoid Aroma Profiling during â€œShine Muscatâ€• (<i>Vitis labrusca</i> Ã— <i>V. vinifera</i>) Grape Berry Development Reveals Coordinate Regulation of MEP Pathway and Terpene Synthase Gene Expression. Journal of Agricultural and Food Chemistry, 2021, 69, 1413-1429.	2.4	25
7318	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. Communications Biology, 2021, 4, 104.	2.0	27
7319	Transcriptome analysis reveals salinity responses in four Tartary buckwheat cultivars. Journal of Plant Biochemistry and Biotechnology, 2021, 30, 564-578.	0.9	6
7320	Identification of Differentially Expressed Genes and Lipid Metabolism Signaling Pathways between Muscle and Fat Tissues in Broiler Chickens. Journal of Poultry Science, 2021, 58, 131-137.	0.7	6
7321	Genetic changes of Plasmodium vivax tempers host tissue-specific responses in Anopheles stephensi. Current Research in Immunology, 2021, 2, 12-22.	1.2	8
7322	Insights from the cDNA and EST analysis of Antrodia cinnamomea. Bioinformation, 2021, 17, 109-118.	0.2	0
7323	Zone of Interaction Between the Parasite and the Host: Protein Profile of the Body Cavity Fluid of Gasterosteus aculeatus L. Infected with the Cestode Schistocephalus solidus (Muller, 1776). Acta Parasitologica, 2021, 66, 569-583.	0.4	4
7324	The Characteristics of Chemosensory and Opsin Genes in Newly Emerged and Sexually Mature Agrilus planipennis, an Important Quarantine Forest Beetle. Frontiers in Genetics, 2020, 11, 604757.	1.1	2
7325	Immune Responses to Gram-Negative Bacteria in Hemolymph of the Chinese Horseshoe Crab, Tachypleus tridentatus. Frontiers in Immunology, 2020, 11, 584808.	2.2	11
7326	Transcriptomic analysis reveals key transcription factors associated to drought tolerance in a wild papaya (Carica papaya) genotype. PLoS ONE, 2021, 16, e0245855.	1.1	10
7327	A De Novo Transcriptomics Approach Reveals Genes Involved in Thrips Tabaci Resistance to Spinosad. Insects, 2021, 12, 67.	1.0	7
7328	Analysis of Differentially Expressed Genes of<i>Chrysoperla sinica</i>Related to Flight Capacity by Transcriptome. Journal of Insect Science, 2021, 21, .	0.6	4
7329	ITRAQ-based quantitative proteomic analysis of Fusarium moniliforme (Fusarium verticillioides) in response to Phloridzin inducers. Proteome Science, 2021, 19, 2.	0.7	4
7330	Transcriptome-based analysis of salt-related genes during the sprout stage of common bean (<i>Phaseolus vulgaris</i>) under salt stress conditions. Biotechnology and Biotechnological Equipment, 2021, 35, 1086-1098.	0.5	14

#	Article	IF	Citations
7331	Application of an optimized annotation pipeline to the <i>Cryptococcus deuterogattii</i> genome reveals dynamic primary metabolic gene clusters and genomic impact of RNAi loss. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	16
7332	De novo transcriptomic analysis and identification of EST-SSR markers in Stephanandra incisa. Scientific Reports, 2021, 11, 1059.	1.6	10
7333	Comparative Analysis of Transcriptome and sRNAs Expression Patterns in the Brachypodium distachyonâ€"Magnaporthe oryzae Pathosystems. International Journal of Molecular Sciences, 2021, 22, 650.	1.8	16
7334	Quantitative proteomics analysis of Angiostrongylus vasorum-induced alterations in dog serum sheds light on the pathogenesis of canine angiostrongylosis. Scientific Reports, 2021, 11, 283.	1.6	12
7335	Identification and characterization of MeERF genes and their targets in pathogen response by cassava (Manihot esculenta). Crop Journal, 2021, , .	2.3	2
7336	Comprehensive identification and expression analysis of. Functional Plant Biology, 2021, 48, 1039-1052.	1.1	8
7338	Temporal patterns of imidacloprid resistance throughout a growing season in <i>Leptinotarsa decemlineata</i> populations. Pest Management Science, 2017, 73, 641-650.	1.7	17
7339	The Gossypium Transcriptome. , 2009, , 157-185.		4
7340	Legume Pangenome Construction Using an Iterative Mapping and Assembly Approach. Methods in Molecular Biology, 2020, 2107, 35-47.	0.4	7
7341	Roles for Text Mining in Protein Function Prediction. Methods in Molecular Biology, 2014, 1159, 95-108.	0.4	15
7342	Impact of Next-Generation Technologies on Exploring Socioeconomically Important Parasites and Developing New Interventions. Methods in Molecular Biology, 2015, 1247, 437-474.	0.4	9
7343	Methods for RNA Profiling of Gravi-Responding Plant Tissues. Methods in Molecular Biology, 2015, 1309, 91-117.	0.4	2
7344	The Mobilome: Metagenomic Analysis of Circular Plasmids, Viruses, and Other Extrachromosomal Elements. Methods in Molecular Biology, 2020, 2075, 253-264.	0.4	6
7345	Global Quantitative Proteomics Using Spectral Counting: An Inexpensive Experimental and Bioinformatics Workflow for Deep Proteome Coverage. Methods in Molecular Biology, 2014, 1072, 171-183.	0.4	3
7346	Forward Genetics in Setaria viridis. Plant Genetics and Genomics: Crops and Models, 2017, , 303-322.	0.3	1
7347	Pochonia chlamydosporia: Multitrophic Lifestyles Explained by a Versatile Genome. , 2017, , 197-207.		7
7348	Clustering of Gene Expression Profiles Applied to Marine Research. Lecture Notes in Computer Science, 2013, , 453-462.	1.0	1
7349	Pyrenophora tritici-repentis: A Plant Pathogenic Fungus with Global Impact. , 2014, , 1-39.		20

#	Article	IF	Citations
7350	Crop Genome Annotation: A Case Study for the Brassica rapa Genome. Compendium of Plant Genomes, 2015, , 53-64.	0.3	1
7351	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
7352	Transcriptome analysis of Botrytis cinerea in response to tea tree oil and its two characteristic components. Applied Microbiology and Biotechnology, 2020, 104, 2163-2178.	1.7	33
7354	Transcriptomic analyses reveal novel genes with sexually dimorphic expression in Takifugu rubripes brain during gonadal sex differentiation. Genes and Genomics, 2020, 42, 425-439.	0.5	5
7355	De novo assembly and microsatellite marker development of the transcriptome of the endangered Brachymystax lenok tsinlingensis. Genes and Genomics, 2020, 42, 727-734.	0.5	4
7356	Differential gene expression patterns related to lipid metabolism in response to ocean acidification in larvae and juveniles of Atlantic cod. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2020, 247, 110740.	0.8	7
7357	An improved draft of the pigeonpea (Cajanus cajan (L.) Millsp.) genome. Data in Brief, 2018, 16, 376-380.	0.5	11
7358	De novo transcriptome analysis of the mussel Perna viridis after exposure to the toxic dinoflagellate Prorocentrum lima. Ecotoxicology and Environmental Safety, 2020, 192, 110265.	2.9	25
7359	Global Analysis of Gene Expression Profiles Provides Novel Insights into the Development and Evolution of the Large Crustacean Eriocheir sinensis. Genomics, Proteomics and Bioinformatics, 2020, 18, 443-454.	3.0	5
7360	Identification of potential therapeutic targets in Neisseria gonorrhoeae by an in-silico approach. Journal of Theoretical Biology, 2020, 490, 110172.	0.8	8
7361	Towards the identification of ancestrally shared regenerative mechanisms across the Metazoa: A Transcriptomic case study in the Demosponge Halisarca caerulea. Marine Genomics, 2018, 37, 135-147.	0.4	31
7362	Bio-denitrification performance enhanced by graphene-facilitated iron acquisition. Water Research, 2020, 180, 115916.	5.3	70
7363	Gonadal transcriptomic analysis of the mud crab Scylla olivacea infected with rhizocephalan parasite Sacculina beauforti. Genomics, 2020, 112, 2959-2969.	1.3	13
7364	A chromosome-level reference genome of non-heading Chinese cabbage [Brassica campestris (syn.) Tj ETQq1 1 0.784314 rgBT /Overlo	2.9	51
7365	MicroRNA and mRNA interactions coordinate the immune response in non-lethal heat stressed Litopenaeus vannamei against AHPND-causing Vibrio parahaemolyticus. Scientific Reports, 2020, 10, 787.	1.6	19
7366	Red versus green leaves: transcriptomic comparison of foliar senescence between two Prunus cerasifera genotypes. Scientific Reports, 2020, 10, 1959.	1.6	8
7367	Population structure and genetic diversity in red clover (Trifolium pratense L.) germplasm. Scientific Reports, 2020, 10, 8364.	1.6	19
7368	Evidence for the Involvement of Vernalization-related Genes in the Regulation of Cold-induced Ripening in â€˜Dâ€™Anjouâ€™ and â€˜Bartlettâ€™ Pear Fruit. Scientific Reports, 2020, 10, 8478.	1.6	10

#	Article	IF	Citations
7369	De novo transcriptome assembly of fluorine accumulator tea plant Camellia sinensis with fluoride treatments. Scientific Data, 2018, 5, 180194.	2.4	6
7370	Comprehensive analysis of long noncoding RNA and mRNA in five colorectal cancer tissues and five normal tissues. Bioscience Reports, 2020, 40, .	1.1	4
7371	<i>Mycena</i> genomes resolve the evolution of fungal bioluminescence. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31267-31277.	3.3	30
7372	Involvement of programmed cell death in suppression of the number of root nodules formed in soybean induced by Bradyrhizobium infection. Soil Science and Plant Nutrition, 2017, 63, 561-577.	0.8	5
7373	Approaches to Fungal Genome Annotation. Mycology, 2011, 2, 118-141.	2.0	109
7374	The genome sequence of tetraploid sweet basil, <i>Ocimum basilicum</i> L., provides tools for advanced genome editing and molecular breeding. DNA Research, 2020, 27, .	1.5	16
7375	A high-quality <i>de novo</i> genome assembly of one swamp eel (<i>Monopterus albus</i>) strain with PacBio and Hi-C sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, 1-9.	0.8	15
7376	Unbiased Subgenome Evolution in Allotetraploid Species of<i>Ephedra</i>and Its Implications for the Evolution of Large Genomes in Gymnosperms. Genome Biology and Evolution, 2021, 13, .	1.1	19
7377	Chromosomal-Level Genome Assembly of Silver Sillago (Sillago sihama). Genome Biology and Evolution, 2021, 13, .	1.1	6
7378	Prey sensing and response in a nematode-trapping fungus is governed by the MAPK pheromone response pathway. Genetics, 2021, 217, .	1.2	30
7379	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. GigaScience, 2020, 9, .	3.3	19
7380	The Full-Length Transcriptome of Spartina alterniflora Reveals the Complexity of High Salt Tolerance in Monocotyledonous Halophyte. Plant and Cell Physiology, 2020, 61, 882-896.	1.5	25
7381	Mixta gen. nov., a new genus in the Erwiniaceae. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1396-1407.	0.8	53
7382	Comprehensive annotation of Glossina pallidipes salivary gland hypertrophy virus from Ethiopian tsetse flies: a proteogenomics approach. Journal of General Virology, 2016, 97, 1010-1031.	1.3	24
7383	Suppressive activity of a viral histone H4 against two host chromatin remodelling factors: lysine demethylase and SWI/SNF. Journal of General Virology, 2016, 97, 2780-2796.	1.3	4
7384	Transcriptome changes associated with Tomato spotted wilt virus infection in various life stages of its thrips vector, Frankliniella fusca (Hinds). Journal of General Virology, 2017, 98, 2156-2170.	1.3	40
7385	Comparative analysis of the genomes of clinical isolates of Mycobacterium avium subsp. hominissuis regarding virulence-related genes. Journal of Medical Microbiology, 2017, 66, 1063-1075.	0.7	11
7386	Genomic epidemiology of a national outbreak of post-surgical Mycobacterium abscessus wound infections in Brazil. Microbial Genomics, 2017, 3, e000111.	1.0	22

#	Article	IF	Citations
7387	Metagenomic assembly of new (sub)polar Cyanobacteria and their associated microbiome from non-axenic cultures. Microbial Genomics, 2018, 4, .	1.0	23
7388	Assessing the impact, genomics and evolution of type II secretion across a large, medically important genus: the Legionella type II secretion paradigm. Microbial Genomics, 2019, 5, .	1.0	26
7389	Mycoparasitism illuminated by genome and transcriptome sequencing of Coniothyrium minitans, an important biocontrol fungus of the plant pathogen Sclerotinia sclerotiorum. Microbial Genomics, 2020, 6, .	1.0	15
7390	Transcriptional analysis of mating and pre-infection stages of the anther smut, Microbotryum lychnidis-dioicae. Microbiology (United Kingdom), 2017, 163, 410-420.	0.7	10
7391	Variable virulence phenotype of Xenorhabdus bovienii (Î³-Proteobacteria: Enterobacteriaceae) in the absence of their vector hosts. Microbiology (United Kingdom), 2017, 163, 510-522.	0.7	19
7392	CAR gene cluster and transcript levels of carotenogenic genes in Rhodotorula mucilaginosa. Microbiology (United Kingdom), 2018, 164, 78-87.	0.7	21
7489	A chromosomeâ€scale genome assembly of <i>Antheraea pernyi</i> (Saturniidae, Lepidoptera). Molecular Ecology Resources, 2020, 20, 1372-1383.	2.2	20
7490	Use of the synergist piperonyl butoxide can slow the development of <i>alpha</i>â€cypermethrin resistance in the whitefly <i>Bemisia tabaci</i>. Insect Molecular Biology, 2017, 26, 152-163.	1.0	12
7491	Hepatopancreatic multi-transcript expression patterns in the crayfish Cherax quadricarinatus during the moult cycle. Insect Molecular Biology, 2007, .	1.0	1
7492	Genomics, environment and balancing selection in behaviourally bimodal populations: The caribou case. Molecular Ecology, 2019, 28, 1946-1963.	2.0	18
7493	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i>. Plant Biotechnology Journal, 2018, 16, 1265-1274.	4.1	217
7494	Diversification of true water bugs revealed by transcriptomeâ€based phylogenomics. Systematic Entomology, 2021, 46, 339-356.	1.7	16
7495	Complete Genome Sequence of an Australian Strain of the Lichen-Forming Fungus Endocarpon pusillum (Hedwig). Microbiology Resource Announcements, 2020, 9, .	0.3	4
7499	In silico discovery of terpenoid metabolism in Cannabis sativa. F1000Research, 2017, 6, 107.	0.8	3
7500	The evolution and future of carbonate precipitation in marine invertebrates: Witnessing extinction or documenting resilience in the Anthropocene?. Elementa, 2014, 2, .	1.1	16
7501	Comparative Developmental Transcriptomics Reveals Rewiring of a Highly Conserved Gene Regulatory Network during a Major Life History Switch in the Sea Urchin Genus Heliocidaris. PLoS Biology, 2016, 14, e1002391.	2.6	78
7502	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	1.5	98
7503	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen Pseudocercospora fijiensis (Synonym Mycosphaerella fijiensis) Genomes Reveal Clues for Disease Control. PLoS Genetics, 2016, 12, e1005876.	1.5	77

#	ARTICLE	IF	CITATIONS
7504	Opposing functions of Fng1 and the Rpd3 HDAC complex in H4 acetylation in Fusarium graminearum. PLoS Genetics, 2020, 16, e1009185.	1.5	24
7505	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). PLoS Neglected Tropical Diseases, 2008, 2, e301.	1.3	44
7506	Stage- and Gender-Specific Proteomic Analysis of Brugia malayi Excretory-Secretory Products. PLoS Neglected Tropical Diseases, 2008, 2, e326.	1.3	134
7507	Whole Genome Sequencing of Mycobacterium africanum Strains from Mali Provides Insights into the Mechanisms of Geographic Restriction. PLoS Neglected Tropical Diseases, 2016, 10, e0004332.	1.3	41
7508	Influence of the Microenvironment in the Transcriptome of Leishmania infantum Promastigotes: Sand Fly versus Culture. PLoS Neglected Tropical Diseases, 2016, 10, e0004693.	1.3	17
7509	Proteomic Analysis of Excretory-Secretory Products of Mesocestoides corti Metacestodes Reveals Potential Suppressors of Dendritic Cell Functions. PLoS Neglected Tropical Diseases, 2016, 10, e0005061.	1.3	28
7510	Differential Protein Expression in the Hemolymph of Bithynia siamensis goniomphalos Infected with Opisthorchis viverrini. PLoS Neglected Tropical Diseases, 2016, 10, e0005104.	1.3	12
7511	Quantitative label-free proteomic analysis of human urine to identify novel candidate protein biomarkers for schistosomiasis. PLoS Neglected Tropical Diseases, 2017, 11, e0006045.	1.3	22
7512	Transcriptome of Pneumocystis carinii during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.	1.1	58
7513	Rapid Annotation of Anonymous Sequences from Genome Projects Using Semantic Similarities and a Weighting Scheme in Gene Ontology. PLoS ONE, 2009, 4, e4619.	1.1	33
7514	Defining Global Neuroendocrine Gene Expression Patterns Associated with Reproductive Seasonality in Fish. PLoS ONE, 2009, 4, e5816.	1.1	39
7515	Proteomic Analysis of Tardigrades: Towards a Better Understanding of Molecular Mechanisms by Anhydrobiotic Organisms. PLoS ONE, 2010, 5, e9502.	1.1	58
7516	Rapid Dopaminergic Modulation of the Fish Hypothalamic Transcriptome and Proteome. PLoS ONE, 2010, 5, e12338.	1.1	33
7517	The Distribution of GYR- and YLP-Like Motifs in Drosophila Suggests a General Role in Cuticle Assembly and Other Protein-Protein Interactions. PLoS ONE, 2010, 5, e12536.	1.1	17
7518	A Compendium of Canine Normal Tissue Gene Expression. PLoS ONE, 2011, 6, e17107.	1.1	36
7519	Deciphering the Role of RND Efflux Transporters in Burkholderia cenocepacia. PLoS ONE, 2011, 6, e18902.	1.1	68
7520	Gene Expression Rhythms in the Mussel Mytilus galloprovincialis (Lam.) across an Annual Cycle. PLoS ONE, 2011, 6, e18904.	1.1	89
7521	The Organophosphate Chlorpyrifos Interferes with the Responses to 17Î²-Estradiol in the Digestive Gland of the Marine Mussel Mytilus galloprovincialis. PLoS ONE, 2011, 6, e19803.	1.1	49

#	Article	IF	Citations
7522	Identification of Genes Directly Involved in Shell Formation and Their Functions in Pearl Oyster, Pinctada fucata. PLoS ONE, 2011, 6, e21860.	1.1	98
7523	First Transcriptome of the Testis-Vas Deferens-Male Accessory Gland and Proteome of the Spermatophore from Dermacentor variabilis (Acari: Ixodidae). PLoS ONE, 2011, 6, e24711.	1.1	55
7524	Profiling the Trypanosoma cruzi Phosphoproteome. PLoS ONE, 2011, 6, e25381.	1.1	68
7525	Examination of Triacylglycerol Biosynthetic Pathways via De Novo Transcriptomic and Proteomic Analyses in an Unsequenced Microalga. PLoS ONE, 2011, 6, e25851.	1.1	198
7526	Development and Characterization of Microsatellite Markers for the Cape Gooseberry Physalis peruviana. PLoS ONE, 2011, 6, e26719.	1.1	45
7527	Microarray-Based Transcriptomic Analysis of Differences between Long-Term Gregarious and Solitarious Desert Locusts. PLoS ONE, 2011, 6, e28110.	1.1	36
7528	Metatranscriptomics Reveals the Diversity of Genes Expressed by Eukaryotes in Forest Soils. PLoS ONE, 2012, 7, e28967.	1.1	149
7529	Red and Green Algal Origin of Diatom Membrane Transporters: Insights into Environmental Adaptation and Cell Evolution. PLoS ONE, 2011, 6, e29138.	1.1	44
7530	SNP Discovery and Development of a High-Density Genotyping Array for Sunflower. PLoS ONE, 2012, 7, e29814.	1.1	100
7531	Transcriptome Analysis of the Model Protozoan, Tetrahymena thermophila, Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
7532	De Novo Transcriptome of Safflower and the Identification of Putative Genes for Oleosin and the Biosynthesis of Flavonoids. PLoS ONE, 2012, 7, e30987.	1.1	56
7533	Annotation of the Transcriptome from Taenia pisiformis and Its Comparative Analysis with Three Taeniidae Species. PLoS ONE, 2012, 7, e32283.	1.1	32
7534	De-Novo Assembly and Analysis of the Heterozygous Triploid Genome of the Wine Spoilage Yeast Dekkera bruxellensis AWRI1499. PLoS ONE, 2012, 7, e33840.	1.1	110
7535	Digital Gene Expression Analysis Based on Integrated De Novo Transcriptome Assembly of Sweet Potato [Ipomoea batatas (L.) Lam.]. PLoS ONE, 2012, 7, e36234.	1.1	156
7536	Insecticide Resistance Mechanisms in the Green Peach Aphid Myzus persicae (Hemiptera: Aphididae) I: A Transcriptomic Survey. PLoS ONE, 2012, 7, e36366.	1.1	133
7537	Sequencing and Analysis of the Mediterranean Amphioxus (Branchiostoma lanceolatum) Transcriptome. PLoS ONE, 2012, 7, e36554.	1.1	42
7538	Microarray Analysis of Gene Regulations and Potential Association with Acephate-Resistance and Fitness Cost in Lygus lineolaris. PLoS ONE, 2012, 7, e37586.	1.1	26
7539	RNA-Seq Analysis of the Sclerotinia homoeocarpa â€“ Creeping Bentgrass Pathosystem. PLoS ONE, 2012, 7, e41150.	1.1	33

#	ARTICLE	IF	CITATIONS
7540	Novel Insights into the Transcriptome of Dirofilaria immitis. PLoS ONE, 2012, 7, e41639.	1.1	15
7541	De Novo Sequencing of Hypericum perforatum Transcriptome to Identify Potential Genes Involved in the Biosynthesis of Active Metabolites. PLoS ONE, 2012, 7, e42081.	1.1	45
7542	Phylogenomic Resolution of Paleozoic Divergences in Harvestmen (Arachnida, Opiliones) via Analysis of Next-Generation Transcriptome Data. PLoS ONE, 2012, 7, e42888.	1.1	57
7543	Heart of Endosymbioses: Transcriptomics Reveals a Conserved Genetic Program among Arbuscular Mycorrhizal, Actinorhizal and Legume-Rhizobial Symbioses. PLoS ONE, 2012, 7, e44742.	1.1	77
7544	Deep Sequencing of the Transcriptomes of Soybean Aphid and Associated Endosymbionts. PLoS ONE, 2012, 7, e45161.	1.1	44
7545	The Social Brain: Transcriptome Assembly and Characterization of the Hippocampus from a Social Subterranean Rodent, the Colonial Tuco-Tuco (Ctenomys sociabilis). PLoS ONE, 2012, 7, e45524.	1.1	21
7546	Comparative proteome analysis of Milnesium tardigradum in early embryonic state versus adults in active and anhydrobiotic state. PLoS ONE, 2012, 7, e45682.	1.1	31
7547	Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	28
7548	A Complex Set of Sex Pheromones Identified in the Cuttlefish Sepia officinalis. PLoS ONE, 2012, 7, e46531.	1.1	7
7549	Transcriptome Sequencing and De Novo Analysis for Ma Bamboo (Dendrocalamus latiflorus Munro) Using the Illumina Platform. PLoS ONE, 2012, 7, e46766.	1.1	104
7550	Transcriptome and Gene Expression Analysis of the Rice Leaf Folder, Cnaphalocrosis medinalis. PLoS ONE, 2012, 7, e47401.	1.1	59
7551	Combining Next-Generation Sequencing and Microarray Technology into a Transcriptomics Approach for the Non-Model Organism Chironomus riparius. PLoS ONE, 2012, 7, e48096.	1.1	32
7552	Characterization of Chicken Spleen Transcriptome after Infection with Salmonella enterica Serovar Enteritidis. PLoS ONE, 2012, 7, e48101.	1.1	77
7553	Genetic Responses Induced in Olive Roots upon Colonization by the Biocontrol Endophytic Bacterium Pseudomonas fluorescens PICF7. PLoS ONE, 2012, 7, e48646.	1.1	60
7554	Deep Sequencing Reveals Differences in the Transcriptional Landscapes of Fibers from Two Cultivated Species of Cotton. PLoS ONE, 2012, 7, e48855.	1.1	37
7555	Identification of Novel and Differentially Expressed MicroRNAs of Dairy Goat Mammary Gland Tissues Using Solexa Sequencing and Bioinformatics. PLoS ONE, 2012, 7, e49463.	1.1	70
7556	Coral Thermal Tolerance: Tuning Gene Expression to Resist Thermal Stress. PLoS ONE, 2012, 7, e50685.	1.1	140
7557	Early Differential Gene Expression in Haemocytes from Resistant and Susceptible Biomphalaria glabrata Strains in Response to Schistosoma mansoni. PLoS ONE, 2012, 7, e51102.	1.1	66

#	ARTICLE	IF	CITATIONS
7558	Bioinformatic Inference of Specific and General Transcription Factor Binding Sites in the Plant Pathogen Phytophthora infestans. PLoS ONE, 2012, 7, e51295.	1.1	13
7559	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree Pongamia pinnata. PLoS ONE, 2012, 7, e51687.	1.1	73
7560	Ocean Acidification Affects Redox-Balance and Ion-Homeostasis in the Life-Cycle Stages of Emiliania huxleyi. PLoS ONE, 2012, 7, e52212.	1.1	72
7561	SOLiD-SAGE of Endophyte-Infected Red Fescue Reveals Numerous Effects on Host Transcriptome and an Abundance of Highly Expressed Fungal Secreted Proteins. PLoS ONE, 2012, 7, e53214.	1.1	76
7562	Comparative Transcriptome Analysis of the Accessory Sex Gland and Testis from the Chinese Mitten Crab (Eriocheir sinensis). PLoS ONE, 2013, 8, e53915.	1.1	54
7563	De novo Transcriptome Sequencing Reveals a Considerable Bias in the Incidence of Simple Sequence Repeats towards the Downstream of â€˜Pre-miRNAsâ€™ of Black Pepper. PLoS ONE, 2013, 8, e56694.	1.1	51
7564	De Novo Assembly of Mud Loach (Misgurnus anguillicaudatus) Skin Transcriptome to Identify Putative Genes Involved in Immunity and Epidermal Mucus Secretion. PLoS ONE, 2013, 8, e56998.	1.1	59
7565	Genes Related to Ion-Transport and Energy Production Are Upregulated in Response to CO2-Driven pH Decrease in Corals: New Insights from Transcriptome Analysis. PLoS ONE, 2013, 8, e58652.	1.1	152
7566	Transcriptome Profiling of Chironomus kiinensis under Phenol Stress Using Solexa Sequencing Technology. PLoS ONE, 2013, 8, e58914.	1.1	18
7567	In-Depth Tanscriptomic Analysis on Giant Freshwater Prawns. PLoS ONE, 2013, 8, e60839.	1.1	32
7568	Nutrigenomics in Arma chinensis: Transcriptome Analysis of Arma chinensis Fed on Artificial Diet and Chinese Oak Silk Moth Antheraea pernyi Pupae. PLoS ONE, 2013, 8, e60881.	1.1	36
7569	Exploiting the Transcriptome of Euphrates Poplar, Populus euphratica (Salicaceae) to Develop and Characterize New EST-SSR Markers and Construct an EST-SSR Database. PLoS ONE, 2013, 8, e61337.	1.1	34
7570	Transcriptomic and Proteomic Responses of Sweetpotato Whitefly, Bemisia tabaci, to Thiamethoxam. PLoS ONE, 2013, 8, e61820.	1.1	58
7571	Next-Generation Sequencing of the Chrysanthemum nankingense (Asteraceae) Transcriptome Permits Large-Scale Unigene Assembly and SSR Marker Discovery. PLoS ONE, 2013, 8, e62293.	1.1	107
7572	Analysis of the Transcriptome of Blowfly Chrysomya megacephala (Fabricius) Larvae in Responses to Different Edible Oils. PLoS ONE, 2013, 8, e63168.	1.1	16
7573	Characterization of Pythium Transcriptome and Gene Expression Analysis at Different Stages of Fermentation. PLoS ONE, 2013, 8, e65552.	1.1	6
7574	Analysis of the Olive Fruit Fly Bactrocera oleae Transcriptome and Phylogenetic Classification of the Major Detoxification Gene Families. PLoS ONE, 2013, 8, e66533.	1.1	55
7575	Transcriptome Profiling of Radish (Raphanus sativus L.) Root and Identification of Genes Involved in Response to Lead (Pb) Stress with Next Generation Sequencing. PLoS ONE, 2013, 8, e66539.	1.1	106

#	ARTICLE	IF	CITATIONS
7576	Transcriptional Response of the Mussel Mytilus galloprovincialis (Lam.) following Exposure to Heat Stress and Copper. PLoS ONE, 2013, 8, e66802.	1.1	91
7577	Strategies for Wheat Stripe Rust Pathogenicity Identified by Transcriptome Sequencing. PLoS ONE, 2013, 8, e67150.	1.1	110
7578	Male-Biased Genes in Catfish as Revealed by RNA-Seq Analysis of the Testis Transcriptome. PLoS ONE, 2013, 8, e68452.	1.1	71
7579	The Plastid Genome of Najas flexilis: Adaptation to Submersed Environments Is Accompanied by the Complete Loss of the NDH Complex in an Aquatic Angiosperm. PLoS ONE, 2013, 8, e68591.	1.1	98
7580	Differential Gene Expression in Response to Papaya ringspot virus Infection in Cucumis metuliferus Using cDNA- Amplified Fragment Length Polymorphism Analysis. PLoS ONE, 2013, 8, e68749.	1.1	8
7581	Tracing the Transcriptomic Changes in Synthetic Trigenomic allohexaploids of Brassica Using an RNA-Seq Approach. PLoS ONE, 2013, 8, e68883.	1.1	39
7582	Exploring Early Micronutrient Deficiencies in Rainbow Trout (Oncorhynchus mykiss) by Next-Generation Sequencing Technology â€“ From Black Box to Functional Genomics. PLoS ONE, 2013, 8, e69461.	1.1	16
7583	Exploring the Host Parasitism of the Migratory Plant-Parasitic Nematode Ditylenchus destuctor by Expressed Sequence Tags Analysis. PLoS ONE, 2013, 8, e69579.	1.1	30
7584	A Lover and a Fighter: The Genome Sequence of an Entomopathogenic Nematode Heterorhabditis bacteriophora. PLoS ONE, 2013, 8, e69618.	1.1	89
7585	De Novo Assembly and Characterization of Two Transcriptomes Reveal Multiple Light-Mediated Functions in the Scallop Eye (Bivalvia: Pectinidae). PLoS ONE, 2013, 8, e69852.	1.1	32
7586	SNP Discovery in European Anchovy (Engraulis encrasicolus, L) by High-Throughput Transcriptome and Genome Sequencing. PLoS ONE, 2013, 8, e70051.	1.1	38
7587	Microarray Analysis of Gene Expression Profiles of Schistosoma japonicum Derived from Less-Susceptible Host Water Buffalo and Susceptible Host Goat. PLoS ONE, 2013, 8, e70367.	1.1	8
7588	De Novo Assembly and Characterization of the Transcriptome, and Development of SSR Markers in Wax Gourd (Benicasa hispida). PLoS ONE, 2013, 8, e71054.	1.1	47
7589	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast Hortaea werneckii. PLoS ONE, 2013, 8, e71328.	1.1	96
7590	Transcriptome Characteristics and Six Alternative Expressed Genes Positively Correlated with the Phase Transition of Annual Cambial Activities in Chinese Fir (Cunninghamia lanceolata (Lamb.) Hook). PLoS ONE, 2013, 8, e71562.	1.1	26
7591	Transcriptome and Peptidome Characterisation of the Main Neuropeptides and Peptidic Hormones of a Euphausiid: The Ice Krill, Euphausia crystallorophias. PLoS ONE, 2013, 8, e71609.	1.1	57
7592	Transcriptome Analysis of Chlorantraniliprole Resistance Development in the Diamondback Moth Plutella xylostella. PLoS ONE, 2013, 8, e72314.	1.1	68
7593	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

#	ARTICLE	IF	CITATIONS
7594	SNP Discovery by Illumina-Based Transcriptome Sequencing of the Olive and the Genetic Characterization of Turkish Olive Genotypes Revealed by AFLP, SSR and SNP Markers. PLoS ONE, 2013, 8, e73674.	1.1	90
7595	Transcriptome and Expression Profile Analysis of Highly Resistant and Susceptible Banana Roots Challenged with Fusarium oxysporum f. sp. cubense Tropical Race 4. PLoS ONE, 2013, 8, e73945.	1.1	78
7596	Transcriptome Profile of the Green Odorous Frog (Odorrana margaretae). PLoS ONE, 2013, 8, e75211.	1.1	33
7597	Comparative Analysis of Latex Transcriptome Reveals Putative Molecular Mechanisms Underlying Super Productivity of Hevea brasiliensis. PLoS ONE, 2013, 8, e75307.	1.1	32
7598	Generation and Analysis of a Large-Scale Expressed Sequence Tag Database from a Full-Length Enriched cDNA Library of Developing Leaves of Gossypium hirsutum L. PLoS ONE, 2013, 8, e76443.	1.1	10
7599	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
7600	Transcriptome Analysis of Nautilus and Pygmy Squid Developing Eye Provides Insights in Lens and Eye Evolution. PLoS ONE, 2013, 8, e78054.	1.1	5
7601	Transcriptome Sequencing and Analysis of the Fast Growing Shoots of Moso Bamboo (Phyllostachys) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	94
7602	Mining Genes Involved in Insecticide Resistance of Liposcelis bostrychophila Badonnel by Transcriptome and Expression Profile Analysis. PLoS ONE, 2013, 8, e79878.	1.1	18
7603	Transcriptome Analysis of Leaf Tissue of Raphanus sativus by RNA Sequencing. PLoS ONE, 2013, 8, e80350.	1.1	26
7604	Transcriptome Analysis of Medicinal Plant Salvia miltiorrhiza and Identification of Genes Related to Tanshinone Biosynthesis. PLoS ONE, 2013, 8, e80464.	1.1	111
7605	Transcriptome Analysis of Salicornia europaea under Saline Conditions Revealed the Adaptive Primary Metabolic Pathways as Early Events to Facilitate Salt Adaptation. PLoS ONE, 2013, 8, e80595.	1.1	41
7606	Sequencing and De Novo Assembly of the Transcriptome of the Glassy-Winged Sharpshooter (Homalodisca vitripennis). PLoS ONE, 2013, 8, e81681.	1.1	15
7607	The Genome Sequence of the Fungal Pathogen Fusarium virguliforme That Causes Sudden Death Syndrome in Soybean. PLoS ONE, 2014, 9, e81832.	1.1	50
7608	Early Transcriptional Response of Soybean Contrasting Accessions to Root Dehydration. PLoS ONE, 2013, 8, e83466.	1.1	27
7609	Transcriptome Analysis of Houttuynia cordata Thunb. by Illumina Paired-End RNA Sequencing and SSR Marker Discovery. PLoS ONE, 2014, 9, e84105.	1.1	42
7610	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
7611	The Discovery of phiAGATE, A Novel Phage Infecting Bacillus pumilus, Leads to New Insights into the Phylogeny of the Subfamily Spounavirinae. PLoS ONE, 2014, 9, e86632.	1.1	29

#	ARTICLE	IF	CITATIONS
7612	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
7613	Transcriptome Profile of Trichoderma harzianum IOC-3844 Induced by Sugarcane Bagasse. PLoS ONE, 2014, 9, e88689.	1.1	41
7614	Single-Nucleotide Polymorphism Markers from De-Novo Assembly of the Pomegranate Transcriptome Reveal Germplasm Genetic Diversity. PLoS ONE, 2014, 9, e88998.	1.1	70
7615	Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. PLoS ONE, 2014, 9, e89323.	1.1	70
7616	Carbohydrate Availability Regulates Virulence Gene Expression in Streptococcus suis. PLoS ONE, 2014, 9, e89334.	1.1	48
7617	A Systems Biology Approach to the Characterization of Stress Response in Dermacentor reticulatus Tick Unfed Larvae. PLoS ONE, 2014, 9, e89564.	1.1	72
7618	Transcriptomics of the Interaction between the Monopartite Phloem-Limited Geminivirus Tomato Yellow Leaf Curl Sardinia Virus and Solanum lycopersicum Highlights a Role for Plant Hormones, Autophagy and Plant Immune System Fine Tuning during Infection. PLoS ONE, 2014, 9, e89951.	1.1	77
7619	Transcriptome Immune Analysis of the Invasive Beetle Octodonta nipae (Maulik) (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2014, 9, e91482.	1.1	26
7620	A Framework Phylogeny of the American Oak Clade Based on Sequenced RAD Data. PLoS ONE, 2014, 9, e93975.	1.1	215
7621	Characterization of the Miiuy Croaker (Miichthys miiuy) Transcriptome and Development of Immune-Relevant Genes and Molecular Markers. PLoS ONE, 2014, 9, e94046.	1.1	63
7622	A Draft Genome of the Honey Bee Trypanosomatid Parasite Crithidia mellificae. PLoS ONE, 2014, 9, e95057.	1.1	60
7623	The Effect of Exposure to a High-Fat Diet on MicroRNA Expression in the Liver of Blunt Snout Bream (Megalobrama amblycephala). PLoS ONE, 2014, 9, e96132.	1.1	41
7624	The Mitochondrial Genome of the Leaf-Cutter Ant Atta laevigata: A Mitogenome with a Large Number of Intergenic Spacers. PLoS ONE, 2014, 9, e97117.	1.1	37
7625	Characterization of Natural Antisense Transcript, Sclerotia Development and Secondary Metabolism by Strand-Specific RNA Sequencing of Aspergillus flavus. PLoS ONE, 2014, 9, e97814.	1.1	13
7626	Proteomic Identification of Novel Differentiation Plasma Protein Markers in Hypobaric Hypoxia-Induced Rat Model. PLoS ONE, 2014, 9, e98027.	1.1	33
7627	Oak Root Response to Ectomycorrhizal Symbiosis Establishment: RNA-Seq Derived Transcript Identification and Expression Profiling. PLoS ONE, 2014, 9, e98376.	1.1	45
7628	A Survey of Innovation through Duplication in the Reduced Genomes of Twelve Parasites. PLoS ONE, 2014, 9, e99213.	1.1	7
7629	CELLO2GO: A Web Server for Protein subCELlular LOcalization Prediction with Functional Gene Ontology Annotation. PLoS ONE, 2014, 9, e99368.	1.1	357

#	ARTICLE	IF	CITATIONS
7630	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. PLoS ONE, 2014, 9, e99720.	1.1	66
7631	Comparison of the Transcriptomes of Ginger (Zingiber officinale Rosc.) and Mango Ginger (Curcuma) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	50
7632	Evaluation of Reference Genes for Quantitative Real-Time PCR in Oil Palm Elite Planting Materials Propagated by Tissue Culture. PLoS ONE, 2014, 9, e99774.	1.1	21
7633	RNA-Seq Analysis Implicates Detoxification Pathways in Ovine Mycotoxin Resistance. PLoS ONE, 2014, 9, e99975.	1.1	10
7634	Response of the Hepatic Transcriptome to Aflatoxin B1 in Domestic Turkey (Meleagris gallopavo). PLoS ONE, 2014, 9, e100930.	1.1	28
7635	De Novo Transcriptomes of a Mixotrophic and a Heterotrophic Ciliate from Marine Plankton. PLoS ONE, 2014, 9, e101418.	1.1	29
7636	De Novo Assembly and Transcriptome Analysis of the Rubber Tree (Hevea brasiliensis) and SNP Markers Development for Rubber Biosynthesis Pathways. PLoS ONE, 2014, 9, e102665.	1.1	113
7637	Molecular Characterization and Differential Expression of Olfactory Genes in the Antennae of the Black Cutworm Moth Agrotis ipsilon. PLoS ONE, 2014, 9, e103420.	1.1	66
7638	De Novo Transcriptomes of Olfactory Epithelium Reveal the Genes and Pathways for Spawning Migration in Japanese Grenadier Anchovy (Coilia nasus). PLoS ONE, 2014, 9, e103832.	1.1	20
7639	A Comprehensive Reference Transcriptome Resource for the Common House Spider Parasteatoda tepidariorum. PLoS ONE, 2014, 9, e104885.	1.1	57
7640	Large-Scale Phylogenetic Classification of Fungal Chitin Synthases and Identification of a Putative Cell-Wall Metabolism Gene Cluster in Aspergillus Genomes. PLoS ONE, 2014, 9, e104920.	1.1	18
7641	De Novo Assembly and Characterization of the Fruit Transcriptome of Chinese Jujube (Ziziphus jujuba) Tj ETQq1 1 0.784314 rgBT /Overl 2014, 9, e106438.	1.1	27
7642	QTL Analysis and Candidate Gene Mapping for the Polyphenol Content in Cider Apple. PLoS ONE, 2014, 9, e107103.	1.1	33
7643	Identification and Expression of Fructose-1,6-Bisphosphate Aldolase Genes and Their Relations to Oil Content in Developing Seeds of Tea Oil Tree (Camellia oleifera). PLoS ONE, 2014, 9, e107422.	1.1	44
7644	Transcriptome Sequencing and Identification of Cold Tolerance Genes in Hardy Corylus Species (C.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	14
7645	Transcriptome Analysis of the Trachinotus ovatus: Identification of Reproduction, Growth and Immune-Related Genes and Microsatellite Markers. PLoS ONE, 2014, 9, e109419.	1.1	42
7646	In-Depth Transcriptome Analysis of the Red Swamp Crayfish Procambarus clarkii. PLoS ONE, 2014, 9, e110548.	1.1	62
7647	Effects of Changes in Food Supply at the Time of Sex Differentiation on the Gonadal Transcriptome of Juvenile Fish. Implications for Natural and Farmed Populations. PLoS ONE, 2014, 9, e111304.	1.1	7

#	ARTICLE	IF	CITATIONS
7648	Comparative Genomics to Delineate Pathogenic Potential in Non-O157 Shiga Toxin-Producing Escherichia coli (STEC) from Patients with and without Haemolytic Uremic Syndrome (HUS) in Norway. PLoS ONE, 2014, 9, e111788.	1.1	41
7649	Characterization of Flower-Bud Transcriptome and Development of Genic SSR Markers in Asian Lotus (Nelumbo nucifera Gaertn.). PLoS ONE, 2014, 9, e112223.	1.1	15
7650	De Novo Assembly and Characterization of the Transcriptome of Seagrass Zostera marina Using Illumina Paired-End Sequencing. PLoS ONE, 2014, 9, e112245.	1.1	36
7651	RNA-Seq Analysis of Quercus pubescens Leaves: De Novo Transcriptome Assembly, Annotation and Functional Markers Development. PLoS ONE, 2014, 9, e112487.	1.1	49
7652	Comparative Analysis of Predicted Plastid-Targeted Proteomes of Sequenced Higher Plant Genomes. PLoS ONE, 2014, 9, e112870.	1.1	8
7653	Comparison of the Transcriptome between Two Cotton Lines of Different Fiber Color and Quality. PLoS ONE, 2014, 9, e112966.	1.1	26
7654	Gene Expression of Protein-Coding and Non-Coding RNAs Related to Polyembryogenesis in the Parasitic Wasp, Copidosoma floridanum. PLoS ONE, 2014, 9, e114372.	1.1	5
7655	Gene Expression of Corals in Response to Macroalgal Competitors. PLoS ONE, 2014, 9, e114525.	1.1	10
7656	Identification of Regulatory Genes Implicated in Continuous Flowering of Longan (Dimocarpus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	1.1	26
7657	Transcriptome Sequencing and Characterization of Japanese Scallop Patinopecten yessoensis from Different Shell Color Lines. PLoS ONE, 2015, 10, e0116406.	1.1	51
7658	RNA Sequencing of Populus x canadensis Roots Identifies Key Molecular Mechanisms Underlying Physiological Adaption to Excess Zinc. PLoS ONE, 2015, 10, e0117571.	1.1	18
7659	Deep mRNA Sequencing of the Tritonia diomedea Brain Transcriptome Provides Access to Gene Homologues for Neuronal Excitability, Synaptic Transmission and Peptidergic Signalling. PLoS ONE, 2015, 10, e0118321.	1.1	24
7660	Transcriptomic Analysis of American Ginseng Seeds during the Dormancy Release Process by RNA-Seq. PLoS ONE, 2015, 10, e0118558.	1.1	19
7661	Comparative Transcriptome Analysis of Anthurium â€œAlbamaâ€•and Its Anthocyanin-Loss Mutant. PLoS ONE, 2015, 10, e0119027.	1.1	17
7662	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
7663	Whole-Genome Analysis Revealed the Positively Selected Genes during the Differentiation of indica and Temperate japonica Rice. PLoS ONE, 2015, 10, e0119239.	1.1	15
7664	Transcriptomic Signatures in Seeds of Apple (Malus domestica L. Borkh) during Fruitlet Abscission. PLoS ONE, 2015, 10, e0120503.	1.1	19
7665	Chemosensory Gene Families in Adult Antennae of Anomala corpulenta Motschulsky (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	66

#	ARTICLE	IF	CITATIONS
7666	DeepSAGE Based Differential Gene Expression Analysis under Cold and Freeze Stress in Seabuckthorn (Hippophae rhamnoides L.). PLoS ONE, 2015, 10, e0121982.	1.1	26
7667	Comparative Whole-Genome Analysis of Clinical Isolates Reveals Characteristic Architecture of Mycobacterium tuberculosis Pangenome. PLoS ONE, 2015, 10, e0122979.	1.1	49
7668	Unraveling 14-3-3 Proteins in C4 Panicoids with Emphasis on Model Plant Setaria italica Reveals Phosphorylation-Dependent Subcellular Localization of RS Splicing Factor. PLoS ONE, 2015, 10, e0123236.	1.1	37
7669	MicroRNA-Like Small RNAs Prediction in the Development of Antrodia cinnamomea. PLoS ONE, 2015, 10, e0123245.	1.1	35
7670	Comparative Proteome Analysis of Multi-Layer Cocoon of the Silkworm, Bombyx mori. PLoS ONE, 2015, 10, e0123403.	1.1	34
7671	Analyses of the Complete Genome and Gene Expression of Chloroplast of Sweet Potato [Ipomoea batata]. PLoS ONE, 2015, 10, e0124083.	1.1	42
7672	De Novo Transcriptome Analysis to Identify Anthocyanin Biosynthesis Genes Responsible for Tissue-Specific Pigmentation in Zoysiagrass (Zoysia japonica Steud.). PLoS ONE, 2015, 10, e0124497.	1.1	27
7673	Transcriptome Profiling Reveals the Regulatory Mechanism Underlying Pollination Dependent and Parthenocarpic Fruit Set Mainly Mediated by Auxin and Gibberellin. PLoS ONE, 2015, 10, e0125355.	1.1	51
7674	Whole-Transcriptome Analysis of Differentially Expressed Genes in the Vegetative Buds, Floral Buds and Buds of Chrysanthemum morifolium. PLoS ONE, 2015, 10, e0128009.	1.1	54
7675	Male- and Female-Biased Gene Expression of Olfactory-Related Genes in the Antennae of Asian Corn Borer, Ostrinia furnacalis (GuenÃ©e) (Lepidoptera: Crambidae). PLoS ONE, 2015, 10, e0128550.	1.1	33
7676	High-Throughput Sequencing and De Novo Assembly of Red and Green Forms of the Perilla frutescens var. crispa Transcriptome. PLoS ONE, 2015, 10, e0129154.	1.1	40
7677	An Interspecies Comparative Analysis of the Predicted Secretomes of the Necrotrophic Plant Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS ONE, 2015, 10, e0130534.	1.1	72
7678	Transcriptome Response Signatures Associated with the Overexpression of a Mitochondrial Uncoupling Protein (AtUCP1) in Tobacco. PLoS ONE, 2015, 10, e0130744.	1.1	11
7679	Metatranscriptome Analysis of Fig Flowers Provides Insights into Potential Mechanisms for Mutualism Stability and Gall Induction. PLoS ONE, 2015, 10, e0130745.	1.1	24
7680	Seasonal Variation in the Skin Transcriptome of Common Bottlenose Dolphins (Tursiops truncatus) from the Northern Gulf of Mexico. PLoS ONE, 2015, 10, e0130934.	1.1	25
7681	Transcriptome-Based Identification of Highly Similar Odorant-Binding Proteins among Neotropical Stink Bugs and Their Egg Parasitoid. PLoS ONE, 2015, 10, e0132286.	1.1	25
7682	Comparative Transcriptome Analysis Reveals Sex-Biased Gene Expression in Juvenile Chinese Mitten Crab Eriocheir sinensis. PLoS ONE, 2015, 10, e0133068.	1.1	42
7683	Transcriptomic Analysis of Paeonia delavayi Wild Population Flowers to Identify Differentially Expressed Genes Involved in Purple-Red and Yellow Petal Pigmentation. PLoS ONE, 2015, 10, e0135038.	1.1	36

#	ARTICLE	IF	CITATIONS
7684	A Catalog of Proteins Expressed in the AG Secreted Fluid during the Mature Phase of the Chinese Mitten Crabs (Eriocheir sinensis). PLoS ONE, 2015, 10, e0136266.	1.1	3
7685	In-Depth Duodenal Transcriptome Survey in Chickens with Divergent Feed Efficiency Using RNA-Seq. PLoS ONE, 2015, 10, e0136765.	1.1	36
7686	Comparative Physiological and Proteomic Analysis Reveals the Leaf Response to Cadmium-Induced Stress in Poplar (Populus yunnanensis). PLoS ONE, 2015, 10, e0137396.	1.1	23
7687	Genome-Wide Transcription Study of Cryptococcus neoformans H99 Clinical Strain versus Environmental Strains. PLoS ONE, 2015, 10, e0137457.	1.1	16
7688	Ovarian Transcriptome Analysis of Portunus trituberculatus Provides Insights into Genes Expressed during Phase III and IV Development. PLoS ONE, 2015, 10, e0138862.	1.1	20
7689	Rice-Infecting Pseudomonas Genomes Are Highly Accessorized and Harbor Multiple Putative Virulence Mechanisms to Cause Sheath Brown Rot. PLoS ONE, 2015, 10, e0139256.	1.1	10
7690	Molecular Characterization and Differential Expression of an Olfactory Receptor Gene Family in the White-Backed Planthopper Sogatella furcifera Based on Transcriptome Analysis. PLoS ONE, 2015, 10, e0140605.	1.1	21
7691	A Diversity of Conserved and Novel Ovarian MicroRNAs in the Speckled Wood (Pararge aegeria). PLoS ONE, 2015, 10, e0142243.	1.1	21
7692	Global Transcriptome Analysis of the Tentacle of the Jellyfish Cyanea capillata Using Deep Sequencing and Expressed Sequence Tags: Insight into the Toxin- and Degenerative Disease-Related Transcripts. PLoS ONE, 2015, 10, e0142680.	1.1	31
7693	Genome-Wide Identification of MicroRNAs in Leaves and the Developing Head of Four Durum Genotypes during Water Deficit Stress. PLoS ONE, 2015, 10, e0142799.	1.1	43
7694	Transcriptome Analysis of Blunt Snout Bream (Megalobrama amblycephala) Reveals Putative Differential Expression Genes Related to Growth and Hypoxia. PLoS ONE, 2015, 10, e0142801.	1.1	20
7695	454 Pyrosequencing of Olive (Olea europaea L.) Transcriptome in Response to Salinity. PLoS ONE, 2015, 10, e0143000.	1.1	37
7696	Identification and Comparative Expression Profiles of Chemoreception Genes Revealed from Major Chemoreception Organs of the Rice Leaf Folder, Cnaphalocrocis medinalis (Lepidoptera: Pyralidae). PLoS ONE, 2015, 10, e0144267.	1.1	32
7697	Whole Transcriptome Analysis Provides Insights into Molecular Mechanisms for Molting in Litopenaeus vannamei. PLoS ONE, 2015, 10, e0144350.	1.1	86
7698	Label-Free Quantitative Proteomic Analysis of Puccinia psidii Uredospores Reveals Differences of Fungal Populations Infecting Eucalyptus and Guava. PLoS ONE, 2016, 11, e0145343.	1.1	18
7699	Using RNA-seq to Profile Gene Expression of Spikelet Development in Response to Temperature and Nitrogen during Meiosis in Rice (Oryza sativa L.). PLoS ONE, 2015, 10, e0145532.	1.1	12
7700	De Novo Transcriptome and Expression Profile Analysis to Reveal Genes and Pathways Potentially Involved in Cantharidin Biosynthesis in the Blister Beetle Mylabris cichorii. PLoS ONE, 2016, 11, e0146953.	1.1	15
7701	Development of a Genomic Resource and Quantitative Trait Loci Mapping of Male Calling Traits in the Lesser Wax Moth, Achroia grisella. PLoS ONE, 2016, 11, e0147014.	1.1	3

#	ARTICLE	IF	CITATIONS
7702	De Novo Transcriptome Assembly of the Chinese Swamp Buffalo by RNA Sequencing and SSR Marker Discovery. PLoS ONE, 2016, 11, e0147132.	1.1	43
7703	Proteomic Analysis of the Schistosoma mansoni Miracidium. PLoS ONE, 2016, 11, e0147247.	1.1	34
7704	Transcriptomic Analysis of Tea Plant Responding to Drought Stress and Recovery. PLoS ONE, 2016, 11, e0147306.	1.1	67
7705	Use of De Novo Transcriptome Libraries to Characterize a Novel Oleaginous Marine Chlorella Species during the Accumulation of Triacylglycerols. PLoS ONE, 2016, 11, e0147527.	1.1	16
7706	Transcriptome and Expression Patterns of Chemosensory Genes in Antennae of the Parasitoid Wasp Chouioia cunea. PLoS ONE, 2016, 11, e0148159.	1.1	53
7707	Complete mitochondrial genome of the Verticillium-wilt causing plant pathogen Verticillium nonalfalfae. PLoS ONE, 2016, 11, e0148525.	1.1	19
7708	Sequencing, De Novo Assembly, and Annotation of the Transcriptome of the Endangered Freshwater Pearl Bivalve, Cristaria plicata, Provides Novel Insights into Functional Genes and Marker Discovery. PLoS ONE, 2016, 11, e0148622.	1.1	61
7709	Comparative Analysis of Lacinutrix Genomes and Their Association with Bacterial Habitat. PLoS ONE, 2016, 11, e0148889.	1.1	9
7710	De Novo Transcriptome Assembly and Characterization for the Widespread and Stress-Tolerant Conifer Platycladus orientalis. PLoS ONE, 2016, 11, e0148985.	1.1	39
7711	De Novo Transcriptome Analysis of Medicinally Important Plantago ovata Using RNA-Seq. PLoS ONE, 2016, 11, e0150273.	1.1	28
7712	Salt-Responsive Transcriptome Profiling of Suaeda glauca via RNA Sequencing. PLoS ONE, 2016, 11, e0150504.	1.1	57
7713	Genome-Wide Association Studies of Anthracnose and Angular Leaf Spot Resistance in Common Bean (Phaseolus vulgaris L.). PLoS ONE, 2016, 11, e0150506.	1.1	89
7714	Characterization of the Kenaf (Hibiscus cannabinus) Global Transcriptome Using Illumina Paired-End Sequencing and Development of EST-SSR Markers. PLoS ONE, 2016, 11, e0150548.	1.1	16
7715	Genetic Divergence between Camellia sinensis and Its Wild Relatives Revealed via Genome-Wide SNPs from RAD Sequencing. PLoS ONE, 2016, 11, e0151424.	1.1	72
7716	A First Insight into the Genome of the Filter-Feeder Mussel Mytilus galloprovincialis. PLoS ONE, 2016, 11, e0151561.	1.1	124
7717	Profiling Ethylene-Responsive Genes Expressed in the Latex of the Mature Virgin Rubber Trees Using cDNA Microarray. PLoS ONE, 2016, 11, e0152039.	1.1	18
7718	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
7719	Identification of Immune-Related Genes and Development of SSR/SNP Markers from the Spleen Transcriptome of Schizothorax prenanti. PLoS ONE, 2016, 11, e0152572.	1.1	21

#	ARTICLE	IF	CITATIONS
7720	Quantitative RT-PCR Gene Evaluation and RNA Interference in the Brown Marmorated Stink Bug. PLoS ONE, 2016, 11, e0152730.	1.1	39
7721	Identification of Multiple Stress Responsive Genes by Sequencing a Normalized cDNA Library from Sea-Land Cotton (Gossypium barbadense L.). PLoS ONE, 2016, 11, e0152927.	1.1	33
7722	Transcript Analysis and Regulative Events during Flower Development in Olive (Olea europaea L.). PLoS ONE, 2016, 11, e0152943.	1.1	55
7723	Transcriptome Analysis Revealed Changes of Multiple Genes Involved in Haliotis discus hannai Innate Immunity during Vibrio parahemolyticus Infection. PLoS ONE, 2016, 11, e0153474.	1.1	32
7724	Sticky Genomes: Using NGS Evidence to Test Hybrid Speciation Hypotheses. PLoS ONE, 2016, 11, e0154911.	1.1	8
7725	Comparative Transcriptome Analysis of Bombyx mori (Lepidoptera) Larval Midgut Response to BmNPV in Susceptible and Near-Isogenic Resistant Strains. PLoS ONE, 2016, 11, e0155341.	1.1	36
7726	Transcriptome Sequencing of Chemically Induced Aquilaria sinensis to Identify Genes Related to Agarwood Formation. PLoS ONE, 2016, 11, e0155505.	1.1	28
7727	Deciphering the Molecular Variations of Pine Wood Nematode Bursaphelenchus xylophilus with Different Virulence. PLoS ONE, 2016, 11, e0156040.	1.1	37
7728	Transcriptome Analysis of the Sydney Rock Oyster, Saccostrea glomerata: Insights into Molluscan Immunity. PLoS ONE, 2016, 11, e0156649.	1.1	42
7729	Transcriptome Sequencing and Analysis for Culm Elongation of the Worldâ€™s Largest Bamboo (Dendrocalamus sinicus). PLoS ONE, 2016, 11, e0157362.	1.1	20
7730	Transcriptome Analysis of the Innate Immunity-Related Complement System in Spleen Tissue of Ctenopharyngodon idella Infected with Aeromonas hydrophila. PLoS ONE, 2016, 11, e0157413.	1.1	85
7731	Deep Sequencing-Based Transcriptome Analysis Reveals the Regulatory Mechanism of Bemisia tabaci (Hemiptera: Aleyrodidae) Nymph Parasitized by Encarsia sophia (Hymenoptera: Aphelinidae). PLoS ONE, 2016, 11, e0157684.	1.1	1
7732	Linking Genes and Brain Development of Honeybee Workers: A Whole-Transcriptome Approach. PLoS ONE, 2016, 11, e0157980.	1.1	21
7733	Transcriptome and Degradome of microRNAs and Their Targets in Response to Drought Stress in the Plants of a Diploid and Its Autotetraploid Paulownia australis. PLoS ONE, 2016, 11, e0158750.	1.1	9
7734	Transcriptome Analysis of Capsicum Chlorosis Virus-Induced Hypersensitive Resistance Response in Bell Capsicum. PLoS ONE, 2016, 11, e0159085.	1.1	27
7735	Genic and Intergenic SSR Database Generation, SNPs Determination and Pathway Annotations, in Date Palm (Phoenix dactylifera L.). PLoS ONE, 2016, 11, e0159268.	1.1	29
7736	Comparative Transcriptome Analysis of Resistant and Susceptible Common Bean Genotypes in Response to Soybean Cyst Nematode Infection. PLoS ONE, 2016, 11, e0159338.	1.1	54
7737	Comparative Analysis of the Chrysanthemum Leaf Transcript Profiling in Response to Salt Stress. PLoS ONE, 2016, 11, e0159721.	1.1	14

#	Article	IF	Citations
7738	Identification and Characterization of Microsatellite Loci in Maqui (Aristotelia chilensis [Molina]) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	1.1	17
7739	Transcriptome Analysis of Storage Roots and Fibrous Roots of the Traditional Medicinal Herb Callerya speciosa (Champ.) ScHot. PLoS ONE, 2016, 11, e0160338.	1.1	19
7740	A Proteomic Approach to Lipo-Chitooligosaccharide and Thuricin 17 Effects on Soybean GerminationUnstressed and Salt Stress. PLoS ONE, 2016, 11, e0160660.	1.1	48
7741	Comparative Methylome Analysis of the Occasional Ruminant Respiratory Pathogen Bibersteinia trehalosi. PLoS ONE, 2016, 11, e0161499.	1.1	6
7742	Transcriptional Differences between Diapausing and Non-Diapausing D. montana Females Reared under the Same Photoperiod and Temperature. PLoS ONE, 2016, 11, e0161852.	1.1	32
7743	Differential Communications between Fungi and Host Plants Revealed by Secretome Analysis of Phylogenetically Related Endophytic and Pathogenic Fungi. PLoS ONE, 2016, 11, e0163368.	1.1	20
7744	Leaf Transcriptome Sequencing for Identifying Genic-SSR Markers and SNP Heterozygosity in Crossbred Mango Variety â€˜Amrapaliâ€™ (Mangifera indica L.). PLoS ONE, 2016, 11, e0164325.	1.1	25
7745	The Role of the Trypanosoma cruzi TcNRBD1 Protein in Translation. PLoS ONE, 2016, 11, e0164650.	1.1	10
7746	Transcriptome Analysis and Comparison of Marmota monax and Marmota himalayana. PLoS ONE, 2016, 11, e0165875.	1.1	9
7747	Transcriptome Analysis of the Chrysanthemum Foliar Nematode, Aphelenchoides ritzemabosi (Aphelenchida: Aphelenchoididae). PLoS ONE, 2016, 11, e0166877.	1.1	4
7748	Overexpressed Proteins in Hypervirulent Clade 8 and Clade 6 Strains of Escherichia coli O157:H7 Compared to E. coli O157:H7 EDL933 Clade 3 Strain. PLoS ONE, 2016, 11, e0166883.	1.1	12
7749	Deep, Staged Transcriptomic Resources for the Novel Coleopteran Models Atrachya menetriesi and Callosobruchus maculatus. PLoS ONE, 2016, 11, e0167431.	1.1	7
7750	Perigone Lobe Transcriptome Analysis Provides Insights into Rafflesia cantleyi Flower Development. PLoS ONE, 2016, 11, e0167958.	1.1	13
7751	Genetic Diversity and Population Structure of Whitebark Pine (Pinus albicaulis Engelm.) in Western North America. PLoS ONE, 2016, 11, e0167986.	1.1	34
7752	Comparative Transcriptomic Study of Muscle Provides New Insights into the Growth Superiority of a Novel Grouper Hybrid. PLoS ONE, 2016, 11, e0168802.	1.1	38
7753	Physiological Characterization and Comparative Transcriptome Analysis of White and Green Leaves of Ananas comosus var. bracteatus. PLoS ONE, 2017, 12, e0169838.	1.1	32
7754	Transcriptome Profiling to Understand the Effect of Citrus Rootstocks on the Growth of â€˜Shatangjuâ€™ Mandarin. PLoS ONE, 2017, 12, e0169897.	1.1	27
7755	Comparative analysis of sterol acquisition in the oomycetes Saprolegnia parasitica and Phytophthora infestans. PLoS ONE, 2017, 12, e0170873.	1.1	27

#	Article	IF	Citations
7756	De novo transcriptome sequencing and analysis of male, pseudo-male and female yellow perch, Perca flavescens. PLoS ONE, 2017, 12, e0171187.	1.1	14
7757	Genomic sequence of 'Candidatus Liberibacter solanacearum' haplotype C and its comparison with haplotype A and B genomes. PLoS ONE, 2017, 12, e0171531.	1.1	39
7758	Identification and expression profile analysis of odorant binding protein and chemosensory protein genes in Bemisia tabaci MED by head transcriptome. PLoS ONE, 2017, 12, e0171739.	1.1	57
7759	De novo assembly, characterization and annotation for the transcriptome of Sarcocheilichthys sinensis. PLoS ONE, 2017, 12, e0171966.	1.1	12
7760	Domestication drive the changes of immune and digestive system of Eurasian perch (Perca fluviatilis). PLoS ONE, 2017, 12, e0172903.	1.1	12
7761	The microRNA repertoire of Tibetan naked carp Gymnocypris przewalskii: A case study in Schizothoracinae fish on the Tibetan Plateau. PLoS ONE, 2017, 12, e0174534.	1.1	15
7762	Transcriptomic profiling of taproot growth and sucrose accumulation in sugar beet (Beta vulgaris L.) at different developmental stages. PLoS ONE, 2017, 12, e0175454.	1.1	28
7763	Transcriptome analysis of creeping bentgrass exposed to drought stress and polyamine treatment. PLoS ONE, 2017, 12, e0175848.	1.1	22
7764	Global gene expression profiling related to temperature-sensitive growth abnormalities in interspecific crosses between tetraploid wheat and Aegilops tauschii. PLoS ONE, 2017, 12, e0176497.	1.1	4
7765	Transcriptome analysis of Phytophthora litchii reveals pathogenicity arsenals and confirms taxonomic status. PLoS ONE, 2017, 12, e0178245.	1.1	18
7766	Comparative transcription analysis of different Antirrhinum phyllotaxy nodes identifies major signal networks involved in vegetative-reproductive transition. PLoS ONE, 2017, 12, e0178424.	1.1	3
7767	Assessing the impact of Benzo[a]pyrene on Marine Mussels: Application of a novel targeted low density microarray complementing classical biomarker responses. PLoS ONE, 2017, 12, e0178460.	1.1	53
7768	Antennal transcriptome analysis of the piercing moth Oraesia emarginata (Lepidoptera: Noctuidae). PLoS ONE, 2017, 12, e0179433.	1.1	18
7769	PpTFDB: A pigeonpea transcription factor database for exploring functional genomics in legumes. PLoS ONE, 2017, 12, e0179736.	1.1	13
7770	Seasonal differences in the testicular transcriptome profile of free-living European beavers (Castor) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	13
7771	Functional differentiation and spatial-temporal co-expression networks of the NBS-encoding gene family in Jilin ginseng, Panax ginseng C.A. Meyer. PLoS ONE, 2017, 12, e0181596.	1.1	13
7772	Characterization of the genome of a phylogenetically distinct tospovirus and its interactions with the local lesion-induced host Chenopodium quinoa by whole-transcriptome analyses. PLoS ONE, 2017, 12, e0182425.	1.1	11
7773	High-density genetic linkage map construction by F2 populations and QTL analysis of early-maturity traits in upland cotton (Gossypium hirsutum L.). PLoS ONE, 2017, 12, e0182918.	1.1	40

#	ARTICLE	IF	CITATIONS
7774	Association of gene expression with biomass content and composition in sugarcane. PLoS ONE, 2017, 12, e0183417.	1.1	26
7775	Allergen homologs in the Euroglyphus maynei draft genome. PLoS ONE, 2017, 12, e0183535.	1.1	15
7776	De novo transcriptome assembly and analysis of differential gene expression in response to drought in European beech. PLoS ONE, 2017, 12, e0184167.	1.1	28
7777	A tree of life based on ninety-eight expressed genes conserved across diverse eukaryotic species. PLoS ONE, 2017, 12, e0184276.	1.1	5
7778	A draft genome sequence of the rose black spot fungus Diplocarpon rosae reveals a high degree of genome duplication. PLoS ONE, 2017, 12, e0185310.	1.1	8
7779	De novo transcriptome sequencing and assembly from apomictic and sexual Eragrostis curvula genotypes. PLoS ONE, 2017, 12, e0185595.	1.1	30
7780	The transcriptomes of cave and surface populations of Gammarus minus (Crustacea: Amphipoda) provide evidence for positive selection on cave downregulated transcripts. PLoS ONE, 2017, 12, e0186173.	1.1	27
7781	De novo RNA sequencing transcriptome of Rhododendron obtusum identified the early heat response genes involved in the transcriptional regulation of photosynthesis. PLoS ONE, 2017, 12, e0186376.	1.1	24
7782	Integrated mRNA and microRNA transcriptome analyses reveal regulation of thermal acclimation in Gymnocypris przewalskii: A case study in Tibetan Schizothoracine fish. PLoS ONE, 2017, 12, e0186433.	1.1	25
7783	Identification and characterization of intestine microRNAs and targets in red swamp crayfish, Procambarus clarkii infected with white spot syndrome virus. PLoS ONE, 2017, 12, e0187760.	1.1	5
7784	The genomes of Crithidia bombi and C. expoeki, common parasites of bumblebees. PLoS ONE, 2018, 13, e0189738.	1.1	26
7785	De Novo characterization of transcriptomes from two North American Papaipema stem-borers (Lepidoptera: Noctuidae). PLoS ONE, 2018, 13, e0191061.	1.1	6
7786	Draft genome sequence of the New Jersey aster yellows strain of â€˜Candidatus Phytoplasma asterisâ€™. PLoS ONE, 2018, 13, e0192379.	1.1	17
7787	Pheromone expression reveals putative mechanism of unisexuality in a saprobic ascomycete fungus. PLoS ONE, 2018, 13, e0192517.	1.1	16
7788	De novo transcriptomic analysis of leaf and fruit tissue of Cornus officinalis using Illumina platform. PLoS ONE, 2018, 13, e0192610.	1.1	19
7789	Cross-species multiple environmental stress responses: An integrated approach to identify candidate genes for multiple stress tolerance in sorghum (Sorghum bicolor (L.) Moench) and related model species. PLoS ONE, 2018, 13, e0192678.	1.1	24
7790	Transcriptome analysis of embryonic domains in Norway spruce reveals potential regulators of suspensor cell death. PLoS ONE, 2018, 13, e0192945.	1.1	17
7791	Sequence analysis of the potato aphid Macrosiphum euphorbiae transcriptome identified two new viruses. PLoS ONE, 2018, 13, e0193239.	1.1	14

#	Article	IF	Citations
7793	Proteomics of extracellular vesicles produced by Granulicatella adiacens, which causes infective endocarditis. PLoS ONE, 2020, 15, e0227657.	1.1	11
7794	Comparative transcriptome analysis of flower bud transition and functional characterization of EjAGL17 involved in regulating floral initiation in loquat. PLoS ONE, 2020, 15, e0239382.	1.1	6
7795	Comparative transcriptome and metabolome analyses of two strawberry cultivars with different storability. PLoS ONE, 2020, 15, e0242556.	1.1	16
7796	A conserved set of maternal genes? Insights from a molluscan transcriptome. International Journal of Developmental Biology, 2014, 58, 501-511.	0.3	28
7797	Identification and expression pattern analysis of chemosensory receptor genes in the Macrocentrus cingulum (Hymenoptera: Braconidae) antennae. European Journal of Entomology, 0, 113, 76-83.	1.2	12
7798	Repairing vertex labels under neighborhood constraints. Proceedings of the VLDB Endowment, 2014, 7, 987-998.	2.1	29
7799	Stress response of the black coral <i>Leiopathes glaberrima</i> when exposed to sub-lethal amounts of crude oil and dispersant. Elementa, 2017, 5, .	1.1	6
7800	In-depth transcriptome reveals the potential biotechnological application of Bothrops jararaca venom gland. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2020, 26, e20190058.	0.8	4
7802	Proteomic Profiling Reveals New Insights into the Allergomes of Anisakis simplex, Pseudoterranova decipiens, and Contracaecum osculatum. Journal of Parasitology, 2020, 106, 572.	0.3	22
7803	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
7804	De novo Analysis of Heortia vitessoides (Lepidoptera: Crambidae) Transcriptome and Identification of Putative Cytochrome P450 Monooxygenase Genes. Journal of Entomological Science, 2019, 54, 293.	0.2	2
7805	Higher expression of somatic repair genes in long-lived ant queens than workers. Aging, 2016, 8, 1940-1951.	1.4	28
7806	The whole transcriptome regulation as a function of mitochondrial polymorphisms and aging in Caenorhabditis elegans. Aging, 2020, 12, 2453-2470.	1.4	12
7807	Quantitative proteomics reveals molecular mechanism of gamabufotalin and its potential inhibition on Hsp90 in lung cancer. Oncotarget, 2016, 7, 76551-76564.	0.8	24
7808	Genome-wide gene expression analysis in the amphioxus, Branchiostoma belcheri after poly (I: C) challenge using strand-specific RNA-seq. Oncotarget, 2017, 8, 108392-108405.	0.8	3
7809	Genome-wide comparison of the protein-coding repertoire reveals fast evolution of immune-related genes in cephalochordates and Osteichthyes superclass. Oncotarget, 2018, 9, 83-95.	0.8	14
7810	Differentially expressed full-length, fusion and novel isoforms transcripts-based signature of well-differentiated keratinized oral squamous cell carcinoma. Oncotarget, 2020, 11, 3227-3243.	0.8	9
7811	Differential Gene Expression of Resistant and Susceptible Sweetpotato Plants after Infection with the Causal Agents of Sweet Potato Virus Disease. Journal of the American Society for Horticultural Science, 2009, 134, 658-666.	0.5	27

#	Article	IF	Citations
7812	A Transcriptomic Analysis of Sensitive and Tolerant Citrus Rootstocks under Natural Iron Deficiency Conditions. Journal of the American Society for Horticultural Science, 2013, 138, 487-498.	0.5	8
7813	Identification of MicroRNAs and Their Targets Involved in Paeonia rockii Petal Variegation Using High-throughput Sequencing. Journal of the American Society for Horticultural Science, 2019, 144, 118-129.	0.5	5
7814	Transcriptome Analysis of Chrysanthemum lavandulifolium Response to Salt Stress and Overexpression a K+ Transport ClAKT Gene-enhanced Salt Tolerance in Transgenic Arabidopsis. Journal of the American Society for Horticultural Science, 2019, 144, 219-235.	0.5	4
7815	Detoxification-related gene expression accompanies anhydrobiosis in the foliar nematode (Aphelenchoides fragariae). Journal of Nematology, 2020, 52, 1-12.	0.4	4
7816	Wide Cross-Species RNA-Seq Comparison Reveals Convergent Molecular Mechanisms Involved in Nickel Hyperaccumulation Across Angiosperms. SSRN Electronic Journal, 0, , .	0.4	1
7817	In silico mining and characterization of simple sequence repeats (SSRs) from Euphorbia esula expressed sequence tags (ESTs): A potential crop for biofuel. Plant OMICS, 2017, 10, 53-63.	0.4	1
7818	Transcriptome Profiles of Populus euphratica upon Heat Shock stress. Current Genomics, 2014, 15, 326-340.	0.7	19
7819	Identification of Plant Protein Kinases in Response to Abiotic and Biotic Stresses Using SuperSAGE. Current Protein and Peptide Science, 2011, 12, 643-656.	0.7	14
7820	Systems Biology Approaches Reveal a Multi-stress Responsive WRKY Transcription Factor and Stress Associated Gene Co-expression Networks in Chickpea. Current Bioinformatics, 2019, 14, 591-601.	0.7	6
7821	EST-SSR Analysis and Cross-species Transferability Study in Lavandula. Bio-protocol, 2016, 6, .	0.2	1
7822	Development and characterization of microsatellite markers for Osyris lanceolata Hochst. & Steud., an endangered African sandalwood tree species. Tropical Plant Research, 2016, 3, 701-703.	0.4	4
7823	Gene expression profiling and expression analysis of freshwater shrimp (Neocaridina denticulata) Tj ETQq1 1 0.784314 rgBT /Overlock Environmental Biology, 2018, 39, 51-57.	0.2	11
7824	De novo characterization of the Lycium ruthenicum transcriptome and analysis of its digital gene expression profiles during fruit development and ripening. Archives of Biological Sciences, 2017, 69, 181-190.	0.2	2
7825	Genome-wide in silico identification, characterization and transcriptional analysis of the family of growth-regulating factors in common bean (Phaseolus vulgaris L.) subjected to polyethylene glycol-induced drought stress. Archives of Biological Sciences, 2017, 69, 5-14.	0.2	9
7826	Differential Expression of Hyperhydricity Responsive Peach miRNAs. Journal of Integrative Bioinformatics, 2016, 13, 308.	1.0	5
7827	Whole-genome sequencing of leopard coral grouper (<i>Plectropomus leopardus</i>) and exploration of regulation mechanism of skin color and adaptive evolution. Zoological Research, 2020, 41, 328-340.	0.9	33
7828	Physiological Response of Pacific Abalone (Haliotis discus hannai) Hepatopancreas to Heat Stress. Journal of Shellfish Research, 2019, 38, 417.	0.3	4
7829	Blue Mussel (Genus Mytilus) Transcriptome Response to Simulated Climate Change in the Gulf of Maine. Journal of Shellfish Research, 2019, 38, 587.	0.3	8

#	ARTICLE	IF	CITATIONS
7830	The Molecular Basis of Osmoregulation and Physiological Processes Associated with Salinity Changes in the Chinese Mitten Crab Eriocheir sinensis. Journal of Shellfish Research, 2019, 38, 643.	0.3	4
7831	Potential and Pitfalls of the DNA Metabarcoding Analyses for the Dietary Study of the Large Japanese Wood Mouse Apodemus speciosus on Seto Inland Sea Islands. Mammal Study, 2019, 44, 221.	0.2	9
7832	Transcriptome analysis deciphers the mechanisms of exogenous nitric oxide action on the response of melon leaves to chilling stress. Biologia Plantarum, 0, 64, 465-472.	1.9	10
7833	Draft Genome of Toxocara canis, a Pathogen Responsible for Visceral Larva Migrans. Korean Journal of Parasitology, 2016, 54, 751-758.	0.5	5
7834	Development of molecular resources for the Chinese horseshoe crab Tachypleus tridentatus. Aquatic Biology, 2015, 24, 17-24.	0.5	1
7835	Seasonal and spatial influences on gene expression in Antarctic krill Euphausia superba. Marine Ecology - Progress Series, 2012, 467, 61-75.	0.9	27
7836	Identification of molecular markers associated with starvation in female Calanus sinicus (Copepoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	4
7837	Refinement of Draft Genome Assemblies of Pigeonpea (Cajanus cajan). Frontiers in Genetics, 2020, 11, 607432.	1.1	5
7838	Silent Witness: Dual-Species Transcriptomics Reveals Epithelial Immunological Quiescence to Helminth Larval Encounter and Fostered Larval Development. Frontiers in Immunology, 2018, 9, 1868.	2.2	13
7839	Stimulation of Mytilus galloprovincialis Hemocytes With Different Immune Challenges Induces Differential Transcriptomic, miRNomic, and Functional Responses. Frontiers in Immunology, 2020, 11, 606102.	2.2	17
7840	CusS-CusR Two-Component System Mediates Tigecycline Resistance in Carbapenem-Resistant Klebsiella pneumoniae. Frontiers in Microbiology, 2019, 10, 3159.	1.5	19
7841	Differential Gene Expression between Leaf and Rhizome in Atractylodes lancea: A Comparative Transcriptome Analysis. Frontiers in Plant Science, 2016, 7, 348.	1.7	34
7843	The Developmental Transcriptome of Bagworm, Metisa plana (Lepidoptera: Psychidae) and Insights into Chitin Biosynthesis Genes. Genes, 2021, 12, 7.	1.0	4
7844	Whole-Transcriptome RNA Sequencing Reveals the Global Molecular Responses and CeRNA Regulatory Network of mRNAs, lncRNAs, miRNAs and circRNAs in Response to Salt Stress in Sugar Beet (Beta) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	46
7845	Comparative Analysis Delineates the Transcriptional Resistance Mechanisms for Pod Borer Resistance in the Pigeonpea Wild Relative Cajanus scarabaeoides (L.) Thouars. International Journal of Molecular Sciences, 2021, 22, 309.	1.8	13
7848	Abiotic Stressâ€Related Expressed Sequence Tags from the Diploid Strawberry Fragaria vesca f. semperflorens. Plant Genome, 2011, 4, .	1.6	7
7849	A New Panel of SNP Markers for the Individual Identification of North American Pumas. Journal of Fish and Wildlife Management, 2016, 7, 13-27.	0.4	23
7850	Phosphate Solubilization and Gene Expression of Phosphate-Solubilizing Bacterium Burkholderia multivorans WS-FJ9 under Different Levels of Soluble Phosphate. Journal of Microbiology and Biotechnology, 2017, 27, 844-855.	0.9	51

#	Article	IF	Citations
7851	Potential diagnostic implications of miR-144 overexpression in human oesophageal cancer. Indian Journal of Medical Research, 2016, 143, 91.	0.4	13
7852	Methotrexate combined with methylprednisolone for the recovery of motor function and differential gene expression in rats with spinal cord injury. Neural Regeneration Research, 2017, 12, 1507.	1.6	13
7853	Differential gene and protein expression between rat tibial nerve and common peroneal nerve during Wallerian degeneration. Neural Regeneration Research, 2019, 14, 2183.	1.6	11
7854	A Systems Level Comparison of Mycobacterium tuberculosis, Mycobacterium leprae and Mycobacterium smegmatis Based on Functional Interaction Network Analysis. Journal of Bacteriology & Parasitology, 2013, 04, .	0.2	9
7855	Differential Gene Expression Profiling in Bed Bug (Cimex Lectularius L.) Fed on Ibuprofen and Caffeine in Reconstituted Human Blood. Entomology, Ornithology, & Herpetology: Current Research, 2015, 04, .	0.1	3
7856	Identification of NaHCO3 Stress Responsive Proteins in Dunaliella salina HTBS using iTRAQ-based Analysis. Journal of Proteomics and Bioinformatics, 2016, 09, .	0.4	2
7857	Megafiller: A Retrofitted Protein Function Predictor for Filling Gaps in Metabolic Networks. Journal of Proteomics and Bioinformatics, 0, s9, .	0.4	5
7858	Transcriptome Analysis of Reaction Wood in Gymnosperms by Next-Generation Sequencing. American Journal of Plant Sciences, 2014, 05, 2785-2798.	0.3	7
7859	Transcriptome Analysis of Ten-DPA Fiber in an Upland Cotton (&lt;i&gt;Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 427 American Journal of Plant Sciences, 2017, 08, 2530-2553.	0.3	8
7860	Insights into Seasonal Dormancy of Perennial Herbaceous Forages. American Journal of Plant Sciences, 2017, 08, 2650-2680.	0.3	7
7861	Water Stress Responsive Differential Methylation of Organellar Genomes of <i>Zea mays</i> Z59. American Journal of Plant Sciences, 2020, 11, 1077-1100.	0.3	3
7862	Transcriptome analysis of the &lt;i&gt;Tityus serrulatus&lt;/i&gt; scorpion venom gland. Open Journal of Genetics, 2012, 02, 210-220.	0.1	58
7863	Identification and characterization of differentially expressed genes during incompatible interaction between the foliar rust Melampsora larici-populina and poplar. Genetics and Molecular Research, 2014, 13, 2082-2093.	0.3	5
7864	Transcriptome analysis of the grass carp (Ctenopharyngodon idella) using 454 pyrosequencing methodology for gene and marker discovery. Genetics and Molecular Research, 2015, 14, 19249-19263.	0.3	9
7865	Transcriptome Sequencing and Analysis of Changes Associated with Insecticide Resistance in the Dengue Mosquito (Aedes aegypti) in Vietnam. American Journal of Tropical Medicine and Hygiene, 2019, 100, 1240-1248.	0.6	27
7866	Genetic diversity analysis of<i>Glycyrrhiza uralensis</i>using 8 novel polymorphic microsatellite markers. Journal of Plant Biotechnology, 2016, 43, 174-180.	0.1	10
7867	Transcriptome-based identification of water-deficit stress responsive genes in the tea plant,Camellia sinensis. Journal of Plant Biotechnology, 2016, 43, 302-310.	0.1	12
7868	Development of Reproducible EST-derived SSR Markers and Assessment of Genetic Diversity in Panax ginseng Cultivars and Related Species. Journal of Ginseng Research, 2011, 35, 399-412.	3.0	49

#	ARTICLE	IF	CITATIONS
7869	DNA Microarray and Gene Ontology Enrichment Analysis Reveals That a Mutation in opsX Affects Virulence and Chemotaxis in Xanthomonas oryzae pv. oryzae. Plant Pathology Journal, 2016, 32, 190-200.	0.7	3
7870	Ovarian transcriptomic analysis of Shan Ma ducks at peak and late stages of egg production. Asian-Australasian Journal of Animal Sciences, 2017, 30, 1215-1224.	2.4	21
7871	Bioinformatics as a Tool for the Structural and Evolutionary Analysis of Proteins. , 0, , .		7
7872	Novel expressed sequence tag- simple sequence repeats (EST-SSR) markers characterized by new bioinformatic criteria reveal high genetic similarity in sugarcane (Saccharum spp.) breeding lines. African Journal of Biotechnology, 2012, 11, .	0.3	2
7873	In silico comparative analysis of EST-SSRs in three cotton genomes. African Journal of Biotechnology, 2012, 11, .	0.3	4
7874	EuDBase: An online resource for automated EST analysis pipeline (ESTFrontier) and database for red seaweed Eucheuma denticulatum. Bioinformation, 2011, 7, 157-162.	0.2	1
7875	Mining functional microsatellites in legume unigenes. Bioinformation, 2011, 7, 264-270.	0.2	9
7876	Analysis of expressed sequence tags (ESTs) from cocoa (Theobroma cacao L) upon infection with Phytophthora megakarya. Bioinformation, 2012, 8, 65-69.	0.2	8
7877	Genome sequence and comparative analysis of Avibacterium paragallinarum. Bioinformation, 2013, 9, 528-536.	0.2	11
7878	BBGD454: A database for transcriptome analysis of blueberry using 454 sequences. Bioinformation, 2013, 9, 883-886.	0.2	4
7879	Computer aided gene mining for gingerol biosynthesis. Bioinformation, 2015, 11, 316-321.	0.2	3
7880	Optimizing k-mer size using a variant grid search to enhance de novo genome assembly. Bioinformation, 2016, 12, 36-40.	0.2	5
7881	Data enabled prediction analysis assigns folate/biopterin transporter (BT1) family to 36 hypothetical membrane proteins in Leishmania donovani. Bioinformation, 2019, 15, 697-708.	0.2	2
7882	Extending MapMan Ontology to Tobacco for Visualization of Gene Expression. Dataset Papers in Biology, 2013, 2013, 1-7.	0.5	4
7883	Evolution of insect olfactory receptors. ELife, 2014, 3, e02115.	2.8	249
7884	The extraembryonic serosa is a frontier epithelium providing the insect egg with a full-range innate immune response. ELife, 2014, 3, .	2.8	68
7885	Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of Albugo candida, a generalist parasite. ELife, 2015, 4, .	2.8	71
7886	Comparative genomics explains the evolutionary success of reef-forming corals. ELife, 2016, 5, .	2.8	169

#	Article	IF	Citations
7887	Symbiont-induced odorant binding proteins mediate insect host hematopoiesis. ELife, 2017, 6, .	2.8	125
7888	Metabolic co-dependence drives the evolutionarily ancient Hydraâ€“Chlorella symbiosis. ELife, 2018, 7, .	2.8	47
7889	Plantâ€“necrotroph co-transcriptome networks illuminate a metabolic battlefield. ELife, 2019, 8, .	2.8	46
7890	Seminal fluid compromises visual perception in honeybee queens reducing their survival during additional mating flights. ELife, 2019, 8, .	2.8	21
7891	Natural selection and repeated patterns of molecular evolution following allopatric divergence. ELife, 2019, 8, .	2.8	18
7892	<i>Clostridium manihotivorum</i>sp. nov., a novel mesophilic anaerobic bacterium that produces cassava pulp-degrading enzymes. PeerJ, 2020, 8, e10343.	0.9	12
7893	Comparative analysis of tissue-specific transcriptomes in the funnel-web spider<i>Macrothele calpeiana</i>(Araneae, Hexathelidae). PeerJ, 2015, 3, e1064.	0.9	14
7894	Unbiased high-throughput characterization of mussel transcriptomic responses to sublethal concentrations of the biotoxin okadaic acid. PeerJ, 2015, 3, e1429.	0.9	15
7895	RNA-Seq of the Caribbean reef-building coral<i>Orbicella faveolata</i>(Scleractinia-Merulinidae) under bleaching and disease stress expands models of coral innate immunity. PeerJ, 2016, 4, e1616.	0.9	56
7896	Gene expression changes in diapause or quiescent potato cyst nematode,<i>Globodera pallida</i>, eggs after hydration or exposure to tomato root diffusate. PeerJ, 2016, 4, e1654.	0.9	8
7897	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ, 2013, 1, e167.	0.9	159
7898	A<i>de novo</i>transcriptome of the Malpighian tubules in non-blood-fed and blood-fed Asian tiger mosquitoes<i>Aedes albopictus</i>: insights into diuresis, detoxification, and blood meal processing. PeerJ, 2016, 4, e1784.	0.9	49
7899	Identification and temporal expression of putative circadian clock transcripts in the amphipod crustacean<i>Talitrus saltator</i>. PeerJ, 2016, 4, e2555.	0.9	19
7900	Genomic insight into pathogenicity of dematiaceous fungus<i>Corynespora cassiicola</i>. PeerJ, 2017, 5, e2841.	0.9	37
7901	Transcriptome analyses provide insights into the difference of alkaloids biosynthesis in the Chinese goldthread (<i>Coptis chinensis</i> Franch.) from different biotopes. PeerJ, 2017, 5, e3303.	0.9	19
7902	Transcriptome analysis reveals the regulation of brassinosteroids on petal growth in <i>Gerbera hybrida</i>. PeerJ, 2017, 5, e3382.	0.9	30
7903	Characterization of the transcriptome and EST-SSR development in <i>Boea clarkeana</i>, a desiccation-tolerant plant endemic to China. PeerJ, 2017, 5, e3422.	0.9	8
7904	A practical guide to build<i>de-novo</i>assemblies for single tissues of non-model organisms: the example of a Neotropical frog. PeerJ, 2017, 5, e3702.	0.9	16

#	ARTICLE	IF	CITATIONS
7905	Identification and analysis of CYP450 genes from transcriptome of<i> Lonicera japonica</i> and expression analysis of chlorogenic acid biosynthesis related CYP450s. PeerJ, 2017, 5, e3781.	0.9	18
7906	Transcriptome sequencing reveals high isoform diversity in the ant <i>Formica exsecta</i>. PeerJ, 2017, 5, e3998.	0.9	7
7907	Evaluating the adaptive evolutionary convergence of carnivorous plant taxa through functional genomics. PeerJ, 2018, 6, e4322.	0.9	6
7908	Investigating the molecular basis for heterophylly in the aquatic plant<i>Potamogeton octandrus</i>(Potamogetonaceae) with comparative transcriptomics. PeerJ, 2018, 6, e4448.	0.9	16
7909	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
7910	Multi-omic profiling to assess the effect of iron starvation in<i>Streptococcus pneumoniae</i>TIGR4. PeerJ, 2018, 6, e4966.	0.9	6
7911	Application of EST-SSR markers developed from the transcriptome of <i>Torreya grandis</i> (Taxaceae), a threatened nut-yielding conifer tree. PeerJ, 2018, 6, e5606.	0.9	39
7912	<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
7913	Identification, expression, and phylogenetic analyses of terpenoid biosynthesis-related genes in secondary xylem of loblolly pine (<i>Pinus taeda</i> L.) based on transcriptome analyses. PeerJ, 2019, 7, e6124.	0.9	15
7914	Whole-genome comparisons of <i>Penicillium</i> spp. reveals secondary metabolic gene clusters and candidate genes associated with fungal aggressiveness during apple fruit decay. PeerJ, 2019, 7, e6170.	0.9	16
7915	Genome organization and molecular characterization of the three<i>Formica exsecta</i>virusesâ€"FeV1, FeV2 and FeV4. PeerJ, 2019, 6, e6216.	0.9	13
7916	Mantle transcriptome sequencing of <i>Mytilus</i> spp. and identification of putative biomineralization genes. PeerJ, 2019, 6, e6245.	0.9	21
7917	Comparative analysis of the liver transcriptome in the red-eared slider <i>Trachemys scripta elegans</i> under chronic salinity stress. PeerJ, 2019, 7, e6538.	0.9	7
7918	Transcriptome sequencing and comparative analysis of adult ovary and testis identify potential gonadal maintenance-related genes in<i>Mauremys reevesii</i>with temperature-dependent sex determination. PeerJ, 2019, 7, e6557.	0.9	18
7919	Comparative genomic analysis of the IDD genes in five Rosaceae species and expression analysis in Chinese white pear (<i>Pyrus bretschneideri</i>). PeerJ, 2019, 7, e6628.	0.9	8
7920	Identification of the GRAS gene family in the <i> Brassica juncea</i> genome provides insight into its role in stem swelling in stem mustard. PeerJ, 2019, 7, e6682.	0.9	19
7921	Shared genomic outliers across two divergent population clusters of a highly threatened seagrass. PeerJ, 2019, 7, e6806.	0.9	29
7922	Transcriptome analysis of<i>Chelidonium majus</i>elaiosomes and seeds provide insights into fatty acid biosynthesis. PeerJ, 2019, 7, e6871.	0.9	4

#	ARTICLE	IF	CITATIONS
7923	Plasticity of gene expression according to salinity in the testis of broodstock and F1 black-chinned tilapia,<i>Sarotherodon melanotheron heudelotii</i>. PeerJ, 2014, 2, e702.	0.9	7
7924	Genome-wide analyses of the bHLH gene family reveals structural and functional characteristics in the aquatic plant <i>Nelumbo nucifera</i>. PeerJ, 2019, 7, e7153.	0.9	26
7925	Comparative transcriptomic and proteomic analyses of the green and white parts of chimeric leaves in Ananas comosus var. bracteatus. PeerJ, 2019, 7, e7261.	0.9	10
7926	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
7927	Genome-wide identification, characterization and expression analysis of the HD-Zip gene family in the stem development of the woody plant <i>Prunus mume</i>. PeerJ, 2019, 7, e7499.	0.9	13
7928	Identification of a native<i>Bacillus thuringiensis</i>strain from Sri Lanka active against Dipel-resistant<i>Plutella xylostella</i>. PeerJ, 2019, 7, e7535.	0.9	15
7929	Identification and characterization of hirudin-HN, a new thrombin inhibitor, from the salivary glands of<i>Hirudo nipponia</i>. PeerJ, 2019, 7, e7716.	0.9	18
7930	The complete chloroplast genome of <i>Dendrobium nobile</i>, an endangered medicinal orchid from north-east India and its comparison with related <i>Dendrobium</i> species. PeerJ, 2019, 7, e7756.	0.9	9
7931	Warm seawater temperature promotes substrate colonization by the blue coral, Heliopora coerulea. PeerJ, 2019, 7, e7785.	0.9	12
7932	Genome-wide identification of C2H2 zinc-finger genes and their expression patterns under heat stress in tomato (<i>Solanum lycopersicum</i> L.). PeerJ, 2019, 7, e7929.	0.9	18
7933	Genetic divergence between populations of feral and domestic forms of a mosquito disease vector assessed by transcriptomics. PeerJ, 2015, 3, e807.	0.9	17
7934	Warm temperatures, cool sponges: the effect of increased temperatures on the Antarctic sponge<i>Isodictya</i>sp.. PeerJ, 2019, 7, e8088.	0.9	22
7935	The Polycyclic Aromatic Hydrocarbon (PAH) degradation activities and genome analysis of a novel strain<i>Stenotrophomonas sp</i>. Pemsol isolated from Mexico. PeerJ, 2020, 8, e8102.	0.9	26
7936	A new insight to biomarkers related to resistance in survived-white spot syndrome virus challenged giant tiger shrimp,Penaeus monodon. PeerJ, 2019, 7, e8107.	0.9	11
7937	Proteogenomic analysis of pitaya reveals cold stress-related molecular signature. PeerJ, 2020, 8, e8540.	0.9	15
7938	The complete chloroplast genomes of seventeen <i>Aegilops tauschii</i>: genome comparative analysis and phylogenetic inference. PeerJ, 2020, 8, e8678.	0.9	16
7939	Genome-wide investigation of WRKY transcription factors in Tartary buckwheat (<i>Fagopyrum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1	0.9	15
7940	First transcriptome analysis of bryozoan Fredericella sultana, the primary host of myxozoan parasite Tetracapsuloides bryosalmonae. PeerJ, 2020, 8, e9027.	0.9	9

#	ARTICLE	IF	CITATIONS
7941	Genome-wide analysis of the superoxide dismutase (SOD) gene family in <i>Zostera marina</i> and expression profile analysis under temperature stress. PeerJ, 2020, 8, e9063.	0.9	17
7942	Identification and expression pattern of chemosensory genes in the transcriptome of <i>Propsilocerus akamusi</i>. PeerJ, 2020, 8, e9584.	0.9	5
7943	Plastid transit peptidesâ€"where do they come from and where do they all belong? Multi-genome and pan-genomic assessment of chloroplast transit peptide evolution. PeerJ, 2020, 8, e9772.	0.9	13
7944	Genome-wide identification and expression analyses of R2R3-MYB transcription factor genes from two Orchid species. PeerJ, 2020, 8, e9781.	0.9	14
7946	Transcriptional Profiling of Soft-rot Resistant Transgenic Chinese Cabbage (Brassica rapa L.) Constitutively Overexpressing a Human Cathelicidin Antimicrobial Peptide (hCAP18/LL-37). Plant Breeding and Biotechnology, 2013, 1, 80-90.	0.3	3
7947	Expression of Heat Shock Proteins by Heat Stress in Soybean. Plant Breeding and Biotechnology, 2017, 5, 344-353.	0.3	8
7948	Pathogenic Variability. , 2021, , 159-232.		0
7949	Dead-End Hybridization in Walnut Trees Revealed by Large-Scale Genomic Sequence Data. Molecular Biology and Evolution, 2022, 39, .	3.5	21
7950	High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. DNA Research, 2021, 28, .	1.5	11
7951	Transcriptomic and Biochemical Analysis Reveal Integrative Pathways Between Carbon and Nitrogen Metabolism in Guzmania monostachia (Bromeliaceae) Under Drought. Frontiers in Plant Science, 2021, 12, 715289.	1.7	2
7952	Cys-SH based quantitative redox proteomics of salt induced response in sugar beet monosomic addition line M14. , 2021, 62, 16.		5
7953	Transcriptome analysis of Clavibacter michiganensis subsp. michiganensis-infected tomatoes: a role of salicylic acid in the host response. BMC Plant Biology, 2021, 21, 476.	1.6	17
7954	Population genomics provides insights into the population structure and temperature-driven adaptation of Collichthys lucidus. BMC Genomics, 2021, 22, 729.	1.2	3
7955	Chromosome-Level Genome Assembly of Cyrtotrachelus buqueti and Mining of Its Specific Genes. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	2
7957	RNAseq-based gene expression profiling of the <i>Anopheles funestus</i> pyrethroid-resistant strain FUMOZ highlights the predominant role of the duplicated <i>CYP6P9a/b</i> cytochrome P450s. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	10
7958	Chromosomeâ€scale genome assembly of <i>Castanopsis tibetana</i> provides a powerful comparative framework to study the evolution and adaptation of Fagaceae trees. Molecular Ecology Resources, 2022, 22, 1178-1189.	2.2	6
7959	Stage Specificity, the Dynamic Regulators and the Unique Orchid Arundina graminifolia. International Journal of Molecular Sciences, 2021, 22, 10935.	1.8	3
7960	Use of Acetic Acid to Partially Replace Lactic Acid for Decontamination against Escherichia coli O157:H7 in Fresh Produce and Mechanism of Action. Foods, 2021, 10, 2406.	1.9	7

#	Article	IF	Citations
7961	Characterization of Basal Transcriptomes Identifies Potential Metabolic and Virulence-Associated Adaptations Among Diverse Nontyphoidal Salmonella enterica Serovars. Frontiers in Microbiology, 2021, 12, 730411.	1.5	4
7962	Transcriptome Analysis Reveals the Complex Molecular Mechanisms of Brassica napusâ€“Sclerotinia sclerotiorum Interactions. Frontiers in Plant Science, 2021, 12, 716935.	1.7	8
7963	Transcriptional expression changes during compensatory plasticity in theÂterminal ganglion of the adult cricket Gryllus bimaculatus. BMC Genomics, 2021, 22, 742.	1.2	4
7964	Analysis of the early response to spinal cord injury identified a key role for mTORC1 signaling in the activation of neural stem progenitor cells. Npj Regenerative Medicine, 2021, 6, 68.	2.5	4
7965	Transcriptomic analysis of blackberry plant (Rubus spp.) reveals a comprehensive metabolic network involved in fruit ripening process. Biologia (Poland), 2021, 76, 3827-3840.	0.8	2
7966	Transcriptome analysis reveals differing response and tolerance mechanism of EPSPS and GAT genes among transgenic soybeans. Molecular Biology Reports, 2021, 48, 7351-7360.	1.0	2
7967	Comprehensive Analyses of NAC Transcription Factor Family in Almond (Prunus dulcis) and Their Differential Gene Expression during Fruit Development. Plants, 2021, 10, 2200.	1.6	3
7968	An Emiliania huxleyi pan-transcriptome reveals basal strain specificity in gene expression patterns. Scientific Reports, 2021, 11, 20795.	1.6	7
7969	Transcriptome Analyses of Leaves Reveal That Hexanoic Acid Priming Differentially Regulate Gene Expression in Contrasting Coffea arabica Cultivars. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	1
7970	Frequent germplasm exchanges drive the high genetic diversity of Chinese-cultivated common apricot germplasm. Horticulture Research, 2021, 8, 215.	2.9	16
7971	Discovery of alternatively spliced isoforms and long non-coding RNA in full length brain transcriptomes of anadromous Hilsa shad, Tenualosa ilisha (Hamilton, 1822). Molecular Biology Reports, 2021, 48, 7333-7342.	1.0	3
7972	Transcriptional changes involved in kumquat (Fortunella spp) defense response to Xanthomonas citri subsp. citri in early stages of infection. Physiological and Molecular Plant Pathology, 2021, 116, 101729.	1.3	4
7973	Improving the Genome Annotation of Rhizoctonia solani Using Proteogenomics. Current Genomics, 2021, 22, 373-383.	0.7	1
7974	Identification of Candidate Olfactory Genes in Scolytus schevyrewi Based on Transcriptomic Analysis. Frontiers in Physiology, 2021, 12, 717698.	1.3	4
7975	De novo Assembly and Analysis of Tissue-Specific Transcriptomes of the Edible Red Sea Urchin Loxechinus albus Using RNA-Seq. Biology, 2021, 10, 995.	1.3	2
7976	Full-Length SMRT Transcriptome Sequencing and SSR Analysis of Bactrocera dorsalis (Hendel). Insects, 2021, 12, 938.	1.0	7
7977	Characterization and fine mapping of a lesion mimic mutant (Lm5) with enhanced stripe rust and powdery mildew resistance in bread wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 2022, 135, 421-438.	1.8	5
7978	Transcriptional analysis of the response of nectarine fruit to low-temperature stress in cold storage. Food Biotechnology, 2021, 35, 349-373.	0.6	1

#	ARTICLE	IF	CITATIONS
7979	Cytokinin Inhibits Fungal Development and Virulence by Targeting the Cytoskeleton and Cellular Trafficking. MBio, 2021, 12, e0306820.	1.8	10
7980	Metabolome and Transcriptome Analysis of Liver and Oocytes of Schizothorax oâ€™connori Raised in Captivity. Frontiers in Genetics, 2021, 12, 677066.	1.1	1
7981	The use of high-throughput sequencing to investigate the diversity of defense protein genes of cucumber inoculated with Cucumber green mottle mosaic virus. Acta Horticulturae, 2021, , 335-340.	0.1	0
7982	Parallel introgression, not recurrent emergence, explains apparent elevational ecotypes of polyploid Himalayan snowtrout. Royal Society Open Science, 2021, 8, 210727.	1.1	3
7983	Accuracies of genomic predictions for disease resistance of striped catfish to <i>Edwardsiella ictaluri</i> using artificial intelligence algorithms. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	10
7984	Integrated analysis of mRNA-seq and miRNA-seq reveals the advantage of polyploid Solidago canadensis in sexual reproduction. BMC Plant Biology, 2021, 21, 462.	1.6	2
7985	Comparative transcriptomic analysis reveals the gonadal development-related gene response to environmental temperature in Mauremys mutica. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2021, 40, 100925.	0.4	3
7986	The contributions of fliG gene to the pathogenicity of Pseudomonas plecoglossicida and pathogen-host interactions with Epinephelus coioides. Fish and Shellfish Immunology, 2021, 119, 238-248.	1.6	12
7987	Identification of bHLH genes through genome-wide association study and antisense expression of ZjbHLH076/ZjICE1 influence tolerance to low temperature and salinity in Zoysia japonica. Plant Science, 2021, 313, 111088.	1.7	11
7988	Methods for Gene Ontology Annotation. , 2007, 406, 495-520.		8
7989	Partitional Clustering of Protein Sequences â€“ An Inductive Logic Programming Approach. Lecture Notes in Computer Science, 2009, , 1001-1004.	1.0	1
7990	Evolutionary Signature of Information Transfer Complexity in Cellular Membrane Proteomes. Genomics and Informatics, 2009, 7, 111-121.	0.4	1
7991	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0
7992	Evolutionary Dynamics in the Aphid Genome: Search for Genes Under Positive Selection and Detection of Gene Family Expansions. , 2010, , 133-142.		1
7993	Analysis and functional annotation of expressed sequence tags from the diesel tree (<i>Copaifera) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.5	1
7994	EST Analysis Pipeline: Use of Distributed Computing Resources. Methods in Molecular Biology, 2011, 722, 103-120.	0.4	0
7995	Visual Gene Ontology Based Knowledge Discovery in Functional Genomics. , 0, , .		1
7996	Protein Homology Analysis for Function Prediction with Parallel Sub-Graph Isomorphism. , 2011, , 129-144.		0

#	Article	IF	Citations
7997	Expressed Sequence Tag Analysis of the Erythrocytic Stage ofPlasmodium berghei. Korean Journal of Parasitology, 2011, 49, 221.	0.5	0
7998	Prediction and comparative analysis of secretory proteins of <I>Meloidogyne incognita</I> and <I>Meloidogyne hapla</I>. Hunan Nong Ye Da Xue Xue Bao = Journal of Hunan Agricultural University, 2011, 37, 376-380.	0.0	0
8001	Proteomic analysis of visceral and subcutaneous adipose tissue in goats. , 2012, , 181-184.		0
8004	Genetics and Molecular Biology of Olives. , 2013, , 129-161.		1
8005	MG289 in <i>Mycoplasma genitalium</i> Enhances Microbial Invasion and Bacterial Persistence in Benign Human Prostate Cells. Open Journal of Urology, 2013, 03, 232-245.	0.0	0
8006	MOLECULAR TECHNOLOGY FOR DEVELOPING DURABLE RESISTANCE TO THE SUGAR BEET ROOT MAGGOT (TETANOPS MYOPAEFORMIS). , 0, , .		0
8007	De novo assembly and annotation of the grey reindeer lichen (Cladonia rangiferina) transcriptome. EMBnet Journal, 2013, 19, 51.	0.2	1
8008	Suspension-Cultured Plant Cells as a Tool to Analyze the Extracellular Proteome. Methods in Molecular Biology, 2014, 1072, 407-433.	0.4	0
8009	Advances in Greengram and Blackgram Genomics. , 2014, , 155-184.		3
8010	Alternaria Comparative Genomics: The Secret Life of Rots. , 2014, , 45-63.		3
8011	Functional Annotation of Proteins by a Novel Method Using Weight and Feature Selection. Lecture Notes in Electrical Engineering, 2014, , 785-797.	0.3	0
8012	Overexpression of the soybean transcription factor GmDof4 significantly enhances the lipid content of. Biotechnology for Biofuels, 2014, 7, 128.	6.2	50
8014	Bioinformatics Analysis of Diguanylate Cyclases and c-di-GMP-Specific Phosphodiesterases from Xanthomonas Species. Hans Journal of Computational Biology, 2014, 04, 68-82.	0.0	0
8015	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
8022	Transcriptome Sequencing and Analysis of Wild Pear (<i>Pyrus trilocularis</i>) using the Illumina Platform. Vegetos, 2015, 28, 1.	0.8	1
8025	Mangomics: Information Systems Supporting Advanced Mango Breeding. , 2015, , 281-307.		0
8026	Phenotypic and Transcriptomic Analysis of Nicotiana benthamiana Expressing Cucumber mosaic virus 2b gene. Research in Plant Disease, 2015, 21, 186-192.	0.3	0
8027	Transcriptional Analysis of Maize Resistance against Fusarium graminearum. Acta Agronomica Sinica(China), 2016, 42, 1122.	0.1	0

#	Article	IF	Citations
8028	Substantial Downregulation of Myogenic Transcripts in Skeletal Muscle of Atlantic Cod during the Spawning Period. PLoS ONE, 2016, 11, e0148374.	1.1	1
8029	Construction of a Full-length cDNA Library from Cardamine manshurica Nakai and Characterization of EST Dataset. Korean Journal of Agricultural Science, 2016, 43, 33-39.	0.2	0
8032	Genome-wide transcriptome profiling of Gossypium spp. roots during early growth after infection with Rotylenchulus reniformis. Plant OMICS, 2016, 9, 198-204.	0.4	0
8034	Bioinformatics - Updated Features and Applications. , 2016, , .		4
8036	Complete genome sequence of a cold-adapted humic acid degrading bacterium Pedobacter sp. PAMC 27299 from the Antarctic seashore. Korean Journal of Microbiology, 2016, 52, 388-390.	0.2	0
8039	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
8042	Expression profiling of Chrysanthemum crassum under salinity stress and the initiation of morphological changes. PLoS ONE, 2017, 12, e0175972.	1.1	2
8055	Molecular modeling and simulation of three important components of Plant Pathogen Interaction cascade in Vigna mungo. Bioinformation, 2017, 13, 323-326.	0.2	1
8062	Expressed sequence tags (ESTs)â€“based computational identification of novel and conserved microRNAs in turmeric (Curcuma longa L.). Journal of Applied Biotechnology & Bioengineering, 2018, 5, .	0.0	0
8064	Big Data Analysis Techniques for Visualization of Genomics in Medicinal Plants. Advances in Data Mining and Database Management Book Series, 2018, , 749-781.	0.4	0
8067	The Spatio-Temporal Control of Zygotic Genome Activation. SSRN Electronic Journal, 0, , .	0.4	1
8068	Transcriptomic Analysis of Flower Development in the Bamboo Phyllostachys violascens (Poaceae:) Tj ETQq1 1 0.784314 rgBT /Overlock	1.0	0
8073	In Silico Analysis of Mobilome Response to Salt Stress in Phaseolus vulgaris L.. TÃ¼rkiye TarÄ±msal AraÅŸtÄ±rmalar Dergisi, 0, , .	0.5	0
8074	Genome-Wide Identification of Genes, Transcription Factors and Transposable Elements in Sesame (Sesamum indicum L.). International Journal of Current Microbiology and Applied Sciences, 2018, 7, 2362-2366.	0.0	1
8077	Genomic and Transcriptomic Sequencing and Analysis Approaches. Middle Black Sea Journal of Health Science, 0, , 34-42.	0.2	0
8078	SEQUENCE ANALYSIS OF INSECTICIDE RESISTANCE AND DETOXIFICATION RELATED GENES IN Spodoptera littoralis(LEPIDOPTERA: NOCTUIDAE). Agrofor, 2018, 2, .	0.1	0
8082	Genetic effect in leaf and xylem transcriptome variations among Eucalyptus urophylla x grandis hybrids in field conditions. Silvae Genetica, 2018, 67, 57-65.	0.4	3
8088	Isolation and characterisation of SSR markers in tongkat ali (Eurycoma longifolia) using next-generation sequencing approach. Journal of Tropical Forest Science, 2018, 30, 279-291.	0.1	0

#	Article	IF	Citations
8097	IDENTIFICACIÃ“N DE LAS PROTEÃNAS INTEGRALES DE MEMBRANA CONSIDERADAS FACTORES DE PATOGENICIDAD EN LA BACTERIA INTRACELULAR Candidatus Hepatobacter penaei MEDIANTE ANÃLISIS BIOINFORMÃTICO. Biotecnia, 2018, 20, 117-126.	0.1	0
8098	Identification and Characterization of Biomineralization-Related Genes. , 2019, , 23-248.		0
8102	The draft genome sequence of the Japanese honey bee, Apis cerana japonica (Hymenoptera: Apidae). European Journal of Entomology, 0, 115, 650-657.	1.2	6
8104	A carnivorous plant genetic map: pitcher/insect-capture QTL on a genetic linkage map of<i>Sarracenia</i>. Life Science Alliance, 2018, 1, e201800146.	1.3	2
8112	Big Data Analysis Techniques for Visualization of Genomics in Medicinal Plants. , 2019, , 804-837.		0
8117	Metabolic pathways analysis and identification of heat response genes of pineapple [Ananas comosus (L.) Merr.] fruit affected by elevated postharvest temperature. Pakistan Journal of Botany, 2019, 51, .	0.2	0
8118	Blood transcriptome resources of chinstrap (Pygoscelis antarcticus) and gentoo (Pygoscelis papua) penguins from the South Shetland Islands, Antarctica. Genomics and Informatics, 2019, 17, e5.	0.4	1
8135	In Silico Prediction of Cell Wall Remodeling Genes in Tomato, Banana, Melon and Grape. International Journal of Life Sciences and Biotechnology, 2019, 2, 108-121.	0.2	2
8144	Transcriptome-wide identification and characterization of the Sox gene family and microsatellites for Corbicula fluminea. PeerJ, 2019, 7, e7770.	0.9	1
8146	Oomycete metabarcoding reveals the presence of <i>Lagenidium</i> spp. in phytotelmata. PeerJ, 2019, 7, e7903.	0.9	4
8147	Molecular response to cold storage in fruit of two zucchini cultivars differing in their chilling sensitivity. Acta Horticulturae, 2019, , 187-194.	0.1	0
8153	Networks of Function and Shared Ancestry Provide Insights into Diversification of Histone Fold Domain in the Plant Kingdom. Studies in Computational Intelligence, 2020, , 789-801.	0.7	0
8154	Identification of novel EST-SSR markers from the de novo transcriptome sequence and application in persimmon (Diospyros L.). European Journal of Horticultural Science, 2019, , 302-309.	0.3	1
8162	Evaluation of Genetic Diversity of <i>Toxicodendron vernicifluum</i> Planted in Japan Using EST-SSR and Genetic SSR Markers. Journal of the Japanese Forest Society, 2019, 101, 298-304.	0.1	1
8172	Draft Genome Sequence of Clostridium sp. Strain FP1, with Similarity to Clostridium tagluense , Isolated from Spoiled Lamb. Microbiology Resource Announcements, 2020, 9, .	0.3	3
8179	Integrated transcriptome and microRNA profiles analysis reveals molecular mechanisms underlying the consecutive monoculture problem of Polygonatum odoratum. Cellular and Molecular Biology, 2020, 66, 47-52.	0.3	5
8184	Use of Chouâ€™s 5-steps rule to predict the subcellular localization of gram-negative and gram-positive bacterial proteins by multi-label learning based on gene ontology annotation and profile alignment. Journal of Integrative Bioinformatics, 2021, 18, 51-79.	1.0	7
8186	Identification of QTLs for chilling and heat requirements for bud dormancy release in Prunus mume and their co-localization with the DAM6 eQTL. Acta Horticulturae, 2020, , 585-592.	0.1	0

#	Article	IF	Citations
8193	Multi-species transcriptomics reveals evolutionary diversity in the mechanisms regulating shrimp tail muscle excitation-contraction coupling. Gene, 2020, 752, 144765.	1.0	4
8195	Mitochondrial Genomics of Six Cacao Pathogens From the Basidiomycete Family Marasmiaceae. Frontiers in Microbiology, 2021, 12, 752094.	1.5	5
8196	Beneficial worm allies warn plants of parasite attack belowground and reduce aboveground herbivore preference and performance. Molecular Ecology, 2021, , .	2.0	5
8197	Transcriptome and Metabolome Analyses Reveal Potential Salt Tolerance Mechanisms Contributing to Maintenance of Water Balance by the Halophytic Grass Puccinellia nuttalliana. Frontiers in Plant Science, 2021, 12, 760863.	1.7	11
8198	Genome and systems biology of <i>Melilotus albus</i> provides insights into coumarins biosynthesis. Plant Biotechnology Journal, 2022, 20, 592-609.	4.1	24
8199	QTL MAPPING OF BROOMRAPE (OROBANCHE CUMANA WALLR.) RESISTANCE IN SUNFLOWER (HELIANTHUS) Tj ETQq1 1 0.784314 rg	0.2	1
8200	The Angiostrongylus vasorum Excretory/Secretory and Surface Proteome Contains Putative Modulators of the Host Coagulation. Frontiers in Cellular and Infection Microbiology, 2021, 11, 753320.	1.8	8
8202	Transcriptome analyses of Ditylenchus destructor in responses to cold and desiccation stress. Genetics and Molecular Biology, 2020, 43, e20180057.	0.6	0
8204	Comparative Transcriptome Analysis of the Ovary and Testis in Noble Scallop (Chlamys nobilis). Pakistan Journal of Zoology, 2020, 53, .	0.1	1
8205	De novo assembly, annotation, marker discovery, and genetic diversity of the Stipa breviflora Griseb. (Poaceae) response to grazing. PLoS ONE, 2020, 15, e0244222.	1.1	4
8206	Genomics- and Metabolomics-Based Investigation of the Deep-Sea Sediment-Derived Yeast, Rhodotorula mucilaginosa 50-3-19/20B. Marine Drugs, 2021, 19, 14.	2.2	15
8208	High levels of glucose alter Physcomitrella patens metabolism and trigger a differential proteomic response. PLoS ONE, 2020, 15, e0242919.	1.1	0
8209	Comparative transcriptome and iTRAQ-based proteome analysis in mature leaves of Brassica carinata provides insights into the purple leaf color diversity. Journal of Horticultural Science and Biotechnology, 2021, 96, 444-455.	0.9	1
8210	Whole transcriptome sequencing and analysis of jute (Corchorus olitorius) fiber cell. Journal of Bioscience and Agriculture Research, 2020, 26, 2204-2010.	0.2	1
8211	In-depth secretome analysis of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in infected wheat uncovers effector functions. Bioscience Reports, 2020, 40, .	1.1	6
8213	Residual Effects Caused by a Past Mycovirus Infection in Fusarium circinatum. Forests, 2021, 12, 11.	0.9	3
8217	Flower transcriptome dynamics during nectary development in pepper (Capsicum annuum L.). Genetics and Molecular Biology, 2020, 43, e20180267.	0.6	3
8223	Isolation, Characterization, and Biotechnological Potential of Native Microalgae From the Peruvian Amazon. , 0, , .		2

#	ARTICLE	IF	CITATIONS
8225	Comparative analysis of diverse toxins from a new pharmaceutical centipede, <italic>Scolopendra mojiangica</italic>. Zoological Research, 2020, 41, 138-147.	0.9	5
8226	Graph Based Automatic Protein Function Annotation Improved by Semantic Similarity. Lecture Notes in Computer Science, 2020, , 261-272.	1.0	1
8227	Skin transcriptional profiles in Oophaga poison frogs. Genetics and Molecular Biology, 2020, 43, e20190401.	0.6	1
8228	How does secondary hypogonadism affect the spermatozoa proteome? Lessons from a porcine animal model. Reproduction, Fertility and Development, 2020, , .	0.1	0
8232	Discovery of Neuropeptides in the Ganglia of the Pacific Abalone Haliotis discus hannai Using Long-Read Transcriptome Analysis. Journal of Shellfish Research, 2020, 39, 99.	0.3	4
8233	Kr-h1 maintains distinct caste-specific neurotranscriptomes in response to socially regulated hormones. Cell, 2021, 184, 5807-5823.e14.	13.5	27
8234	Effects of rrm1 on NNV Resistance Revealed by RNA-seq and Gene Editing. Marine Biotechnology, 2021, 23, 854-869.	1.1	4
8235	Effects of nitrogen levels on gene expression and amino acid metabolism in Welsh onion. BMC Genomics, 2021, 22, 803.	1.2	5
8236	Targeted transcriptomics reveals signatures of large-scale independent origins and concerted regulation of effector genes in Radopholus similis. PLoS Pathogens, 2021, 17, e1010036.	2.1	2
8237	Deep transcriptomic study reveals the role of cell wall biosynthesis and organization networks in the developing shell of peanut pod. BMC Plant Biology, 2021, 21, 509.	1.6	4
8239	Transcriptome-Wide Gene Expression Plasticity in Stipa grandis in Response to Grazing Intensity Differences. International Journal of Molecular Sciences, 2021, 22, 11882.	1.8	5
8240	Different Early Responses of Laminariales to an Endophytic Infection Provide Insights About Kelp Host Specificity. Frontiers in Marine Science, 2021, 8, .	1.2	5
8241	RhWRKY33 Positively Regulates Onset of Floral Senescence by Responding to Wounding- and Ethylene-Signaling in Rose Plants. Frontiers in Plant Science, 2021, 12, 726797.	1.7	9
8242	Identification and Functional Analysis of lncRNAs Responsive to Hypoxia in Eospalax fontanierii. Current Issues in Molecular Biology, 2021, 43, 1889-1905.	1.0	0
8243	Transcriptome profiling reveals the novel immunometabolism-related genes against WSSV infection from Fenneropenaeus merguiensis. Fish and Shellfish Immunology, 2022, 120, 31-44.	1.6	7
8244	BarH1 regulates odorant-binding proteins expression and olfactory perception of Monochamus alternatus Hope. Insect Biochemistry and Molecular Biology, 2022, 140, 103677.	1.2	5
8245	Metabolite Diversity and Metabolic Genome-Wide Marker Association Studies (Mgwas) for Health Benefiting Nutritional Traits in Pearl Millet Grains. Cells, 2021, 10, 3076.	1.8	14
8246	Characterization and analysis of transcriptome complexity using SMRT-Seq combined with RNA-Seq for a better understanding of Acanthogobius ommaturus in response to temperature stress. International Journal of Biological Macromolecules, 2021, 193, 1551-1561.	3.6	6

#	Article	IF	Citations
8247	Candidate Effectors of Plasmodiophora brassicae Pathotype 5X During Infection of Two Brassica napus Genotypes. Frontiers in Microbiology, 2021, 12, 742268.	1.5	7
8249	Protein Homology Analysis for Function Prediction with Parallel Sub-Graph Isomorphism. , 0, , 386-399.		2
8250	Handling and Interpreting Gene Groups. , 2007, , 69-84.		0
8256	In silico Characterization of bHLH Transcription Factor Genes in the Genome of Rainbow Trout (Oncorhynchus mykiss). Marine Science and Technology Bulletin, 0, , .	0.2	0
8259	Transcriptome-wide single nucleotide polymorphisms related to electric organ discharge differentiation among African weakly electric fish species. PLoS ONE, 2020, 15, e0240812.	1.1	2
8263	Kin recognition: Neurogenomic response to mate choice and sib mating avoidance in a parasitic wasp. PLoS ONE, 2020, 15, e0241128.	1.1	0
8266	De novo transcriptome analysis of <i>Cnidium monnieri</i> (L.) Cuss and detection of genes related to coumarin biosynthesis. PeerJ, 2020, 8, e10157.	0.9	9
8267	Genome-wide transcription analysis of histidine-related cataract in Atlantic salmon (Salmo salar L). Molecular Vision, 2009, 15, 1332-50.	1.1	15
8268	Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. Molecular Vision, 2010, 16, 72-8.	1.1	29
8269	A microarray analysis of gene expression patterns during early phases of newt lens regeneration. Molecular Vision, 2013, 19, 135-45.	1.1	17
8270	Induction of Glutaredoxin Expression in Response to Desiccation Stress in the Foliar Nematode Aphelenchoides fragariae. Journal of Nematology, 2012, 44, 370-6.	0.4	3
8271	Identification and differential expression of microRNAs in 1, 25-dihydroxyvitamin D3-induced osteogenic differentiation of human adipose-derived mesenchymal stem cells. American Journal of Translational Research (discontinued), 2017, 9, 4856-4871.	0.0	8
8272	Comparative Functional Study of Thioester-containing Related Proteins in the Recently Sequenced Genome of. Iranian Journal of Parasitology, 2018, 13, 79-88.	0.6	2
8273	Development of Novel Polymorphic EST-SSR Markers from the Cranberry Fruit Transcriptome. Iranian Journal of Biotechnology, 2021, 19, e2499.	0.3	1
8274	Introduction to basics of bioinformatics. , 2022, , 1-15.		5
8275	Genome assembly and annotation. , 2022, , 49-66.		0
8276	Metabolic responses to air-exposure stress of the Chinese mitten crab (Eriocheir sinensis) revealed by a combined analysis of metabolome and transcriptome. Aquaculture, 2022, 548, 737710.	1.7	8
8277	Mitochondrial proteomics reveals new insights into embryogenic competence acquisition in Carica papaya L. callus. Journal of Proteomics, 2022, 252, 104434.	1.2	2

#	Article	IF	Citations
8278	Effect of creatine and EDTA supplemented diets on European seabass (Dicentrarchus labrax) allergenicity, fish muscle quality and omics fingerprint. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 41, 100941.	0.4	5
8280	Transciptome Analysis Molecular Mechanism of Starch Synthesis During Tuber Development in Chinese Yam (Dioscorea opposita). Journal of Biobased Materials and Bioenergy, 2021, 15, 589-597.	0.1	3
8281	Transcriptomic survey reveals multiple adaptation mechanisms in response to nitrogen deprivation in marine Porphyridium cruentum. PLoS ONE, 2021, 16, e0259833.	1.1	1
8282	Small RNA sequencing reveals various microRNAs involved in piperine biosynthesis in black pepper (Piper nigrum L.). BMC Genomics, 2021, 22, 838.	1.2	6
8283	Identification of essential genes involved in metabolismâ€based resistance mechanism to <scp>fenoxapropâ€<i>P</i></scp>â€ethyl in <i>Polypogon fugax</i>. Pest Management Science, 2022, 78, 1164-1175.	1.7	12
8284	Global survey of alternative splicing and gene modules associated with fertility regulation in a thermosensitive genic male sterile wheat. Journal of Experimental Botany, 2022, 73, 2157-2174.	2.4	3
8285	Diversity, multifaceted evolution, and facultative saprotrophism in the European Batrachochytrium salamandrivorans epidemic. Nature Communications, 2021, 12, 6688.	5.8	11
8286	Olfactory dysfunction and potential mechanisms caused by volatile organophosphate dichlorvos in the silkworm as a model animal. Journal of Hazardous Materials, 2022, 425, 127940.	6.5	9
8287	Separate the wheat from the chaff: genomic scan for local adaptation in the red coral Corallium rubrum. , 0, 1, .		7
8290	Whole-transcriptome sequencing reveals a vernalization-related ceRNA regulatory network in chinese cabbage (Brassica campestris L. ssp. pekinensis). BMC Genomics, 2021, 22, 819.	1.2	13
8291	De novo assembly, transcriptome characterization and marker discovery in Indian major carp, Labeo rohita through pyrosequencing. Genetica, 2022, 150, 59-66.	0.5	1
8294	Establishment of Hostâ€"Algal Endosymbioses: Genetic Response to Symbiont Versus Prey in a Sponge Host. Genome Biology and Evolution, 2021, 13, .	1.1	5
8295	Genome-Wide Association Mapping for Heat and Drought Adaptive Traits in Pea. Genes, 2021, 12, 1897.	1.0	11
8296	Anakinra restores cellular proteostasis by coupling mitochondrial redox balance to autophagy. Journal of Clinical Investigation, 2022, 132, .	3.9	7
8297	Integration of transcriptomics and network analysis reveals co-expressed genes in Frankliniella occidentalis larval guts that respond to tomato spotted wilt virus infection. BMC Genomics, 2021, 22, 810.	1.2	9
8298	Comparative Transcriptomics and Gene Knockout Reveal Virulence Factors of Arthrinium phaeospermum in Bambusa pervariabilis Ã— Dendrocalamopsis grandis. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	7
8299	A high-resolution genome of an euryhaline and eurythermal rhinogoby (Rhinogobius similis Gill 1895). G3: Genes, Genomes, Genetics, 2021, , .	0.8	1
8300	Rapidly evolving genetic features for desert adaptations in Stipagrostis pennata. BMC Genomics, 2021, 22, 846.	1.2	0

#	Article	IF	Citations
8301	Inoculation with Arbuscular Mycorrhizal Fungi Reinforces Tea Plantâ€™s Tolerance to Salinity. Journal of Plant Growth Regulation, 2022, 41, 3498-3517.	2.8	5
8302	Effect of Berberine Hydrochloride Treatment on Transcriptomic Response in Gill Tissue of Charybdis japonica Infected With Aeromonas hydrophila. Frontiers in Marine Science, 2021, 8, .	1.2	1
8303	Transcriptome Profiling of the Salt Stress Response in the Leaves and Roots of Halophytic Eutrema salsugineum. Frontiers in Genetics, 2021, 12, 770742.	1.1	18
8304	Genome-Wide Identification of Long Non-Coding RNAs and Their Potential Functions in Poplar Growth and Phenylalanine Biosynthesis. Frontiers in Genetics, 2021, 12, 762678.	1.1	5
8305	Genome sequencing of the multicellular alga Astrephomene provides insights into convergent evolution of germ-soma differentiation. Scientific Reports, 2021, 11, 22231.	1.6	7
8306	Transcriptomic Analysis of Listeria monocytogenes in Response to Bile Under Aerobic and Anaerobic Conditions. Frontiers in Microbiology, 2021, 12, 754748.	1.5	2
8308	Genome-wide transcriptome analysis of the early developmental stages of Echinococcus granulosus protoscoleces reveals extensive alternative splicing events in the spliceosome pathway. Parasites and Vectors, 2021, 14, 574.	1.0	3
8309	Arbuscular Mycorrhizal Fungus Alters Root System Architecture in Camellia sinensis L. as Revealed by RNA-Seq Analysis. Frontiers in Plant Science, 2021, 12, 777357.	1.7	10
8310	<i>In silico</i> analysis of diversity, specificity and molecular evolution of <i>Stenotrophomonas</i> phages. Environmental Microbiology Reports, 2022, 14, 422-430.	1.0	3
8311	Development and Application of EST-SSR Markers in Cephalotaxus oliveri From Transcriptome Sequences. Frontiers in Genetics, 2021, 12, 759557.	1.1	7
8312	A High-Density Genetic Linkage Map and Fine Mapping of QTL For Feed Conversion Efficiency in Common Carp (Cyprinus carpio). Frontiers in Genetics, 2021, 12, 778487.	1.1	2
8313	Genetic mapping reveals complex architecture and candidate genes involved in common bean response to <i>Meloidogyne incognita</i> infection. Plant Genome, 2022, 15, e20161.	1.6	4
8314	Long-read assembly and comparative evidence-based reanalysis of <i>Cryptosporidium</i> genome sequences reveal expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. Genome Research, 2022, 32, 203-213.	2.4	26
8315	Transcriptomic Analysis Reveals the Positive Role of Abscisic Acid in Endodormancy Maintenance of Leaf Buds of Magnolia wufengensis. Frontiers in Plant Science, 2021, 12, 742504.	1.7	3
8316	Sexual diversification of splicing regulation during embryonic development in honeybees (<i>Apis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	3
8317	Pan-genome Analyses of 3 Strains of <i>Inonotus obliquus</i> and Prediction of Polysaccharide and Terpenoid Genes. Natural Product Communications, 2021, 16, 1934578X2110609.	0.2	0
8318	Effect of actinorhizal root exudates on the proteomes of Frankia soli NRRL B-16219, a strain colonizing the root tissues of its actinorhizal host via intercellular pathway. Research in Microbiology, 2022, 173, 103900.	1.0	5
8319	Transcriptome analysis provides insights into the root response of Chinese fir to phosphorus deficiency. BMC Plant Biology, 2021, 21, 525.	1.6	9

#	ARTICLE	IF	CITATIONS
8320	Distinct and essential roles of bZIP transcription factors in the stress response and pathogenesis in Alternaria alternata. Microbiological Research, 2022, 256, 126915.	2.5	11
8321	Integrated de novo Analysis of Transcriptional and Metabolic Variations in Salt-Treated Solenostemma argel Desert Plants. Frontiers in Plant Science, 2021, 12, 744699.	1.7	3
8323	Tissue-specific transcriptome for Rheum tanguticum reveals candidate genes related to the anthraquinones biosynthesis. Physiology and Molecular Biology of Plants, 2021, 27, 2487-2501.	1.4	6
8324	Integrative genome, transcriptome, microRNA, and degradome analysis of water dropwort (Oenanthe) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	31
8325	De novo leaf transcriptome of a triploid linalool chemotype of Lippia alba (Mill.) N.E.Br. ex Britton & P. Wilson. Revista Brasileira De Botanica, 2021, 44, 889-901.	0.5	2
8326	Recombinant Production and Characterization of a New Toxin from Cryptops iheringi Centipede Venom Revealed by Proteome and Transcriptome Analysis. Toxins, 2021, 13, 858.	1.5	4
8327	Roles of a Cryptochrome in Carbon Fixation and Sucrose Metabolism in the Liverwort Marchantia polymorpha. Cells, 2021, 10, 3387.	1.8	2
8328	Integrative Transcriptomics and Proteomics Analyses to Reveal the Developmental Regulation of Metorchis orientalis: A Neglected Trematode With Potential Carcinogenic Implications. Frontiers in Cellular and Infection Microbiology, 2021, 11, 783662.	1.8	1
8329	Single-cell RNA-seq profiling of individual Biomphalaria glabrata immune cells with a focus on immunologically relevant transcripts. Immunogenetics, 2022, 74, 77-98.	1.2	10
8330	Phenotypic responses and potential genetic mechanism of lepidopteran insects under exposure to graphene oxide. Ecotoxicology and Environmental Safety, 2021, 228, 113008.	2.9	6
8331	Reannotation of Mycoplasma hyopneumoniae hypothetical proteins revealed novel potential virulence factors. Microbial Pathogenesis, 2022, 162, 105344.	1.3	4
8334	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
8335	Drafting Penicillium oxalicum calcineurin-CrzA pathway by combining the analysis of phenotype, transcriptome, and endogenous proteinâ€"protein interactions. Fungal Genetics and Biology, 2022, 158, 103652.	0.9	2
8336	De novo Transcriptome Assembly of Senna occidentalis Sheds Light on the Anthraquinone Biosynthesis Pathway. Frontiers in Plant Science, 2021, 12, 773553.	1.7	4
8337	Sex-biased dynamics of three-spined stickleback (Gasterosteus aculeatus) gene expression patterns. Genomics, 2022, 114, 266-277.	1.3	4
8338	High Throughput Identification of the Potential Antioxidant Peptides in Ophiocordyceps sinensis. Molecules, 2022, 27, 438.	1.7	5
8339	Metabolic Processes Are Differentially Regulated During Wild-Type and Attenuated Dengue Virus Infection in Aedes aegypti. American Journal of Tropical Medicine and Hygiene, 2022, , .	0.6	0
8340	Whole genome analysis and functional characterization of a novel Bacillus thuringiensis (Bt 62) isolate against sugarcane white grub Holotrichia serrata (F). Genomics, 2022, 114, 185-195.	1.3	2

#	ARTICLE	IF	CITATIONS
8341	H3K9me2 genome-wide distribution in the holocentric insect Spodoptera frugiperda (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.3	1
8342	A global phosphoproteomics analysis of adult Fasciola gigantica by LCâ€“MS/MS. Parasitology Research, 2022, , 1.	0.6	1
8343	Stage specific comparative transcriptomic analysis to reveal gene networks regulating iron and zinc content in pearl millet [Pennisetum glaucum (L.) R. Br.]. Scientific Reports, 2022, 12, 276.	1.6	11
8344	Identification, Characterization, and Expression Analysis of Spondin-Like and Fasciclin-Like Genes in Neopyropia yezoensis, A Marine Red Alga. Phycology, 2022, 2, 45-59.	1.7	4
8346	Dynamic transcriptome analysis of ovarian follicles in artificial maturing Japanese eel (Anguilla) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582	0.9	3
8347	Transcriptomic analysis of Bombyx mori corpora allata with comparison to prothoracic glands in the final instar larvae. Gene, 2022, 813, 146095.	1.0	2
8348	17-(Allylamino)-17-demethoxygeldanamycin treatment induces the accumulation of heat shock proteins and alleviates senescence in broccoli. Postharvest Biology and Technology, 2022, 186, 111818.	2.9	5
8349	Proteomic profiling of royal jelly produced by Apis mellifera L. exposed to food containing herbicide-based glyphosate. Chemosphere, 2022, 292, 133334.	4.2	7
8352	In Silico Approaches in Bioremediation Research and Advancements. , 2022, , 221-238.		1
8353	De Novo Transcriptome Assembly and SNP Discovery for the Development of dCAPS Markers in Oat. Agronomy, 2022, 12, 184.	1.3	3
8354	The genome of lowâ€chill Chinese plum â€œSanyueliâ€•(<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. Molecular Ecology Resources, 2022, 22, 1919-1938.	2.2	11
8355	Comparative Genomics Reveals Evolutionary Drivers of Sessile Life and Left-right Shell Asymmetry in Bivalves. Genomics, Proteomics and Bioinformatics, 2022, 20, 1078-1091.	3.0	8
8357	Identification of Key Genes Related to Postnatal Testicular Development Based on Transcriptomic Data of Testis in Hu Sheep. Frontiers in Genetics, 2021, 12, 773695.	1.1	4
8358	Expression level of B- and C-class MADS-box genes is associated with the petaloidy of stamens in cultivated amaryllis (<i>Hippeastrum hybridum</i>). Journal of Horticultural Science and Biotechnology, 2022, 97, 211-223.	0.9	3
8359	The complex <scp>Tup1â€Cyc8</scp> bridges transcription factor <scp>ClrB</scp> and putative histone methyltransferase <scp>LaeA</scp> to activate the expression of cellulolytic genes. Molecular Microbiology, 2022, 117, 1002-1022.	1.2	6
8360	Deletion of all three MAP kinase genes results in severe defects in stress responses and pathogenesis in Fusarium graminearum. Stress Biology, 2022, 2, 1.	1.5	14
8361	Transcriptome Analysis of Detoxification-Related Genes in <i>Spodoptera frugiperda</i> (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10	0.6	11
8362	Identification of Genes Associated with Stress Tolerance of High Ethanolâ€“Producing Saccharomyces cerevisiae Strain, NCIM3186, by Differential Gene Expression Analysis. Bioenergy Research, 0, , 1.	2.2	4

#	ARTICLE	IF	CITATIONS
8363	Mechanism of molecules crosstalk and the critical role of jasmonic acid on triterpenoid synthesis in Cyclocarya Paliurus cells under Aspergillus niger elicitor. Journal of Plant Biochemistry and Biotechnology, 2022, 31, 864-879.	0.9	1
8364	Genome-wide identification and characterization of the bHLH gene family in an ornamental woody plant Prunus mume. Horticultural Plant Journal, 2022, 8, 531-544.	2.3	19
8365	Comparative transcriptome analysis reveals variations of bioactive constituents in Lonicera japonica flowers under salt stress. Plant Physiology and Biochemistry, 2022, 173, 87-96.	2.8	8
8366	Genome diversity of domesticated Acinetobacter baumannii ATCC 19606T strains. Microbial Genomics, 2022, 8, .	1.0	7
8367	Genome-wide identification and characterization of functionally relevant microsatellite markers from transcription factor genes of Tea (Camellia sinensis (L.) O. Kuntze). Scientific Reports, 2022, 12, 201.	1.6	11
8368	Quantitative Insights into the Contribution of Nematocysts to the Adaptive Success of Cnidarians Based on Proteomic Analysis. Biology, 2022, 11, 91.	1.3	2
8369	Response of Poplar Leaf Transcriptome to Changed Management and Environmental Conditions in Pure and Mixed with Black Locust Stands. Forests, 2022, 13, 147.	0.9	1
8370	Transcriptome analysis of Auricularia fibrillifera fruit-body responses to drought stress and rehydration. BMC Genomics, 2022, 23, 58.	1.2	9
8371	Integration of Aspergillus niger transcriptomic profile with metabolic model identifies potential targets to optimise citric acid production from lignocellulosic hydrolysate. , 2022, 15, 4.		3
8373	Transcriptome profiling reveals that foliar water uptake occurs with C3 and crassulacean acid metabolism facultative photosynthesis in Tamarix ramosissima under extreme drought. AoB PLANTS, 2022, 14, plab060.	1.2	3
8374	Comparative physiological and transcriptomic profiles reveal regulatory mechanisms of soft rot disease resistance in Amorphophallus spp.. Physiological and Molecular Plant Pathology, 2022, 118, 101807.	1.3	7
8375	Chromosome-level genome assembly of Bactrocera dorsalis reveals its adaptation and invasion mechanisms. Communications Biology, 2022, 5, 25.	2.0	17
8378	Novel Bacteriophages Show Activity against Selected Australian Clinical Strains of Pseudomonas aeruginosa. Microorganisms, 2022, 10, 210.	1.6	6
8379	Comparative Transcriptome Provides a New Insight into Floral Regulation and Defense Response Against Phytoplasma in Sesame (Sesamum indicum L.). Plant Molecular Biology Reporter, 2022, 40, 446-457.	1.0	1
8380	Unraveling the Genome Sequence of Plant Growth Promoting Aspergillus niger (CSR3) Provides Insight into the Synthesis of Secondary Metabolites and Its Comparative Genomics. Journal of Fungi (Basel, Switzerland), 2022, 8, 107.	1.5	7
8381	Means, motive and opportunity for biological invasions: Genetic introgression in a fungal pathogen. Molecular Ecology, 2023, 32, 2428-2442.	2.0	10
8382	ESTâ€“SSR Marker Development and Full-Length Transcriptome Sequence Analysis of Tiger Lily (Lilium) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.5	6
8383	A chromosome-level genome assembly of an alpine plant <i>Crucihimalaya lasiocarpa</i> provides insights into high-altitude adaptation. DNA Research, 2022, 29, .	1.5	13

#	ARTICLE	IF	CITATIONS
8384	Pathogen resistance in Sphagneticola trilobata (Singapore daisy): molecular associations and differentially expressed genes in response to disease from a widespread fungus. Genetica, 2022, 150, 13.	0.5	2
8385	Gene-Set Enrichment Analysis for Identifying Genes and Biological Activities Associated with Growth Traits in Dromedaries. Animals, 2022, 12, 184.	1.0	1
8386	Full-length transcriptome sequencing of Heliocidaris crassispina using PacBio single-molecule real-time sequencing. Fish and Shellfish Immunology, 2022, 120, 507-514.	1.6	8
8387	Comparative transcriptome analysis of long non coding RNA (lncRNA) in RTG-2Âcells infected by infectious hematopoietic necrosis virus. Fish and Shellfish Immunology, 2022, 120, 314-324.	1.6	5
8388	Identification of Pueraria spp. through DNA barcoding and comparative transcriptomics. BMC Plant Biology, 2022, 22, 10.	1.6	7
8389	Transcriptome Analysis of Different Sections of Rhizome in Polygonatum sibiricum Red. and Mining Putative Genes Participate in Polysaccharide Biosynthesis. Biochemical Genetics, 2022, 60, 1547-1566.	0.8	8
8390	Long-read transcriptome sequencing provides insight into lignan biosynthesis during fruit development in Schisandra chinensis. BMC Genomics, 2022, 23, 17.	1.2	10
8391	GAAP: A GUI-based Genome Assembly and Annotation Package. Current Genomics, 2022, 23, 77-82.	0.7	3
8392	Wounding response in Porifera (sponges) activates ancestral signaling cascades involved in animal healing, regeneration, and cancer. Scientific Reports, 2022, 12, 1307.	1.6	13
8393	Genome Resequencing Reveals Rapid, Repeated Evolution in the Colorado Potato Beetle. Molecular Biology and Evolution, 2022, 39, .	3.5	31
8394	Antennal transcriptome analysis of chemosensory genes in the cowpea beetle, Callosobruchus maculatus (F.). PLoS ONE, 2022, 17, e0262817.	1.1	7
8395	Targeted search for scaling genes reveals matrix metalloproteinase 3 as a scaler of the dorsal-ventral pattern in Xenopus laevis embryos. Developmental Cell, 2022, 57, 95-111.e12.	3.1	6
8396	Partitiâ€like viruses from African armyworm increase larval and pupal mortality of a novel host: the Egyptian cotton leafworm. Pest Management Science, 2022, 78, 1529-1537.	1.7	4
8397	Transcriptomic Analysis of Morphology Regulatory Mechanisms of Microparticles to Paraisaria dubia in Submerged Fermentation. Applied Biochemistry and Biotechnology, 2022, 194, 4333-4347.	1.4	7
8398	Organ-Specific Gene Expression Reveals the Role of the Cymbidium ensifolium-miR396/Growth-Regulating Factors Module in Flower Development of the Orchid Plant Cymbidium ensifolium. Frontiers in Plant Science, 2021, 12, 799778.	1.7	9
8399	Systemic effects of <i>Tuber melanosporum</i> inoculation in two <i>Corylus avellana</i> genotypes. Tree Physiology, 2022, 42, 1463-1480.	1.4	1
8400	A cluster of transcripts identifies a transition stage initiating leafy head growth in heading morphotypes of <i>Brassica</i>. Plant Journal, 2022, 110, 688-706.	2.8	7
8401	Understanding saffron biology using omics- and bioinformatics tools: stepping towards a better Crocus phenome. Molecular Biology Reports, 2022, 49, 5325-5340.	1.0	10

#	ARTICLE	IF	CITATIONS
8402	TIP41L, a putative candidate gene conferring both seed size and boll weight, was fine-mapped in an introgression line of Gossypium hirsutum-Gossypium arboreum. Plant Science, 2022, 317, 111197.	1.7	1
8403	Differential gene expression and chemical patterns of an intertidal crab inhabiting a polluted port and an adjacent marine protected area. Science of the Total Environment, 2022, 822, 153463.	3.9	7
8404	Comparative transcriptome reveals the thermal stress response differences between Heilongjiang population and Xinjiang population of Lota lota. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100960.	0.4	3
8405	Transcriptome analysis of Holotrichia oblita reveals differentially expressed unigenes related to reproduction and development under different photoperiods. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100959.	0.4	0
8406	Population structure and signals of local adaptation in <i>Eugenia uniflora</i> (Myrtaceae), a widely distributed species in the Atlantic Forest. Botanical Journal of the Linnean Society, 2023, 201, 100-113.	0.8	3
8407	Identification of Olfactory Genes in Monochamus saltuarius and Effects of Bursaphelenchus xylophilus Infestation on Their Expression. Forests, 2022, 13, 258.	0.9	5
8408	Chromosomal genome and population genetic analyses to reveal genetic architecture, breeding history and genes related to cadmium accumulation in Lentinula edodes. BMC Genomics, 2022, 23, 120.	1.2	9
8410	Characterization and phylogenetic analysis of the complete mitochondrial genome of the pathogenic fungus Ilyonectria destructans. Scientific Reports, 2022, 12, 2359.	1.6	4
8411	Identification of genes involved in drought tolerance in seedlings of the desert grass, Psammochloa villosa (Poaceae), based on full-length isoform sequencing and de novo assembly from short reads. Journal of Plant Physiology, 2022, 271, 153630.	1.6	2
8412	Comparison of lncRNA Expression in the Uterus between Periods of Embryo Implantation and Labor in Mice. Animals, 2022, 12, 399.	1.0	3
8413	Screening of Differentially Expressed Genes and Localization Analysis of Female Gametophyte at the Free Nuclear Mitosis Stage in Pinus tabuliformis Carr.. International Journal of Molecular Sciences, 2022, 23, 1915.	1.8	0
8414	Physio-Morphological, Biochemical and Transcriptomic Analyses Provide Insights Into Drought Stress Responses in Mesona chinensis Benth. Frontiers in Plant Science, 2022, 13, 809723.	1.7	6
8415	Characterized Gene Repertoires and Functional Gene Reference for Forensic Entomology: Genomic and Developmental Transcriptomic Analysis of <i>Aldrichina grahami</i> (Diptera: Calliphoridae). Journal of Medical Entomology, 2022, 59, 810-819.	0.9	2
8418	Silencing of Opisthorchis viverrini Tetraspanin Gene Expression Results in Reduced Secretion of Extracellular Vesicles. Frontiers in Cellular and Infection Microbiology, 2022, 12, 827521.	1.8	10
8419	RNA-Seq analysis reveals the role of MYB12, MYB111 and MBW complex repressors in regulation of flavonoid biosynthesis in stigmas of saffron (Crocus sativus L.) flowers. Acta Physiologiae Plantarum, 2022, 44, 1.	1.0	4
8420	Seaweeds influence oyster microbiota and disease susceptibility. Journal of Animal Ecology, 2022, 91, 805-818.	1.3	4
8421	SUMOylation of Translationally Regulated Tumor Protein Modulates Its Immune Function. Frontiers in Immunology, 2022, 13, 807097.	2.2	1
8423	Genomic Characterization of the Titan-like Cell Producing Naganishia tulchinskyi, the First Novel Eukaryote Isolated from the International Space Station. Journal of Fungi (Basel, Switzerland), 2022, 8, 165.	1.5	5

#	ARTICLE	IF	CITATIONS
8424	Transcriptome Responses to Defined Insecticide Selection Pressures in the German Cockroach (Blattella germanica L.). Frontiers in Physiology, 2021, 12, 816675.	1.3	7
8426	Changes in Gene Expression in Leaves of Cacao Genotypes Resistant and Susceptible to Phytophthora palmivora Infection. Frontiers in Plant Science, 2021, 12, 780805.	1.7	6
8427	Seascape genomics of coastal bottlenose dolphins along strong gradients of temperature and salinity. Molecular Ecology, 2022, 31, 2223-2241.	2.0	14
8428	Genome-wide identification and characterization of NLR genes in lamprey (Lethenteron reissneri) and their responses to lipopolysaccharide/poly(I:C) challenge. Molecular Immunology, 2022, 143, 122-134.	1.0	5
8429	Characterization of Bioactivities and Biosynthesis of Angucycline/Angucyclinone Derivatives Derived from Gephyromycinifex aptenodytis gen. nov., sp. nov.. Marine Drugs, 2022, 20, 34.	2.2	11
8430	Isolation, characterization and mapping of genes differentially expressed during fibre development between Gossypium hirsutum and G. barbadense by cDNA-SRAP. Journal of Genetics, 2013, 92, 175-81.	0.4	5
8431	Root transcripts associated with arsenic accumulation in hyperaccumulator Pteris vittata. Journal of Biosciences, 2018, 43, 105-115.	0.5	1
8432	Transcriptome profiling of coriander: a dual purpose crop unravels stem gall resistance genes. Journal of Genetics, 2019, 98, .	0.4	4
8433	Transcriptome-wide identification and profiling of miRNAs in a stress-tolerant conifer. Journal of Biosciences, 2020, 45, .	0.5	1
8434	Modern Approaches for Transcriptome Analyses in Plants. Advances in Experimental Medicine and Biology, 2021, 1346, 11-50.	0.8	0
8435	&lt;i&gt;In silico&lt;/i&gt; Analysis of the Entire &lt;i&gt;P. glaucum&lt;/i&gt; Genome Identifies Regulatory Genes of the bZIP Family Modulated in Response Pathways to Water Stress. American Journal of Plant Sciences, 2022, 13, 277-293.	0.3	2
8438	Stage Specific Comparative Transcriptomic Analysis to Reveal Gene Networks Regulating Iron and Zinc Content in Pearl Millet [Pennisetum Glaucum (L.) R. Br.]. SSRN Electronic Journal, 0, , .	0.4	0
8439	Architectural features of planning and development of data processing soft-ware for the sequencing process. InteraktivnaÃ¢ Nauka, 2022, , 52-55.	0.0	0
8440	Convergent consequences of parthenogenesis on stick insect genomes. Science Advances, 2022, 8, eabg3842.	4.7	27
8441	Non-Coding RNA Analyses of Seasonal Cambium Activity in Populus tomentosa. Cells, 2022, 11, 640.	1.8	10
8442	Identification and characterization of genome-wide resistance gene analogs (RGAs) of durian (Durio) Tj ETQq1 1 0.784314 rgBT /Overlo	1.5	10
8443	Transcriptome Characterization of the Roles of Abscisic Acid and Calcium Signaling during Water Deficit in Garlic. Applied Sciences (Switzerland), 2022, 12, 2440.	1.3	1
8444	Haloterrigena gelatinilytica sp. nov., a new extremely halophilic archaeon isolated from salt-lake. Archives of Microbiology, 2022, 204, 176.	1.0	1

#	Article	IF	Citations
8445	The transcriptomic responses of blunt snout bream (Megalobrama amblycephala) to acute hypoxia stress alone, and in combination with bortezomib. BMC Genomics, 2022, 23, 162.	1.2	8
8446	Genome Analysis of the Broad Host Range Necrotroph Nalanthamala psidii Highlights Genes Associated With Virulence. Frontiers in Plant Science, 2022, 13, 811152.	1.7	1
8447	Transcriptional regulation of metal metabolism- and nutrient absorption-related genes in Eucalyptus grandis by arbuscular mycorrhizal fungi at different zinc concentrations. BMC Plant Biology, 2022, 22, 76.	1.6	9
8448	Complete genome sequence of biocontrol strain Paenibacillus peoriae HJ-2 and further analysis of its biocontrol mechanism. BMC Genomics, 2022, 23, 161.	1.2	6
8449	Cadmium Exposure Alters Rhizospheric Microbial Community and Transcriptional Expression of Vetiver Grass. Frontiers in Plant Science, 2022, 13, 808844.	1.7	2
8450	Comparative Transcriptome Analysis Reveals Sex-Biased Expression of Hormone-Related Genes at an Early Stage of Sex Differentiation in Red Bayberry (Morella rubra). Horticulturae, 2022, 8, 183.	1.2	3
8451	Population genetics and microevolution of clinical <i>Candida glabrata</i> reveals recombinant sequence types and hyper-variation within mitochondrial genomes, virulence genes, and drug targets. Genetics, 2022, 221, .	1.2	11
8452	Development of SNP Marker Sets for Marker-Assisted Background Selection in Cultivated Cucumber Varieties. Agronomy, 2022, 12, 487.	1.3	1
8453	Binding sites of miRNA on the overexpressed genes of oral cancer using 7mer-seed match. Molecular and Cellular Biochemistry, 2022, 477, 1507-1526.	1.4	0
8454	Chromosome-level genome assembly of a xerophytic plant, <i>Haloxylon ammodendron</i>. DNA Research, 2022, 29, .	1.5	15
8455	Comparative Transcriptome Analysis of Bt Resistant and Susceptible Strains in Ostrinia furnacalis (GuenÃ©e) (Lepidoptera: Crambidae). Agriculture (Switzerland), 2022, 12, 298.	1.4	1
8456	Whole-transcriptome analysis and construction of an anther development-related ceRNA network in Chinese cabbage (Brassica campestris L. ssp. pekinensis). Scientific Reports, 2022, 12, 2667.	1.6	4
8458	Comparative Transcriptomic Analysis Provides Insight into the Key Regulatory Pathways and Differentially Expressed Genes in Blueberry Flower Bud Endo- and Ecodormancy Release. Horticulturae, 2022, 8, 176.	1.2	2
8460	Identification of Odorant-Binding and Chemosensory Protein Genes in Mythimna separata Adult Brains Using Transcriptome Analyses. Frontiers in Physiology, 2022, 13, 839559.	1.3	4
8461	Study of Dimorphism Transition Mechanism of Tremella fuciformis Based on Comparative Proteomics. Journal of Fungi (Basel, Switzerland), 2022, 8, 242.	1.5	1
8462	The byssal-producing glands and proteins of the silverlip pearl oyster <i>Pinctada maxima</i> (Jameson, 1901). Biofouling, 2022, 38, 186-206.	0.8	0
8463	New insights into flowering date in <i>Prunus</i>: fine mapping of a major QTL in sweet cherry. Horticulture Research, 2022, 9, .	2.9	8
8464	Transcriptome analysis of genes associated with autolysis of Coprinus comatus. Scientific Reports, 2022, 12, 2476.	1.6	0

#	Article	IF	Citations
8465	Genome-wide association studies dissect the genetic architecture of seed shape and size in common bean. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	4
8466	Mechanisms of Oogenesis-Related Long Non-coding RNAs in Porcine Ovaries Treated With Recombinant Pig Follicle-Stimulating Hormone. Frontiers in Veterinary Science, 2021, 8, 838703.	0.9	1
8467	Full-length transcriptome analysis of multiple organs and identification of adaptive genes and pathways in Mikania micrantha. Scientific Reports, 2022, 12, 3272.	1.6	0
8469	Sugarcane Transcriptomics in Response to Abiotic and Biotic Stresses: A Review. Sugar Tech, 2022, 24, 1295-1318.	0.9	5
8470	Comparative Transcriptome Reveals the Molecular Regulation Mechanism of Charybdis japonica to High- and Low-Temperature Stresses. Frontiers in Marine Science, 2022, 9, .	1.2	5
8471	Genome-wide identification of the SWEET gene family in <i>Phaseolus vulgaris</i> L. and their patterns of expression under abiotic stress. Journal of Plant Interactions, 2022, 17, 390-403.	1.0	8
8472	Antennal Transcriptome Analysis Reveals Differentially Expressed Olfactory Genes Between Male and Female Citrus Longhorn Beetle Anoplophora chinensis (Forster) (Coleoptera: Cerambycidae). Journal of the Kansas Entomological Society, 2022, 94, .	0.1	0
8473	Transcriptome analyses reveal the expression profile of genes related to lignan biosynthesis in Anthriscus sylvestris L. Hoffm. Gen. Physiology and Molecular Biology of Plants, 2022, 28, 333-346.	1.4	1
8474	iTRAQ-Based Proteome Profiling of Differentially Expressed Proteins in Insulin-Resistant Human Hepatocellular Carcinoma. Frontiers in Cell and Developmental Biology, 2022, 10, 836041.	1.8	0
8475	Transcriptome profile analysis reveals the emamectin benzoate-induced genes associated with olfaction and metabolic detoxification in <i>Spodoptera exigua</i> HÃ¼bner (Lepidoptera: noctuidae). International Journal of Transgender Health, 2022, 15, 340-357.	1.1	1
8476	Strong parallel differential gene expression induced by hatchery rearing weakly associated with methylation signals in adult Coho Salmon (<i>O. kisutch</i>). Genome Biology and Evolution, 2022, , .	1.1	4
8477	Single nucleotide polymorphism discovery and functional annotation analysis of blackberry fruit. Trees - Structure and Function, 0, , 1.	0.9	1
8478	Analysis of Competing Endogenous RNAs and MicroRNAs in Tea (<i>Camellia sinensis</i>) Leaves During Infection by the Leaf Spot Pathogen <i>Pestalotiopsis trachicarpicola</i>. Molecular Plant-Microbe Interactions, 2022, 35, 432-438.	1.4	2
8479	Nitrate/ammonium-responsive microRNA-mRNA regulatory networks affect root system architecture in Populusâ€‰Ã—â€‰canescens. BMC Plant Biology, 2022, 22, 96.	1.6	7
8480	A chromosomeâ€•level genome assembly of <i>Paracymoriza distinctalis</i> (Lepidoptera: Crambidae:) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.6	0
8481	RNA-Seq and Gene Regulatory Network Analyses Uncover Candidate Genes in the Early Defense to Two Hemibiotrophic Colletorichum spp. in Strawberry. Frontiers in Genetics, 2021, 12, 805771.	1.1	3
8482	New Insights into the Toxin Diversity and Antimicrobial Activity of the â€œFire Coralâ€•Millepora complanata. Toxins, 2022, 14, 206.	1.5	5
8483	Label-free quantitative proteomics of maize roots from different root zones provides insight into proteins associated with enhance water uptake. BMC Genomics, 2022, 23, 184.	1.2	6

#	ARTICLE	IF	CITATIONS
8485	Cold stress after swimming fatigue decreases immunity-related gene expression in the spleen of the Chinese sucker. Fish and Shellfish Immunology, 2022, 122, 455-464.	1.6	1
8486	Janus Kinase Mediates Faster Recovery From Sevoflurane Anesthesia Than Isoflurane Anesthesia in the Migratory Locusts. Frontiers in Physiology, 2022, 13, 806746.	1.3	0
8487	Transcriptome Analysis of Apples in High-Temperature Treatments Reveals a Role of MdLBD37 in the Inhibition of Anthocyanin Accumulation. International Journal of Molecular Sciences, 2022, 23, 3766.	1.8	3
8488	Prospection of putative genes for digestive enzymes based on functional genome of the hepatopancreas of Amazon river prawn. Acta Scientiarum - Animal Sciences, 0, 44, e53894.	0.3	1
8489	New Insight on Vitality Differences for the Penaeid Shrimp, Fenneropenaeus chinensis, in Low Salinity Environment Through Transcriptomics. Frontiers in Ecology and Evolution, 2022, 10, .	1.1	1
8490	Differential gene expression in Eucalyptus clones in response to nutrient deficiency. Tree Genetics and Genomes, 2022, 18, 1.	0.6	1
8491	The alternative splicing landscape of a coral reef fish during a marine heatwave. Ecology and Evolution, 2022, 12, e8738.	0.8	3
8492	Structure and biosynthesis of carotenoids produced by a novel Planococcus sp. isolated from South Africa. Microbial Cell Factories, 2022, 21, 43.	1.9	4
8493	Integrated transcriptomic and proteomic analyses for the characterization of parathyroid oxyphil cells in uremic patients. Amino Acids, 2022, 54, 749-763.	1.2	3
8495	Full-Length Transcriptome Sequences Provide Insight Into Hermaphroditism of Freshwater Pearl Mussel Hyriopsis schlegelii. Frontiers in Genetics, 2022, 13, 868742.	1.1	6
8496	Full-length transcriptome analysis of <i>Adiantum flabellulatum</i> gametophyte. PeerJ, 2022, 10, e13079.	0.9	5
8497	Rapid evolution fuels transcriptional plasticity to ocean acidification. Global Change Biology, 2022, 28, 3007-3022.	4.2	23
8498	Genome-wide SNP and InDel analysis of three Philippine mango species inferred from whole-genome sequencing. Journal of Genetic Engineering and Biotechnology, 2022, 20, 46.	1.5	5
8499	Inflorescence Transcriptome Sequencing and Development of New EST-SSR Markers in Common Buckwheat (Fagopyrum esculentum). Plants, 2022, 11, 742.	1.6	6
8500	Sequencing and Functional Annotation of Competing Endogenous RNAs and MicroRNAs in Tea Leaves During Infection by <i>Lasiodiplodia theobromae</i>. PhytoFrontiers, 2022, 2, 307-313.	0.8	3
8501	Polyphasic Identification and Genomic Insights of Leptothermofonsia sichuanensis gen. sp. nov., a Novel Thermophilic Cyanobacteria Within Leptolyngbyaceae. Frontiers in Microbiology, 2022, 13, 765105.	1.5	11
8502	Genome-Wide Identification of the Long Noncoding RNAs of Tribolium castaneum in Response to Terpinen-4-ol Fumigation. Insects, 2022, 13, 283.	1.0	4
8503	Comparative Analysis of Blood Transcriptome in the Yangtze Finless Porpoise (Neophocaena) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	0

#	ARTICLE	IF	CITATIONS
8504	Schistosoma japonicum translationally controlled tumour protein, which is associated with the development of female worms, as a target for control of schistosomiasis. International Journal for Parasitology, 2022, 52, 569-579.	1.3	7
8505	Transcriptional Profiles of a Foliar Fungal Endophyte (<i>Pestalotiopsis</i> , Ascomycota) and Its Bacterial Symbiont (<i>Luteibacter</i> , <i>Gammaproteobacteria</i>) Reveal Sulfur Exchange and Growth Regulation during Early Phases of Symbiotic Interaction. MSystems, 2022, 7, e0009122.	1.7	11
8506	The regulatory role of CARBON STARVED ANTHER-mediated photoperiod-dependent male fertility in rice. Plant Physiology, 2022, 189, 955-971.	2.3	3
8507	Transcriptome Analysis of Populus euphratica under Salt Treatment and PeERF1 Gene Enhances Salt Tolerance in Transgenic Populus alba Ã— Populus glandulosa. International Journal of Molecular Sciences, 2022, 23, 3727.	1.8	6
8508	Global gene expression responses of Atlantic salmon skin to Moritella viscosa. Scientific Reports, 2022, 12, 4622.	1.6	7
8509	Gill and Liver Transcript Expression Changes Associated With Gill Damage in Atlantic Salmon (Salmo) Tj ETQq1 1 0.784314 rgBT /Overlo	2.2	8
8510	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. Genome Biology, 2022, 23, 75.	3.8	15
8511	Transcriptomic analysis of pea aphids (<i>Acyrthosiphon pisum</i>) treated with plant extracts from endophyteâ€containing drunken horse grass. Journal of Applied Entomology, 0, , .	0.8	0
8512	Tracking of Diversity and Evolution in the Brown Rot Fungi Monilinia fructicola, Monilinia fructigena, and Monilinia laxa. Frontiers in Microbiology, 2022, 13, 854852.	1.5	14
8513	Transcriptome analysis of Tamarix ramosissima leaves in response to NaCl stress. PLoS ONE, 2022, 17, e0265653.	1.1	9
8514	Transcriptome Analysis Reveals a Gene Expression Pattern That Contributes to Sugarcane Bud Propagation Induced by Indole-3-Butyric Acid. Frontiers in Plant Science, 2022, 13, 852886.	1.7	5
8515	De novo assembly and analysis of Polygonatum cyrtonema Hua and identification of genes involved in polysaccharide and saponin biosynthesis. BMC Genomics, 2022, 23, 195.	1.2	6
8517	Chromosome-Scale Assembly and Characterization of the Albino Northern Snakehead, Channa argus var. (Teleostei: Channidae) Genome. Frontiers in Marine Science, 2022, 9, .	1.2	1
8518	Efficiently whole-genomic mutagenesis approach by ARTP in blunt snout bream (Megalobrama) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	4
8519	Genome sequencing of a predominant clonal lineage of the grain aphid Sitobion avenae. Insect Biochemistry and Molecular Biology, 2022, 143, 103742.	1.2	4
8520	Accumulation of functional metabolites and transcriptomics in postharvest fumeâ€drying and airâ€drying process in rhubarb. Journal of the Science of Food and Agriculture, 2022, , .	1.7	0
8521	Complete Genome Sequence of Brevibacterium frigoritolerans Ant232, Isolated from Antarctic Snow. Microbiology Resource Announcements, 2022, , e0015222.	0.3	2
8522	Comparative genomic analyses reveal cis-regulatory divergence after polyploidization in cotton. Crop Journal, 2022, , .	2.3	0

#	Article	IF	Citations
8523	Intraspecific hybridization as a mitigation strategy of low salinity in marine bivalve noble scallop Chlamys nobilis. Aquaculture, 2022, 552, 738037.	1.7	5
8524	Transcriptomes analysis of Pichia kudriavzevii UniMAP 3â€“1 in response to acetic acid supplementation in glucose and xylose medium at elevated fermentation temperature. Process Biochemistry, 2022, 118, 41-51.	1.8	5
8525	Proteomic analysis of the periodontal pathogen Prevotella intermedia secretomes in biofilm and planktonic lifestyles. Scientific Reports, 2022, 12, 5636.	1.6	7
8526	Draft Genome Sequence of Paenibacillus sonchi IIRRBNF1, a Nitrogen-Fixing and Plant Growth-Promoting Bacterium Isolated from Rice Rhizosphere. Microbiology Resource Announcements, 2022, 11, e0012622.	0.3	1
8527	Multiâ€omics reveal differentiation and maintenance of dimorphic flowers in an alpine plant on the Qinghaiâ€Tibet Plateau. Molecular Ecology, 2023, 32, 1411-1424.	2.0	7
8528	Comparative Proteomics Reveals the Difference in Root Cold Resistance between Vitis. riparia Ã— V. labrusca and Cabernet Sauvignon in Response to Freezing Temperature. Plants, 2022, 11, 971.	1.6	1
8529	Predict the role of lncRNA in kidney aging based on RNA sequencing. BMC Genomics, 2022, 23, 254.	1.2	5
8530	The role of microRNA-4723-5p regulated by c-myc in triple-negative breast cancer. Bioengineered, 2022, 13, 9097-9105.	1.4	1
8532	Establishment of the Y-linked Dmrt1Y as the candidate sex determination gene in spotbanded scat (Selenotoca multifasciata). Aquaculture Reports, 2022, 23, 101085.	0.7	0
8533	Fatty acid synthases and desaturases are essential for the biosynthesis of <i>Î±</i>â€linolenic acid and metamorphosis in a major mulberry pest, <i>Glyphodes pyloalis</i> walker (<scp>Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	4
8534	Transcriptome Profiling in the Marine Red Alga Neopyropia yezoensis Under Light/Dark Cycle. Marine Biotechnology, 2022, 24, 393-407.	1.1	3
8535	Brain transcriptome response to Streptococcus agalactiae infection and the heterogeneous regulation of neuropeptides on immune response in tilapia, Oreochromis niloticus. Aquaculture, 2022, 555, 738222.	1.7	4
8536	Purification and characterization of antifungal lipopeptide produced by Bacillus velezensis isolated from raw honey. PLoS ONE, 2022, 17, e0266470.	1.1	12
8537	Heavy oil exposure suppresses antiviral activities in Japanese flounder Paralichthys olivaceus infected with viral hemorrhagic septicemia virus (VHSV). Fish and Shellfish Immunology, 2022, , .	1.6	0
8538	Infection of the entomopathogenic fungus <i>Metarhizium rileyi</i> suppresses cellular immunity and activates humoral antibacterial immunity of the host <i>Spodoptera frugiperda</i>. Pest Management Science, 2022, 78, 2828-2837.	1.7	9
8539	The chromosome-level genome assembly of <i>Gentiana dahurica</i> (Gentianaceae) provides insights into gentiopicroside biosynthesis. DNA Research, 2022, 29, .	1.5	12
8540	SNP Discovery Using BSR-Seq Approach for Spot Blotch Resistance in Wheat (Triticum aestivum L.), an Essential Crop for Food Security. Frontiers in Genetics, 2022, 13, 859676.	1.1	4
8541	Feedlot diets containing different starch levels and additives change the cecal proteome involved in cattleâ€™s energy metabolism and inflammatory response. Scientific Reports, 2022, 12, 5691.	1.6	5

#	Article	IF	Citations
8542	Comprehensive transcriptome profiling and functional analysis of the meagre (Argyrosomus regius) immune system. Fish and Shellfish Immunology, 2022, 123, 506-520.	1.6	2
8543	Transcriptomic and proteomic analysis of Chinese rare minnow (Gobiocypris rarus) larvae in response to acute waterborne cadmium or mercury stress. Aquatic Toxicology, 2022, 246, 106134.	1.9	8
8544	Sequencing and de novo transcriptome assembly for discovering regulators of gene expression in Jack (Artocarpus heterophyllus). Genomics, 2022, 114, 110356.	1.3	1
8545	Transcriptome analysis of the mantle tissue of Pinctada fucata with red and black shells under salinity stress. Gene, 2022, 823, 146367.	1.0	3
8546	Genomeâ€“wide transcriptional response of contrasting genotypes of industrial crop castor to As(V) stress: Identification of genes and mechanisms associated with As(V) tolerance. Industrial Crops and Products, 2022, 179, 114678.	2.5	2
8547	De novo transcriptome analysis identifies key genes involved in dehydration stress response in kodo millet (Paspalum scrobiculatum L.). Genomics, 2022, 114, 110347.	1.3	8
8548	Transcriptional and translational perturbation in abiotic stress induced physiological activities and metabolic pathway networks in spongy tissue disorder of mango fruit. Postharvest Biology and Technology, 2022, 188, 111880.	2.9	5
8550	Transcriptomic studies of solventogenic clostridia, Clostridium acetobutylicum and Clostridium beijerinckii. Biotechnology Advances, 2022, 58, 107889.	6.0	6
8551	Transcriptomics Reveals Host-Dependent Differences of Polysaccharides Biosynthesis in Cynomorium songaricum. Molecules, 2022, 27, 44.	1.7	4
8552	CottonGen: The Community Database for Cotton Genomics, Genetics, and Breeding Research. Plants, 2021, 10, 2805.	1.6	42
8553	Genomic Traces of the Fruit Fly Anastrepha obliqua Associated with Its Polyphagous Nature. Insects, 2021, 12, 1116.	1.0	8
8554	Transcriptomic Analysis Reveals Regulatory Networks for Osmotic Water Stress and Rewatering Response in the Leaves of Ginkgo biloba. Forests, 2021, 12, 1705.	0.9	3
8555	Integrative Analyses of Biochemical Properties and Transcriptome Reveal the Dynamic Changes in Leaf Senescence of Tobacco (Nicotiana tabacum L.). Frontiers in Genetics, 2021, 12, 790167.	1.1	5
8556	Proteomics Investigations of Potential Protein Biomarkers in Sera of Rabbits Infected With Schistosoma japonicum. Frontiers in Cellular and Infection Microbiology, 2021, 11, 784279.	1.8	9
8558	Insights into the Host-Pathogen Interaction Pathways through RNA-Seq Analysis of Lens culinaris Medik. in Response to Rhizoctonia bataticola Infection. Genes, 2022, 13, 90.	1.0	18
8560	The TOR kinase pathway is relevant for nitrogen signaling and antagonism of the mycoparasite Trichoderma atroviride. PLoS ONE, 2021, 16, e0262180.	1.1	7
8561	Transcriptome analysis of potential flocculation-related genes in Streptomyces sp. hsn06 with flocculation activity on Chlorella vulgaris biomass. Archives of Microbiology, 2022, 204, 41.	1.0	0
8562	RNA-sequencing identifies novel transcriptomic signatures in intestinal failure-associated liver disease. Journal of Pediatric Surgery, 2022, 57, 158-165.	0.8	6

#	Article	IF	Citations
8563	Potato leafroll virus reduces Buchnera aphidocola titer and alters vector transcriptome responses. Scientific Reports, 2021, 11, 23931.	1.6	10
8564	Mechanisms underlying Clostridium pasteurianumâ€™s metabolic shift when grown with Geobacter sulfurreducens. Applied Microbiology and Biotechnology, 2022, 106, 865-876.	1.7	3
8565	Cryptosporidium felis differs from other Cryptosporidium spp. in codon usage. Microbial Genomics, 2021, 7, .	1.0	3
8566	Ploidy level enhances the photosynthetic capacity of a tetraploid variety of <i>Acer buergerianum</i> Miq.. PeerJ, 2021, 9, e12620.	0.9	5
8567	The developmentally dynamic microRNA transcriptome of <i>Glossina pallidipes</i> tsetse flies, vectors of animal trypanosomiasis. Bioinformatics Advances, 2022, 2, .	0.9	1
8568	Planting Season Impacts Sugarcane Stem Development, Secondary Metabolite Levels, and Natural Antisense Transcription. Cells, 2021, 10, 3451.	1.8	6
8569	Genetic insights into the regulatory pathways for continuous flowering in a unique orchid Arundina graminifolia. BMC Plant Biology, 2021, 21, 587.	1.6	11
8570	Characterization of Long Non-Coding RNAs in the Bollworm, Helicoverpa zea, and Their Possible Role in Cry1Ac-Resistance. Insects, 2022, 13, 12.	1.0	8
8571	Comparative Transcriptome Analysis of the Anthers from the Cytoplasmic Male-Sterile Pepper Line HZ1A and Its Maintainer Line HZ1B. Horticulturae, 2021, 7, 580.	1.2	2
8572	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	1.7	1
8573	Genome-Wide Identification of Stress-Associated Proteins (SAPs) Encoding A20/AN1 Zinc Finger in Almond (Prunus dulcis) and Their Differential Expression during Fruit Development. Plants, 2022, 11, 117.	1.6	3
8574	Genetic variability and genomeâ€wide marker association studies for starch traits contributing to low glycaemic index in pearl millet. Food and Energy Security, 2022, 11, .	2.0	6
8575	Identification of novel microRNAs in Rous sarcoma Virus (RSV) and their target sites in tumor suppressor genes of chicken. Infection, Genetics and Evolution, 2021, 96, 105139.	1.0	2
8576	Shrimp immune response: A transcriptomic perspective. Reviews in Aquaculture, 2022, 14, 1136-1149.	4.6	12
8577	Cytological, Biochemical, and Transcriptomic Analyses of a Novel Yellow Leaf Variation in a Paphiopedilum (Orchidaceae) SCBG COP15. Genes, 2022, 13, 71.	1.0	4
8578	Developmental gene regulatory network connections predicted by machine learning from gene expression data alone. PLoS ONE, 2021, 16, e0261926.	1.1	2
8579	Development of Disease-Resistance-Associated Microsatellite DNA Markers for Selective Breeding of Tilapia (Oreochromis spp.) Farmed in Taiwan. Genes, 2022, 13, 99.	1.0	9
8580	Genome sequencing and transcriptome analyses provide insights into the origin and domestication of water caltrop (<i>Trapa</i> spp., Lythraceae). Plant Biotechnology Journal, 2022, 20, 761-776.	4.1	16

#	Article	IF	Citations
8581	Mutations in PpAGO3 Lead to Enhanced Virulence of Phytophthora parasitica by Activation of 25â€"26â€‰nt sRNA-Associated Effector Genes. Frontiers in Microbiology, 2022, 13, 856106.	1.5	0
8582	Identification of key proteins in hostâ€"pathogen interactions between Mycobacterium tuberculosis and Homo sapiens: A systematic network theoretical approach. Healthcare Analytics, 2022, 2, 100052.	2.6	8
8583	Oogenesis and lipid metabolism in the deep-sea sponge Phakellia ventilabrum (Linnaeus, 1767). Scientific Reports, 2022, 12, 6317.	1.6	8
8585	Transcriptome Profiling Reveals a Petunia Transcription Factor, PhCOL4, Contributing to Antiviral RNA Silencing. Frontiers in Plant Science, 2022, 13, 876428.	1.7	1
8586	The grapevine aspartic protease gene family: characterization and expression modulation in response to Plasmopara viticola. Journal of Plant Research, 2022, 135, 501-515.	1.2	1
8587	Comparative transcriptome analysis provides insights into the molecular mechanisms of high-frequency hearing differences between the sexes of Odorrana tormota. BMC Genomics, 2022, 23, 296.	1.2	3
8588	Multi-locus genome-wide association studies (ML-GWAS) reveal novel genomic regions associated with seedling and adult plant stage leaf rust resistance in bread wheat (Triticum aestivum L.). Heredity, 2022, 128, 434-449.	1.2	15
8589	Pathogen exposure leads to a transcriptional downregulation of core cellular functions that may dampen the immune response in a macroalga. Molecular Ecology, 2022, 31, 3468-3480.	2.0	3
8590	Gene expression profiles provide insights into the survival strategies in deep-sea mussel (Bathymodiolus platifrons) of different developmental stages. BMC Genomics, 2022, 23, 311.	1.2	2
8591	Transcriptomic Analysis of Cadmium Stressed Tamarix hispida Revealed Novel Transcripts and the Importance of Abscisic Acid Network. Frontiers in Plant Science, 2022, 13, 843725.	1.7	7
8592	Find My Way to You: A Comparative Study of Antennal Sensilla and Olfactory Genes in Slug Moth With Different Diet Ranges (Lepidoptera: Limacodidae). Frontiers in Ecology and Evolution, 2022, 10, .	1.1	0
8593	Composition and abundance of midgut surface proteins in the Asian citrus psyllid, Diaphorina citri. Journal of Proteomics, 2022, 261, 104580.	1.2	6
9478	Identification of Two Major QTLs in Brassica napus Lines With Introgressed Clubroot Resistance From Turnip Cultivar ECD01. Frontiers in Plant Science, 2021, 12, 785989.	1.7	12
9479	A chromosome-level reference genome of <i>Ensete glaucum</i> gives insight into diversity and chromosomal and repetitive sequence evolution in the Musaceae. GigaScience, 2022, 11, .	3.3	19
9480	Responses to Submergence and Recovery in Seedlings of the Rheophyte Dyckia Brevifolia (Bromeliaceae). SSRN Electronic Journal, 0, , .	0.4	0
9481	Fuel source shift or cost reduction: Context-dependent adaptation strategies in closely related <i>Neodon fuscus</i> and <i>Lasiopodomys brandtii</i> against hypoxia. Zoological Research, 2022, 43, 497-513.	0.9	0
9482	Bioinformatics-assisted multiomics approaches to improve the agronomic traits in cotton. , 2022, , 233-251.		1
9483	Genome informatics: present status and future prospects in agriculture. , 2022, , 47-59.		0

#	ARTICLE	IF	CITATIONS
9484	Functional genomics tools for studying microbe-mediated stress tolerance in plants. , 2022, , 175-204.		1
9485	Transcriptome Sequencing of the Pale Anemones (Exaiptasia diaphana) Revealed Functional Peptide Gene Resources of Sea Anemone. Frontiers in Marine Science, 2022, 9, .	1.2	7
9486	Allelic Polymorphisms of Killer Immunoglobulin-Like Receptor Genes in Malay and Orang Asli Populations of Peninsular Malaysia. Human Immunology, 2022, , .	1.2	2
9487	Comparative Lipidome and Transcriptome Provide Novel Insight Into Polyunsaturated Fatty Acids Metabolism of the Sea Urchin. Frontiers in Marine Science, 2022, 9, .	1.2	1
9488	Climate Warming Since the Holocene Accelerates Westâ€"East Communication for the Eurasian Temperate Water Strider Species <i>Aquarius paludum</i>. Molecular Biology and Evolution, 2022, 39, .	3.5	4
9489	Identification of Known and Novel Arundo donax L. MicroRNAs and Their Targets Using High-Throughput Sequencing and Degradome Analysis. Life, 2022, 12, 651.	1.1	1
9490	Constitutive expression of <i>SlMX1</i> gene improves fruit yield and quality, health-promoting compounds, fungal resistance and delays ripening in transgenic tomato plants. Journal of Plant Interactions, 2022, 17, 517-536.	1.0	7
9491	Integrative analysis of metabolome and transcriptome reveals the improvements of seed quality in vegetable soybean (Glycine max (L.) Merr.). Phytochemistry, 2022, 200, 113216.	1.4	8
9492	The Genome-Wide Identification of Long Non-Coding RNAs Involved in Floral Thermogenesis in Nelumbo nucifera Gaertn. International Journal of Molecular Sciences, 2022, 23, 4901.	1.8	0
9493	Genome-Wide Analyses of MADS-Box Genes in Humulus lupulus L. Reveal Potential Participation in Plant Development, Floral Architecture, and Lupulin Gland Metabolism. Plants, 2022, 11, 1237.	1.6	7
9494	Fungal secondary metabolites in food and pharmaceuticals in the era of multi-omics. Applied Microbiology and Biotechnology, 2022, 106, 3465-3488.	1.7	33
9495	Hybrid Assembly and Annotation of the Genome of the Indian Punica granatum, a Superfood. Frontiers in Genetics, 2022, 13, .	1.1	4
9496	Identification and Characterization of Circular RNAs in Brassica rapa in Response to Plasmodiophora brassicae. International Journal of Molecular Sciences, 2022, 23, 5369.	1.8	4
9497	Thiamine functions as a key activator for modulating plant health and broadâ€spectrum tolerance in cotton. Plant Journal, 2022, 111, 374-390.	2.8	11
9499	Comparative RNA-Seq analysis to understand anthocyanin biosynthesis and regulations in <i>Curcuma alismatifolia</i>. Folia Horticulturae, 2022, 34, 65-83.	0.6	1
9500	Survival Characteristics and Transcriptomic Analyses Reveal the Adaptive Response of the Aquatic Pathogen Non-O1/O139 Vibrio cholerae to Starvation Stress. Microbiology Spectrum, 2022, 10, e0193921.	1.2	3
9501	A comparative study indicates vertical inheritance and horizontal gene transfer of arsenic resistance-related genes in eukaryotes. Molecular Phylogenetics and Evolution, 2022, 173, 107479.	1.2	4
9502	Chromosome-level genome assembly of <i>Mentha longifolia</i> L. reveals gene organization underlying disease resistance and essential oil traits. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	8

#	Article	IF	Citations
9503	Leaf and rhizome transcriptome assembly and expression analysis of genes involved in terpene biosynthesis in Dioscorea opposita. Journal of Plant Biochemistry and Biotechnology, 0, , 1.	0.9	0
9505	Identification and bioinformatic characterization of rare variants of Rhododendron canescens architecture genes. Euphytica, 2022, 218, 1.	0.6	0
9506	Transcriptome Analysis of Antennal Chemosensory Genes in Curculio Dieckmanni Faust. (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.3	0
9507	Chromosome-level genome assembly of Asian yellow pond turtle (Mauremys mutica) with temperature-dependent sex determination system. Scientific Reports, 2022, 12, 7905.	1.6	7
9508	Protein sequence databases generated from metagenomics and public databases produced similar soil metaproteomic results of microbial taxonomic and functional changes. Pedosphere, 2022, 32, 507-520.	2.1	0
9509	Leveraging lncRNA-miRNA-mRNA network to reveal anti-Spiroplasma eriocheiris infection mechanisms in Macrobrachium nipponense. Aquaculture, 2022, 557, 738286.	1.7	4
9510	Proteomics and Co-expression Network Analysis Reveal the Importance of Hub Proteins and Metabolic Pathways in Nicotine Synthesis and Accumulation in Tobacco (Nicotiana tabacum L.). Frontiers in Plant Science, 2022, 13, 860455.	1.7	5
9511	Comparative transcriptome profiling of high and low oil yielding Santalum album L. PLoS ONE, 2022, 17, e0252173.	1.1	0
9512	Integration of the transcriptome and proteome provides insights into the mechanism calcium regulated of Ulva prolifera in response to high-temperature stress. Aquaculture, 2022, 557, 738344.	1.7	6
9513	Small RNA sequencing and identification of papaya (Carica papaya L.) miRNAs with potential cross-kingdom human gene targets. Molecular Genetics and Genomics, 2022, 297, 981-997.	1.0	7
9514	Absence of increased genomic variants in the cyanobacterium Chroococcidiopsis exposed to Mars-like conditions outside the space station. Scientific Reports, 2022, 12, 8437.	1.6	12
9515	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i>, the western spadefoot toad. DNA Research, 2022, 29, .	1.5	1
9516	Transcriptome and metabolome reveal the accumulation of secondary metabolites in different varieties of Cinnamomum longepaniculatum. BMC Plant Biology, 2022, 22, 243.	1.6	13
9517	Pea aphid winged and wingless males exhibit reproductive, gene expression, and lipid metabolism differences. Current Research in Insect Science, 2022, 2, 100039.	0.8	3
9518	Gene Co-expression Network and Regression Analysis Identify the Transcriptomic, Physiological, and Biochemical Indicators of the Response of Alpine Woody Plant Rhododendron rex to Drought Stress. Frontiers in Plant Science, 2022, 13, .	1.7	2
9519	Transcriptomic analysis identifies differentially expressed genes in purple tender shoots and green mature leaves of Zijuan tea. Czech Journal of Food Sciences, 2022, 40, 210-220.	0.6	0
9521	Ancient Origins of Cytoskeletal Crosstalk: Spectraplakin-like Proteins Precede the Emergence of Cortical Microtubule Stabilization Complexes as Crosslinkers. International Journal of Molecular Sciences, 2022, 23, 5594.	1.8	3
9522	Mitochondrial dysfunction associated with ascorbate synthesis in plants. Plant Physiology and Biochemistry, 2022, 185, 55-68.	2.8	7

#	Article	IF	Citations
9523	Identification and characterization of conserved miRNAs from Gossypium hirsutum. Ecological Genetics and Genomics, 2022, 24, 100125.	0.3	0
9525	Identification and Characterization of Chemosensory Receptors in the Pheromone Gland-Ovipositor of Spodoptera frugiperda (J. E. Smith). Insects, 2022, 13, 481.	1.0	3
9526	Pathogenic Process-Associated Transcriptome Analysis of Stemphylium lycopersici from Tomato. International Journal of Genomics, 2022, 2022, 1-12.	0.8	1
9527	Integrating metabolomics and transcriptomics to unveil the spatiotemporal distribution of macrocyclic diterpenoids and candidate genes involved in ingenol biosynthesis in the medicinal plant Euphorbia lathyris L.. Industrial Crops and Products, 2022, 184, 115096.	2.5	6
9528	Transcriptomics in Plant. , 2022, , 99-127.		1
9529	The reference genome and full-length transcriptome of pakchoi provide insights into cuticle formation and heat adaption. Horticulture Research, 2022, 9, .	2.9	8
9530	Genome Assembly and Evolutionary Analysis of the Mandarin Duck <i>Aix galericulata</i> Reveal Strong Genome Conservation among Ducks. Genome Biology and Evolution, 2022, 14, .	1.1	1
9531	Identification of Differentially Expressed Genes in Resistant Tetraploid Wheat (Triticum turgidum) under Sitobion avenae (F.) Infestation. International Journal of Molecular Sciences, 2022, 23, 6012.	1.8	1
9532	Transcriptome analysis of<i>Mythimna separata</i>: De novo assembly and detection of genes related to betaâ€cypermethrin resistance. Archives of Insect Biochemistry and Physiology, 2022, 111, .	0.6	1
9534	RNA-seq analysis and transcriptome assembly of Salicornia neei reveals a powerful system for ammonium detoxification. Electronic Journal of Biotechnology, 2022, 58, 70-81.	1.2	1
9535	Comparative transcriptomic analysis of genes in the triterpene saponin biosynthesis pathway in leaves and roots of <i>Ardisia kteniophylla</i> A. DC., a plant used in traditional Chinese medicine. Ecology and Evolution, 2022, 12, .	0.8	1
9536	Physiological and Metabolic Response of Arthrospira maxima to Organophosphates. Microorganisms, 2022, 10, 1063.	1.6	2
9537	Phototransduction in a marine sponge provides insights into the origin of animal vision. IScience, 2022, 25, 104436.	1.9	1
9538	Whole transcriptome analysis provides new insight on immune response mechanism of golden pompano (Trachinotus ovatus) to Amyloodinium ocellatum infestation. Aquaculture, 2022, 560, 738396.	1.7	7
9539	Full-Length Transcriptome Sequencing Analysis and Characterization of Gene Isoforms Involved in Flavonoid Biosynthesis in the Seedless Kiwifruit Cultivar â€˜Chengxiangâ€™ (Actinidia arguta). Diversity, 2022, 14, 424.	0.7	2
9542	Comparative Transcriptomics of Gonads Reveals the Molecular Mechanisms Underlying Gonadal Development in Giant Freshwater Prawns (Macrobrachium rosenbergii). Journal of Marine Science and Engineering, 2022, 10, 737.	1.2	4
9543	A complete inventory of long-chain polyunsaturated fatty acid biosynthesis pathway enzymes in the miniaturized cyprinid Paedocypris micromegethes. Fish Physiology and Biochemistry, 0, , .	0.9	0
9544	Volatile Organic Compounds of Streptomyces sp. TOR3209 Stimulated Tobacco Growth by Up-Regulating the Expression of Genes Related to Plant Growth and Development. Frontiers in Microbiology, 2022, 13, .	1.5	3

#	ARTICLE	IF	CITATIONS
9545	Comparative Transcriptomics and Metabolites Analysis of Two Closely Related Euphorbia Species Reveal Environmental Adaptation Mechanism and Active Ingredients Difference. Frontiers in Plant Science, 2022, 13, .	1.7	5
9546	Full-Length Transcriptome Sequencing and Comparative Transcriptomic Analyses Provide Comprehensive Insight Into Molecular Mechanisms of Cellulose and Lignin Biosynthesis in Cunninghamia lanceolata. Frontiers in Plant Science, 2022, 13, .	1.7	4
9547	Proteomics-based analysis of potential therapeutic targets in patients with peritoneal dialysis-associated peritonitis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, , 140796.	1.1	0
9548	The Transcription Factor MdERF78 Is Involved in ALA-Induced Anthocyanin Accumulation in Apples. Frontiers in Plant Science, 2022, 13, .	1.7	10
9549	Drought Stress Mitigating Morphological, Physiological, Biochemical, and Molecular Responses of Guava (Psidium guajava L.) Cultivars. Frontiers in Plant Science, 2022, 13, .	1.7	8
9550	Integrative transcriptome and proteome analyses of Trichoderma longibrachiatum LC and its cellulase hyper-producing mutants generated by heavy ion mutagenesis reveal the key genes involved in cellulolytic enzymes regulation. , 2022, 15, .		6
9551	Key Role of Heat Shock Protein Expression Induced by Ampicillin in Citrus Defense against Huanglongbing: A Transcriptomics Study. Agronomy, 2022, 12, 1356.	1.3	2
9552	Cloning and homologous characterization of geranylgeranyl pyrophosphate synthase (GGPPS) from Withania somnifera revealed alterations in metabolic flux towards gibberellic acid biosynthesis. Planta, 2022, 256, .	1.6	5
9553	Leaf transcriptome profiling of contrasting sugarcane genotypes for drought tolerance under field conditions. Scientific Reports, 2022, 12, .	1.6	5
9554	Identification of the Key Genes Associated with Different Hair Types in the Inner Mongolia Cashmere Goat. Animals, 2022, 12, 1456.	1.0	7
9555	Effects of low salinity on hemolymph osmolality and transcriptome of the Iwagaki oyster, Crassostrea nippona. Fish and Shellfish Immunology, 2022, 126, 211-216.	1.6	7
9556	Extreme freeze-tolerance in cryophilic tardigrades relies on controlled ice formation but does not involve significant change in transcription. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 271, 111245.	0.8	8
9557	Fiber-specific overexpression of GhACO1 driven by E6 promoter improves cotton fiber quality and yield. Industrial Crops and Products, 2022, 185, 115134.	2.5	7
9565	Genome-Wide Identification of Genes Enabling Accurate Prediction of Hybrid Performance from Parents Across Environments and Populations for Gene-Based Breeding in Maize. SSRN Electronic Journal, 0, , .	0.4	0
9566	Integrated mRNA and miRNA Transcriptome Analysis Suggests a Regulatory Network for UVâ€"B-Controlled Terpenoid Synthesis in Fragrant Woodfern (Dryopteris fragrans). International Journal of Molecular Sciences, 2022, 23, 5708.	1.8	6
9567	Linked-Read Sequencing of Eight Falcons Reveals a Unique Genomic Architecture in Flux. Genome Biology and Evolution, 2022, 14, .	1.1	3
9568	Integrated Transcriptomic and Proteomic Analyses Uncover the Regulatory Mechanisms of Myricaria laxiflora Under Flooding Stress. Frontiers in Plant Science, 0, 13, .	1.7	3
9569	Intra-Species Genomic Variation in the Pine Pathogen Fusarium circinatum. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlock	1.5	4

#	Article	IF	Citations
9570	Identification of a Novel Densovirus in Aphid, and Uncovering the Possible Antiviral Process During Its Infection. Frontiers in Immunology, 0, 13, .	2.2	4
9572	Molecular basis of intraspecific differentiation for heavy metal tolerance in the copper moss Scopelophila cataractae. Environmental and Experimental Botany, 2022, 201, 104970.	2.0	4
9573	Transcriptome Profiling of the Leaf Spot Pathogen, <i>Pestalotiopsis trachicarpicola</i>, and Its Host, Tea (<i>Camellia sinensis</i>), During Infection. Plant Disease, 2022, 106, 2247-2252.	0.7	4
9575	SMRT Sequencing Reveals Candidate Genes and Pathways With Medicinal Value in Cipangopaludina chinensis. Frontiers in Genetics, 0, 13, .	1.1	1
9576	Comparative Genomic Analyses Provide Insight Into the Pathogenicity of Metschnikowia bicuspidata LNES0119. Frontiers in Microbiology, 0, 13, .	1.5	7
9577	Identification of Genes Related to Hair Follicle Cycle Development in Inner Mongolia Cashmere Goat by WGCNA. Frontiers in Veterinary Science, 0, 9, .	0.9	9
9578	Antennal transcriptome analysis of olfactory genes and tissue expression profiling of odorant binding proteins in Semanotus bifasciatus (cerambycidae: coleoptera). BMC Genomics, 2022, 23, .	1.2	5
9579	Human Follicular Mites: Ectoparasites Becoming Symbionts. Molecular Biology and Evolution, 2022, 39, .	3.5	6
9580	Transcriptome Analysis and Identification of a Female-Specific SSR Marker in Pistacia chinensis Based on Illumina Paired-End RNA Sequencing. Genes, 2022, 13, 1024.	1.0	3
9581	Astaxanthin and eicosapentaenoic acid production by S4, a new mutant strain of Nannochloropsis gaditana. Microbial Cell Factories, 2022, 21, .	1.9	9
9582	Adaptation insights from comparative transcriptome analysis of two Opisthopappus species in the Taihang mountains. BMC Genomics, 2022, 23, .	1.2	3
9583	Accumulation of endosymbiont genomes in an insect autosome followed by endosymbiont replacement. Current Biology, 2022, 32, 2786-2795.e5.	1.8	8
9584	Functional Heterogeneity of the Young and Old Duplicate Genes in Tung Tree (Vernicia fordii). Frontiers in Plant Science, 0, 13, .	1.7	1
9585	Transcript Complexity and New Insights of Restorer Line in CMS-D8 Cotton Through Full-Length Transcriptomic Analysis. Frontiers in Plant Science, 0, 13, .	1.7	1
9586	Genomic and transcriptomic analyses of Bacillus methylotrophicus NJ13 reveal a molecular response strategy combating Ilyonectria robusta causing ginseng rusty root rot. Biological Control, 2022, , 104972.	1.4	6
9587	Co-Expression Analysis Reveals Differential Expression of Homologous Genes Associated with Specific Terpenoid Biosynthesis in Rehmannia glutinosa. Genes, 2022, 13, 1092.	1.0	3
9588	Integrated Methylome and Transcriptome Analysis Provides Insights into the DNA Methylation Underlying the Mechanism of Cytoplasmic Male Sterility in Kenaf (Hibiscus cannabinus L.). International Journal of Molecular Sciences, 2022, 23, 6864.	1.8	3
9589	Comparative Small RNA and Degradome Sequencing Provides Insights into Antagonistic Interactions in the Biocontrol Fungus Clonostachys rosea. Applied and Environmental Microbiology, 2022, 88, .	1.4	5

#	Article	IF	Citations
9590	MicroSugar: A database of comprehensive miRNA target prediction framework for sugarcane (Saccharum officinarum L.). Genomics, 2022, , 110420.	1.3	1
9591	piRNA-like small RNAs target transposable elements in a Clade IV parasitic nematode. Scientific Reports, 2022, 12, .	1.6	4
9592	De novo assembly provides new insights into the evolution of Elaeagnus angustifolia L.. Plant Methods, 2022, 18, .	1.9	3
9593	The Role of Intestinal Microbial Metabolites in the Immunity of Equine Animals Infected With Horse Botflies. Frontiers in Veterinary Science, 0, 9, .	0.9	2
9594	Comparative Transcriptome Analysis Provides Insights Into the Mechanism by Which 2,4-Dichlorophenoxyacetic Acid Improves Thermotolerance in Lentinula edodes. Frontiers in Microbiology, 0, 13, .	1.5	2
9595	Draft genome sequence and functional analysis of Lysinibacillus xylanilyticus t26, a plant growth-promoting bacterium isolated from Capsicum chinense rhizosphere. Journal of Biosciences, 2022, 47, .	0.5	2
9596	A Transcriptomic Atlas Underlying Developmental Plasticity of Seasonal Forms of <i>Bicyclus anynana</i> Butterflies. Molecular Biology and Evolution, 2022, 39, .	3.5	9
9597	Phylogenomic and functional characterization of an evolutionary conserved cytochrome P450-based insecticide detoxification mechanism in bees. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	31
9598	Physiological and Transcriptomic Responses of Illicium difengpi to Drought Stress. Sustainability, 2022, 14, 7479.	1.6	4
9599	Integrated metabolomic and transcriptomic analysis reveals variation in the metabolites and genes of <scp><i>Platycodon grandiflorus</i></scp> roots from different regions. Phytochemical Analysis, 2022, 33, 982-994.	1.2	3
9600	Sugarcane Root Transcriptome Analysis Revealed the Role of Plant Hormones in the Colonization of an Endophytic Diazotroph. Frontiers in Microbiology, 0, 13, .	1.5	3
9601	Genome structure and evolutionary history of frankincense producing Boswellia sacra. IScience, 2022, 25, 104574.	1.9	3
9602	Comparative genomics analysis of Bacillus velezensis LOH112 isolated from a nonagenarian provides insights into its biocontrol and probiotic traits. Gene, 2022, 835, 146644.	1.0	4
9603	Differential responses of bloom-forming Ulva intestinalis and economically important Gracilariopsis lemaneiformis to marine heatwaves under changing nitrate conditions. Science of the Total Environment, 2022, 840, 156591.	3.9	13
9604	Deciphering key regulators of Inonotus hispidus petroleum ether extract involved in anti-tumor through whole transcriptome and proteome analysis in H22 tumor-bearing mice model. Journal of Ethnopharmacology, 2022, 296, 115468.	2.0	8
9605	Effect of Climate Change on Abiotic Stress Response Gene Networks in Arabidopsis thaliana. , 2022, , 149-172.		2
9607	Transcriptional and Toxic Responses to Saxitoxin Exposure in the Marine Copepod Tigriopus Japonicus Hye-Min Kang, Jihoon Lee, Yeon-Ju Lee, Yeun Park, Euihyeon Lee, A-Young Shin, Jeonghoon Han, Hyi-Seung Lee, Jong Seok Lee, and Kyun-Woo Lee* Marine Biotechnology Research Center, Korea Institute of Ocean Science and Technology, Busan 49111, South Korea. SSRN Electronic Journal, 0, , .	0.4	0
9608	Conserved secreted effectors contribute to endophytic growth and multihost plant compatibility in a vascular wilt fungus. Plant Cell, 2022, 34, 3214-3232.	3.1	20

#	ARTICLE	IF	CITATIONS
9609	The Genome of the Marine Alga Ulva compressa (Chlorophyta) Reveals Protein-Coding Genes with Similarity to Plants and Green Microalgae, but Also to Animal, Bacterial, and Fungal Genes. International Journal of Molecular Sciences, 2022, 23, 7279.	1.8	8
9610	High-Temperature Stress Effect on the Red Cusk-Eel (Geypterus chilensis) Liver: Transcriptional Modulation and Oxidative Stress Damage. Biology, 2022, 11, 990.	1.3	8
9612	Chromosomal Assembly of the Hexagrammos agrammus Genome via Third-Generation DNA Sequencing and Hi-C Technology. Frontiers in Marine Science, 0, 9, .	1.2	0
9613	Systematic Functional Annotation Workflow for Insects. Insects, 2022, 13, 586.	1.0	12
9614	Functional characteristics of EST-SSR markers available for Scots pine. Mathematical Biology and Bioinformatics, 2022, 17, 82-155.	0.1	2
9615	Genome-Wide Evolutionary Analysis of Putative Non-Specific Herbicide Resistance Genes and Compilation of Core Promoters between Monocots and Dicots. Genes, 2022, 13, 1171.	1.0	5
9616	Proteomic Profiling of Black Coral (Antipatharia) Skeleton Reveals Hundreds of Skeleton-Associated Proteins Across Two Taxa. Frontiers in Marine Science, 0, 9, .	1.2	1
9617	Genome Assembly and Analysis of the Flavonoid and Phenylpropanoid Biosynthetic Pathways in Fingerroot Ginger (Boesenbergia rotunda). International Journal of Molecular Sciences, 2022, 23, 7269.	1.8	1
9618	Draft Genome of Tanacetum Coccineum: Genomic Comparison of Closely Related Tanacetum-Family Plants. International Journal of Molecular Sciences, 2022, 23, 7039.	1.8	1
9619	Transcriptome sequencing and signal transduction for the enhanced tanshinone production in <i>Salvia miltiorrhiza</i> hairy roots induced by <i>Trichoderma atroviride</i> D16 polysaccharide fraction. Bioscience, Biotechnology and Biochemistry, 0, , .	0.6	2
9620	Differentially Expressed Transcription Factors during Male and Female Cone Development in Pinus halepensis. Agronomy, 2022, 12, 1588.	1.3	2
9621	The Chromosome-Level Genome of Elaeagnus moorcroftii Wall., an Economically and Ecologically Important Tree Species in Drylands. Diversity, 2022, 14, 468.	0.7	3
9622	New insights into cypermethrin insecticide resistance mechanisms of <i>Culex pipiens pallens</i> by proteome analysis. Pest Management Science, 2022, 78, 4579-4588.	1.7	2
9623	Salinity Fluctuation on the Genetic Regulatory Mechanisms of the Crustacean, Charybdis japonica. Frontiers in Marine Science, 0, 9, .	1.2	3
9624	Analysis of Transcriptome and Terpene Constituents of Scots Pine Genotypes Inherently Resistant or Susceptible to Heterobasidion annosum. Frontiers in Plant Science, 0, 13, .	1.7	1
9626	Transcriptome Dynamics of an Oyster Larval Response to a Conspecific Cue-Mediated Settlement Induction in the Pacific Oyster Crassostrea gigas. Diversity, 2022, 14, 559.	0.7	3
9627	Ripening of Pomegranate Skin as Revealed by Developmental Transcriptomics. Cells, 2022, 11, 2215.	1.8	2
9629	Chromosomeâ€level genome assembly defines femaleâ€biased genes associated with sex determination and differentiation in the human blood fluke <i>Schistosoma japonicum</i>. Molecular Ecology Resources, 0, , .	2.2	1

#	Article	IF	Citations
9632	Identification of Chemosensory Genes, Including Candidate Pheromone Receptors, in Phauda flammans (Walker) (Lepidoptera: Phaudidae) Through Transcriptomic Analyses. Frontiers in Physiology, 0, 13, .	1.3	4
9633	Plant Foraging Strategies Driven by Distinct Genetic Modules: Cross-Ecosystem Transcriptomics Approach. Frontiers in Plant Science, 0, 13, .	1.7	0
9634	Toxicological and transcriptomic effects in <i>Mythimna separata</i> (Lepidoptera: Noctuidae) exposed to chlorantraniliprole and functional characterization of glutathione Sâ€transferases. Pest Management Science, 2022, 78, 4517-4532.	1.7	9
9635	Transcriptome of the coralline alga Calliarthron tuberculosum (Corallinales, Rhodophyta) reveals convergent evolution of a partial lignin biosynthesis pathway. PLoS ONE, 2022, 17, e0266892.	1.1	4
9637	SbWRKY55 regulates sorghum response to saline environment by its dual role in abscisic acid signaling. Theoretical and Applied Genetics, 2022, 135, 2609-2625.	1.8	7
9638	Differentiation and Temperature Adaptation of Pampus Echinogaster Based on Genome-Wide SNPs. Frontiers in Marine Science, 0, 9, .	1.2	1
9639	Transcriptomic Insight into Viviparous Growth in Water Lily. BioMed Research International, 2022, 2022, 1-18.	0.9	0
9640	Identification and Functional Prediction of Poplar Root circRNAs Involved in Treatment With Different Forms of Nitrogen. Frontiers in Plant Science, 0, 13, .	1.7	2
9641	Sex-Specific Transcriptomic Differences in the Immune Cells of a Key Atlantic-Mediterranean Sea Urchin. Frontiers in Marine Science, 0, 9, .	1.2	1
9642	Partial root-zone simulated drought induces greater flavonoid accumulation than full root-zone simulated water deficiency in the leaves of Ginkgo biloba. Environmental and Experimental Botany, 2022, 201, 104998.	2.0	9
9643	Revealing the difference of Î±-amylase and CYP6AE76 gene between polyphagous Conogethes punctiferalis and oligophagous C. pinicolalis by multiple-omics and molecular biological technique. BMC Genomics, 2022, 23, .	1.2	1
9644	Comparison of gene expression profiles among caste differentiations in the termite Reticulitermes speratus. Scientific Reports, 2022, 12, .	1.6	8
9645	Transcriptional responses in Ecklonia cava to short-term exposure to polycyclic aromatic hydrocarbons. Molecular and Cellular Toxicology, 2022, 18, 629-636.	0.8	2
9646	Transcriptional responses are oriented towards different components of the rearing environment in two Drosophila sibling species. BMC Genomics, 2022, 23, .	1.2	5
9647	Transcriptome comparison for identification of pigmentation-related genes in different color varieties of Siamese fighting fish Betta splendens. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, , 101014.	0.4	1
9648	Gene function prediction in five model eukaryotes exclusively based on gene relative location through machine learning. Scientific Reports, 2022, 12, .	1.6	1
9649	Full-Length Transcriptome Sequencing Reveals Alternative Splicing and lncRNA Regulation during Nodule Development in Glycine max. International Journal of Molecular Sciences, 2022, 23, 7371.	1.8	6
9650	A panâ€genome and chromosomeâ€length reference genome of narrowâ€leafed lupin (<i>Lupinus) Tj ETQq1 1 0.784314 rgBT /Over Journal, 0, , .	2.8	9

#	ARTICLE	IF	CITATIONS
9651	Transcriptome-wide characterization, evolutionary analysis, and expression pattern analysis of the NF-Y transcription factor gene family and salt stress response in Panax ginseng. BMC Plant Biology, 2022, 22, .	1.6	7
9652	Dynamicity of histone H3K27ac and H3K27me3 modifications regulate the cold-responsive gene expression in Oryza sativa L. ssp. indica. Genomics, 2022, 114, 110433.	1.3	10
9654	Spruce gigaâ€genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. Plant Journal, 2022, 111, 1469-1485.	2.8	17
9655	Patterns of gene expression in ovaries of sexual vs. asexual lineages of a freshwater snail. Frontiers in Ecology and Evolution, 0, 10, .	1.1	0
9656	Integrated Analysis of Single-Molecule Real-Time Sequencing and Next-Generation Sequencing Eveals Insights into Drought Tolerance Mechanism of Lolium multiflorum. International Journal of Molecular Sciences, 2022, 23, 7921.	1.8	4
9657	Transcriptional profiling between yellow- and black-seeded Brassica napus reveals molecular modulations on flavonoid and fatty acid content. Journal of Integrative Agriculture, 2022, 21, 2211-2226.	1.7	5
9658	Comparative transcriptome analysis on the mangrove Acanthus ilicifolius and its two terrestrial relatives provides insights into adaptation to intertidal habitats. Gene, 2022, 839, 146730.	1.0	3
9659	Responses to submergence and recovery in seedlings of the rheophyte Dyckia brevifolia (Bromeliaceae). Environmental and Experimental Botany, 2022, 201, 104984.	2.0	1
9660	In silico identification of rice and human miRNAs sequences within tRFs of Oryza sativa and expression analysis of rice tRFs with their corresponding miRNAs. South African Journal of Botany, 2022, 149, 487-495.	1.2	0
9661	Transcriptome and Metabonomic Analysis of Tamarix ramosissima Potassium (K+) Channels and Transporters in Response to NaCl Stress. Genes, 2022, 13, 1313.	1.0	12
9662	Comparative transcriptome analysis revealed candidate genes involved in fruiting body development and sporulation in Ganoderma lucidum. Archives of Microbiology, 2022, 204, .	1.0	7
9663	Multi-Locus Genome-Wide Association Studies to Characterize Fusarium Head Blight (FHB) Resistance in Hard Winter Wheat. Frontiers in Plant Science, 0, 13, .	1.7	5
9664	Comparative transcriptome analysis unveiling reactive oxygen species scavenging system of Sonneratia caseolaris under salinity stress. Frontiers in Plant Science, 0, 13, .	1.7	5
9665	An apple somatic mutation of delayed fruit maturation date is primarily caused by a retrotransposon insertionâ€associated large deletion. Plant Journal, 2022, 111, 1609-1625.	2.8	4
9666	The SWC4 subunit of the SWR1 chromatin remodeling complex is involved in varying virulence of<i>Metarhizium brunneum</i>isolates offering role of epigenetic regulation of pathogenicity. Virulence, 2022, 13, 1252-1269.	1.8	5
9667	Gene expression profiling before and after internode culture for adventitious shoot formation in ipecac. BMC Plant Biology, 2022, 22, .	1.6	1
9668	Differential Transcriptomic Profiles Following Stimulation with Lipopolysaccharide in Intestinal Organoids from Dogs with Inflammatory Bowel Disease and Intestinal Mast Cell Tumor. Cancers, 2022, 14, 3525.	1.7	20
9670	Analysis of Growth Phases of Enterotoxigenic Escherichia coli Reveals a Distinct Transition Phase before Entry into Early Stationary Phase with Shifts in Tryptophan, Fucose, and Putrescine Metabolism and Degradation of Neurotransmitter Precursors. Microbiology Spectrum, 2022, 10, .	1.2	5

#	Article	IF	Citations
9671	Whole genome sequencing of the multidrug-resistant Chryseobacterium indologenes isolated from a patient in Brazil. Frontiers in Medicine, 0, 9, .	1.2	7
9672	Chromosome-level genome of Tibetan naked carp (<i>Gymnocypris przewalskii</i>) provides insights into Tibetan highland adaptation. DNA Research, 2022, 29, .	1.5	9
9673	The genome of the mustard hill coral, Porites astreoides. GigaByte, 0, 2022, 1-12.	0.0	4
9674	RNA-Seq Provides Insights into the Mechanisms Underlying Ilyonectria robusta Responding to Secondary Metabolites of Bacillus methylotrophicus NJ13. Journal of Fungi (Basel, Switzerland), 2022, 8, 779.	1.5	2
9675	Fatty Acid Accumulations and Transcriptome Analyses Under Different Treatments in a Model Microalga Euglena gracilis. Frontiers in Chemical Engineering, 0, 4, .	1.3	0
9676	Transcriptome analysis reveals candidate genes related to steroid alkaloid biosynthesis in <i>Fritillaria anhuiensis</i>. Physiologia Plantarum, 2022, 174, .	2.6	2
9677	Blood transcriptome analysis revealing aging gene expression profiles in red panda. PeerJ, 0, 10, e13743.	0.9	0
9678	Validated Growth Rate-Dependent Regulation of Lipid Metabolism in Yarrowia lipolytica. International Journal of Molecular Sciences, 2022, 23, 8517.	1.8	8
9679	Jasmonic acid pretreatment improves salt tolerance of wheat by regulating hormones biosynthesis and antioxidant capacity. Frontiers in Plant Science, 0, 13, .	1.7	6
9680	Cytokinin Regulates Energy Utilization in Botrytis cinerea. Microbiology Spectrum, 2022, 10, .	1.2	4
9681	Identification of Heat-Tolerant Genes in Non-Reference Sequences in Rice by Integrating Pan-Genome, Transcriptomics, and QTLs. Genes, 2022, 13, 1353.	1.0	2
9682	Functional Annotation, Prediction of <i>Cis</i> Target Gene for the Sequence of mRNAs, and Candidate Long Noncoding RNAs from Tea (<i>Camellia sinensis</i> var. <i>sinensis</i>) Leaves During Infection by the Fungal Pathogen <i>EpicoccumÂnigrum</i>. PhytoFrontiers, 0, , .	0.8	0
9683	Osmoregulatory strategies of estuarine fish Scatophagus argus in response to environmental salinity changes. BMC Genomics, 2022, 23, .	1.2	2
9686	24-Epibrassinolide Promotes Fatty Acid Accumulation and the Expression of Related Genes in Styrax tonkinensis Seeds. International Journal of Molecular Sciences, 2022, 23, 8897.	1.8	5
9687	Transcriptome Analysis of Eggplant under Salt Stress: AP2/ERF Transcription Factor SmERF1 Acts as a Positive Regulator of Salt Stress. Plants, 2022, 11, 2205.	1.6	15
9688	Molecular mechanisms underlying iron and phosphorus co-limitation responses in the nitrogen-fixing cyanobacterium <i>Crocosphaera</i>. ISME Journal, 2022, 16, 2702-2711.	4.4	9
9690	Shewanella shenzhenensis sp. nov., a novel Fe(III)-reducing bacterium with abundant possible cytochrome genes, isolated from mangrove sediment. Antonie Van Leeuwenhoek, 2022, 115, 1245-1252.	0.7	2
9691	A Polyketide Synthetase Gene Cluster Is Responsible for Antibacterial Activity of <i>Burkholderia contaminans</i> MS14. Phytopathology, 2023, 113, 11-20.	1.1	2

#	Article	IF	Citations
9692	Analysis of Amino Acids in the Roots of Tamarix ramosissima by Application of Exogenous Potassium (K+) under NaCl Stress. International Journal of Molecular Sciences, 2022, 23, 9331.	1.8	8
9693	Comparative Transcriptome Analysis Reveals Gene Expression Differences in Eggplant (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.9	3
9694	The cAMP-PKA pathway regulates prey sensing and trap morphogenesis in the nematode-trapping fungus <i>Arthrobotrys oligospora</i>. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
9695	Transcriptome-wide N6-methyladenosine (m6A) methylation in soybean under Meloidogyne incognita infection. ABIOTECH, 0, , .	1.8	2
9696	Comparative transcriptome analysis reveals the nonâ€neuronal cholinergic system in the ovary of the oriental armyworm, <i>Mythimna separata</i> Walker (Lepidoptera: Noctuidae). Pest Management Science, 2022, 78, 5220-5233.	1.7	3
9697	Deciphering the transcriptomic response of <i>Ilyonectria robusta</i> in relation to ginsenoside Rg1 treatment and the development of ginseng rusty root rot. FEMS Microbiology Letters, 2022, 369, .	0.7	3
9698	TinoTranscriptDB: A Database of Transcripts and Microsatellite Markers of Tinospora cordifolia, an Important Medicinal Plant. Genes, 2022, 13, 1433.	1.0	7
9699	Comparative transcriptome and metabolome analyses identified the mode of sucrose degradation as a metabolic marker for early vegetative propagation in bulbs of <i>Lycoris</i>. Plant Journal, 2022, 112, 115-134.	2.8	13
9700	Transcriptomic Response of the Diazotrophic Bacteria Gluconacetobacter diazotrophicus Strain PAL5 to Iron Limitation and Characterization of the fur Regulatory Network. International Journal of Molecular Sciences, 2022, 23, 8533.	1.8	3
9701	Whole genome assembly of the armored loricariid catfish Ancistrus triradiatus highlights herbivory signatures. Molecular Genetics and Genomics, 2022, 297, 1627-1642.	1.0	1
9702	Characterization and analysis of the promoter region of monodehydroascorbate reductase 4 (CpMDAR4) in papaya. Plant Reproduction, 0, , .	1.3	0
9704	Comparative Transcriptome Analysis of Deep-Rooting and Shallow-Rooting Potato (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.6	1
9705	Whole-genome analysis of hard winter wheat germplasm identifies genomic regions associated with spike and kernel traits. Theoretical and Applied Genetics, 2022, 135, 2953-2967.	1.8	7
9706	Characterization of â€˜<i>QTL-hotspot</i>â€™ introgression lines reveals physiological mechanisms and candidate genes associated with drought adaptation in chickpea. Journal of Experimental Botany, 2022, 73, 7255-7272.	2.4	20
9708	Developmental RNA-Seq transcriptomics of haploid germ cells and spermatozoa uncovers novel pathways associated with teleost spermiogenesis. Scientific Reports, 2022, 12, .	1.6	3
9709	Identification of a genomic region containing genes involved in resistance to four pathotypes of <i>Plasmodiophora brassicae</i> in <i>Brassica rapa</i> turnip ECD02. Plant Genome, 2022, 15, .	1.6	2
9710	Pulmonate slug evolution is reflected in the de novo genome of Arion vulgaris Moquin-Tandon, 1855. Scientific Reports, 2022, 12, .	1.6	2
9712	Comparative Transcriptome Analysis on the Regulatory Mechanism of Thoracic Ganglia in Eriocheir sinensis at Post-Molt and Inter-Molt Stages. Life, 2022, 12, 1181.	1.1	2

#	Article	IF	Citations
9713	Cystathionine Gamma-Lyase Regulate Psilocybin Biosynthesis in Gymnopilus dilepis Mushroom via Amino Acid Metabolism Pathways. Journal of Fungi (Basel, Switzerland), 2022, 8, 870.	1.5	0
9714	A pan-Zea genome map for enhancing maize improvement. Genome Biology, 2022, 23, .	3.8	21
9715	Transcriptome profiling of Toona ciliata young stems in response to Hypsipyla robusta Moore. Frontiers in Plant Science, 0, 13, .	1.7	1
9716	Transcriptome and biochemical response to 60Co gamma radiation exposure on the grafted seedlings of Paeonia suffruticosa. Acta Physiologiae Plantarum, 2022, 44, .	1.0	1
9718	De novo transcriptome assembly reveals characteristics of flower sex determination of Excoecaria agallocha. Annals of Forest Science, 2022, 79, .	0.8	0
9719	Distinct composition and amplification dynamics of transposable elements in sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). Plant Journal, 2022, 112, 172-192.	2.8	2
9720	Insights into adaptive divergence of Japanese mantis shrimp Oratosquilla oratoria inferred from comparative analysis of full-length transcriptomes. Frontiers in Marine Science, 0, 9, .	1.2	3
9721	Effects of Exogenous Potassium (K+) Application on the Antioxidant Enzymes Activities in Leaves of Tamarix ramosissima under NaCl Stress. Genes, 2022, 13, 1507.	1.0	3
9722	Transcriptome analysis of different life-history stages and screening of male-biased genes in Daphnia sinensis. BMC Genomics, 2022, 23, .	1.2	3
9723	Endophytic bacterium Bacillus aryabhattai induces novel transcriptomic changes to stimulate plant growth. PLoS ONE, 2022, 17, e0272500.	1.1	10
9724	Comparative transcriptome analysis, unfolding the pathways regulating the seed-size trait in cultivated lentil (Lens culinaris Medik.). Frontiers in Genetics, 0, 13, .	1.1	9
9725	Adaptive radiation in Orinus, an endemic alpine grass of the Qinghai-Tibet Plateau, based on comparative transcriptomic analysis. Journal of Plant Physiology, 2022, 277, 153786.	1.6	1
9726	Characterization of a new Bacillus velezensis as a powerful biocontrol agent against tomato gray mold. Pesticide Biochemistry and Physiology, 2022, 187, 105199.	1.6	9
9727	Genome-wide identification of genes enabling accurate prediction of hybrid performance from parents across environments and populations for gene-based breeding in maize. Plant Science, 2022, 324, 111424.	1.7	2
9728	Identification of candidate genes associated with sex differentiation and determination of gender diphasic plant Lilium apertum (Liliaceae). Scientia Horticulturae, 2022, 306, 111431.	1.7	1
9729	Common and novel metabolic pathways related ESTs were upregulated in three date palm cultivars to ameliorate drought stress. Scientific Reports, 2022, 12, .	1.6	2
9730	Integrative functional analysis uncovers metabolic differences between Candida species. Communications Biology, 2022, 5, .	2.0	4
9731	Single-molecule Real-time (SMRT) Sequencing Facilitates Transcriptome Research and Genome Annotation of the Fish Sillago sinica. Marine Biotechnology, 2022, 24, 1002-1013.	1.1	1

#	Article	IF	Citations
9732	FgCsn12 Is Involved in the Regulation of Ascosporogenesis in the Wheat Scab Fungus Fusarium graminearum. International Journal of Molecular Sciences, 2022, 23, 10445.	1.8	1
9733	High-Density Genetic Linkage Map Construction and QTLs Identification Associated with Four Leaf-Related Traits in Ladyâ€™s Slipper Orchids (Paphiopedilum concolor Ã— Paphiopedilum hirsutissimum). Horticulturae, 2022, 8, 842.	1.2	3
9734	A butterfly pan-genome reveals that a large amount of structural variation underlies the evolution of chromatin accessibility. Genome Research, 2022, 32, 1862-1875.	2.4	10
9735	Transcriptome analysis of the spleen provides insight into the immunoregulation of Scortum barcoo under Streptococcus agalactiae infection. Ecotoxicology and Environmental Safety, 2022, 245, 114095.	2.9	8
9736	Contribution of anthocyanin and polyunsaturated fatty acid biosynthesis to cold tolerance during bud sprouting in tree peony. Industrial Crops and Products, 2022, 188, 115563.	2.5	2
9737	Butanol production from Thai traditional beverage (Sato) factory wastewater using newly isolated Clostridium beijerinckii CUEA02. Biochemical Engineering Journal, 2022, 187, 108648.	1.8	1
9738	Biocontrol of antifungal volatiles produced by Ceriporia lacerate HG2011 against citrus fruit rot incited by Penicillium spp.. Postharvest Biology and Technology, 2022, 194, 112094.	2.9	6
9739	Mitochondrial DNA polymorphisms in COX1 affect the lifespan of Caenorhabditis elegans through nuclear gene dct-15. Gene, 2022, 845, 146776.	1.0	1
9740	Enhancement of an efficient enzyme cocktail from Penicillium consortium on biodegradation of pretreated poplar. Chemical Engineering Journal, 2023, 452, 139352.	6.6	8
9741	Transcriptomic and metabolomic analyses reveal that MYB transcription factors regulate anthocyanin synthesis and accumulation in the disc florets of the anemone form of chrysanthemum morifolium. Scientia Horticulturae, 2023, 307, 110847.	1.7	6
9742	Comparative maternal protein profiling of mouse biparental and uniparental embryos. GigaScience, 2022, 11, .	3.3	3
9743	Transcriptome analysis identifies key genes involved in anthocyanin biosynthesis in black and purple fruits (<i>Lycium ruthenicum</i> Murr. L). Biotechnology and Biotechnological Equipment, 2022, 36, 553-560.	0.5	2
9744	Determining transcriptomic response of kidneys of olive flounder to viral hemorrhagic septicemia virus infection using next-generation sequencing. Aquaculture, 2023, 562, 738886.	1.7	1
9745	Analysis of the ASR and LP3 homologous gene families reveal positive selection acting on LP3-3 gene. Gene, 2023, 850, 146935.	1.0	2
9746	Epidemiology of Plasmid Lineages Mediating the Spread of Extended-Spectrum Beta-Lactamases among Clinical Escherichia coli. MSystems, 2022, 7, .	1.7	6
9747	Genomic Variations in the Tea Leafhopper Reveal the Basis of Its Adaptive Evolution. Genomics, Proteomics and Bioinformatics, 2022, 20, 1092-1105.	3.0	5
9748	Transcriptional Memory in Taraxacum mongolicum in Response to Long-Term Different Grazing Intensities. Plants, 2022, 11, 2251.	1.6	1
9749	Effects of Nutrient Elements on Growth and Expression of Insect-Defense Response Genes in Zanthoxylum bungeanum Maxim. Forests, 2022, 13, 1365.	0.9	2

#	Article	IF	Citations
9750	Gene expression and phytohormone levels in the asymptomatic and symptomatic phases of infection in potato tubers inoculated with Dickeya solani. PLoS ONE, 2022, 17, e0273481.	1.1	0
9751	Characterization and Comparison of Eye Development and Phototransduction Genes in Deep- and Shallow-Water Shrimp Alvinocaris longirostris and Palaemon carinicauda. Diversity, 2022, 14, 653.	0.7	2
9752	Comparative genome analysis unravels pathogenicity of Xanthomonas albilineans causing sugarcane leaf scald disease. BMC Genomics, 2022, 23, .	1.2	2
9753	Transcriptome analysis of five different tissues of bitter gourd (Momordica charantia L.) fruit identifies full-length genes involved in seed oil biosynthesis. Scientific Reports, 2022, 12, .	1.6	0
9754	Genome-wide analysis reveals allelic variation and chromosome copy number variation in paromomycin-resistant Leishmania donovani. Parasitology Research, 2022, 121, 3121-3132.	0.6	1
9755	Exploration of the regulatory mechanisms of regeneration, anti-oxidation, anti-aging and the immune response at the post-molt stage of Eriocheir sinensis. Frontiers in Physiology, 0, 13, .	1.3	0
9756	Terpenoids and their gene regulatory networks in Opisthopappus taihangensis â€˜Taihang Mingzhuâ€™ as detected by transcriptome and metabolome analyses. Frontiers in Plant Science, 0, 13, .	1.7	2
9757	Transcriptome analysis of the response to thyroid hormone in <i>Xenopus</i> neural stem and progenitor cells. Developmental Dynamics, 2023, 252, 294-304.	0.8	2
9758	Insights of auxin signaling F-box genes in wheat (Triticum aestivum L.) and their dynamic expression during the leaf rust infection. Protoplasma, 2023, 260, 723-739.	1.0	2
9759	Analysis of the Antennal Transcriptome and Identification of Tissue-specific Expression of Olfactory-related Genes in <i>Micromelalopha troglodyta</i> (Lepidoptera: Notodontidae). Journal of Insect Science, 2022, 22, .	0.6	0
9760	Physiological and transcriptional responses of seed germination to moderate drought in Apocynum venetum. Frontiers in Ecology and Evolution, 0, 10, .	1.1	2
9761	Meta-transcriptomic comparison of two sponge holobionts feeding on coral- and macroalgal-dissolved organic matter. BMC Genomics, 2022, 23, .	1.2	4
9762	Transcriptomic and proteomic analyses provide insights into the adaptive responses to the combined impact of salinity and alkalinity in Gymnocypris przewalskii. Bioresources and Bioprocessing, 2022, 9, .	2.0	3
9763	Differential effects of arbuscular mycorrhizal fungi on three saltâ€tolerant grasses under cadmium and salt stress. Land Degradation and Development, 2023, 34, 506-520.	1.8	5
9764	A non specific Lipid Transfer Protein with potential functions in infection and nodulation. Molecular Plant-Microbe Interactions, 0, , .	1.4	3
9765	Analysis of genome and methylation changes in Chinese indigenous chickens over time provides insight into species conservation. Communications Biology, 2022, 5, .	2.0	5
9766	Transcriptional Dynamics Induced by Diapause Hormone in the Silkworm, Bombyx mori. Biology, 2022, 11, 1313.	1.3	2
9767	Sequence Data, Functional Annotation, and Relationship Analysis Between mRNAs and Long Noncoding RNAs from Tea Leaves During Infection by the Fungal Pathogen <i>Epicoccum sorghinum</i>. Molecular Plant-Microbe Interactions, 2022, 35, 875-879.	1.4	0

#	Article	IF	Citations
9768	Integrated Metabolites and Transcriptomics at Different Growth Stages Reveal Polysaccharide and Flavonoid Biosynthesis in Cynomorium songaricum. International Journal of Molecular Sciences, 2022, 23, 10675.	1.8	1
9769	Identification of Putative Neuropeptides That Alter the Behaviour of Schistosoma mansoni Cercariae. Biology, 2022, 11, 1344.	1.3	1
9770	Transcriptional regulation of proanthocyanidin biosynthesis pathway genes and transcription factors in Indigofera stachyodes Lindl. roots. BMC Plant Biology, 2022, 22, .	1.6	0
9772	Comparative transcriptomics analyses of chemosensory genes of antenna in male red swamp crayfish Procambarus clarkii. Frontiers in Ecology and Evolution, 0, 10, .	1.1	3
9773	De novo transcriptome analysis of high-salinity stress-induced antioxidant activity and plant phytohormone alterations in Sesuvium portulacastrum. Frontiers in Plant Science, 0, 13, .	1.7	6
9774	Mycobacterium Time-Series Genome Analysis Identifies AAC2â€² as a Potential Drug Target with Naloxone Showing Potential Bait Drug Synergism. Molecules, 2022, 27, 6150.	1.7	7
9775	Whole-Genome Sequencing and Comparative Genomics Analysis of the Wild Edible Mushroom (Gomphus purpuraceus) Provide Insights into Its Potential Food Application and Artificial Domestication. Genes, 2022, 13, 1628.	1.0	4
9777	WGCNA Identifies a Comprehensive and Dynamic Gene Co-Expression Network That Associates with Smut Resistance in Sugarcane. International Journal of Molecular Sciences, 2022, 23, 10770.	1.8	18
9778	Bacillus velezensis strain Ag75 as a new multifunctional agent for biocontrol, phosphate solubilization and growth promotion in maize and soybean crops. Scientific Reports, 2022, 12, .	1.6	14
9779	Biochemical indices, gene expression, and SNPs associated with salinity adaptation in juvenile chum salmon (<i>Oncorhynchus keta</i>) as determined by comparative transcriptome analysis. PeerJ, 0, 10, e13585.	0.9	2
9780	Full-Length Transcriptome Sequencing Combined with RNA-Seq to Analyze Genes Related to Terpenoid Biosynthesis in Cinnamomum burmannii. Current Issues in Molecular Biology, 2022, 44, 4197-4215.	1.0	1
9781	Characterization of differentially expressed and lipid metabolism-related lncRNA-mRNA interaction networks during the growth of liver tissue through rabbit models. Frontiers in Veterinary Science, 0, 9, .	0.9	0
9782	Mining the Roles of Cucumber DUF966 Genes in Fruit Development and Stress Response. Plants, 2022, 11, 2497.	1.6	3
9783	Transcriptome sequencing and DEG analysis in different developmental stages of floral buds induced by potassium chlorate in <i>Dimocarpus longan</i>. Plant Biotechnology, 2022, 39, 259-272.	0.5	0
9784	Non-photoperiodic transition of female cannabis seedlings from juvenile to adult reproductive stage. Plant Reproduction, 0, , .	1.3	6
9785	Genome resequencing and transcriptome profiling reveal molecular evidence of tolerance to water deficit in barley. Journal of Advanced Research, 2023, 49, 31-45.	4.4	3
9786	Transcriptome analysis of mangrove-isolated Chlorella vulgaris UMT-M1 reveals insights for vigorous growth and lipid accumulation through reduced salinity. Algal Research, 2022, 67, 102833.	2.4	3
9787	Urbanization drives adaptive evolution in a Neotropical bird. Environmental Epigenetics, 0, , .	0.9	0

#	Article	IF	Citations
9788	Evolution of isoformâ€level gene expression patterns across tissues during lotus species divergence. Plant Journal, 2022, 112, 830-846.	2.8	1
9789	Dynamic Transcriptional Landscape of Grass Carp (Ctenopharyngodon idella) Reveals Key Transcriptional Features Involved in Fish Development. International Journal of Molecular Sciences, 2022, 23, 11547.	1.8	2
9790	Nutritional Component Analyses in Different Varieties of Actinidia eriantha Kiwifruit by Transcriptomic and Metabolomic Approaches. International Journal of Molecular Sciences, 2022, 23, 10217.	1.8	5
9791	Antagonistic potential of Trichoderma as a biocontrol agent against Sclerotinia asari. Frontiers in Microbiology, 0, 13, .	1.5	3
9792	Combined transcriptome and metabolite profiling analyses provide insights into the chronic toxicity of carbaryl and acetamiprid to Apis mellifera larvae. Scientific Reports, 2022, 12, .	1.6	3
9793	<i>De novo</i> genome assembly of the medicinal plant <i>Gentiana macrophylla</i> provides insights into the genomic evolution and biosynthesis of iridoids. DNA Research, 2022, 29, .	1.5	10
9794	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of Citrus grandis â€˜Tomentosaâ€™. Plant Science, 2022, 325, 111489.	1.7	7
9795	Comprehensive collection of genes and comparative analysis of full-length transcriptome sequences from Japanese larch (Larix kaempferi) and Kuril larch (Larix gmelinii var. japonica). BMC Plant Biology, 2022, 22, .	1.6	4
9797	Toxicity of chronic waterborne zinc exposure in the hepatopancreas of white shrimp Litopenaeus vannamei. Chemosphere, 2022, 309, 136553.	4.2	8
9798	Transcriptional and toxic responses to saxitoxin exposure in the marine copepod Tigriopus japonicus. Chemosphere, 2022, 309, 136464.	4.2	0
9799	GlycAP, a glycoproteomic analysis platform for site-specific N-glycosylation research. International Journal of Mass Spectrometry, 2022, 482, 116947.	0.7	1
9800	Profiling and Functional Analysis of long non-coding RNAs in yak healthy and atretic follicles. Animal Reproduction, 2022, 19, .	0.4	0
9801	Transcriptomic alterations in roots of two contrasting Coffea arabica cultivars after hexanoic acid priming. Frontiers in Genetics, 0, 13, .	1.1	1
9802	Identification of Arginine Phosphorylation in Mycolicibacterium smegmatis. Microbiology Spectrum, 2022, 10, .	1.2	6
9804	Survival virulent characteristics and transcriptomic analyses of Vibrio mimicus exposed to starvation. Frontiers in Marine Science, 0, 9, .	1.2	1
9805	A combined polygenic score of 21,293 rare and 22 common variants improves diabetes diagnosis based on hemoglobin A1C levels. Nature Genetics, 2022, 54, 1609-1614.	9.4	20
9806	Deciphering the mechanism of anhydrobiosis in the entomopathogenic nematode Heterorhabditis indica through comparative transcriptomics. PLoS ONE, 2022, 17, e0275342.	1.1	0
9807	Whole-Genome Sequencing and Transcriptome Analysis of Ganoderma lucidum Strain Yw-1-5 Provides New Insights into the Enhanced Effect of Tween80 on Exopolysaccharide Production. Journal of Fungi (Basel, Switzerland), 2022, 8, 1081.	1.5	4

#	Article	IF	Citations
9808	Effects of Glutamine Starvation on SHVV Replication by Quantitative Proteomics Analysis. Fishes, 2022, 7, 315.	0.7	0
9809	Quantitative Data-Independent Acquisition Mass Spectrometry Proteomics and Weighted Correlation Network Analysis of Plasma Samples for the Discovery of Chronic Kidney Disease-Specific Atherosclerosis Risk Factors. DNA and Cell Biology, 0, , .	0.9	0
9810	Potential Role of Lysine Acetylation in Antibiotic Resistance of Escherichia coli. MSystems, 2022, 7, .	1.7	4
9811	Identification of Schistosoma mansoni miracidia attractant candidates in infected Biomphalaria glabrata using behaviour-guided comparative proteomics. Frontiers in Immunology, 0, 13, .	2.2	2
9812	Characterization of <i>Pseudomonas</i> sp. NIBR-H-19, an Antimicrobial Secondary Metabolite Producer Isolated from the Gut of Korean Native Sea Roach, <i>Ligia exotica</i>. Journal of Microbiology and Biotechnology, 2022, 32, 1416-1426.	0.9	0
9813	De novo full length transcriptome analysis and gene expression profiling to identify genes involved in phenylethanol glycosides biosynthesis in Cistanche tubulosa. BMC Genomics, 2022, 23, .	1.2	5
9814	Genome-Wide Survey and Analysis of Microsatellites in Waterlily, and Potential for Polymorphic Marker Development. Genes, 2022, 13, 1782.	1.0	0
9815	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. Nature Communications, 2022, 13, .	5.8	28
9816	Data-independent acquisition-based quantitative proteomic analysis of m.3243A>G MELAS reveals novel potential pathogenesis and therapeutic targets. Medicine (United States), 2022, 101, e30938.	0.4	0
9817	Genome Resource of Rhizoctonia solani anastomosis group 4 strain AG4-JY, a pathomycete of sheath blight of foxtail millet. Plant Disease, 0, , .	0.7	0
9818	Insight into the regulatory networks underlying the high lipid perennial ryegrass growth under different irradiances. PLoS ONE, 2022, 17, e0275503.	1.1	1
9819	Transcriptome analysis of MYB transcription factors family and PgMYB genes involved in salt stress resistance in Panax ginseng. BMC Plant Biology, 2022, 22, .	1.6	8
9821	CuGenDBv2: an updated database for cucurbit genomics. Nucleic Acids Research, 2023, 51, D1457-D1464.	6.5	33
9822	EpichloÃ« seed transmission efficiency is influenced by plant defense response mechanisms. Frontiers in Plant Science, 0, 13, .	1.7	3
9823	Whole-Genome Sequencing of <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> Strain Race-4 Infecting Cucumber in China. Plant Disease, 2023, 107, 1210-1213.	0.7	1
9824	High-quality genome resource of a novel Venturiaceae sp. KMAF11, isolated from diseased Colobanthus quitensis, an Antarctic flowering plant. Plant Disease, 0, , .	0.7	0
9827	De-novo genome assembly and annotation of sobaity seabream Sparidentex hasta. Frontiers in Genetics, 0, 13, .	1.1	1
9828	Transcriptome analysis of hepatopancreas and gills of Palaemon gravieri under salinity stress. Gene, 2023, 851, 147013.	1.0	0

#	Article	IF	Citations
9829	Transcriptome profiling of lung immune responses potentially related to acute respiratory distress syndrome in forest musk deer. BMC Genomics, 2022, 23, .	1.2	0
9830	Transcriptome Analysis of Persian Oak (Quercus brantii L.) Decline Using RNA-seq Technology. Biochemical Genetics, 0, , .	0.8	0
9831	Comparative proteomic profiles of Schistosoma japonicum male worms derived from single-sex and bisexual infections. International Journal for Parasitology, 2022, 52, 815-828.	1.3	3
9833	Integrated Analysis of Transcriptome and microRNA Profile Reveals the Toxicity of Euphorbia Factors toward Human Colon Adenocarcinoma Cell Line Caco-2. Molecules, 2022, 27, 6931.	1.7	2
9834	Genome-Wide Analysis and Characterization of SABATH Gene Family in Phaseolus vulgaris Genotypes Subject to Melatonin under Drought and Salinity Stresses. Plant Molecular Biology Reporter, 2023, 41, 242-259.	1.0	5
9835	Next Generation Sequencing and Comparative Genomic Analysis Reveal Extreme Plasticity of Two Burkholderia glumae Strains HN1 and HN2. Pathogens, 2022, 11, 1265.	1.2	0
9836	CRISPR-based oligo recombineering prioritizes apicomplexan cysteines for drug discovery. Nature Microbiology, 2022, 7, 1891-1905.	5.9	13
9837	De Novo Assembly of a Sarcocarp Transcriptome Set Identifies AaMYB1 as a Regulator of Anthocyanin Biosynthesis in Actinidia arguta var. purpurea. International Journal of Molecular Sciences, 2022, 23, 12120.	1.8	0
9838	Transcriptome Sequencing Reveals Pathways Related to Proliferation and Differentiation of Shitou Goose Myoblasts. Animals, 2022, 12, 2956.	1.0	5
9840	HiFi chromosome-scale diploid assemblies of the grape rootstocks 110R, Kober 5BB, and 101â€“14 Mgt. Scientific Data, 2022, 9, .	2.4	6
9841	GPI-Anchored Protein Homolog IcFBR1 Functions Directly in Morphological Development of Isaria cicadae. Journal of Fungi (Basel, Switzerland), 2022, 8, 1152.	1.5	1
9842	PacBio full-length sequencing integrated with RNA-seq reveals the molecular mechanism of waterlogging and its recovery in Paeonia ostii. Frontiers in Plant Science, 0, 13, .	1.7	1
9843	In silico genomic analysis of the potential probiotic Lactiplantibacillus pentosus CF2-10N reveals promising beneficial effects with health promoting properties. Frontiers in Microbiology, 0, 13, .	1.5	6
9845	Increased levels of cell wall degrading enzymes and peptidases are associated with aggressiveness in a virulent isolate of Pyrenophora teres f. maculata. Journal of Plant Physiology, 2022, 279, 153839.	1.6	2
9846	Deep into the Apoplast: Grapevine and <i>Plasmopara viticola</i> Proteomes Reveal the Secret Beneath Host and Pathogen Communication at 6 h After Contact. Phytopathology, 2023, 113, 893-903.	1.1	2
9847	Immune function modulation during artificial ovarian maturation in Japanese eel (Anguilla japonica): A transcriptome profiling approach. Fish and Shellfish Immunology, 2022, 131, 662-671.	1.6	3
9848	Polystyrene microplastic ingestion induces the damage in digestive gland of Amphioctopus fangsiao at the physiological, inflammatory, metabolome and transcriptomic levels. Environmental Pollution, 2022, 315, 120480.	3.7	7
9849	Full-Length Transcriptome Analysis of Cultivated and Wild Tetraploid Peanut. Phyton, 2023, 92, 439-453.	0.4	0

#	Article	IF	Citations
9850	Whole transcriptome analysis identifies full-length genes for neoandrographolide biosynthesis from Andrographis alata, an alternate source for antiviral compounds. Gene, 2023, 851, 146981.	1.0	1
9851	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (Scatophagus tetracanthus). Aquaculture, 2023, 563, 739023.	1.7	1
9852	Proteome analysis of Campylobacter jejuni poultry strain 2704 survival during 45Âmin exposure to peracetic acid. International Journal of Food Microbiology, 2023, 385, 110000.	2.1	1
9853	Comparing adventitious root-formation and graft-unification abilities in clones of Argania spinosa. Frontiers in Plant Science, 0, 13, .	1.7	2
9854	Morphological and transcriptomic analysis revealing morphological variations and genetic clues in one <i>Lentinula edodes</i> abnormal browning strain. Journal of Basic Microbiology, 0, , .	1.8	0
9855	Transcriptome Profiling of the Resistance Response of Musa acuminata subsp. burmannicoides, var. Calcutta 4 to Pseudocercospora musae. International Journal of Molecular Sciences, 2022, 23, 13589.	1.8	3
9856	Effects of trichothecene production by Trichoderma arundinaceum isolates from bean-field soils on the defense response, growth and development of bean plants (Phaseolus vulgaris). Frontiers in Plant Science, 0, 13, .	1.7	1
9857	Avirulent phenotype promotes <i>Bordetella pertussis</i> adaptation to the intramacrophage environment. Emerging Microbes and Infections, 2023, 12, .	3.0	3
9858	Transcriptome Profiling of Stem-Differentiating Xylem in Response to Abiotic Stresses Based on Hybrid Sequencing in Cunninghamia lanceolata. International Journal of Molecular Sciences, 2022, 23, 13986.	1.8	1
9859	Population structure of sumac (Rhus coriaria L.) from TÃ¼rkiye based on transcriptome-developed SSR marker. Genetic Resources and Crop Evolution, 0, , .	0.8	0
9860	A high-quality chromosome-level genome assembly of Pelteobagrus vachelli provides insights into its environmental adaptation and population history. Frontiers in Genetics, 0, 13, .	1.1	0
9861	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. Frontiers in Veterinary Science, 0, 9, .	0.9	7
9862	Silybum marianum chemotype differentiation is genetically determined by factors involved in silydianin biosynthesis. Journal of Applied Research on Medicinal and Aromatic Plants, 2023, 32, 100442.	0.9	0
9864	New Insights into the Mechanism of Trichoderma virens-Induced Developmental Effects on Agrostis stolonifera Disease Resistance against Dollar Spot Infection. Journal of Fungi (Basel, Switzerland), 2022, 8, 1186.	1.5	1
9865	Improved assembly and annotation of the sesame genome. DNA Research, 2022, 29, .	1.5	11
9866	Transcriptome and Phenotype Integrated Analysis Identifies Genes Controlling Ginsenoside Rb1 Biosynthesis and Reveals Their Interactions in the Process in Panax ginseng. International Journal of Molecular Sciences, 2022, 23, 14016.	1.8	3
9867	lncRNA HHIP-AS1/HHIP modulates osteogenic differentiation of BM-MSCs by regulating Hedgehog signaling pathway. Aging, 2022, 14, 8839-8855.	1.4	2
9868	Decoding the microbiome and metabolome of the <i>Panchagavya</i>â€"An indigenous fermented bioâ€formulation. , 2022, 1, .		4

#	Article	IF	Citations
9869	Revealing the mechanisms of the bioactive ingredients accumulation in Polygonatum cyrtonema by multiomics analyses. Frontiers in Plant Science, 0, 13, .	1.7	2
9870	Transcriptomic and metabolomic integration to assess the response of gilthead sea bream (Sparus) Tj ETQq1 1 0.784314 rgBT /Overlock	3.7	2
9871	Integrated Genomic and Transcriptomic Elucidation of Flowering in Garlic. International Journal of Molecular Sciences, 2022, 23, 13876.	1.8	1
9872	RNA-Sequencing of Heterorhabditis nematodes to identify factors involved in symbiosis with Photorhabdus bacteria. BMC Genomics, 2022, 23, .	1.2	1
9873	Genomeâ€scale signatures of adaptive gene expression changes in an invasive seaweed <i>Gracilaria vermiculophylla</i>. Molecular Ecology, 2023, 32, 613-627.	2.0	3
9874	Ice plant root plasma membrane aquaporins are regulated by clathrin-coated vesicles in response to salt stress. Plant Physiology, 2023, 191, 199-218.	2.3	3
9875	De Novo Transcriptome Assembly and Analysis of Longevity Genes Using Subterranean Termite (Reticulitermes chinensis) Castes. International Journal of Molecular Sciences, 2022, 23, 13660.	1.8	1
9876	Transcriptomic and phenotype analysis revealed the role of rpoS in stress resistance and virulence of pathogenic Enterobacter cloacae from Macrobrachium rosenbergii. Frontiers in Microbiology, 0, 13, .	1.5	1
9877	Transcription level differences in Taxus wallichiana var. mairei elicited by Ce3+, Ce4+ and methyl jasmonate. Frontiers in Plant Science, 0, 13, .	1.7	0
9878	Phenotypic and Differential Gene Expression Analyses of Phase Transition in Oedaleus asiaticus under High-Density Population Stress. Insects, 2022, 13, 1034.	1.0	0
9879	Genome based phylogeny and virulence factor analysis of mastitis causing Escherichia coli isolated from Indian cattle. Indian Journal of Animal Sciences, 2021, 90, 1577-1583.	0.1	1
9880	Betalain accumulation and de novo transcriptome sequencing reveal the potential to increase bioactive compounds in Alternanthera sessilis elicited by methyl jasmonate. Acta Physiologiae Plantarum, 2023, 45, .	1.0	3
9881	Temporal transcriptome of tomato elucidates the signaling pathways of induced systemic resistance and systemic acquired resistance activated by Chaetomium globosum. Frontiers in Genetics, 0, 13, .	1.1	0
9882	Adaptation of Helicoverpa armigera to Soybean Peptidase Inhibitors Is Associated with the Transgenerational Upregulation of Serine Peptidases. International Journal of Molecular Sciences, 2022, 23, 14301.	1.8	3
9883	Tyrosine promotes anthocyanin biosynthesis in pansy (<i>Viola Ã— wittrockiana</i>) by inducing ABA synthesis. , 2022, 1, 1-12.		0
9884	Analyzing toxicological effects of AsIII and AsV to Chlamys farreri by integrating transcriptomic and metabolomic approaches. Marine Pollution Bulletin, 2023, 186, 114385.	2.3	2
9885	The genome sequence of the Neotropical brown stink bug, Euschistus heros provides insights into population structure, demographic history and signatures of adaptation. Insect Biochemistry and Molecular Biology, 2023, 152, 103890.	1.2	3
9886	Hepatopancreatic transcriptome profiles reveal the effects of toxic dietary concentrations of selenium on the immunity and growth of juvenile abalone Haliotis discus hannai. Aquaculture Reports, 2023, 28, 101449.	0.7	0

#	Article	IF	Citations
9887	Transcriptome profile analysis reveals the regulation mechanism of pistil abortion in Handeliodendron bodinieri. Scientia Horticulturae, 2023, 310, 111697.	1.7	2
9888	Dataset from de novo transcriptome assembly of Myristica fatua leaves using MinION nanopore sequencer. Data in Brief, 2023, 46, 108838.	0.5	4
9889	Differential gene expression analysis in the scallop Argopecten purpuratus exposed to altered pH and temperature conditions in an upwelling-influenced farming area. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 45, 101046.	0.4	0
9890	Effects of short-term exposure to volatile pesticide dichlorvos on the olfactory systems in Spodoptera litura: Calcium homeostasis, synaptic plasticity and apoptosis. Science of the Total Environment, 2023, 864, 161050.	3.9	2
9891	De-novo transcriptome assembly for discovery of putative microsatellite markers and transcription factors in black pepper (Piper nigrum). , 2019, 89, .		0
9892	Diversity in Expression Biases of Lineage-Specific Genes During Development and Anhydrobiosis Among Tardigrade Species. Evolutionary Bioinformatics, 2022, 18, 117693432211402.	0.6	1
9893	Comparative transcriptome and proteome analysis of lily clones inoculated with <i>Fusarium oxysporum</i> f. sp. <i>lilii</i>. Ornamental Plant Research, 2022, 2, 1-10.	0.2	0
9894	Analysis of the Antioxidant Mechanism of Tamarix ramosissima Roots under NaCl Stress Based on Physiology, Transcriptomic and Metabolomic. Antioxidants, 2022, 11, 2362.	2.2	2
9895	Identification of the Genes Encoding B3 Domain-Containing Proteins Related to Vernalization of Beta vulgaris. Genes, 2022, 13, 2217.	1.0	2
9896	Comprehensive profiling of epigenetic modifications in fast-growing Moso bamboo shoots. Plant Physiology, 2023, 191, 1017-1035.	2.3	6
9897	Complete Genome Sequence Data of Novel <i>Streptomyces angustmyceticus</i> Strain CQUSa03, a Potential Biological Control Agent for Potato Oomycete and Fungal Diseases. Plant Disease, 2023, 107, 1609-1612.	0.7	2
9898	Divergence and introgression among the <i>virilis</i> group of <i>Drosophila</i>. Evolution Letters, 2022, 6, 537-551.	1.6	4
9899	Transcriptomic Signature of Horseshoe Crab Carcinoscorpius rotundicauda Hemocytesâ€™ Response to Lipopolysaccharides. Current Issues in Molecular Biology, 2022, 44, 5866-5878.	1.0	1
9900	An Intestinal Symbiotic Bacterial Strain of Oscheius chongmingensis Modulates Host Viability at Both Global and Post-Transcriptional Levels. International Journal of Molecular Sciences, 2022, 23, 14692.	1.8	0
9901	Genome Sequence Resource for <i>Cercospora rodmanii</i> J1, a Potential Biological Control Agent for Water Hyacinth. Phytopathology, 2022, 112, 2462-2465.	1.1	0
9903	Combined analysis of transcriptomics and metabolomics revealed complex metabolic genes for diterpenoids biosynthesis in different organs of Anoectochilus roxburghii. Chinese Herbal Medicines, 2022, , .	1.2	0
9904	Full-length transcriptome and metabolite analysis reveal reticuline epimerase-independent pathways for benzylisoquinoline alkaloids biosynthesis in Sinomenium acutum. Frontiers in Plant Science, 0, 13, .	1.7	0
9905	Comparative Transcriptome Analysis of MeJA Responsive Enzymes Involved in Phillyrin Biosynthesis of Forsythia suspensa. Metabolites, 2022, 12, 1143.	1.3	1

#	ARTICLE	IF	CITATIONS
9906	Global transcriptomic analysis reveals candidate genes associated with different phosphorus acquisition strategies among soybean varieties. Frontiers in Plant Science, 0, 13, .	1.7	3
9907	Improving automatic GO annotation with semantic similarity. BMC Bioinformatics, 2022, 23, .	1.2	3
9908	Spatial Venomicsâ"€Cobra Venom System Reveals Spatial Differentiation of Snake Toxins by Mass Spectrometry Imaging. Journal of Proteome Research, 2023, 22, 26-35.	1.8	4
9909	Transcriptome sequencing reveals potential key genes of cellular changes during the first rapid growth stage of jujube fruit size. New Zealand Journal of Crop and Horticultural Science, 0, , 1-15.	0.7	0
9910	Investigation and Expression Analysis of R2R3-MYBs and Anthocyanin Biosynthesis-Related Genes during Seed Color Development of Common Bean (Phaseolus vulgaris). Plants, 2022, 11, 3386.	1.6	4
9911	Transcriptome analysis and development of EST-SSR markers in Anoectochilus emeiensis (Orchidaceae). PLoS ONE, 2022, 17, e0278551.	1.1	0
9912	Identification of Candidate Genes Associated with Pulp Color by Transcriptomic Analysis of â€˜Huaxiuâ€™ Plum (Prunus salicina Lindl.) during Fruit-Ripening. Current Issues in Molecular Biology, 2022, 44, 6368-6384.	1.0	2
9913	Comparative genomics of five <i>Valsa</i> species gives insights on their pathogenicity evolution. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	0
9914	The microbiome buffers tadpole hosts from heat stress: a hologenomic approach to understand hostâ€"microbe interactions under warming. Journal of Experimental Biology, 2023, 226, .	0.8	9
9915	Differential gene expression associated with flower development of mango (Mangifera indica L.) varieties with different shelf-life. Gene Expression Patterns, 2023, 47, 119301.	0.3	0
9916	Whole-transcriptome analyses of Sorghum leaves identify key mRNAs and ncRNAs associated with GA3-mediated alleviation of salt stress. Frontiers in Plant Science, 0, 13, .	1.7	1
9917	The chromosome-level genome assembly of goldstripe ponyfish (Karalla daura) reveals its similarity to Chinese sillago on contracted immune gene families. Frontiers in Marine Science, 0, 9, .	1.2	0
9918	Integration of transcriptomic and metabolomic profiling of encystation in Cryptocaryon irritans regulated by rapamycin. Veterinary Parasitology, 2023, 314, 109868.	0.7	0
9919	Improving the quality of barren rocky soil by culturing sweetpotato, with special reference to plant-microbes-soil interactions. Microbiological Research, 2023, 268, 127294.	2.5	2
9920	The Current Developments in Medicinal Plant Genomics Enabled the Diversification of Secondary Metabolitesâ€™ Biosynthesis. International Journal of Molecular Sciences, 2022, 23, 15932.	1.8	15
9921	Long non-coding RNAs as the regulatory hubs in rice response to salt stress. Scientific Reports, 2022, 12, .	1.6	7
9922	Molecular evolution and signatures of selective pressures on Bos, focusing on the Nelore breed (Bos) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	0
9923	Whole-transcriptome analyses of sheep embryonic testicular cells infected with the bluetongue virus. Frontiers in Immunology, 0, 13, .	2.2	1

#	Article	IF	Citations
9924	Full-Length Transcriptome of Myotis pilosus as a Reference Resource and Mining of Auditory and Immune Related Genes. International Journal of Molecular Sciences, 2023, 24, 62.	1.8	0
9925	Abscisic acid affects the floret numbers of inflorescence by regulating indole-3-acetic acid transport and accumulation in Lavandula angustifolia. Biologia Plantarum, 0, 66, 298-307.	1.9	0
9927	Selective sweeps linked to the colonization of novel habitats and climatic changes in a wild tomato species. New Phytologist, 0, , .	3.5	3
9928	Diverse infective and lytic machineries identified in genome analysis of tailed coliphages against broad spectrum multidrug-resistant Escherichia coli. International Microbiology, 0, , .	1.1	1
9929	Multiomic Approaches Reveal Hormonal Modulation and Nitrogen Uptake and Assimilation in the Initial Growth of Maize Inoculated with Herbaspirillum seropedicae. Plants, 2023, 12, 48.	1.6	7
9930	High-quality chromosome-level genome assembly of Pacific cod, Gadus macrocephalus. Frontiers in Marine Science, 0, 9, .	1.2	0
9931	Role of exogenous abscisic acid in freezing tolerance of mangrove Kandelia obovata under natural frost condition at near 32Â°N. BMC Plant Biology, 2022, 22, .	1.6	4
9932	An alternative pathway to plant cold tolerance in the absence of vacuolar invertase activity. Plant Journal, 2023, 113, 327-341.	2.8	4
9933	Cross-Talk between Transcriptome Analysis and Dynamic Changes of Carbohydrates Identifies Stage-Specific Genes during the Flower Bud Differentiation Process of Chinese Cherry (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 41	0.8	1
9934	Hedgehog signaling regulates Wolffian duct development through the primary cilium. Biology of Reproduction, 2023, 108, 241-257.	1.2	0
9935	First chromosome scale genomes of ithomiine butterflies (Nymphalidae: Ithomiini): Comparative models for mimicry genetic studies. Molecular Ecology Resources, 2023, 23, 872-885.	2.2	1
9936	A long-read and short-read transcriptomics approach provides the first high-quality reference transcriptome and genome annotation for <i>Pseudotsuga menziesii</i> (Douglas-fir). G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	1
9937	Genome-wide identification, characterization, and evolutionary analysis of NBS genes and their association with disease resistance in Musa spp.. Functional and Integrative Genomics, 2023, 23, .	1.4	2
9938	FgSnt1 of the Set3 HDAC complex plays a key role in mediating the regulation of histone acetylation by the cAMP-PKA pathway in Fusarium graminearum. PLoS Genetics, 2022, 18, e1010510.	1.5	1
9939	Transcriptional Responses for Biosynthesis of Triterpenoids in Exogenous Inducers Treated Inonotus Hispidus Using RNA-Seq. Molecules, 2022, 27, 8541.	1.7	0
9941	De novo transcriptome sequencing of Impatiens uliginosa and the analysis of candidate genes related to spur development. BMC Plant Biology, 2022, 22, .	1.6	0
9942	Integrating unsupervised language model with triplet neural networks for protein gene ontology prediction. PLoS Computational Biology, 2022, 18, e1010793.	1.5	10
9945	Transcriptome analysis of the muscle of fastâ€•and slowâ€growing phoenix barb (<i>Spinibarbus) Tj ETQq1 1 0.784314 rgBT /Overloc	0.7	2

#	ARTICLE	IF	CITATIONS
9947	IdentificaciÃ³n de proteÃnas en Candidatus Liberibacter asiaticus para desarrollar un mÃ©todo de detecciÃ³n inmunoenzimÃ¡tico. Revista Mexicana De Ciencias Agricolas, 2022, 13, 1489-1494.	0.0	0
9948	Comparison of structural variants detected by PacBio-CLR and ONT sequencing in pear. BMC Genomics, 2022, 23, .	1.2	2
9950	Transcriptome and metabolome profiling provide insights into hormone-mediated enhanced growth in autotetraploid seedlings of banana (Musa spp.). Frontiers in Sustainable Food Systems, 0, 6, .	1.8	0
9951	Transcriptome analysis of largemouth bass (Micropterus salmoides) challenged with LPS and polyI:C. Fish and Shellfish Immunology, 2023, 133, 108534.	1.6	2
9952	A Genome-Wide View of the Transcriptome Dynamics of Fresh-Cut Potato Tubers. Genes, 2023, 14, 181.	1.0	3
9953	Combined Metabolome and Transcriptome Analyses Unveil the Molecular Mechanisms of Fruit Acidity Variation in Litchi (Litchi chinensis Sonn.). International Journal of Molecular Sciences, 2023, 24, 1871.	1.8	4
9954	Transcriptional and Physiological Analysis Reveal New Insights into the Regulation of Fertilization (N,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Journal of Molecular Sciences, 2023, 24, 1522.	1.8	3
9955	Saxitoxins-producing potential of the marine dinoflagellate Alexandrium affine and its environmental implications revealed by toxins and transcriptome profiling. Marine Environmental Research, 2023, 185, 105874.	1.1	5
9956	Genome Sequence Resource of <i>Ustilago crameri</i>, a Fungal Pathogen Causing Millet Smut Disease of Foxtail Millet. Plant Disease, 2023, 107, 546-548.	0.7	1
9958	Identification of multiple novel genetic mechanisms that regulate chilling tolerance in Arabidopsis. Frontiers in Plant Science, 0, 13, .	1.7	0
9959	Secretome of Paenibacillus sp. S-12 provides an insight about its survival and possible pathogenicity. Folia Microbiologica, 0, , .	1.1	0
9960	Comparative transcriptomic analyzes of human lung epithelial cells infected with wild-type SARS-CoV-2 and its variant with a 12-bp missing in the E gene. Frontiers in Microbiology, 0, 13, .	1.5	2
9961	Transcriptome Analysis of Rhododendron liliiflorum H. LÃ©v. Flower Colour Differences. Horticulturae, 2023, 9, 82.	1.2	3
9962	Arbuscular mycorrhizal fungus alleviates anthracnose disease in tea seedlings. Frontiers in Plant Science, 0, 13, .	1.7	6
9964	Codon Usage Provide Insights into the Adaptation of Rice Genes under Stress Condition. International Journal of Molecular Sciences, 2023, 24, 1098.	1.8	4
9965	Comprehensive Transcriptome Profiling Uncovers Molecular Mechanisms and Potential Candidate Genes Associated with Heat Stress Response in Chickpea. International Journal of Molecular Sciences, 2023, 24, 1369.	1.8	5
9966	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome. Plant Journal, 2023, 113, 787-801.	2.8	4
9967	Comparative transcriptome analyses of three Gentiana species provides signals for the molecular footprints of selection effects and the phylogenetic relationships. Molecular Genetics and Genomics, 0, , .	1.0	0

#	ARTICLE	IF	CITATIONS
9968	Isolation and Characterization of Bacteria from Natural Hot Spring and Insights into the Thermophilic Cellulase Production. Current Microbiology, 2023, 80, .	1.0	3
9969	Comparative analysis of root anatomical structure, chemical components and differentially expressed genes between early bolting and unbolting in Peucedanum praeruptorum Dunn. Genomics, 2023, 115, 110557.	1.3	5
9970	Large-Scale Chromosomal Changes Lead to Genome-Level Expression Alterations, Environmental Adaptation, and Speciation in the Gayal (<i>Bos frontalis</i>). Molecular Biology and Evolution, 2023, 40, .	3.5	5
9971	Differentially expressed genes in head kidney of Pelteobagrus fulvidraco following Vibrio cholerae challenge. Frontiers in Immunology, 0, 13, .	2.2	2
9972	Comparative transcriptomic analysis of early fruit development in eggplant (Solanum melongena L.) and functional characterization of SmOVATE5. Plant Cell Reports, 0, , .	2.8	2
9973	Transcriptomic differences between bleached and unbleached hydrozoan <i>Millepora complanata</i> following the 2015-2016 ENSO in the Mexican Caribbean. PeerJ, 0, 11, e14626.	0.9	0
9974	flgC gene is involved in the virulence regulation of Pseudomonas plecoglossicida and affects the immune response of Epinephelus coioides. Fish and Shellfish Immunology, 2023, 132, 108512.	1.6	9
9975	Transcriptomic exploration of the Coleopteran wings reveals insight into the evolution of novel structures associated with the beetle elytron. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2023, 340, 197-213.	0.6	2
9976	Isolation and Characterization of SPOTTED LEAF42 Encoding a Porphobilinogen Deaminase in Rice. Plants, 2023, 12, 403.	1.6	0
9977	Full-length transcriptome analysis of two chemotype and functional characterization of genes related to sesquiterpene biosynthesis in Atractylodes lancea. International Journal of Biological Macromolecules, 2023, 225, 1543-1554.	3.6	5
9979	Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. Journal of Fungi (Basel, Switzerland), 2023, 9, 126.	1.5	2
9980	Transcriptome Dataset of Strawberry (Fragaria Ã— ananassa Duch.) Leaves Using Oxford Nanopore Sequencing under LED Irradiation and Application of Methyl Jasmonate and Methyl Salicylate Hormones Treatment. Data, 2023, 8, 22.	1.2	3
9982	The Integrated mRNA and miRNA Approach Reveals Potential Regulators of Flowering Time in Arundina graminifolia. International Journal of Molecular Sciences, 2023, 24, 1699.	1.8	3
9983	A chromosomeâ€level genome assembly enables the identification of the follicule stimulating hormone receptor as the master sexâ€determining gene in the flatfish <i>Solea senegalensis</i>. Molecular Ecology Resources, 2023, 23, 886-904.	2.2	9
9984	Genomic divergence and introgression among three Populus species. Molecular Phylogenetics and Evolution, 2023, 180, 107686.	1.2	5
9985	De novo transcriptome analysis of bagworm Metisa plana from highly infested oil palm estate in Perak revealed detoxification genes and potential insecticide targets. Journal of Asia-Pacific Entomology, 2023, 26, 102039.	0.4	1
9986	De Novo Assembly, Characterization and Comparative Transcriptome Analysis of the Mature Gonads in Spinibarbus hollandi. Animals, 2023, 13, 166.	1.0	6
9987	Genome-Wide Identification of the Hypericum perforatum WRKY Gene Family Implicates HpWRKY85 in Drought Resistance. International Journal of Molecular Sciences, 2023, 24, 352.	1.8	4

#	Article	IF	Citations
9988	Molecular machineries of ciliogenesis, cell survival, and vasculogenesis are differentially expressed during regeneration in explants of the demosponge Halichondria panicea. BMC Genomics, 2022, 23, .	1.2	3
9989	Validation of Novel spot blotch disease resistance alleles identified in unexplored wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock	1.6	2
9990	Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. Frontiers in Immunology, 0, 13, .	2.2	3
9991	Transcriptome profiling reveals the roles of pigment formation mechanisms in yellow Paeonia delavayi flowers. Molecular Genetics and Genomics, 2023, 298, 375-387.	1.0	4
9992	The redlegged earth mite draft genome provides new insights into pesticide resistance evolution and demography in its invasive Australian range. Journal of Evolutionary Biology, 2023, 36, 381-398.	0.8	5
9993	Characterization and acceleration of genome shuffling and ploidy reduction in synthetic allopolyploids by genome sequencing and editing. Nucleic Acids Research, 2023, 51, 198-217.	6.5	5
9994	R2R3 MYB transcription factor SbMYBHv33 negatively regulates sorghum biomass accumulation and salt tolerance. Theoretical and Applied Genetics, 2023, 136, .	1.8	5
9995	Effects of Dietary Vitamin E on Intramuscular Fat Deposition and Transcriptome Profile of the Pectoral Muscle of Broilers. Journal of Poultry Science, 2023, 60, n/a.	0.7	3
9996	Chromosome-scale genomics, metabolomics, and transcriptomics provide insight into the synthesis and regulation of phenols in Vitis adenoclada grapes. Frontiers in Plant Science, 0, 14, .	1.7	1
9997	Complete genome sequencing of nematode Aphelenchoides besseyi, an economically important pest causing rice white-tip disease. Phytopathology Research, 2023, 5, .	0.9	3
9998	Genomeâ€wide identification and characterization of exapted transposable elements in the large genome of sunflower (<i>Helianthus annuus</i> L.). Plant Journal, 2023, 113, 734-748.	2.8	3
9999	Identification and expression analyses of the olfactoryâ€related genes in different tissues' transcriptome of a predacious soldier beetle, <i>Podabrus annulatus</i> (Coleoptera, Cantharidae). Archives of Insect Biochemistry and Physiology, 2023, 112, .	0.6	3
10000	Grapevine-Associated Lipid Signalling Is Specifically Activated in an Rpv3 Background in Response to an Aggressive P. viticola Pathovar. Cells, 2023, 12, 394.	1.8	1
10002	Multi-Omic Profiling, Structural Characterization, and Potent Inhibitor Screening of Evasion-Related Proteins of a Parasitic Nematode, Haemonchus contortus, Surviving Vaccine Treatment. Biomedicines, 2023, 11, 411.	1.4	1
10003	Identification of Differential-Expressed Genes in Banana-Biostimulant Interaction Using Suppression Subtractive Hybridization. Agronomy, 2023, 13, 415.	1.3	1
10004	Stage-Specific Transcriptomes of the Mussel Mytilus coruscus Reveals the Developmental Program for the Planktonic to Benthic Transition. Genes, 2023, 14, 287.	1.0	2
10005	Revealing the mode of action of Phenylalanine application in inducing fruit resistance to fungal pathogens. Postharvest Biology and Technology, 2023, 199, 112298.	2.9	4
10006	Comparative genomic and functional annotation of Pseudomonas spp. genomes responsible for blue discoloration of Brazilian fresh soft cheese. International Dairy Journal, 2023, 140, 105605.	1.5	1

#	Article	IF	Citations
10007	Comparative gene analysis of beer tolerant and sensitive Lactobacillus brevis. Food Science and Technology, 0, 43, .	0.8	0
10008	Identification of Conserved and Novel MicroRNAs with their Targets in Garden Pea (<i>Pisum) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.6	1
10009	The interaction between the histone acetyltransferase complex Hat1â€Hat2 and transcription factor AmyR provides a molecular brake to regulate amylase gene expression. Molecular Microbiology, 2023, 119, 471-491.	1.2	3
10010	Genomic divergence between two sister <i>Medicago</i> species triggered by the quaternary climatic oscillations on the Qinghaiâ€“Tibet plateau and northern China. Molecular Ecology, 2023, 32, 3118-3132.	2.0	1
10011	Chromosome-scale genome assembly of marigold (Tagetes erecta L.): An ornamental plant and feedstock for industrial lutein production. Horticultural Plant Journal, 2023, 9, 1119-1130.	2.3	2
10012	Secretome analysis of the phytopathogen Macrophomina phaseolina cultivated in liquid medium supplemented with and without soybean leaf infusion. Fungal Biology, 2023, , .	1.1	1
10013	Effects of heat and hyposalinity on the gene expression in Acropora pruinosa larvae. Frontiers in Marine Science, 0, 10, .	1.2	2
10014	Comparative transcriptome analysis revealed genes involved in the sexual size dimorphisms and expressed sequence tag-Simple Sequence Repeat loci validation in Odorrana graminea. Frontiers in Ecology and Evolution, 0, 11, .	1.1	0
10015	Acute temperature stresses trigger liver transcriptome and microbial community remodeling in largemouth bass (Micropterus salmoides). Aquaculture, 2023, 573, 739573.	1.7	7
10016	Sexual dimorphism-related gene expression analysis based on the transcriptome in Gynaephora qinghaiensis, a pest of grassland on the Qinghai-Tibet Plateau. Journal of Asia-Pacific Entomology, 2023, 26, 102083.	0.4	0
10017	The genome sequence and demographic history of <i>Przewalskia tangutica</i> (Solanaceae), an endangered alpine plant on the Qinghaiâ€“Tibet Plateau. DNA Research, 2023, 30, .	1.5	1
10018	Comparative protein analysis of two maize genotypes with contrasting tolerance to low temperature. BMC Plant Biology, 2023, 23, .	1.6	4
10019	Physiological and transcriptome analysis reveals key genes and molecular basis into heterosis of kenaf (Hibiscus cannabinus L.) under drought stress. Environmental and Experimental Botany, 2023, 209, 105293.	2.0	1
10020	Functional characterization of differentially expressed proteins coming from unisexual and bisexual infected Schistosoma japonicum female worms. Experimental Parasitology, 2023, 248, 108504.	0.5	3
10021	Identification of genes responsible for the social skill in the earthworm, Eudrilus eugeniae. Gene Reports, 2023, 31, 101774.	0.4	0
10022	Integration of environmental signatures and omics-based approaches on the European flounder to assist with health assessment of estuarine ecosystems in Brittany, France. Science of the Total Environment, 2023, 878, 163195.	3.9	2
10023	Transcriptomic analysis of Mythimna separata ovaries and identification of genes involved in reproduction. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2023, 46, 101075.	0.4	0
10024	Complete genome sequence of Lactobacillus fermentum 9-4, a purine-degrading Lactobacillus probiotic isolated from Chinese fermented rice-flour noodles. Journal of Future Foods, 2023, 3, 169-174.	2.0	1

#	Article	IF	Citations
10025	Transcriptome and weighted gene co-expression network analysis of jujube (Ziziphus jujuba Mill.) fruit reveal putative genes involved in proanthocyanin biosynthesis and regulation. Food Science and Human Wellness, 2023, 12, 1557-1570.	2.2	3
10026	Transcriptome analysis identifies differentially expressed genes involved in lignin biosynthesis in barley. International Journal of Biological Macromolecules, 2023, 236, 123940.	3.6	1
10027	Sources, bioaccumulation, and toxicity mechanisms of cadmium in Chlamys farreri. Journal of Hazardous Materials, 2023, 453, 131395.	6.5	1
10028	Differential protein response to different light quality conditions of industrial hemp cultivation based on DIA technology. Industrial Crops and Products, 2023, 197, 116650.	2.5	2
10029	Transcriptome and metabolome reveal the role of flavonoids in poplar resistance to poplar anthracnose. Industrial Crops and Products, 2023, 197, 116537.	2.5	3
10033	Transcriptional alterations associated with overexpression of a chlorogenic acid pathway gene in eggplant fruit. Journal of King Saud University - Science, 2023, 35, 102577.	1.6	0
10034	A pangenome analysis pipeline provides insights into functional gene identification in rice. Genome Biology, 2023, 24, .	3.8	12
10035	Light-Induced Flavonoid Biosynthesis in Sinopodophyllum hexandrum with High-Altitude Adaptation. Plants, 2023, 12, 575.	1.6	4
10036	Contaminants of emerging concern in the Maumee River and their effects on freshwater mussel physiology. PLoS ONE, 2023, 18, e0280382.	1.1	4
10037	RNA-seq analysis reveals the critical role of the novel lncRNA BIANCR in intramuscular adipogenesis through the ERK1/2 signaling pathway. Journal of Animal Science and Biotechnology, 2023, 14, .	2.1	7
10038	De novo transcriptome assembly from the nodal root growth zone of hydrated and water-deficit stressed maize inbred line FR697. Scientific Reports, 2023, 13, .	1.6	2
10039	A novel insight of Picrorhiza kurroa miRNAs in human cystic fibrosis: A transcriptome-wide cross-kingdom study. , 2023, 35, 201153.		1
10040	Transcriptome Analysis of Heat Shock Factor C2a Over-Expressing Wheat Roots Reveals Ferroptosis-like Cell Death in Heat Stress Recovery. International Journal of Molecular Sciences, 2023, 24, 3099.	1.8	3
10041	Susceptibility monitoring and comparative gene expression of susceptible and resistant strains of <i>Spodoptera frugiperda</i> to lambdaâ€cyhalothrin and chlorpyrifos. Pest Management Science, 2023, 79, 2206-2219.	1.7	2
10042	Responses of carbapenemase-producing and non-producing carbapenem-resistant Pseudomonas aeruginosa strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. Frontiers in Microbiology, 0, 13, .	1.5	1
10043	Genome-wide identification and characterization of parthenocarpic fruit set-related gene homologs in cucumber (Cucumis sativus L.). Scientific Reports, 2023, 13, .	1.6	5
10044	Development of unigene-derived SSR markers from RNA-seq data of Uraria lagopodioides (Fabaceae) and their application in the genus Uraria Desv. (Fabaceae). BMC Plant Biology, 2023, 23, .	1.6	0
10045	Transcriptome Analysis Reveals Regulatory Networks and Hub Genes in the Flavonoid Metabolism of Rosa roxburghii. Horticulturae, 2023, 9, 233.	1.2	2

#	Article	IF	Citations
10046	Transcriptomics analysis provides insights into the heat adaptation strategies of an Antarctic bacterium, Cryobacterium sp. SO1. Polar Biology, 2023, 46, 185-197.	0.5	2
10047	Physiological and Transcriptional Responses of Apocynum venetum to Salt Stress at the Seed Germination Stage. International Journal of Molecular Sciences, 2023, 24, 3623.	1.8	1
10048	Exploring conserved and novel MicroRNA-like small RNAs from stress tolerant Trichoderma fusants and parental strains during interaction with fungal phytopathogen Sclerotium rolfsii Sacc.. Pesticide Biochemistry and Physiology, 2023, 191, 105368.	1.6	4
10049	Comparison of microsatellite distribution in the genomes of Pteropus vampyrus and Miniopterus natalensis (Chiroptera). BMC Genomic Data, 2023, 24, .	0.7	1
10051	De Novo SNP Discovery and Genotyping of Masson Pine (Pinus massoniana Lamb.) via Genotyping-by-Sequencing. Forests, 2023, 14, 387.	0.9	0
10052	Differential Expression Genes of the Head Kidney and Spleen in Streptococcus iniae-Infected East Asian Fourfinger Threadfin Fish (Eleutheronema tetradactylum). International Journal of Molecular Sciences, 2023, 24, 3832.	1.8	4
10053	Resequencing of durian genomes reveals large genetic variations among different cultivars. Frontiers in Plant Science, 0, 14, .	1.7	0
10054	Multi-Omics of Circular RNAs and Their Responses to Hormones in Moso Bamboo (<i>Phyllostachys) Tj ETQq1 1 0.784314 rgBT /Over	3.0	1
10055	A Mathematical Analysis of 4IR Innovation Barriers in Developmental Social Workâ€”A Structural Equation Modeling Approach. Mathematics, 2023, 11, 1003.	1.1	9
10056	Liver Transcriptome Analysis Reveals Energy Regulation and Functional Impairment of Onychostoma simaÂDuring Starvation. Marine Biotechnology, 2023, 25, 247-258.	1.1	1
10058	A Klebsiella pneumoniae NDM-1+ bacteriophage: Adaptive polyvalence and disruption of heterogenous biofilms. Frontiers in Microbiology, 0, 14, .	1.5	1
10059	Genome assembly and genetic dissection of a prominent drought-resistant maize germplasm. Nature Genetics, 2023, 55, 496-506.	9.4	17
10060	Enlarged fins of Tibetan catfish provide new evidence of adaptation to high plateau. Science China Life Sciences, 2023, 66, 1554-1568.	2.3	2
10061	Field plus lab experiments help identify freezing tolerance and associated genes in subtropical evergreen broadleaf trees: A case study of Camellia oleifera. Frontiers in Plant Science, 0, 14, .	1.7	3
10062	Transcriptome Profiling Data of Tea Leaves During Infection by the Dark Brown Tea Leaf Spot Pathogen, Epicoccum mackenziei. PhytoFrontiers, 0, , .	0.8	0
10063	Transcript annotation of Chinese sturgeon (Acipenser sinensis) using Iso-seq and RNA-seq data. Scientific Data, 2023, 10, .	2.4	2
10064	Mechanisms of Immune-Related Long Non-Coding RNAs in Spleens of Mice Vaccinated with 23-Valent Pneumococcal Polysaccharide Vaccine (PPV23). Vaccines, 2023, 11, 529.	2.1	0
10065	Temperature-induced modulation of stress-tolerant PGP genes bioprospected from Bacillus sp. IHBT-705 associated with saffron (Crocus sativus) rhizosphere: A natural -treasure trove of microbial biostimulants. Frontiers in Plant Science, 0, 14, .	1.7	4

#	Article	IF	Citations
10066	Full-length transcriptome sequence and SSR marker development for genetic diversity research in yellowfin seabream Acanthopagrus latus. Journal of Oceanology and Limnology, 0, , .	0.6	0
10069	Full-Length Transcriptome of the Great Himalayan Leaf-Nosed Bats (Hipposideros armiger) Optimized Genome Annotation and Revealed the Expression of Novel Genes. International Journal of Molecular Sciences, 2023, 24, 4937.	1.8	0
10071	Analysis of the molecular and biochemical mechanisms involved in the symbiotic relationship between Arbuscular mycorrhiza fungi and Manihot esculenta Crantz. Frontiers in Plant Science, 0, 14, .	1.7	1
10072	Identifying Genes Associated with Female Flower Development of Phellodendron amurense Rupr. Using a Transcriptomics Approach. Genes, 2023, 14, 661.	1.0	2
10073	Data-Independent Acquisition Proteomics Reveals the Effects of Red and Blue Light on the Growth and Development of Moso Bamboo (Phyllostachys edulis) Seedlings. International Journal of Molecular Sciences, 2023, 24, 5103.	1.8	2
10075	Genome-wide identification of bHLH transcription factors and their response to salt stress in Cyclocarya paliurus. Frontiers in Plant Science, 0, 14, .	1.7	2
10076	Full-length transcriptome combined with RNA sequence analysis of Fraxinus chinensis. Genes and Genomics, 2023, 45, 553-567.	0.5	0
10077	A learning experience elicits sexâ€dependent neurogenomic responses in <i>Bicyclus anynana</i> butterflies. Molecular Ecology, 2023, 32, 3220-3238.	2.0	2
10079	Comparative transcriptome analysis reveals the molecular mechanism of heat-tolerance in Neopyropia yezoensis induced by Sargassum horneri extract. Frontiers in Marine Science, 0, 10, .	1.2	3
10080	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. Nature Communications, 2023, 14, .	5.8	12
10082	Isolation of bacteriophages infecting Xanthomonas oryzae pv. oryzae and genomic characterization of novel phage vB_XooS_NR08 for biocontrol of bacterial leaf blight of rice. Frontiers in Microbiology, 0, 14, .	1.5	2
10083	Whole-genome sequencing reveals putative underlying mechanisms of biocontrol capability of IBFCBF-5. Acta Physiologiae Plantarum, 2023, 45, .	1.0	1
10084	Tandem mass tag-based quantitative proteomics analyses of a chicken-original virulent and its attenuated Histomonas meleagridis strain in China. Frontiers in Veterinary Science, 0, 10, .	0.9	2
10085	Transcriptome sequencing of sesame (Sesamum indicum) using Illumina Platform. , 2018, 88, 442-446.		0
10086	Genome-Wide Analysis of Long Non-Coding RNAs Related to UV-B Radiation in the Antarctic Moss Pohlia nutans. International Journal of Molecular Sciences, 2023, 24, 5757.	1.8	1
10087	Axenic in vitro cultivation and genome diploidization of the moss Vesicularia montagnei for horticulture utilization. Frontiers in Plant Science, 0, 14, .	1.7	0
10088	Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. Biology, 2023, 12, 476.	1.3	0
10089	Positive and Relaxed Selective Pressures Have Both Strongly Influenced the Evolution of Cryonotothenioid Fishes during Their Radiation in the Freezing Southern Ocean. Genome Biology and Evolution, 2023, 15, .	1.1	7

#	Article	IF	Citations
10090	Genome assembly of the ectoparasitoid wasp Theocolax elegans. Scientific Data, 2023, 10, .	2.4	1
10092	Study on molecular mechanism of volatiles variation during Bupleurum scorzonerifolium root development based on metabolome and transcriptome analysis. Frontiers in Plant Science, 0, 14, .	1.7	0
10093	Whole transcriptome analysis and construction of a ceRNA regulatory network related to leaf and petiole development in Chinese cabbage (Brassica campestris L. ssp. pekinensis). BMC Genomics, 2023, 24, .	1.2	0
10094	Fast and accurate protein function prediction from sequence through pretrained language model and homology-based label diffusion. Briefings in Bioinformatics, 2023, 24, .	3.2	12
10095	Extensive search of genetic sex markers in Siberian (Acipenser baerii) and Atlantic (A. oxyrinchus) sturgeons. Aquaculture, 2023, 573, 739517.	1.7	1
10096	Transcriptomic responses of the fast-growing bacterium Vibrio natriegens during cold-induced loss of culturability. Applied Microbiology and Biotechnology, 2023, 107, 3009-3019.	1.7	1
10097	Snapshot of four mature quinoa (Chenopodium quinoa) seeds: a shotgun proteomics analysis with emphasis on seed maturation, reserves and early germination. Physiology and Molecular Biology of Plants, 2023, 29, 319-334.	1.4	0
10098	Reference proteomes of five wheat species as starting point for future design of cultivars with lower allergenic potential. Npj Science of Food, 2023, 7, .	2.5	6
10099	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	13
10100	<i>Bifidobacterium longum</i> subsp. <i>infantis</i> utilizes human milk urea to recycle nitrogen within the infant gut microbiome. Gut Microbes, 2023, 15, .	4.3	3
10101	Comparative Transcriptomic Analysis Reveals the Functionally Segmented Intestine in Tunicate Ascidian. International Journal of Molecular Sciences, 2023, 24, 6270.	1.8	2
10102	Chromosomeâ€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>. Plant Journal, 2023, 114, 1490-1505.	2.8	2
10103	The duplicated P450s CYP6P9a/b drive carbamates and pyrethroids cross-resistance in the major African malaria vector Anopheles funestus. PLoS Genetics, 2023, 19, e1010678.	1.5	7
10104	Transposable elements in the transcriptome of the velvetbean caterpillar <i>Anticarsia gemmatalis</i> HÃ¼bner, 1818 (Lepidoptera: Erebidae). Genome, 0, , .	0.9	0
10105	The first genome assembly of the amphibian nematode parasite (Aplectana chamaeleonis). GigaByte, 0, 2023, 1-8.	0.0	0
10106	Shotgun proteomics of quinoa seeds reveals chitinases enrichment under rainfed conditions. Scientific Reports, 2023, 13, .	1.6	5
10107	Identification and characterization of siderophilic biocontrol strain SL-44 combined with whole genome. Environmental Science and Pollution Research, 0, , .	2.7	0
10108	Transcriptomic insights into the immune response of the intestine to Aeromonas veronii infection in northern snakehead (Channa argus). Ecotoxicology and Environmental Safety, 2023, 255, 114825.	2.9	4

#	Article	IF	Citations
10111	Regulatory Networks of lncRNAs, miRNAs, and mRNAs in Response to Heat Stress in Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.8	1
10112	FishGET: A fish gene expression and transcriptome database with improved accuracy and visualization. IScience, 2023, 26, 106539.	1.9	1
10113	The effects of circularly polarized light on mating behavior and gene expression in Anomala corpulenta (Coleoptera: Scarabaeidae). Frontiers in Physiology, 0, 14, .	1.3	0
10114	Identification and Characterization of Development-Related microRNAs in the Red Flour Beetle, Tribolium castaneum. International Journal of Molecular Sciences, 2023, 24, 6685.	1.8	0
10115	Genetic mapping of some key plant architecture traits in Brassica juncea using a doubled haploid population derived from a cross between two distinct lines: vegetable type Tumida and oleiferous Varuna. Theoretical and Applied Genetics, 2023, 136, .	1.8	0
10116	A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. BMC Genomics, 2023, 24, .	1.2	4
10117	Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species. Nature Genetics, 2023, 55, 852-860.	9.4	43
10118	Intracellular metabolomics and microRNAomics unveil new insight into the regulatory network for potential biocontrol mechanism of stressâ€tolerant <i>Trichoâ€</i>fusants interacting with phytopathogen <i>Sclerotium rolfsii</i> Sacc. Journal of Cellular Physiology, 2023, 238, 1288-1307.	2.0	4
10119	Genome Mining and Screening for Secondary Metabolite Production in the Endophytic Fungus Dactylonectria alcacerensis CT-6. Microorganisms, 2023, 11, 968.	1.6	1
10120	Population genomics reveals demographic history and selection signatures of hazelnut (<i>Corylus</i>). Horticulture Research, 0, , .	2.9	0
10121	Comparative Transcriptomic and Proteomic Analyses Provide New Insights into the Tolerance to Cyclic Dehydration in a Lichen Phycobiont. Microbial Ecology, 0, , .	1.4	2
10122	Genomic and transcriptomic analysis of sacred fig (Ficus religiosa). BMC Genomics, 2023, 24, .	1.2	0
10123	A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids. Science Advances, 2023, 9, .	4.7	4
10124	De novo transcriptome assembly of Iphiculus spongiosus Adams & White, 1849 (Decapoda;) Tj ETQq1 1 0.784314 rgBT /Overlock 2023, 62, 102960.	0.4	0
10125	Integrated Metabolome and Transcriptome Analysis Reveals a Potential Mechanism for Water Accumulation Mediated Translucency in Pineapple (Ananas comosus (L.) Merr.) Fruit. International Journal of Molecular Sciences, 2023, 24, 7199.	1.8	3
10126	Transcriptome analysis reveals the molecular mechanisms of adaptation to high temperatures in Gracilaria bailinae. Frontiers in Plant Science, 0, 14, .	1.7	0
10127	Transcriptional Profiling of Populations in the Clam Ruditapes decussatus Suggests Genetically Determined Differentiation in Gene Expression along Parallel Temperature Gradients and between Races of the Atlantic Ocean and West Mediterranean Sea. Fishes, 2023, 8, 203.	0.7	0
10128	Identification of core cuprotosis-correlated biomarkers in abdominal aortic aneurysm immune microenvironment based on bioinformatics. Frontiers in Immunology, 0, 14, .	2.2	1

#	Article	IF	Citations
10129	Transcriptome Analysis of Solanum Virginianum and in Silico Prediction of Antimicrobial Peptides. Pharmacophore, 2023, 14, 1-10.	0.2	0
10130	Long-reads-based transcriptome dataset from leaves of lime, Citrus aurantiifolia (Christm.) Swingle treated by ethephon and abscisic acid. Data in Brief, 2023, 48, 109167.	0.5	1
10131	Transcriptome analysis revealed the synergism of novel rhodethrin inhibition on biofilm architecture, antibiotic resistance and quorum sensing inEnterococcus faecalis. Gene, 2023, 871, 147436.	1.0	4
10132	Comparative Transcriptome Analysis Reveals the Effect of the DHN Melanin Biosynthesis Pathway on the Appressorium Turgor Pressure of the Poplar Anthracnose-Causing Fungus Colletotrichum gloeosporioides. International Journal of Molecular Sciences, 2023, 24, 7411.	1.8	1
10133	MRF: a tool to overcome the barrier of inconsistent genome annotations and perform comparative genomics studies for the largest animal DNA virus. Virology Journal, 2023, 20, .	1.4	1
10134	OsJRL40, a Jacalin-Related Lectin Gene, Promotes Salt Stress Tolerance in Rice. International Journal of Molecular Sciences, 2023, 24, 7441.	1.8	4
10135	Single-sex schistosomiasis: a mini review. Frontiers in Immunology, 0, 14, .	2.2	0
10136	De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (Cedrus atlantica). Frontiers in Plant Science, 0, 14, .	1.7	3
10137	Responses of population structure and genomic diversity to climate change and fishing pressure in a pelagic fish. Global Change Biology, 2023, 29, 4107-4125.	4.2	2
10138	Insights into the Molecular Basis of Huanglongbing Tolerance in Persian Lime (Citrus latifolia Tan.) through a Transcriptomic Approach. International Journal of Molecular Sciences, 2023, 24, 7497.	1.8	2
10139	Genome-wide analyses of LATERAL ORGAN BOUNDARIES in cassava reveal the role of LBD47 in defence against bacterial blight. PLoS ONE, 2023, 18, e0282100.	1.1	2
10140	In Ovo Injection of CHIR-99021 Promotes Feather Follicle Development via Modulating the Wnt Signaling Pathway and Transcriptome in Goose Embryos (Anser cygnoides). Frontiers in Physiology, 0, 13, .	1.3	6
10141	Regulatory network mediated by CmMKK5â€“CmMPK13 cascade response to phosphorus starvation in chrysanthemum. Industrial Crops and Products, 2023, 199, 116730.	2.5	0
10158	Protocols to Study Host-Pathosystems. , 2023, , 831-913.		0
10181	Understanding the Molecular Mechanisms of Orchid Mycorrhizal Symbiosis from Genetic Information. , 2023, , 1-25.		0
10202	VollstÃndige Shotgun-DNA-Metagenomik. , 2023, , 187-200.		0
10220	Pathogenomics of Pathogenic Variability. , 2023, , 595-728.		0
10362	Computational Genomics Approaches for Livestock Improvement and Management. Livestock Diseases and Management, 2023, , 351-376.	0.5	0

#	Article	IF	Citations
10438	Prospects of Bioinformatics and Data Acquirement Tools in Boosting the Application of Phytochemicals in Food Sciences. , 2024, , 281-302.		0