OrthoMCL: Identification of Ortholog Groups for Eukar

Genome Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	DoOP: Databases of Orthologous Promoters, collections of clusters of orthologous upstream sequences from chordates and plants. Nucleic Acids Research, 2004, 33, D86-D90.	6.5	26
2	GeneSyn: a tool for detecting conserved gene order across genomes. Bioinformatics, 2004, 20, 1472-1474.	1.8	12
3	The Iccare web server: an attempt to merge sequence and mapping information for plant and animal species. Nucleic Acids Research, 2004, 32, W429-W434.	6.5	35
4	Curation of the Plasmodium falciparum genome. Trends in Parasitology, 2004, 20, 548-552.	1.5	15
5	Malaria vaccines: if at first you don't succeedâ€¦. Trends in Parasitology, 2004, 20, 604-610.	1.5	27
6	The Origin of Eukaryotes Is Suggested as the Symbiosis of Pyrococcus into Î³-Proteobacteria by Phylogenetic Tree Based on Gene Content. Journal of Molecular Evolution, 2004, 59, 606-619.	0.8	39
7	OrthoDisease: A database of human disease orthologs. Human Mutation, 2004, 24, 112-119.	1.1	56
8	PLANT GENOMICS: The Third Wave. Annual Review of Genomics and Human Genetics, 2004, 5, 443-477.	2.5	68
9	Decoding Cilia Function. Cell, 2004, 117, 527-539.	13.5	484
10	Update on genome completion and annotations: Protein Information Resource. Human Genomics, 2004, 1, 229.	1.4	25
11	Protozoan genomics for drug discovery. Nature Biotechnology, 2005, 23, 1089-1091.	9.4	70
12	Data integration: challenges for drug discovery. Nature Reviews Drug Discovery, 2005, 4, 45-58.	21.5	161
13	A protein interaction network of the malaria parasite Plasmodium falciparum. Nature, 2005, 438, 103-107.	13.7	480
14	Identifying remote protein homologs by network propagation. FEBS Journal, 2005, 272, 5119-5128.	2.2	27
15	Evolutionary sequence analysis of complete eukaryote genomes. BMC Bioinformatics, 2005, 6, 53.	1.2	48
16	Determining functional specificity from protein sequences. Bioinformatics, 2005, 21, 2629-2635.	1.8	17
17	The Arabidopsis genome: A foundation for plant research. Genome Research, 2005, 15, 1632-1642.	2.4	110
18	The Opportunistic Pathogen Toxoplasma gondii Deploys a Diverse Legion of Invasion and Survival Proteins. Journal of Biological Chemistry, 2005, 280, 34233-34244.	1.6	111

#	ARTICLE	IF	CITATIONS
19	Clustering orthologs based on sequence and domain similarities. , 2005, , .		0
20	Comparative interactomics. FEBS Letters, 2005, 579, 1828-1833.	1.3	44
21	Ancient genomic architecture for mammalian olfactory receptor clusters. Genome Biology, 2006, 7, R88.	13.9	47
22	Benchmarking ortholog identification methods using functional genomics data. Genome Biology, 2006, 7, R31.	13.9	139
23	Integration and mining of malaria molecular, functional and pharmacological data: how far are we from a chemogenomic knowledge space?. Malaria Journal, 2006, 5, 110.	0.8	18
24	Combining Bioinformatics and Phylogenetics to Identify Large Sets of Single-Copy Orthologous Genes (COSII) for Comparative, Evolutionary and Systematic Studies: A Test Case in the Euasterid Plant Clade. Genetics, 2006, 174, 1407-1420.	1.2	269
25	Schizosaccharomyces pombe comparative genomics; from sequence to systems. , 0, , 233-285.		21
26	Overview and comparison of ortholog databases. Drug Discovery Today: Technologies, 2006, 3, 137-143.	4.0	24
27	Systematic identification of functional orthologs based on protein network comparison. Genome Research, 2006, 16, 428-435.	2.4	168
28	Comparative Genomics in <i>C. elegans, C. briggsae,</i> and Other <i>Caenorhabditis</i> Species. , 2006, 351, 13-30.		6
29	Dynamic analysis of a genomic island inMagnetospirillumsp. strain AMB-1 reveals how magnetosome synthesis developed. FEBS Letters, 2006, 580, 801-812.	1.3	87
30	The S. purpuratus genome: A comparative perspective. Developmental Biology, 2006, 300, 485-495.	0.9	27
31	The Role of the COG Database in Comparative and Functional Genomics. Current Bioinformatics, 2006, 1, 291-300.	0.7	16
32	How to get the most from fission yeast genome data: a report from the 2006 European Fission Yeast Meeting computing workshop. Yeast, 2006, 23, 905-912.	0.8	3
33	Operon prediction based on SVM. Computational Biology and Chemistry, 2006, 30, 233-240.	1.1	25
34	A phylogenomic gene cluster resource: the Phylogenetically Inferred Groups (PhIGs) database. BMC Bioinformatics, 2006, 7, 201.	1.2	56
35	Evolution of the vertebrate parahox clusters. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2006, 306B, 481-487.	0.6	12
36	OrthoMCL-DB: querying a comprehensive multi-species collection of ortholog groups. Nucleic Acids Research, 2006, 34, D363-D368.	6.5	802

#	ARTICLE	IF	CITATIONS
37	Cross-species comparative toxicogenomics as an aid to safety assessment. Expert Opinion on Drug Metabolism and Toxicology, 2006, 2, 859-874.	1.5	16
38	COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations. Bioinformatics, 2006, 22, 779-788.	1.8	61
39	Automatic clustering of orthologs and inparalogs shared by multiple proteomes. Bioinformatics, 2006, 22, e9-e15.	1.8	227
40	SIMAP: the similarity matrix of proteins. Nucleic Acids Research, 2006, 34, D252-D256.	6.5	44
41	Detecting uber-operons in prokaryotic genomes. Nucleic Acids Research, 2006, 34, 2418-2427.	6.5	33
42	YOGY: a web-based, integrated database to retrieve protein orthologs and associated Gene Ontology terms. Nucleic Acids Research, 2006, 34, W330-W334.	6.5	44
43	Computational modeling of the Plasmodiumfalciparum interactome reveals protein functionon a genome-wide scale. Genome Research, 2006, 16, 542-549.	2.4	91
44	Hierarchical clustering algorithm for comprehensive orthologous-domain classification in multiple genomes. Nucleic Acids Research, 2006, 34, 647-658.	6.5	74
45	TreeFam: a curated database of phylogenetic trees of animal gene families. Nucleic Acids Research, 2006, 34, D572-D580.	6.5	465
46	Heterogeneous Genomic Molecular Clocks in Primates. PLoS Genetics, 2006, 2, e163.	1.5	89
47	Toxoplasma gondii Purine Nucleoside Phosphorylase Biochemical Characterization, Inhibitor Profiles, and Comparison with the Plasmodium falciparum Ortholog. Journal of Biological Chemistry, 2006, 281, 25652-25658.	1.6	34
48	A Systematic Map of Genetic Variation in Plasmodium falciparum. PLoS Pathogens, 2006, 2, e57.	2.1	176
49	Correlated Asymmetry of Sequence and Functional Divergence Between Duplicate Proteins of Saccharomyces cerevisiae. Molecular Biology and Evolution, 2006, 23, 1068-1075.	3.5	68
50	Characterization of five microRNA families in maize. Journal of Experimental Botany, 2006, 57, 2601-2612.	2.4	81
51	Automated data integration for developmental biological research. Development (Cambridge), 2007, 134, 3227-3238.	1.2	8
52	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. PLoS Computational Biology, 2007, 3, e206.	1.5	261
53	OMA Browser Exploring orthologous relations across 352 complete genomes. Bioinformatics, 2007, 23, 2180-2182.	1.8	101
54	Bottleneck Genes and Community Structure in the Cell Cycle Network of S. pombe. PLoS Computational Biology, 2007, 3, e103.	1.5	23

#	Article	IF	Citations
55	Automated Protein Subfamily Identification and Classification. PLoS Computational Biology, 2007, 3, e160.	1.5	110
56	Identification of Cold-Induced Genes in Cereal Crops and Arabidopsis Through Comparative Analysis of Multiple EST Sets. , 2007, , 48-65.		4
57	Automatic genome-wide reconstruction of phylogenetic gene trees. Bioinformatics, 2007, 23, i549-i558.	1.8	129
58	Comparative genome analysis across a kingdom of eukaryotic organisms: Specialization and diversification in the Fungi. Genome Research, 2007, 17, 1809-1822.	2.4	94
59	Comparasite: a database for comparative study of transcriptomes of parasites defined by full-length cDNAs. Nucleic Acids Research, 2007, 35, D431-D438.	6.5	29
60	Immunity genes and their orthologs: a multi-species database. International Immunology, 2007, 19, 1361-1370.	1.8	13
61	eggNOG: automated construction and annotation of orthologous groups of genes. Nucleic Acids Research, 2007, 36, D250-D254.	6.5	428
62	Finding Conserved Gene Order Across Multiple Genomes. Methods in Molecular Biology, 2007, 396, 111-119.	0.4	0
63	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. Briefings in Bioinformatics, 2007, 9, 34-45.	3.2	4
64	Structural RNAs of known and unknown function identified in malaria parasites by comparative genomics and RNA analysis. Rna, 2007, 13, 1923-1939.	1.6	89
65	Identification of Diverse Archaeal Proteins with Class III Signal Peptides Cleaved by Distinct Archaeal Prepilin Peptidases. Journal of Bacteriology, 2007, 189, 772-778.	1.0	139
66	WormBase 2007. Nucleic Acids Research, 2007, 36, D612-D617.	6.5	95
67	Evolutionary conservation of cell migration genes: from nematode neurons to vertebrate neural crest. Genes and Development, 2007, 21, 391-396.	2.7	33
68	MSOAR: A High-Throughput Ortholog Assignment System Based on Genome Rearrangement. Journal of Computational Biology, 2007, 14, 1160-1175.	0.8	67
70	Reactome: An integrated expert model of human molecular processes and access toolkit. Journal of Integrative Bioinformatics, 2007, 4, 286-296.	1.0	0
71	Metabolic peculiarities of Aspergillus niger disclosed by comparative metabolic genomics. Genome Biology, 2007, 8, R182.	13.9	51
72	The human phylome. Genome Biology, 2007, 8, R109.	3.8	150
73	Evolution of the core and pan-genome of Streptococcus: positive selection, recombination, and genome composition. Genome Biology, 2007, 8, R71.	13.9	316

#	ARTICLE	IF	CITATIONS
74	Reactome: a knowledge base of biologic pathways and processes. Genome Biology, 2007, 8, R39.	13.9	539
75	Orthology and Functional Conservation in Eukaryotes. Annual Review of Genetics, 2007, 41, 465-507.	3.2	99
76	ProtozoaDB: dynamic visualization and exploration of protozoan genomes. Nucleic Acids Research, 2007, 36, D547-D552.	6.5	17
77	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. Biology Direct, 2007, 2, 33.	1.9	164
78	Sybil: Methods and Software for Multiple Genome Comparison and Visualization. Methods in Molecular Biology, 2007, 408, 93-108.	0.4	55
79	Assessing Performance of Orthology Detection Strategies Applied to Eukaryotic Genomes. PLoS ONE, 2007, 2, e383.	1.1	362
80	The Apicoplast and Mitochondrion of Toxoplasma gondii. , 2007, , 207-244.		1
81	Comparative biology: beyond sequence analysis. Current Opinion in Biotechnology, 2007, 18, 371-377.	3.3	45
82	Ontology annotation: mapping genomic regions to biological function. Current Opinion in Chemical Biology, 2007, 11, 4-11.	2.8	76
83	Clustering orthologous proteins across phylogenetically distant species. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1113-1122.	1.5	7
84	An essential role for a CD36-related receptor in pheromone detection in Drosophila. Nature, 2007, 450, 289-293.	13.7	504
85	Wholeâ€genome analysis of the ammoniaâ€oxidizing bacterium, <i>Nitrosomonas eutropha</i> C91: implications for niche adaptation. Environmental Microbiology, 2007, 9, 2993-3007.	1.8	150
86	Mining the genomes of plant pathogenic bacteria: how not to drown in gigabases of sequence. Molecular Plant Pathology, 2007, 9, 071031023555001-???.	2.0	2
87	A search engine to identify pathway genes from expression data on multiple organisms. BMC Systems Biology, 2007, 1, 20.	3.0	6
88	OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics. BMC Evolutionary Biology, 2007, 7, 241.	3.2	120
89	Inferring angiosperm phylogeny from EST data with widespread gene duplication. BMC Evolutionary Biology, 2007, 7, S3.	3.2	89
90	cTFbase: a database for comparative genomics of transcription factors in cyanobacteria. BMC Genomics, 2007, 8, 104.	1.2	28
91	C-terminal motif prediction in eukaryotic proteomes using comparative genomics and statistical over-representation across protein families. BMC Genomics, 2007, 8, 191.	1.2	15

#	ARTICLE	IF	CITATIONS
92	Experimental-confirmation and functional-annotation of predicted proteins in the chicken genome. BMC Genomics, 2007, 8, 425.	1.2	16
93	e-Fungi: a data resource for comparative analysis of fungal genomes. BMC Genomics, 2007, 8, 426.	1.2	32
94	Dating the early evolution of plants: detection and molecular clock analyses of orthologs. Molecular Genetics and Genomics, 2007, 278, 393-402.	1.0	103
95	Homology and phylogeny and their automated inference. Die Naturwissenschaften, 2008, 95, 469-481.	0.6	2
96	Evolution and pathogenesis of<i>Staphylococcus aureus</i>: lessons learned from genotyping and comparative genomics. FEMS Microbiology Reviews, 2008, 32, 23-37.	3.9	133
97	The genome of the simian and human malaria parasite Plasmodium knowlesi. Nature, 2008, 455, 799-803.	13.7	338
98	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. Nature Biotechnology, 2008, 26, 909-915.	9.4	1,012
99	Genomic-scale prioritization of drug targets: the TDR Targets database. Nature Reviews Drug Discovery, 2008, 7, 900-907.	21.5	282
100	Clustering of cognate proteins among distinct proteomes derived from multiple links to a single seed sequence. BMC Bioinformatics, 2008, 9, 141.	1.2	8
101	Funybase: a Fungal phylogenomic database. BMC Bioinformatics, 2008, 9, 456.	1.2	60
102	Algorithm of OMA for large-scale orthology inference. BMC Bioinformatics, 2008, 9, 518.	1.2	148
103	Consistent and contrasting properties of lineage-specific genes in the apicomplexan parasites Plasmodium and Theileria. BMC Evolutionary Biology, 2008, 8, 108.	3.2	43
104	Molecular evolution of synonymous codon usage in Populus. BMC Evolutionary Biology, 2008, 8, 307.	3.2	76
105	Multiple genome alignment for identifying the core structure among moderately related microbial genomes. BMC Genomics, 2008, 9, 515.	1.2	25
106	The quest for orthologs: finding the corresponding gene across genomes. Trends in Genetics, 2008, 24, 539-551.	2.9	258
107	Essential Concepts in Toxicogenomics. Methods in Molecular Biology, 2008, , .	0.4	1
108	Large-scale assignment of orthology: back to phylogenetics?. Genome Biology, 2008, 9, 235.	13.9	187
110	Organization and Evolution of the Biological Response to Singlet Oxygen Stress. Journal of Molecular Biology, 2008, 383, 713-730.	2.0	65

#	Article	IF	Citations
111	ArchaeaTF: An integrated database of putative transcription factors in Archaea. Genomics, 2008, 91, 102-107.	1.3	22
112	Saturation and base composition bias explain phylogenomic conflict in Plasmodium. Genomics, 2008, 91, 433-442.	1.3	56
113	Phosphoproteome Analysis of Fission Yeast. Journal of Proteome Research, 2008, 7, 1088-1097.	1.8	173
114	Evolutionary Conservation of Human Drug Targets in Organisms used for Environmental Risk Assessments. Environmental Science & Technology, 2008, 42, 5807-5813.	4.6	475
115	Genomics of bacteria and archaea: the emerging dynamic view of the prokaryotic world. Nucleic Acids Research, 2008, 36, 6688-6719.	6.5	642
116	Graph Clustering Via a Discrete Uncoupling Process. SIAM Journal on Matrix Analysis and Applications, 2008, 30, 121-141.	0.7	466
117	An Algorithm to Cluster Orthologous Proteins across Multiple Genomes. , 2008, , .		0
118	Designating eukaryotic orthology via processed transcription units. Nucleic Acids Research, 2008, 36, 3436-3442.	6.5	4
119	COMPARE, a multi-organism system for cross-species data comparison and transfer of information. Bioinformatics, 2008, 24, 447-449.	1.8	11
120	Patterns of Molecular Evolution in Caenorhabditis Preclude Ancient Origins of Selfing. Genetics, 2008, 178, 2093-2104.	1.2	87
121	AffyTrees: Facilitating Comparative Analysis of Affymetrix Plant Microarray Chips. Plant Physiology, 2008, 146, 377-386.	2.3	10
122	ORTHOFOCUS: PROGRAM FOR IDENTIFICATION OF ORTHOLOGS IN MULTIPLE GENOMES IN FAMILY-FOCUSED STUDIES. Journal of Bioinformatics and Computational Biology, 2008, 06, 811-824.	0.3	6
123	Multiple genome sequences reveal adaptations of a phototrophic bacterium to sediment microenvironments. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18543-18548.	3.3	131
124	A Novel GDP-dependent Pyruvate Kinase Isozyme from Toxoplasma gondii Localizes to Both the Apicoplast and the Mitochondrion. Journal of Biological Chemistry, 2008, 283, 14041-14052.	1.6	44
125	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. Genome Research, 2008, 18, 1944-1954.	2.4	515
126	Logical Identification of an Allantoinase Analog (puuE) Recruited from Polysaccharide Deacetylases. Journal of Biological Chemistry, 2008, 283, 23295-23304.	1.6	62
127	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. Journal of Bioinformatics and Computational Biology, 2008, 06, 573-584.	0.3	10
128	Comparing Patterns of Natural Selection across Species Using Selective Signatures. PLoS Genetics, 2008, 4, e23.	1.5	40

#	Article	IF	Citations
129	Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies. Systematic Biology, 2008, 57, 613-627.	2.7	162
130	Discovering regulatory motifs in the <i>Plasmodium</i> genome using comparative genomics. Bioinformatics, 2008, 24, 1843-1849.	1.8	31
131	Divergence Times in Caenorhabditis and Drosophila Inferred from Direct Estimates of the Neutral Mutation Rate. Molecular Biology and Evolution, 2008, 25, 778-786.	3.5	220
132	Reconstructing ancestral genome content based on symmetrical best alignments and Dollo parsimony. Bioinformatics, 2008, 24, 606-612.	1.8	16
133	Conservation of the Chitin Utilization Pathway in the <i>Vibrionaceae</i>. Applied and Environmental Microbiology, 2008, 74, 44-51.	1.4	211
134	Mammalian Nonsynonymous Sites Are Not Overdispersed: Comparative Genomic Analysis of Index of Dispersion of Mammalian Proteins. Molecular Biology and Evolution, 2008, 25, 634-642.	3.5	6
135	EnsemblCompara GeneTrees: Complete, duplication-aware phylogenetic trees in vertebrates. Genome Research, 2009, 19, 327-335.	2.4	1,058
136	Multigenome DNA sequence conservation identifies <i>Hox cis</i>-regulatory elements. Genome Research, 2008, 18, 1955-1968.	2.4	25
137	Arabidopsis Reactome: A Foundation Knowledgebase for Plant Systems Biology. Plant Cell, 2008, 20, 1426-1436.	3.1	52
138	An approach of orthology detection from homologous sequences under minimum evolution. Nucleic Acids Research, 2008, 36, e110-e110.	6.5	26
140	The Apicomplexan Whole-Genome Phylogeny: An Analysis of Incongruence among Gene Trees. Molecular Biology and Evolution, 2008, 25, 2689-2698.	3.5	105
141	Rickettsia Phylogenomics: Unwinding the Intricacies of Obligate Intracellular Life. PLoS ONE, 2008, 3, e2018.	1.1	175
142	Spindle Assembly Checkpoint Protein Dynamics Reveal Conserved and Unsuspected Roles in Plant Cell Division. PLoS ONE, 2009, 4, e6757.	1.1	61
143	The Core and Pan-Genome of the Vibrionaceae. , 2009, , .		1
144	3D-interologs: A Protein-Protein Interacting Evolution Database across Multiple Species. , 2009, , .		0
145	Towards Improved Reconstruction of Ancestral Gene Order in Angiosperm Phylogeny. Journal of Computational Biology, 2009, 16, 1353-1367.	0.8	12
146	Genome Evolution in Malaria Parasites: I. Core Genome Components. , 2009, , .		0
147	Data integration for plant genomics--exemplars from the integration of Arabidopsis thaliana databases. Briefings in Bioinformatics, 2009, 10, 676-693.	3.2	21

#	ARTICLE	IF	CITATIONS
148	Phylogenomic Analysis Demonstrates a Pattern of Rare and Ancient Horizontal Gene Transfer between Plants and Fungi. Plant Cell, 2009, 21, 1897-1911.	3.1	162
149	Taxon K, a complex within the Burkholderia cepacia complex, comprises at least two novel species, Burkholderia contaminans sp. nov. and Burkholderia lata sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2009, 59, 102-111.	0.8	280
150	Improved criteria and comparative genomics tool provide new insights into grass paleogenomics. Briefings in Bioinformatics, 2009, 10, 619-630.	3.2	63
151	Comparative Genomics Reveal Extensive Transposon-Mediated Genomic Plasticity and Diversity among Potential Effector Proteins within the Genus<i>Coxiella</i>. Infection and Immunity, 2009, 77, 642-656.	1.0	197
152	Pervasive, genome-wide positive selection leading to functional divergence in the bacterial genus <i>Campylobacter</i>. Genome Research, 2009, 19, 1224-1232.	2.4	59
153	Expansion and Diversification of the<i>Populus</i>R2R3-MYB Family of Transcription Factors Â Â. Plant Physiology, 2009, 149, 981-993.	2.3	450
154	Common introns within orthologous genes: software and application to plants. Briefings in Bioinformatics, 2009, 10, 631-644.	3.2	29
155	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. Nucleic Acids Research, 2009, 37, D448-D454.	6.5	49
156	Unraveling Transcriptional Control in Arabidopsis Using cis-Regulatory Elements and Coexpression Networks Â Â. Plant Physiology, 2009, 150, 535-546.	2.3	197
157	Scalable graph clustering using stochastic flows. , 2009, , .		159
158	Disparate Effects of Roscovitine on Renal Tubular Epithelial Cell Apoptosis and Senescence: Implications for Autosomal Dominant Polycystic Kidney Disease. American Journal of Nephrology, 2009, 29, 509-515.	1.4	21
159	An entropy based heuristic model for predicting functional sub-type divisions of protein families. , 2009, , .		0
160	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. Genome Research, 2009, 19, 1722-1731.	2.4	295
161	RiceArrayNet: A Database for Correlating Gene Expression from Transcriptome Profiling, and Its Application to the Analysis of Coexpressed Genes in Rice Â Â Â. Plant Physiology, 2009, 151, 16-33.	2.3	91
162	Cohesive versus Flexible Evolution of Functional Modules in Eukaryotes. PLoS Computational Biology, 2009, 5, e1000276.	1.5	19
163	Phylogenetic and Functional Assessment of Orthologs Inference Projects and Methods. PLoS Computational Biology, 2009, 5, e1000262.	1.5	341
164	The Gene Ontology's Reference Genome Project: A Unified Framework for Functional Annotation across Species. PLoS Computational Biology, 2009, 5, e1000431.	1.5	148
165	Probabilistic Orthology Analysis. Systematic Biology, 2009, 58, 411-424.	2.7	37

#	Article	IF	Citations
166	Deletional Bias across the Three Domains of Life. Genome Biology and Evolution, 2009, 1, 145-152.	1.1	186
167	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. PLoS Genetics, 2009, 5, e1000407.	1.5	129
168	A Comparative Genomics, Network-Based Approach to Understanding Virulence in <i>Vibrio cholerae</i>. Journal of Bacteriology, 2009, 191, 6262-6272.	1.0	10
169	FIGfams: yet another set of protein families. Nucleic Acids Research, 2009, 37, 6643-6654.	6.5	130
170	Genome Sequences of Three<i>Agrobacterium</i>Biovars Help Elucidate the Evolution of Multichromosome Genomes in Bacteria. Journal of Bacteriology, 2009, 191, 2501-2511.	1.0	220
171	Analysis of Ten <i>Brucella</i> Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle. Journal of Bacteriology, 2009, 191, 3569-3579.	1.0	103
172	GENE LOSS UNDER NEIGHBORHOOD SELECTION FOLLOWING WHOLE GENOME DUPLICATION AND THE RECONSTRUCTION OF THE ANCESTRAL POPULUS GENOME. Journal of Bioinformatics and Computational Biology, 2009, 07, 499-520.	0.3	12
173	Genome Sequence of<i>Azotobacter vinelandii</i>, an Obligate Aerobe Specialized To Support Diverse Anaerobic Metabolic Processes. Journal of Bacteriology, 2009, 191, 4534-4545.	1.0	265
174	The origins of apicomplexan sequence innovation. Genome Research, 2009, 19, 1202-1213.	2.4	63
175	Caveat emptor: limitations of the automated reconstruction of metabolic pathways in Plasmodium. Trends in Parasitology, 2009, 25, 37-43.	1.5	42
176	FlyPhy: a phylogenomic analysis platform for Drosophila genes and gene families. BMC Bioinformatics, 2009, 10, 123.	1.2	2
177	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. BMC Bioinformatics, 2009, 10, 154.	1.2	401
178	OrthoSelect: a protocol for selecting orthologous groups in phylogenomics. BMC Bioinformatics, 2009, 10, 219.	1.2	23
179	Comparison of eukaryotic phylogenetic profiling approaches using species tree aware methods. BMC Bioinformatics, 2009, 10, 383.	1.2	16
180	Databases of homologous gene families for comparative genomics. BMC Bioinformatics, 2009, 10, S3.	1.2	118
181	HaMStR: Profile hidden markov model based search for orthologs in ESTs. BMC Evolutionary Biology, 2009, 9, 157.	3.2	269
182	Genome wide evolutionary analyses reveal serotype specific patterns of positive selection in selected Salmonella serotypes. BMC Evolutionary Biology, 2009, 9, 264.	3.2	62
183	Evolution of MIR168 paralogs in Brassicaceae. BMC Evolutionary Biology, 2009, 9, 62.	3.2	21

#	ARTICLE	IF	CITATIONS
184	Evolution from a respiratory ancestor to fill syntrophic and fermentative niches: comparative fenomics of six Geobacteraceae species. BMC Genomics, 2009, 10, 103.	1.2	45
185	ChlamyCyc: an integrative systems biology database and web-portal for Chlamydomonas reinhardtii. BMC Genomics, 2009, 10, 209.	1.2	73
186	Organization and evolution of two SIDER retroposon subfamilies and their impact on the Leishmania genome. BMC Genomics, 2009, 10, 240.	1.2	40
187	Predicting protein-protein interactions in Arabidopsis thaliana through integration of orthology, gene ontology and co-expression. BMC Genomics, 2009, 10, 288.	1.2	120
188	The other side of comparative genomics: genes with no orthologs between the cow and other mammalian species. BMC Genomics, 2009, 10, 604.	1.2	8
189	The complete genome sequence of Xanthomonas albilineans provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae. BMC Genomics, 2009, 10, 616.	1.2	142
190	Identification of mammalian orthologs using local synteny. BMC Genomics, 2009, 10, 630.	1.2	57
191	Genomic and systems evolution in Vibrionaceae species. BMC Genomics, 2009, 10, S11.	1.2	15
192	Computational prediction of essential genes in an unculturable endosymbiotic bacterium, Wolbachia of Brugia malayi. BMC Microbiology, 2009, 9, 243.	1.3	117
193	Proteomes and transcriptomes of the Apicomplexa â€“ Whereâ€™s the message?. International Journal for Parasitology, 2009, 39, 135-143.	1.3	68
194	The NfeD Protein Family and Its Conserved Gene Neighbours Throughout Prokaryotes: Functional Implications for Stomatin-Like Proteins. Journal of Molecular Evolution, 2009, 69, 657-667.	0.8	11
195	Evolutionary constraints on structural similarity in orthologs and paralogs. Protein Science, 2009, 18, 1306-1315.	3.1	58
196	Quantitative RNA expression analysis with Affymetrix Tiling 1.0R arrays identifies new E2F target genes. Plant Journal, 2009, 57, 184-194.	2.8	65
197	Network visualization and analysis of gene expression data using BioLayout Express3D. Nature Protocols, 2009, 4, 1535-1550.	5.5	443
198	Reactome knowledgebase of human biological pathways and processes. Nucleic Acids Research, 2009, 37, D619-D622.	6.5	760
199	Reconstruction of monocotelydoneous proto-chromosomes reveals faster evolution in plants than in animals. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14908-14913.	3.3	144
200	Biodiversity and evolution of primary carbon metabolism in Aspergillus nidulans and other Aspergillus spp.. Fungal Genetics and Biology, 2009, 46, S19-S44.	0.9	93
201	The transcriptional regulation of protein complexes; a cross-species perspective. Genomics, 2009, 94, 369-376.	1.3	18

#	ARTICLE	IF	CITATIONS
202	Vaxign: a web-based vaccine target design program for reverse vaccinology. Procedia in Vaccinology, 2009, 1, 23-29.	0.4	56
203	Aligning Two Genomic Sequences That Contain Duplications. Lecture Notes in Computer Science, 2009, , 98-110.	1.0	1
204	Inferring clocks when lacking rocks: the variable rates of molecular evolution in bacteria. Biology Direct, 2009, 4, 35.	1.9	179
205	Using OrthoCluster for the Detection of Synteny Blocks Among Multiple Genomes. Current Protocols in Bioinformatics, 2009, 27, Unit 6.10 6.10.1-18.	25.8	12
206	Discovery: an interactive resource for the rational selection and comparison of putative drug target proteins in malaria. Malaria Journal, 2009, 8, 178.	0.8	9
207	A systematic classification of Plasmodium falciparum P-loop NTPases: structural and functional correlation. Malaria Journal, 2009, 8, 69.	0.8	10
208	Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. Genome Biology, 2009, 10, R86.	13.9	25
209	The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. Genome Biology, 2009, 10, R58.	13.9	38
210	Detection of Gene Orthology Based on Protein-Protein Interaction Networks. , 2009, , .		4
211	A Novel Heuristic for Local Multiple Alignment of Interspersed DNA Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 180-189.	1.9	14
212	Comparative genomics of the fungal pathogens <i>Candida dubliniensis</i> and <i>Candida albicans</i>. Genome Research, 2009, 19, 2231-2244.	2.4	195
213	Genome Sequences of Escherichia coli B strains REL606 and BL21(DE3). Journal of Molecular Biology, 2009, 394, 644-652.	2.0	316
214	Multi-granularity Parallel Computing in a Genome-Scale Molecular Evolution Application. Lecture Notes in Computer Science, 2009, 5698, 49-59.	1.0	0
215	Comparative Genome Analysis. , 2009, , 33-58.		0
216	A Draft Genome Sequence of <i>Pseudomonas syringae</i> pv. <i>tomato</i> T1 Reveals a Type III Effector Repertoire Significantly Divergent from That of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. Molecular Plant-Microbe Interactions, 2009, 22, 52-62.	1.4	134
217	Historical Constraints on Vertebrate Genome Evolution. Genome Biology and Evolution, 2010, 2, 13-18.	1.1	13
218	Genome-Wide Influence of Indel Substitutions on Evolution of Bacteria of the PVC Superphylum, Revealed Using a Novel Computational Method. Genome Biology and Evolution, 2010, 2, 870-886.	1.1	23
219	The Sequence of a 1.8-Mb Bacterial Linear Plasmid Reveals a Rich Evolutionary Reservoir of Secondary Metabolic Pathways. Genome Biology and Evolution, 2010, 2, 212-224.	1.1	193

#	ARTICLE	IF	CITATIONS
221	Some Algorithmic Challenges in Genome-Wide Ortholog Assignment. Journal of Computer Science and Technology, 2010, 25, 42-52.	0.9	9
222	MSOAR 2.0: Incorporating tandem duplications into ortholog assignment based on genome rearrangement. BMC Bioinformatics, 2010, 11, 10.	1.2	72
223	Scaffold filling, contig fusion and comparative gene order inference. BMC Bioinformatics, 2010, 11, 304.	1.2	50
224	Enrichment of homologs in insignificant BLAST hits by co-complex network alignment. BMC Bioinformatics, 2010, 11, 86.	1.2	8
225	The Potential for pathogenicity was present in the ancestor of the Ascomycete subphylum Pezizomycotina. BMC Evolutionary Biology, 2010, 10, 318.	3.2	4
226	Conservation and divergence of known apicomplexan transcriptional regulons. BMC Genomics, 2010, 11, 147.	1.2	14
227	Drug target prediction and prioritization: using orthology to predict essentiality in parasite genomes. BMC Genomics, 2010, 11, 222.	1.2	76
228	The Alveolate Perkinsus marinus: Biological Insights from EST Gene Discovery. BMC Genomics, 2010, 11, 228.	1.2	92
229	Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of Xanthomonas fuscans subsp. aurantifolii. BMC Genomics, 2010, 11, 238.	1.2	102
230	Genomic organization of eukaryotic tRNAs. BMC Genomics, 2010, 11, 270.	1.2	91
231	The collapse of gene complement following whole genome duplication. BMC Genomics, 2010, 11, 313.	1.2	114
232	Comparative genomics of the family Vibrionaceae reveals the wide distribution of genes encoding virulence-associated proteins. BMC Genomics, 2010, 11, 369.	1.2	14
233	Drawing the line between commensal and pathogenic Gardnerella vaginalis through genome analysis and virulence studies. BMC Genomics, 2010, 11, 375.	1.2	127
234	Evolution of electron transfer out of the cell: comparative genomics of six Geobacter genomes. BMC Genomics, 2010, 11, 40.	1.2	170
235	Orthology confers intron position conservation. BMC Genomics, 2010, 11, 412.	1.2	29
236	YeastWeb: a workset-centric web resource for gene family analysis in yeast. BMC Genomics, 2010, 11, 429.	1.2	1
237	The genome of Geobacter bemidjiensis, exemplar for the subsurface clade of Geobacter species that predominate in Fe(III)-reducing subsurface environments.. BMC Genomics, 2010, 11, 490.	1.2	52
238	Probing the pan-genome of Listeria monocytogenes: new insights into intraspecific niche expansion and genomic diversification. BMC Genomics, 2010, 11, 500.	1.2	74

#	Article	IF	Citations
239	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
240	Relationship between operon preference and functional properties of persistent genes in bacterial genomes. BMC Genomics, 2010, 11, 71.	1.2	24
241	Combining modularity, conservation, and interactions of proteins significantly increases precision and coverage of protein function prediction. BMC Genomics, 2010, 11, 717.	1.2	12
242	FUNGIpath: a tool to assess fungal metabolic pathways predicted by orthology. BMC Genomics, 2010, 11, 81.	1.2	39
243	Core genome components and lineage specific expansions in malaria parasites Plasmodium. BMC Genomics, 2010, 11, S13.	1.2	8
244	3D-interologs: an evolution database of physical protein- protein interactions across multiple genomes. BMC Genomics, 2010, 11, S7.	1.2	34
245	Refining orthologue groups at the transcript level. BMC Genomics, 2010, 11, S11.	1.2	5
246	Vibrio chromosomes share common history. BMC Microbiology, 2010, 10, 137.	1.3	37
247	Dioecious Silene latifolia plants show sexual dimorphism in the vegetative stage. BMC Plant Biology, 2010, 10, 208.	1.6	39
248	Molecular and phylogenetic characterization of the sieve element occlusion gene family in Fabaceae and non-Fabaceaeplants. BMC Plant Biology, 2010, 10, 219.	1.6	61
249	A putative kinase-related protein (PKRP) from Plasmodium berghei mediates infection in the midgut and salivary glands of the mosquito. International Journal for Parasitology, 2010, 40, 979-988.	1.3	3
250	Phylogenomic analysis of 11 complete African swine fever virus genome sequences. Virology, 2010, 400, 128-136.	1.1	134
251	Detection of gene orthology from gene co-expression and protein interaction networks. BMC Bioinformatics, 2010, 11, S7.	1.2	24
252	Global analysis of the rat and human platelet proteome â€" the molecular blueprint for illustrating multiâ€functional platelets and crossâ€species function evolution. Proteomics, 2010, 10, 2444-2457.	1.3	33
253	Characteristics of the genome of <i>Arsenophonus nasoniae</i>, sonâ€killer bacterium of the wasp <i>Nasonia</i>. Insect Molecular Biology, 2010, 19, 75-89.	1.0	94
254	Genome sequence of the model mushroom Schizophyllum commune. Nature Biotechnology, 2010, 28, 957-963.	9.4	490
255	The Genome Sequence of<i>Methanohalophilus mahii</i>SLP^TReveals Differences in the Energy Metabolism among Members of the<i>Methanosarcinaceae</i>Inhabiting Freshwater and Saline Environments. Archaea, 2010, 2010, 1-16.	2.3	35
256	The Human-Bacterial Pathogen Protein Interaction Networks of Bacillus anthracis, Francisella tularensis, and Yersinia pestis. PLoS ONE, 2010, 5, e12089.	1.1	131

#	Article	IF	Citations
257	Comparative Genome Analysis Reveals an Absence of Leucine-Rich Repeat Pattern-Recognition Receptor Proteins in the Kingdom Fungi. PLoS ONE, 2010, 5, e12725.	1.1	31
258	Scaffolding a <i>Caenorhabditis</i> nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747.	2.4	83
259	Host-Interactive Genes in Amerindian<i>Helicobacter pylori</i>Diverge from Their Old World Homologs and Mediate Inflammatory Responses. Journal of Bacteriology, 2010, 192, 3078-3092.	1.0	50
260	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. Bioinformatics, 2010, 26, 1481-1487.	1.8	213
261	Conserved Symbiotic Plasmid DNA Sequences in the Multireplicon Pangenomic Structure of <i>Rhizobium etli</i>. Applied and Environmental Microbiology, 2010, 76, 1604-1614.	1.4	86
262	ProPhylER: A curated online resource for protein function and structure based on evolutionary constraint analyses. Genome Research, 2010, 20, 142-154.	2.4	28
263	Genome Sequence of Lactobacillus crispatus ST1. Journal of Bacteriology, 2010, 192, 3547-3548.	1.0	38
264	Identification of Three Novel Superantigen-Encoding Genes in <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> , <i>szeF</i> , <i>szeN</i> , and <i>szeP</i>. Infection and Immunity, 2010, 78, 4817-4827.	1.0	56
265	Vaxign: The First Web-Based Vaccine Design Program for Reverse Vaccinology and Applications for Vaccine Development. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-15.	3.0	260
266	Genome-Wide Analysis of Ethylene-Responsive Element Binding Factor-Associated Amphiphilic Repression Motif-Containing Transcriptional Regulators in Arabidopsis. Plant Physiology, 2010, 152, 1109-1134.	2.3	262
267	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. Nucleic Acids Research, 2010, 38, D190-D195.	6.5	202
268	Cross-Kingdom Comparison of Transcriptomic Adjustments to Low-Oxygen Stress Highlights Conserved and Plant-Specific Responses. Plant Physiology, 2010, 152, 1484-1500.	2.3	306
269	Comparative Genomics and Transduction Potential of <i>Enterococcus faecalis</i> Temperate Bacteriophages. Journal of Bacteriology, 2010, 192, 1122-1130.	1.0	71
270	Phylogeny of Gammaproteobacteria. Journal of Bacteriology, 2010, 192, 2305-2314.	1.0	317
271	Low-Complexity Regions in Plasmodium falciparum: Missing Links in the Evolution of an Extreme Genome. Molecular Biology and Evolution, 2010, 27, 2198-2209.	3.5	56
272	Gene-oriented ortholog database: a functional comparison platform for orthologous loci. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq002-baq002.	1.4	7
273	Getting Started in Gene Orthology and Functional Analysis. PLoS Computational Biology, 2010, 6, e1000703.	1.5	100
274	Characterizing the Metabolism of Dehalococcoides with a Constraint-Based Model. PLoS Computational Biology, 2010, 6, e1000887.	1.5	46

#	Article	IF	Citations
275	The Extinction Dynamics of Bacterial Pseudogenes. PLoS Genetics, 2010, 6, e1001050.	1.5	146
276	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
277	Reconstruction of the Core and Extended Regulons of Global Transcription Factors. PLoS Genetics, 2010, 6, e1001027.	1.5	62
278	Meeting report: a workshop on Best Practices in Genome Annotation. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq001-baq001.	1.4	18
279	The Impact of Gene Expression Regulation on Evolution of Extracellular Signaling Pathways. Molecular and Cellular Proteomics, 2010, 9, 2666-2677.	2.5	8
280	Construction of a Large Extracellular Protein Interaction Network and Its Resolution by Spatiotemporal Expression Profiling. Molecular and Cellular Proteomics, 2010, 9, 2654-2665.	2.5	37
281	Markov clustering of protein interaction networks with improved balance and scalability. , 2010, , .		59
282	Homology prediction refinement and reconstruction of gene content and order of ancestral bacterial genomes. , 2010, , .		1
283	Evolutionary Relationships of Wild Hominids Recapitulated by Gut Microbial Communities. PLoS Biology, 2010, 8, e1000546.	2.6	464
284	Complex prokaryotic genome structure: rapid evolution of chromosome II. Genome, 2010, 53, 675-687.	0.9	18
285	Reconstructing Gene Histories in Ascomycota Fungi. Methods in Enzymology, 2010, 470, 447-485.	0.4	3
286	PLAZA: A Comparative Genomics Resource to Study Gene and Genome Evolution in Plants. Plant Cell, 2010, 21, 3718-3731.	3.1	243
287	Insights from the Comparison of Plant Genome Sequences. Annual Review of Plant Biology, 2010, 61, 349-372.	8.6	202
288	Large-Scale Comparative Phosphoproteomics Identifies Conserved Phosphorylation Sites in Plants Â Â. Plant Physiology, 2010, 153, 1161-1174.	2.3	361
289	Accumulation, functional annotation, and comparative analysis of expressed sequence tags in eggplant (Solanum melongena L.), the third pole of the genus Solanum species after tomato and potato. Gene, 2010, 450, 76-84.	1.0	39
290	Introducing the bacterial â€˜chromidâ€™: not a chromosome, not a plasmid. Trends in Microbiology, 2010, 18, 141-148.	3.5	337
291	2Ã— genomes - depth does matter. Genome Biology, 2010, 11, R16.	13.9	47
292	Shotgun Proteomic Analysis of Yeast-Elicited California Poppy (Eschscholzia californica) Suspension Cultures Producing Enhanced Levels of Benzophenanthridine Alkaloids. Journal of Proteome Research, 2010, 9, 4337-4345.	1.8	17

#	ARTICLE	IF	CITATIONS
293	Issues with the PipeAlign phylogenomics toolkit in identifying protein subfamilies. , 2010, , .		0
294	Multiple <i>GAL</i> pathway gene clusters evolved independently and by different mechanisms in fungi. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10136-10141.	3.3	144
295	Evolution of biological interaction networks: from models to real data. Genome Biology, 2011, 12, 235.	13.9	37
296	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. Nucleic Acids Research, 2011, 39, W339-W346.	6.5	1,622
297	Spectral Clustering on Neighborhood Kernels with Modified Symmetry for Remote Homology Detection. , 2011, , .		1
298	Identifying positional homologs as bidirectional best hits of sequence and gene context similarity. , 2011, , .		0
299	The what, where, how and why of gene ontology--a primer for bioinformaticians. Briefings in Bioinformatics, 2011, 12, 723-735.	3.2	122
300	Genome sequence and analysis of the tuber crop potato. Nature, 2011, 475, 189-195.	13.7	1,912
302	Classifying Proteins into Functional Groups Based on All-versus-All BLAST of 10 Million Proteins. OMICS A Journal of Integrative Biology, 2011, 15, 513-521.	1.0	11
303	Community Discovery in Social Networks: Applications, Methods and Emerging Trends. , 2011, , 79-113.		62
304	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	1.5	902
305	Phylogenetic Analysis of Protein Sequence Data Using the Randomized Axelerated Maximum Likelihood (<scp>RAXML</scp>) Program. Current Protocols in Molecular Biology, 2011, 96, Unit19.11.	2.9	43
306	Constitutive expression of a grapevine polygalacturonase-inhibiting protein affects gene expression and cell wall properties in uninfected tobacco. BMC Research Notes, 2011, 4, 493.	0.6	30
307	Comparative transcriptome analysis reveals vertebrate phylotypic period during organogenesis. Nature Communications, 2011, 2, 248.	5.8	256
309	The Evolutionary History of YAP and the Hippo/YAP Pathway. Molecular Biology and Evolution, 2011, 28, 2403-2417.	3.5	134
310	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic Xanthomonas spp. Journal of Bacteriology, 2011, 193, 5450-5464.	1.0	189
311	Comparative genomics of the pathogenic ciliate Ichthyophthirius multifiliis, its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. Genome Biology, 2011, 12, R100.	13.9	102
312	A physical map for the Amborella trichopoda genome sheds light on the evolution of angiosperm genome structure. Genome Biology, 2011, 12, R48.	13.9	28

#	Article	IF	Citations
313	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of Trichoderma. Genome Biology, 2011, 12, R40.	3.8	594
314	Using OrthoMCL to Assign Proteins to OrthoMCLâ€DB Groups or to Cluster Proteomes Into New Ortholog Groups. Current Protocols in Bioinformatics, 2011, 35, Unit 6.12.1-19.	25.8	397
315	Inferring Protein Function from Homology Using the Princeton Protein Orthology Database (Pâ€POD). Current Protocols in Bioinformatics, 2011, 33, Unit 6.11.	25.8	4
316	The Monarch Butterfly Genome Yields Insights into Long-Distance Migration. Cell, 2011, 147, 1171-1185.	13.5	509
317	Target identification and validation of novel antimalarials. Future Microbiology, 2011, 6, 693-704.	1.0	30
318	Exploring the genomes: From Arabidopsis to crops. Journal of Plant Physiology, 2011, 168, 3-8.	1.6	15
319	Phylogenomic Evidence for the Presence of a Flagellum and cbb3 Oxidase in the Free-Living Mitochondrial Ancestor. Molecular Biology and Evolution, 2011, 28, 3285-3296.	3.5	124
320	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13212-13217.	3.3	163
321	Plant protein-coding gene families: emerging bioinformatics approaches. Trends in Plant Science, 2011, 16, 558-567.	4.3	31
322	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	3.2	217
323	Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. Plant Genome, 2011, 4, 191-203.	1.6	131
324	Reassessing Domain Architecture Evolution of Metazoan Proteins: Major Impact of Gene Prediction Errors. Genes, 2011, 2, 449-501.	1.0	20
325	Genome Characterization of the Oleaginous Fungus Mortierella alpina. PLoS ONE, 2011, 6, e28319.	1.1	133
326	Targeting Protein-Protein Interactions for Parasite Control. PLoS ONE, 2011, 6, e18381.	1.1	31
327	Evaluating Ortholog Prediction Algorithms in a Yeast Model Clade. PLoS ONE, 2011, 6, e18755.	1.1	84
328	Intracellular Eukaryotic Parasites Have a Distinct Unfolded Protein Response. PLoS ONE, 2011, 6, e19118.	1.1	45
329	Novel Insights into the Diversity of Catabolic Metabolism from Ten Haloarchaeal Genomes. PLoS ONE, 2011, 6, e20237.	1.1	72
330	MultiMSOAR 2.0: An Accurate Tool to Identify Ortholog Groups among Multiple Genomes. PLoS ONE, 2011, 6, e20892.	1.1	16

#	ARTICLE	IF	CITATIONS
331	Genome Sequencing Reveals Unique Mutations in Characteristic Metabolic Pathways and the Transfer of Virulence Genes between V. mimicus and V. cholerae. PLoS ONE, 2011, 6, e21299.	1.1	25
332	Gain, Loss and Divergence in Primate Zinc-Finger Genes: A Rich Resource for Evolution of Gene Regulatory Differences between Species. PLoS ONE, 2011, 6, e21553.	1.1	48
333	Codivergence of Mycoviruses with Their Hosts. PLoS ONE, 2011, 6, e22252.	1.1	46
334	Pseudomonas aeruginosa AES-1 Exhibits Increased Virulence Gene Expression during Chronic Infection of Cystic Fibrosis Lung. PLoS ONE, 2011, 6, e24526.	1.1	31
335	Calculating Orthologs in Bacteria and Archaea: A Divide and Conquer Approach. PLoS ONE, 2011, 6, e28388.	1.1	24
336	Comparative Genomic Analysis of the Streptococcus dysgalactiae Species Group: Gene Content, Molecular Adaptation, and Promoter Evolution. Genome Biology and Evolution, 2011, 3, 168-185.	1.1	52
337	Functional modelling of an equine bronchoalveolar lavage fluid proteome provides experimental confirmation and functional annotation of equine genome sequences. Animal Genetics, 2011, 42, 395-405.	0.6	8
338	Genomeâ€wide Expansion and Expression Divergence of the Basic Leucine Zipper Transcription Factors in Higher Plants with an Emphasis on Sorghum^F. Journal of Integrative Plant Biology, 2011, 53, 212-231.	4.1	157
339	The genome of Theobroma cacao. Nature Genetics, 2011, 43, 101-108.	9.4	656
340	The draft genome of the parasitic nematode Trichinella spiralis. Nature Genetics, 2011, 43, 228-235.	9.4	285
341	The Arabidopsis lyrata genome sequence and the basis of rapid genome size change. Nature Genetics, 2011, 43, 476-481.	9.4	814
342	Ancestral polyploidy in seed plants and angiosperms. Nature, 2011, 473, 97-100.	13.7	1,862
343	Classification and identification of the Burkholderia cepacia complex: Past, present and future. Systematic and Applied Microbiology, 2011, 34, 87-95.	1.2	169
344	Molecular characterization of the uncultivatable hemotropic bacterium Mycoplasma haemofelis. Veterinary Research, 2011, 42, 83.	1.1	15
345	Proteinortho: Detection of (Co-)orthologs in large-scale analysis. BMC Bioinformatics, 2011, 12, 124.	1.2	1,091
346	Horizontal gene transfer in silkworm, Bombyx mori. BMC Genomics, 2011, 12, 248.	1.2	45
347	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	9.4	1,893
348	Horizontal Transfer of a Large and Highly Toxic Secondary Metabolic Gene Cluster between Fungi. Current Biology, 2011, 21, 134-139.	1.8	253

#	Article	IF	Citations
349	Applications of high-throughput sequencing to symbiotic nematodes of the genus Heterorhabditis. Symbiosis, 2011, 55, 111-118.	1.2	8
350	Validation of computational prediction of horizontal gene transfer eventsâ€"XenoCluster. Journal of Supercomputing, 2011, 57, 141-150.	2.4	0
351	Eimeria maxima phosphatidylinositol 4-phosphate 5-kinase: locus sequencing, characterization, and cross-phylum comparison. Parasitology Research, 2011, 108, 611-620.	0.6	1
352	Human and chicken TLR pathways: manual curation and computer-based orthology analysis. Mammalian Genome, 2011, 22, 130-138.	1.0	18
353	Selection-Driven Divergence After Gene Duplication in Arabidopsis thaliana. Journal of Molecular Evolution, 2011, 73, 153-165.	0.8	16
354	A Closer Look at Bacteroides: Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. Microbial Ecology, 2011, 61, 473-485.	1.4	135
355	An EST-based analysis identifies new genes and reveals distinctive gene expression features of Coffea arabica and Coffea canephora. BMC Plant Biology, 2011, 11, 30.	1.6	67
356	Interplay of recombination and selection in the genomes of Chlamydia trachomatis. Biology Direct, 2011, 6, 28.	1.9	70
357	Improving pan-genome annotation using whole genome multiple alignment. BMC Bioinformatics, 2011, 12, 272.	1.2	38
358	An integrative approach to ortholog prediction for disease-focused and other functional studies. BMC Bioinformatics, 2011, 12, 357.	1.2	629
359	Using context to improve protein domain identification. BMC Bioinformatics, 2011, 12, 90.	1.2	44
360	Identification of conserved gene clusters in multiple genomes based on synteny and homology. BMC Bioinformatics, 2011, 12, S18.	1.2	8
361	Phylogenomic reconstruction of lactic acid bacteria: an update. BMC Evolutionary Biology, 2011, 11, 1.	3.2	312
362	Evidence for the additions of clustered interacting nodes during the evolution of protein interaction networks from network motifs. BMC Evolutionary Biology, 2011, 11, 133.	3.2	17
363	Genome fluctuations in cyanobacteria reflect evolutionary, developmental and adaptive traits. BMC Evolutionary Biology, 2011, 11, 187.	3.2	151
364	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. BMC Evolutionary Biology, 2011, 11, 8.	3.2	88
365	Identification, variation and transcription of pneumococcal repeat sequences. BMC Genomics, 2011, 12, 120.	1.2	48
366	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. BMC Genomics, 2011, 12, 146.	1.2	167

#	ARTICLE	IF	CITATIONS
367	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	1.2	49
368	Genome-wide analysis of WRKY gene family in Cucumis sativus. BMC Genomics, 2011, 12, 471.	1.2	236
369	The Cryptosporidium parvum Kinome. BMC Genomics, 2011, 12, 478.	1.2	35
370	Comparative Genomics of Helicobacter pylori and the human-derived Helicobacter bizzozeronii CIII-1 strain reveal the molecular basis of the zoonotic nature of non-pylori gastric Helicobacter infections in humans. BMC Genomics, 2011, 12, 534.	1.2	32
371	De novo assembly of Euphorbia fischeriana root transcriptome identifies prostratin pathway related genes. BMC Genomics, 2011, 12, 600.	1.2	75
372	Preimplantation development regulatory pathway construction through a text-mining approach. BMC Genomics, 2011, 12, S3.	1.2	6
374	Many task computing for orthologous genes identification in protozoan genomes using Hydra. Concurrency Computation Practice and Experience, 2011, 23, 2326-2337.	1.4	8
375	In silico bioinformatic tools for determining core genes from sets of genomes. Drug Development Research, 2011, 72, 147-152.	1.4	0
376	A statistical approach to high-throughput screening of predicted orthologs. Computational Statistics and Data Analysis, 2011, 55, 935-943.	0.7	2
377	Comparative genomics and the role of lateral gene transfer in the evolution of bovine adapted Streptococcus agalactiae. Infection, Genetics and Evolution, 2011, 11, 1263-1275.	1.0	99
378	Resolving the question of trypanosome monophyly: A comparative genomics approach using whole genome data sets with low taxon sampling. Infection, Genetics and Evolution, 2011, 11, 955-959.	1.0	15
379	Horizontal gene transfer facilitated the evolution of plant parasitic mechanisms in the oomycetes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15258-15263.	3.3	225
380	The Transcriptional Response of Listeria monocytogenes during Adaptation to Growth on Lactate and Diacetate Includes Synergistic Changes That Increase Fermentative Acetoin Production. Applied and Environmental Microbiology, 2011, 77, 5294-5306.	1.4	53
381	Parallel evolution of transcriptome architecture during genome reorganization. Genome Research, 2011, 21, 1892-1904.	2.4	58
382	The Comprehensive Phytopathogen Genomics Resource: a web-based resource for data-mining plant pathogen genomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar053-bar053.	1.4	26
383	Phosphate Deprivation in Maize: Genetics and Genomics. Plant Physiology, 2011, 156, 1067-1077.	2.3	83
384	Complete Genome Sequence of Mycoplasma haemofelis, a Hemotropic Mycoplasma. Journal of Bacteriology, 2011, 193, 2060-2061.	1.0	21
385	Evolutionarily Conserved Orthologous Families in Phages Are Relatively Rare in Their Prokaryotic Hosts. Journal of Bacteriology, 2011, 193, 1806-1814.	1.0	45

#	ARTICLE	IF	CITATIONS
386	OrthoDisease: tracking disease gene orthologs across 100 species. Briefings in Bioinformatics, 2011, 12, 463-473.	3.2	16
387	Ortholog identification in the presence of domain architecture rearrangement. Briefings in Bioinformatics, 2011, 12, 413-422.	3.2	28
388	Characterization and Inference of Gene Gain/Loss along Burkholderia Evolutionary History. Evolutionary Bioinformatics, 2011, 7, EBO.S7510.	0.6	10
389	An Enterotoxin-Bearing Pathogenicity Island in Staphylococcus epidermidis. Journal of Bacteriology, 2011, 193, 1854-1862.	1.0	54
390	QuartetS: a fast and accurate algorithm for large-scale orthology detection. Nucleic Acids Research, 2011, 39, e88-e88.	6.5	32
391	Core and Panmetabolism in <i>Escherichia coli</i>. Journal of Bacteriology, 2011, 193, 1461-1472.	1.0	51
392	Result verification, code verification and computation of support values in phylogenetics. Briefings in Bioinformatics, 2011, 12, 270-279.	3.2	5
393	The<i>sieve element occlusion</i>gene family in dicotyledonous plants. Plant Signaling and Behavior, 2011, 6, 151-153.	1.2	22
394	Genome Variation in Cryptococcus gattii, an Emerging Pathogen of Immunocompetent Hosts. MBio, 2011, 2, e00342-10.	1.8	182
395	A Bayesian Approach for Fast and Accurate Gene Tree Reconstruction. Molecular Biology and Evolution, 2011, 28, 273-290.	3.5	110
396	PhyloPro: a web-based tool for the generation and visualization of phylogenetic profiles across Eukarya. Bioinformatics, 2011, 27, 877-878.	1.8	10
397	Integration of sequence-similarity and functional association information can overcome intrinsic problems in orthology mapping across bacterial genomes. Nucleic Acids Research, 2011, 39, e150-e150.	6.5	11
398	dictyBase update 2011: web 2.0 functionality and the initial steps towards a genome portal for the Amoebozoa. Nucleic Acids Research, 2011, 39, D620-D624.	6.5	39
399	Quantifying Nonvertical Inheritance in the Evolution of Legionella pneumophila. Molecular Biology and Evolution, 2011, 28, 985-1001.	3.5	47
400	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i>. Genome Research, 2011, 21, 2129-2142.	2.4	380
401	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509.	3.3	218
402	ReMark: an automatic program for clustering orthologs flexibly combining a Recursive and a Markovclustering algorithms. Bioinformatics, 2011, 27, 1731-1733.	1.8	13
403	Gene Gain and Loss during Evolution of Obligate Parasitism in the White Rust Pathogen of Arabidopsis thaliana. PLoS Biology, 2011, 9, e1001094.	2.6	271

#	ARTICLE	IF	CITATIONS
404	The Genome Sequence of the Leaf-Cutter Ant Atta cephalotes Reveals Insights into Its Obligate Symbiotic Lifestyle. PLoS Genetics, 2011, 7, e1002007.	1.5	231
405	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. PLoS Genetics, 2011, 7, e1002345.	1.5	164
406	The Plant Pathogen Pseudomonas syringae pv. tomato Is Genetically Monomorphic and under Strong Selection to Evade Tomato Immunity. PLoS Pathogens, 2011, 7, e1002130.	2.1	186
407	Comparative and Functional Genomics of Rhodococcus opacus PD630 for Biofuels Development. PLoS Genetics, 2011, 7, e1002219.	1.5	109
408	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen Bursaphelenchus xylophilus. PLoS Pathogens, 2011, 7, e1002219.	2.1	351
409	OMA 2011: orthology inference among 1000 complete genomes. Nucleic Acids Research, 2011, 39, D289-D294.	6.5	185
410	Phylogenomics Reveals an Anomalous Distribution of USP Genes in Metazoans. Molecular Biology and Evolution, 2011, 28, 153-161.	3.5	19
411	An Erythrocyte Cytoskeleton-Binding Motif in Exported Plasmodium falciparum Proteins. Eukaryotic Cell, 2011, 10, 1439-1447.	3.4	31
412	Identifying discriminative classification-based motifs in biological sequences. Bioinformatics, 2011, 27, 1231-1238.	1.8	93
413	Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. Genome Research, 2011, 21, 1882-1891.	2.4	145
414	PETcofold: predicting conserved interactions and structures of two multiple alignments of RNA sequences. Bioinformatics, 2011, 27, 211-219.	1.8	52
415	Jumbled Genomes: Missing Apicomplexan Synteny. Molecular Biology and Evolution, 2011, 28, 2855-2871.	3.5	65
416	Identifying Single Copy Orthologs in Metazoa. PLoS Computational Biology, 2011, 7, e1002269.	1.5	23
417	Horizontal Transfer, Not Duplication, Drives the Expansion of Protein Families in Prokaryotes. PLoS Genetics, 2011, 7, e1001284.	1.5	426
418	Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough. PLoS Biology, 2011, 9, e1000602.	2.6	932
419	Genomic Transition to Pathogenicity in Chytrid Fungi. PLoS Pathogens, 2011, 7, e1002338.	2.1	99
420	Detecting Network Communities: An Application to Phylogenetic Analysis. PLoS Computational Biology, 2011, 7, e1001131.	1.5	21
421	Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga Nannochloropsis oceanica CCMP1779. PLoS Genetics, 2012, 8, e1003064.	1.5	376

#	Article	IF	Citations
422	Predicting and Analyzing Protein Phosphorylation Sites in Plants Using Musite. Frontiers in Plant Science, 2012, 3, 186.	1.7	27
423	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. Viruses, 2012, 4, 3209-3226.	1.5	156
424	The Chordate Proteome History Database. Evolutionary Bioinformatics, 2012, 8, EBO.S9186.	0.6	5
425	The Biofuel Feedstock Genomics Resource: a web-based portal and database to enable functional genomics of plant biofuel feedstock species. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar061.	1.4	22
426	The genome of the heartworm, <i>Dirofilaria immitis</i> , reveals drug and vaccine targets. FASEB Journal, 2012, 26, 4650-4661.	0.2	124
427	Comparative Genomics of the Apicomplexan Parasites Toxoplasma gondii and Neospora caninum: Coccidia Differing in Host Range and Transmission Strategy. PLoS Pathogens, 2012, 8, e1002567.	2.1	206
428	The CanOE Strategy: Integrating Genomic and Metabolic Contexts across Multiple Prokaryote Genomes to Find Candidate Genes for Orphan Enzymes. PLoS Computational Biology, 2012, 8, e1002540.	1.5	32
429	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus Magnaporthe oryzae. PLoS Genetics, 2012, 8, e1002869.	1.5	167
430	ProteinHistorian: Tools for the Comparative Analysis of Eukaryote Protein Origin. PLoS Computational Biology, 2012, 8, e1002567.	1.5	89
431	Evolution and Architecture of the Inner Membrane Complex in Asexual and Sexual Stages of the Malaria Parasite. Molecular Biology and Evolution, 2012, 29, 2113-2132.	3.5	135
432	LegumeIP: an integrative database for comparative genomics and transcriptomics of model legumes. Nucleic Acids Research, 2012, 40, D1221-D1229.	6.5	91
433	Revised Phylogeny and Novel Horizontally Acquired Virulence Determinants of the Model Soft Rot Phytopathogen Pectobacterium wasabiae SCC3193. PLoS Pathogens, 2012, 8, e1003013.	2.1	93
434	Comparative Genomics of Enterococci: Variation in Enterococcus faecalis, Clade Structure in E. faecium, and Defining Characteristics of <i>E</i> .Â <i>gallinarum</i> and <i>E</i> .Â <i>casseliflavus</i>. MBio, 2012, 3, e00318-11.	1.8	259
435	Genome Sequence of Rickettsia conorii subsp. caspia, the Agent of Astrakhan Fever. Journal of Bacteriology, 2012, 194, 4763-4764.	1.0	6
436	Looking Deep Inside: Detection of Low-Abundance Proteins in Leaf Extracts of Arabidopsis and Phloem Exudates of Pumpkin Â. Plant Physiology, 2012, 159, 902-914.	2.3	51
437	Genome Sequence for â€œCandidatus Mycoplasma haemominutum,â€• a Low-Pathogenicity Hemoplasma Species. Journal of Bacteriology, 2012, 194, 905-906.	1.0	13
438	Genomic Comparison of Rickettsia helvetica and Other Rickettsia Species. Journal of Bacteriology, 2012, 194, 2751-2751.	1.0	9
439	Analysis of Genome Content Evolution in PVC Bacterial Super-Phylum: Assessment of Candidate Genes Associated with Cellular Organization and Lifestyle. Genome Biology and Evolution, 2012, 4, 1375-1390.	1.1	51

#	ARTICLE	IF	CITATIONS
440	Causes and Consequences of Genome Expansion in Fungi. Genome Biology and Evolution, 2012, 4, 13-23.	1.1	68
441	ViPR: an open bioinformatics database and analysis resource for virology research. Nucleic Acids Research, 2012, 40, D593-D598.	6.5	610
442	FungiDB: an integrated functional genomics database for fungi. Nucleic Acids Research, 2012, 40, D675-D681.	6.5	321
443	Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species. PLoS ONE, 2012, 7, e37135.	1.1	2,836
444	MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Research, 2012, 40, e49-e49.	6.5	4,252
445	Genome Sequence of Rickettsia conorii subsp. israelensis, the Agent of Israeli Spotted Fever. Journal of Bacteriology, 2012, 194, 5130-5131.	1.0	9
446	Genome Sequence of Rickettsia conorii subsp.<i>indica</i>, the Agent of Indian Tick Typhus. Journal of Bacteriology, 2012, 194, 3288-3289.	1.0	15
447	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. MBio, 2012, 3, e00259-12.	1.8	211
448	Dissecting Plant Genomes with the PLAZA Comparative Genomics Platform Â. Plant Physiology, 2012, 158, 590-600.	2.3	238
449	A Rickettsia Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. Journal of Bacteriology, 2012, 194, 376-394.	1.0	152
450	Accessibility and conservation: General features of bacterial small RNAâ€"mRNA interactions?. RNA Biology, 2012, 9, 954-965.	1.5	56
451	A machine learning framework for trait based genomics. , 2012, , .		3
452	Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research, 2012, 40, D1178-D1186.	6.5	4,204
453	Sequence and Annotation of Rickettsia sibirica sibirica Genome. Journal of Bacteriology, 2012, 194, 2377-2377.	1.0	7
454	Genomic characterization of the <i>Bacillus cereus</i> sensu lato species: Backdrop to the evolution of <i>Bacillus anthracis</i>. Genome Research, 2012, 22, 1512-1524.	2.4	148
455	MIPS PlantsDB: a database framework for comparative plant genome research. Nucleic Acids Research, 2012, 41, D1144-D1151.	6.5	179
456	Molecular Evolution in Nonrecombining Regions of the Drosophila melanogaster Genome. Genome Biology and Evolution, 2012, 4, 278-288.	1.1	51
457	Genome Sequence of Pectobacterium sp. Strain SCC3193. Journal of Bacteriology, 2012, 194, 6004-6004.	1.0	17

#	Article	IF	Citations
458	Comparative Analysis of Genome Sequences Covering the Seven Cronobacter Species. PLoS ONE, 2012, 7, e49455.	1.1	130
459	A framework for readapting and running bioinformatics applications in the cloud. , 2012, , .		0
460	Interkingdom Gene Transfer May Contribute to the Evolution of Phytopathogenicity in <i>Botrytis Cinerea</i>. Evolutionary Bioinformatics, 2012, 8, EBO.S8486.	0.6	8
461	PsRobot: a web-based plant small RNA meta-analysis toolbox. Nucleic Acids Research, 2012, 40, W22-W28.	6.5	448
462	Investigating the Relationship between Topology and Evolution in a Dynamic Nematode Odor Genetic Network. International Journal of Evolutionary Biology, 2012, 2012, 1-8.	1.0	2
463	Listeria monocytogenes Shows Temperature-Dependent and -Independent Responses to Salt Stress, Including Responses That Induce Cross-Protection against Other Stresses. Applied and Environmental Microbiology, 2012, 78, 2602-2612.	1.4	108
464	Elephant Transcriptome Provides Insights into the Evolution of Eutherian Placentation. Genome Biology and Evolution, 2012, 4, 713-725.	1.1	27
465	Genome Sequence of â€œRickettsia sibirica subsp. mongolitimonaeâ€. Journal of Bacteriology, 2012, 194, 2389-2390.	1.0	7
466	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
467	PanOCT: automated clustering of orthologs using conserved gene neighborhood for pan-genomic analysis of bacterial strains and closely related species. Nucleic Acids Research, 2012, 40, e172-e172.	6.5	227
468	The evolution of nitrogen fixation in cyanobacteria. Bioinformatics, 2012, 28, 603-606.	1.8	88
469	Comparative Genomics of Early-Diverging Brucella Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. MBio, 2012, 3, e00246-12.	1.8	37
470	Dynamic Nucleotide-Binding Site and Leucine-Rich Repeat-Encoding Genes in the Grass Family Â Â Â. Plant Physiology, 2012, 159, 197-210.	2.3	132
471	Transcriptional and Metabolic Analysis of Senescence Induced by Preventing Pollination in Maize. Plant Physiology, 2012, 159, 1730-1744.	2.3	90
472	Complete genome sequence of the termite hindgut bacterium Spirochaeta coccoides type strain (SPN1T), reclassification in the genus Sphaerochaeta as Sphaerochaeta coccoides comb. nov. and emendations of the family Spirochaetaceae and the genus Sphaerochaeta. Standards in Genomic Sciences, 2012, 6, 194-209.	1.5	58
473	Generation and analysis of expressed sequence tags in the extreme large genomes Lilium and Tulipa. BMC Genomics, 2012, 13, 640.	1.2	62
474	Complete genome sequence of Polynucleobacter necessarius subsp. asymbioticus type strain (QLW-P1DMWA-1T). Standards in Genomic Sciences, 2012, 6, 1-14.	1.5	30
475	Comparative Genome Analysis of Three Eukaryotic Parasites with Differing Abilities To Transform Leukocytes Reveals Key Mediators of <i>Theileria</i> -Induced Leukocyte Transformation. MBio, 2012, 3, e00204-12.	1.8	64

#	Article	IF	Citations
476	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. Molecular Biology and Evolution, 2012, 29, 3793-3806.	3.5	127
477	The AHL- and BDSF-Dependent Quorum Sensing Systems Control Specific and Overlapping Sets of Genes in Burkholderia cenocepacia H111. PLoS ONE, 2012, 7, e49966.	1.1	70
478	The<i>ASP3</i>locus in<i>Saccharomyces cerevisiae</i>originated by horizontal gene transfer from<i>Wickerhamomyces</i>. FEMS Yeast Research, 2012, 12, 859-863.	1.1	27
479	Making next-generation sequencing work for you: approaches and practical considerations for marker development and phylogenetics. Plant Ecology and Diversity, 2012, 5, 427-450.	1.0	32
480	Automated hierarchical classification of protein domain subfamilies based on functionally-divergent residue signatures. BMC Bioinformatics, 2012, 13, 144.	1.2	11
481	Signal Correlations in Ecological Niches Can Shape the Organization and Evolution of Bacterial Gene Regulatory Networks. Advances in Microbial Physiology, 2012, 61, 1-36.	1.0	6
482	A genome triplication associated with early diversification of the core eudicots. Genome Biology, 2012, 13, R3.	13.9	389
483	Iterative orthology prediction uncovers new mitochondrial proteins and identifies C12orf62 as the human ortholog of COX14, a protein involved in the assembly of cytochrome c oxidase. Genome Biology, 2012, 13, R12.	13.9	100
484	Staphylococcus epidermidis pan-genome sequence analysis reveals diversity of skin commensal and hospital infection-associated isolates. Genome Biology, 2012, 13, R64.	13.9	206
485	Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature, 2012, 491, 705-710.	13.7	983
486	Gene-RiViT: A visualization tool for comparative analysis of gene neighborhoods in prokaryotes. , 2012, , .		3
487	MonarchBase: the monarch butterfly genome database. Nucleic Acids Research, 2012, 41, D758-D763.	6.5	91
488	Ultrafast clustering algorithms for metagenomic sequence analysis. Briefings in Bioinformatics, 2012, 13, 656-668.	3.2	403
489	Analysis of gene expression from the <i>Wolbachia</i> genome of a filarial nematode supports both metabolic and defensive roles within the symbiosis. Genome Research, 2012, 22, 2467-2477.	2.4	155
490	Codon usage patterns and adaptive evolution of marine unicellular cyanobacteria Synechococcus and Prochlorococcus. Molecular Phylogenetics and Evolution, 2012, 62, 206-213.	1.2	35
491	Caldicellulosiruptor Core and Pangenomes Reveal Determinants for Noncellulosomal Thermophilic Deconstruction of Plant Biomass. Journal of Bacteriology, 2012, 194, 4015-4028.	1.0	96
492	The <i>ac53</i> , <i>ac78</i> , <i>ac101</i> , and <i>ac103</i> Genes Are Newly Discovered Core Genes in the Family Baculoviridae. Journal of Virology, 2012, 86, 12069-12079.	1.5	132
493	Update on sumoylation: defining core components of the plant SUMO conjugation system by phylogenetic comparison. New Phytologist, 2012, 195, 23-31.	3.5	75

#	Article	IF	Citations
494	A rootâ€knot nematodeâ€secreted protein is injected into giant cells and targeted to the nuclei. New Phytologist, 2012, 194, 924-931.	3.5	85
495	CORNET 2.0: integrating plant coexpression, proteinâ€"protein interactions, regulatory interactions, gene associations and functional annotations. New Phytologist, 2012, 195, 707-720.	3.5	113
496	Highly conserved lowâ€copy nuclear genes as effective markers for phylogenetic analyses in angiosperms. New Phytologist, 2012, 195, 923-937.	3.5	192
497	Population Genomics of Chlamydia trachomatis: Insights on Drift, Selection, Recombination, and Population Structure. Molecular Biology and Evolution, 2012, 29, 3933-3946.	3.5	94
498	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2012, 22, 1309-1313.	1.8	140
499	SuperPartitions: Detection and classification of orthologs. Gene, 2012, 492, 199-211.	1.0	11
500	QuartetS-DB: a large-scale orthology database for prokaryotes and eukaryotes inferred by evolutionary evidence. BMC Bioinformatics, 2012, 13, 143.	1.2	11
501	A genome-wide study of recombination rate variation in Bartonella henselae. BMC Evolutionary Biology, 2012, 12, 65.	3.2	18
502	Evolution of the metabolic and regulatory networks associated with oxygen availability in two phytopathogenic enterobacteria. BMC Genomics, 2012, 13, 110.	1.2	39
503	A genome-wide study of two-component signal transduction systems in eight newly sequenced mutans streptococci strains. BMC Genomics, 2012, 13, 128.	1.2	31
504	The Physalis peruviana leaf transcriptome: assembly, annotation and gene model prediction. BMC Genomics, 2012, 13, 151.	1.2	52
505	Unique core genomes of the bacterial family vibrionaceae: insights into niche adaptation and speciation. BMC Genomics, 2012, 13, 179.	1.2	24
506	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. BMC Genomics, 2012, 13, 492.	1.2	51
507	Analysis of the Lactobacillus casei supragenome and its influence in species evolution and lifestyle adaptation. BMC Genomics, 2012, 13, 533.	1.2	144
508	Comparative genomics of the classical Bordetella subspecies: the evolution and exchange of virulence-associated diversity amongst closely related pathogens. BMC Genomics, 2012, 13, 545.	1.2	99
509	The complete swine olfactory subgenome: expansion of the olfactory gene repertoire in the pig genome. BMC Genomics, 2012, 13, 584.	1.2	91
510	Comparative genomics of bacteria in the genus Providencia isolated from wild Drosophila melanogaster. BMC Genomics, 2012, 13, 612.	1.2	32
511	The Schistosoma mansoni phylome: using evolutionary genomics to gain insight into a parasiteâ€™s biology. BMC Genomics, 2012, 13, 617.	1.2	28

#	ARTICLE	IF	CITATIONS
512	Transcriptome database resource and gene expression atlas for the rose. BMC Genomics, 2012, 13, 638.	1.2	76
513	Small RNA and transcriptome deep sequencing proffers insight into floral gene regulation in Rosa cultivars. BMC Genomics, 2012, 13, 657.	1.2	49
514	Genomic insights into strategies used by Xanthomonas albilineans with its reduced artillery to spread within sugarcane xylem vessels. BMC Genomics, 2012, 13, 658.	1.2	50
515	Distinct co-evolution patterns of genes associated to DNA polymerase III DnaE and PolC. BMC Genomics, 2012, 13, 69.	1.2	18
516	The genome of Pelobacter carbinolicus reveals surprising metabolic capabilities and physiological features. BMC Genomics, 2012, 13, 690.	1.2	35
517	Identification of common genetic modifiers of neurodegenerative diseases from an integrative analysis of diverse genetic screens in model organisms. BMC Genomics, 2012, 13, 71.	1.2	29
518	Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. BMC Microbiology, 2012, 12, 135.	1.3	126
519	Extensive remodeling of the Pseudomonas syringae pv. avellanae type III secretome associated with two independent host shifts onto hazelnut. BMC Microbiology, 2012, 12, 141.	1.3	67
520	A Multilocus Sequence Typing System (MLST) reveals a high level of diversity and a genetic component to Entamoeba histolytica virulence. BMC Microbiology, 2012, 12, 151.	1.3	47
521	Defining bacterial species in the genomic era: insights from the genus Acinetobacter. BMC Microbiology, 2012, 12, 302.	1.3	188
522	Genomes-based phylogeny of the genus Xanthomonas. BMC Microbiology, 2012, 12, 43.	1.3	71
523	Scheffersomyces stipitis: a comparative systems biology study with the Crabtree positive yeast Saccharomyces cerevisiae. Microbial Cell Factories, 2012, 11, 136.	1.9	57
524	Transcriptome analysis of symptomatic and recovered leaves of geminivirus-infected pepper (Capsicum) Tj ETQq0 0 0 rgBT /Overlock 10	1.4	67
525	A genome-scale metabolic model of the lipid-accumulating yeast Yarrowia lipolytica. BMC Systems Biology, 2012, 6, 35.	3.0	105
526	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. BMC Systems Biology, 2012, 6, 87.	3.0	128
527	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. Advances in Botanical Research, 2012, 64, 383-427.	0.5	11
528	Inferring Orthology and Paralogy. Methods in Molecular Biology, 2012, 855, 259-279.	0.4	87
529	Intrinsically disordered regions have specific functions in mitochondrial and nuclear proteins. Molecular BioSystems, 2012, 8, 247-255.	2.9	13

#	Article	IF	Citations
530	The draft genome of a diploid cotton Gossypium raimondii. Nature Genetics, 2012, 44, 1098-1103.	9.4	935
532	Evolution of Xanthomonas Gene Content: Gene Gain/Loss History and Species Divergence. Journal of Integrative Agriculture, 2012, 11, 954-961.	1.7	2
533	Allele Identification in Assembled Genomic Sequence Datasets. Methods in Molecular Biology, 2012, 888, 197-211.	0.4	2
534	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
536	Known and novel post-transcriptional regulatory sequences are conserved across plant families. Rna, 2012, 18, 368-384.	1.6	77
537	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
538	Environmental Comparative Pharmacology: Theory and Application. Emerging Topics in Ecotoxicology, 2012, , 85-108.	1.5	11
539	From event-labeled gene trees to species trees. BMC Bioinformatics, 2012, 13, .	1.2	29
540	A graph-theoretic approach for inparalog detection. BMC Bioinformatics, 2012, 13, S16.	1.2	5
541	An automated approach for the identification of horizontal gene transfers from complete genomes reveals the rhizome of Rickettsiales. BMC Evolutionary Biology, 2012, 12, 243.	3.2	13
542	Sequencing of mitochondrial genomes of nine Aspergillus and Penicillium species identifies mobile introns and accessory genes as main sources of genome size variability. BMC Genomics, 2012, 13, 698.	1.2	131
543	Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse Escherichia coli genomes. BMC Genomics, 2012, 13, 577.	1.2	205
544	Oocyte-somatic cells interactions, lessons from evolution. BMC Genomics, 2012, 13, 560.	1.2	40
545	Improving N-terminal protein annotation of Plasmodium species based on signal peptide prediction of orthologous proteins. Malaria Journal, 2012, 11, 375.	0.8	3
546	Computational discovery of regulatory elements in a continuous expression space. Genome Biology, 2012, 13, R109.	13.9	8
547	Genome Analysis of a Highly Virulent Serotype 1 Strain of Streptococcus pneumoniae from West Africa. PLoS ONE, 2012, 7, e26742.	1.1	17
548	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. PLoS ONE, 2012, 7, e29847.	1.1	235
549	Comparative Analysis of Gene Content Evolution in Phytoplasmas and Mycoplasmas. PLoS ONE, 2012, 7, e34407.	1.1	47

#	ARTICLE	IF	CITATIONS
550	Identification of Functional Differences in Metabolic Networks Using Comparative Genomics and Constraint-Based Models. PLoS ONE, 2012, 7, e34670.	1.1	41
551	Expression Profiling of Cucumis sativus in Response to Infection by Pseudoperonospora cubensis. PLoS ONE, 2012, 7, e34954.	1.1	54
552	Pseudomonas syringae pv. actinidiae (PSA) Isolates from Recent Bacterial Canker of Kiwifruit Outbreaks Belong to the Same Genetic Lineage. PLoS ONE, 2012, 7, e36518.	1.1	124
553	Gene Repertoire Evolution of Streptococcus pyogenes Inferred from Phylogenomic Analysis with Streptococcus canis and Streptococcus dysgalactiae. PLoS ONE, 2012, 7, e37607.	1.1	37
554	Comparative Geno-Plasticity Analysis of Mycoplasma bovis HB0801 (Chinese Isolate). PLoS ONE, 2012, 7, e38239.	1.1	71
555	Oligonucleotide Primers for Targeted Amplification of Single-Copy Nuclear Genes in Apocritan Hymenoptera. PLoS ONE, 2012, 7, e39826.	1.1	10
556	High Confidence Prediction of Essential Genes in Burkholderia Cenocepacia. PLoS ONE, 2012, 7, e40064.	1.1	60
557	Two Different Secondary Metabolism Gene Clusters Occupied the Same Ancestral Locus in Fungal Dermatophytes of the Arthrodermataceae. PLoS ONE, 2012, 7, e41903.	1.1	9
558	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
559	Decay of Genes Encoding the Oomycete Flagellar Proteome in the Downy Mildew Hyaloperonospora arabidopsidis. PLoS ONE, 2012, 7, e47624.	1.1	24
560	Survey of Endosymbionts in the Diaphorina citri Metagenome and Assembly of a Wolbachia wDi Draft Genome. PLoS ONE, 2012, 7, e50067.	1.1	77
561	Diagnostic Peptide Discovery: Prioritization of Pathogen Diagnostic Markers Using Multiple Features. PLoS ONE, 2012, 7, e50748.	1.1	36
562	Contribution of Lateral Gene Transfers to the Genome Composition and Parasitic Ability of Root-Knot Nematodes. PLoS ONE, 2012, 7, e50875.	1.1	57
563	Molecular Characterization of Cold Adaptation of Membrane Proteins in the Vibrionaceae Core-Genome. PLoS ONE, 2012, 7, e51761.	1.1	18
564	Development of Transcriptomic Resources for Interrogating the Biosynthesis of Monoterpene Indole Alkaloids in Medicinal Plant Species. PLoS ONE, 2012, 7, e52506.	1.1	150
565	Comparative Genomics of Aeschynomene Symbionts: Insights into the Ecological Lifestyle of Nod-Independent Photosynthetic Bradyrhizobia. Genes, 2012, 3, 35-61.	1.0	30
566	REGEN: Ancestral Genome Reconstruction for Bacteria. Genes, 2012, 3, 423-443.	1.0	6
567	Let the Data Do the Talking: Hypothesis Discovery from Large-Scale Data Sets in Real Time. , 0, , 235-257.		0

#	Article	IF	Citations
568	Text mining in livestock animal science: Introducing the potential of text mining to animal sciences 1. Journal of Animal Science, 2012, 90, 3666-3676.	0.2	5
569	Developmental Milestones Punctuate Gene Expression in the Caenorhabditis Embryo. Developmental Cell, 2012, 22, 1101-1108.	3.1	207
570	The banana (Musa acuminata) genome and the evolution of monocotyledonous plants. Nature, 2012, 488, 213-217.	13.7	1,049
571	Comparative and Functional Genomics of Anoxygenic Green Bacteria from the Taxa Chlorobi, Chloroflexi, and Acidobacteria. Advances in Photosynthesis and Respiration, 2012, , 47-102.	1.0	145
572	Large Scale In Silico Identification of MYB Family Genes from Wheat Expressed Sequence Tags. Molecular Biotechnology, 2012, 52, 184-192.	1.3	15
573	Genome sequence of foxtail millet (Setaria italica) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554.	9.4	636
574	Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. Genome Biology and Evolution, 2012, 4, 586-601.	1.1	9
575	Using MCL to Extract Clusters from Networks. Methods in Molecular Biology, 2012, 804, 281-295.	0.4	374
576	Phylogenomic analysis of transcriptome data elucidates coâ€occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). American Journal of Botany, 2012, 99, 397-406.	0.8	94
577	Development of gene-based markers and construction of an integrated linkage map in eggplant by using Solanum orthologous (SOL) gene sets. Theoretical and Applied Genetics, 2012, 125, 47-56.	1.8	61
578	De novo sequencing and a comprehensive analysis of purple sweet potato (Impomoea batatas L.) transcriptome. Planta, 2012, 236, 101-113.	1.6	118
579	Iron transporters in marine prokaryotic genomes and metagenomes. Environmental Microbiology, 2012, 14, 114-128.	1.8	93
580	Exposing the third chromosome of <i>Burkholderia cepacia</i> complex strains as a virulence plasmid. Molecular Microbiology, 2012, 83, 362-378.	1.2	90
581	Postâ€transcriptional regulatory networks play a key role in noise reduction that is conserved from microâ€organisms to mammals. FEBS Journal, 2012, 279, 3501-3512.	2.2	20
582	Genes under positive selection in a model plant pathogenic fungus, Botrytis. Infection, Genetics and Evolution, 2012, 12, 987-996.	1.0	40
583	Conservation of thiolâ€oxidative stress responses regulated by SigR orthologues in actinomycetes. Molecular Microbiology, 2012, 85, 326-344.	1.2	65
584	Comparative coâ€expression analysis in plant biology. Plant, Cell and Environment, 2012, 35, 1787-1798.	2.8	83
585	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. Plant Journal, 2012, 71, 492-502.	2.8	209

#	ARTICLE	IF	CITATIONS
586	BAR expressolog identification: expression profile similarity ranking of homologous genes in plant species. Plant Journal, 2012, 71, 1038-1050.	2.8	102
587	On the cultureâ€independent assessment of the diversity and distribution of <i>Prochlorococcus</i>. Environmental Microbiology, 2012, 14, 567-579.	1.8	11
588	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
589	PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for examining phage diversity. BMC Bioinformatics, 2012, 13, 37.	1.2	21
590	A methodology for detecting the orthology signal in a PPI network at a functional complex level. BMC Bioinformatics, 2012, 13, S18.	1.2	14
591	Genome plasticity and systems evolution in Streptomyces. BMC Bioinformatics, 2012, 13, S8.	1.2	61
592	BBH-LS: an algorithm for computing positional homologs using sequence and gene context similarity. BMC Systems Biology, 2012, 6, S22.	3.0	8
593	Reference genomes and transcriptomes of Nicotiana sylvestris and Nicotiana tomentosiformis. Genome Biology, 2013, 14, R60.	3.8	192
594	Draft genome of the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major forest pest. Genome Biology, 2013, 14, R27.	13.9	260
595	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate Salpingoeca rosetta. Genome Biology, 2013, 14, R15.	13.9	219
596	The SYSCILIA gold standard (SCGSv1) of known ciliary components and its applications within a systems biology consortium. Cilia, 2013, 2, 7.	1.8	160
597	The family based variability in protein family expansion. International Journal of Bioinformatics Research and Applications, 2013, 9, 121.	0.1	0
598	Comparative genome characterization of Achromobacter members reveals potential genetic determinants facilitating the adaptation to a pathogenic lifestyle. Applied Microbiology and Biotechnology, 2013, 97, 6413-6425.	1.7	45
599	Genomic analysis of the biocontrol strain <i><scp>P</scp>seudomonas fluorescens</i>â€...<scp>Pf</scp>29<scp>Arp</scp> with evidence of <scp>T</scp>3<scp>SS</scp> and <scp>T</scp>6<scp>SS</scp> gene expression on plant roots. Environmental Microbiology Reports, 2013, 5, 393-403.	1.0	62
600	Multifactorial diversity sustains microbial community stability. ISME Journal, 2013, 7, 2126-2136.	4.4	176
601	A novel method for cross-species gene expression analysis. BMC Bioinformatics, 2013, 14, 70.	1.2	45
602	JContextExplorer: a tree-based approach to facilitate cross-species genomic context comparison. BMC Bioinformatics, 2013, 14, 18.	1.2	10
603	Structural and evolutionary adaptation of rhoptry kinases and pseudokinases, a family of coccidian virulence factors. BMC Evolutionary Biology, 2013, 13, 117.	3.2	74

#	ARTICLE	IF	CITATIONS
604	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
605	Genomic characterization provides new insight into Salmonella phage diversity. BMC Genomics, 2013, 14, 481.	1.2	80
606	The miniature genome of a carnivorous plant Genlisea aurea contains a low number of genes and short non-coding sequences. BMC Genomics, 2013, 14, 476.	1.2	58
607	Genomic basis of ecological niche divergence among cryptic sister species of non-biting midges. BMC Genomics, 2013, 14, 384.	1.2	25
608	Genomic analysis of the native European Solanum species, S. dulcamara. BMC Genomics, 2013, 14, 356.	1.2	25
609	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
610	Draft genome sequence of the rubber tree Hevea brasiliensis. BMC Genomics, 2013, 14, 75.	1.2	222
611	Genome sequence reveals that Pseudomonas fluorescens F113 possesses a large and diverse array of systems for rhizosphere function and host interaction. BMC Genomics, 2013, 14, 54.	1.2	78
612	Comparative genome analysis of Spiroplasma melliferumIPMB4A, a honeybee-associated bacterium. BMC Genomics, 2013, 14, 22.	1.2	118
613	Draft genome sequence of the male-killing Wolbachia strain wBol1 reveals recent horizontal gene transfers from diverse sources. BMC Genomics, 2013, 14, 20.	1.2	65
614	A new computational approach redefines the subtelomeric vir superfamily of Plasmodium vivax. BMC Genomics, 2013, 14, 8.	1.2	40
615	Draft genome sequence of chickpea (Cicer arietinum) provides a resource for trait improvement. Nature Biotechnology, 2013, 31, 240-246.	9.4	1,049
616	Synthetic circuit of inositol phosphorylceramide synthase in Leishmania: a chemical biology approach. Journal of Chemical Biology, 2013, 6, 51-62.	2.2	4
617	Proteomic Comparison of Historic and Recently Emerged Hypervirulent <i>Clostridium difficile</i> Strains. Journal of Proteome Research, 2013, 12, 1151-1161.	1.8	52
618	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	5.8	244
619	Phylogenomics supports Panpulmonata: Opisthobranch paraphyly and key evolutionary steps in a major radiation of gastropod molluscs. Molecular Phylogenetics and Evolution, 2013, 69, 764-771.	1.2	59
620	The sacred lotus genome provides insights into the evolution of flowering plants. Plant Journal, 2013, 76, 557-567.	2.8	75
621	Orthology relations, symbolic ultrametrics, and cographs. Journal of Mathematical Biology, 2013, 66, 399-420.	0.8	62

#	Article	IF	Citations
622	Genome sequencing identifies Listeria fleischmannii subsp. coloradonensis subsp. nov., isolated from a ranch. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3257-3268.	0.8	46
623	Draft Assembly of the Symbiodinium minutum Nuclear Genome Reveals Dinoflagellate Gene Structure. Current Biology, 2013, 23, 1399-1408.	1.8	488
624	How old is my gene?. Trends in Genetics, 2013, 29, 659-668.	2.9	60
625	Insulin Biosynthetic Interaction Network Component, TMEM24, Facilitates Insulin Reserve Pool Release. Cell Reports, 2013, 4, 921-930.	2.9	38
626	Polygalacturonases from Moniliophthora perniciosa are regulated by fermentable carbon sources and possible post-translational modifications. Fungal Genetics and Biology, 2013, 60, 110-121.	0.9	7
627	Genes encoding FAD-binding proteins in Volvariella volvacea exhibit differential expression in homokaryons and heterokaryons. Microbiological Research, 2013, 168, 533-546.	2.5	13
628	Physical linkage of metabolic genes in fungi is an adaptation against the accumulation of toxic intermediate compounds. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11481-11486.	3.3	82
629	Genome Reduction Promotes Increase in Protein Functional Complexity in Bacteria. Genetics, 2013, 193, 303-307.	1.2	41
630	GET_HOMOLOGUES, a Versatile Software Package for Scalable and Robust Microbial Pangenome Analysis. Applied and Environmental Microbiology, 2013, 79, 7696-7701.	1.4	902
631	BlastGraph: a comparative genomics tool based on BLAST and graph algorithms. Bioinformatics, 2013, 29, 3222-3224.	1.8	10
632	Genomic insights into salt adaptation in a desert poplar. Nature Communications, 2013, 4, 2797.	5.8	286
633	The Genome of the Ctenophore <i>Mnemiopsis leidyi</i> and Its Implications for Cell Type Evolution. Science, 2013, 342, 1242592.	6.0	570
634	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	6.0	743
635	Quantitative synteny scoring improves homology inference and partitioning of gene families. BMC Bioinformatics, 2013, 14, S12.	1.2	32
636	Comparative transcriptomics as a tool for the identification of root branching genes in maize. Plant Biotechnology Journal, 2013, 11, 1092-1102.	4.1	54
637	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (Raphanus spp.). BMC Genomics, 2013, 14, 721.	1.2	16
638	Identifying conserved protein complexes between species by constructing interolog networks. BMC Bioinformatics, 2013, 14, S8.	1.2	34
639	Bolbase: a comprehensive genomics database for Brassica oleracea. BMC Genomics, 2013, 14, 664.	1.2	99

#	ARTICLE	IF	CITATIONS
640	Analysing complex Triticeae genomes â€“ concepts and strategies. Plant Methods, 2013, 9, 35.	1.9	19
641	Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. BMC Genomics, 2013, 14, 611.	1.2	175
642	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. BMC Genomics, 2013, 14, 579.	1.2	186
643	Analysis of cattle olfactory subgenome: the first detail study on the characteristics of the complete olfactory receptor repertoire of a ruminant. BMC Genomics, 2013, 14, 596.	1.2	46
644	kClust: fast and sensitive clustering of large protein sequence databases. BMC Bioinformatics, 2013, 14, 248.	1.2	83
645	Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. BMC Genomics, 2013, 14, 430.	1.2	31
646	The genome of Romanomermis culicivorax: revealing fundamental changes in the core developmental genetic toolkit in Nematoda. BMC Genomics, 2013, 14, 923.	1.2	43
647	Single-cell genomics reveal low recombination frequencies in freshwater bacteria of the SAR11 clade. Genome Biology, 2013, 14, R130.	13.9	74
648	Repertoire, unified nomenclature and evolution of the Type III effector gene set in the Ralstonia solanacearum species complex. BMC Genomics, 2013, 14, 859.	1.2	206
649	Genome sequence and analysis of methylotrophic yeast Hansenula polymorpha DL1. BMC Genomics, 2013, 14, 837.	1.2	81
650	Molecular adaptation of telomere associated genes in mammals. BMC Evolutionary Biology, 2013, 13, 251.	3.2	32
651	Comparative genomics analysis of Streptococcus agalactiae reveals that isolates from cultured tilapia in China are closely related to the human strain A909. BMC Genomics, 2013, 14, 775.	1.2	73
652	Genome sequence of Xanthomonas fuscans subsp. fuscans strain 4834-R reveals that flagellar motility is not a general feature of xanthomonads. BMC Genomics, 2013, 14, 761.	1.2	55
653	Whole-genome sequencing of Oryza brachyantha reveals mechanisms underlying Oryza genome evolution. Nature Communications, 2013, 4, 1595.	5.8	190
654	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). Genome Research, 2013, 23, 396-408.	2.4	832
655	Two Rumex Species from Contrasting Hydrological Niches Regulate Flooding Tolerance through Distinct Mechanisms. Plant Cell, 2013, 25, 4691-4707.	3.1	133
656	Functional Annotation and Comparative Analysis of a Zygopteran Transcriptome. G3: Genes, Genomes, Genetics, 2013, 3, 763-770.	0.8	5
657	The Rhizome of the Multidrug-Resistant Enterobacter aerogenes Genome Reveals How New â€œKiller Bugsâ€•Are Created because of a Sympatric Lifestyle. Molecular Biology and Evolution, 2013, 30, 369-383.	3.5	113

#	ARTICLE	IF	CITATIONS
658	Evolutionary and Population Genomics of the Cavity Causing Bacteria Streptococcus mutans. Molecular Biology and Evolution, 2013, 30, 881-893.	3.5	168
659	The evolutionary landscape of the Mycobacterium tuberculosis genome. Gene, 2013, 518, 187-193.	1.0	8
660	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2898-2903.	3.3	351
661	Co-expression network with proteinâ€"protein interaction and transcription regulation in malaria parasite Plasmodium falciparum. Gene, 2013, 518, 7-16.	1.0	8
662	Clostridium-DTDB: A comprehensive database for potential drug targets of Clostridium difficile. Computers in Biology and Medicine, 2013, 43, 362-367.	3.9	20
663	Multiple ancient horizontal gene transfers and duplications in lepidopteran species. Insect Molecular Biology, 2013, 22, 72-87.	1.0	43
664	Sequencing and annotation of the Ophiostoma ulmigenome. BMC Genomics, 2013, 14, 162.	1.2	40
665	Proposal for a new class within the phylum Proteobacteria , Acidithiobacillia classis nov., with the type order Acidithiobacillales , and emended description of the class Gammaproteobacteria. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2901-2906.	0.8	129
666	Transcriptomic analysis of metabolic function in the giant kelp, <i><scp>M</scp>acrocystis pyrifera</i>, across depth and season. New Phytologist, 2013, 198, 398-407.	3.5	51
667	The draft genome of sweet orange (Citrus sinensis). Nature Genetics, 2013, 45, 59-66.	9.4	837
668	Draft genome of the wheat A-genome progenitor Triticum urartu. Nature, 2013, 496, 87-90.	13.7	700
669	Genome-Based Computational Vaccine Discovery by Reverse Vaccinology. , 2013, , 91-104.		1
670	Assemblyâ€free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. Environmental Microbiology Reports, 2013, 5, 686-696.	1.0	8
671	The draft genome of the fast-growing non-timber forest species moso bamboo (Phyllostachys) Tj ETQq1 1 0.784314 rgBT /Overlock 10	9.4	483
672	Comparative characterization of the virulence gene clusters (lipooligosaccharide [LOS] and capsular) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Campylobacter species. Infection, Genetics and Evolution, 2013, 14, 200-213.	1.0	42
673	Evidence for adaptive evolution of lowâ€temperature stress response genes in a Pooideae grass ancestor. New Phytologist, 2013, 199, 1060-1068.	3.5	37
674	Genome Sequencing and Comparative Genomics in Cereals. , 2013, , 101-126.		0
675	Functional Annotation of Plant Genomes. , 2013, , 155-176.		0

#	Article	IF	Citations
676	Construction of Plastid Reference Proteomes for Maize and <i>Arabidopsis</i> and Evaluation of Their Orthologous Relationships; The Concept of Orthoproteomics. Journal of Proteome Research, 2013, 12, 491-504.	1.8	82
677	Architecture and evolution of a minute plant genome. Nature, 2013, 498, 94-98.	13.7	293
678	SUCCESSIVE GAIN OF INSULATOR PROTEINS IN ARTHROPOD EVOLUTION. Evolution; International Journal of Organic Evolution, 2013, 67, 2945-2956.	1.1	32
679	The genome of Mesobuthus martensii reveals a unique adaptation model of arthropods. Nature Communications, 2013, 4, 2602.	5.8	187
680	FROM PLANT GENOMES TO PROTEIN FAMILIES: COMPUTATIONAL TOOLS. Computational and Structural Biotechnology Journal, 2013, 8, e201307001.	1.9	7
681	Resequencing and Comparative Genomics of <i>Stagonospora nodorum</i>: Sectional Gene Absence and Effector Discovery. G3: Genes, Genomes, Genetics, 2013, 3, 959-969.	0.8	66
684	Comparison and Analysis of the Genomes of Two Aspergillus oryzae Strains. Journal of Agricultural and Food Chemistry, 2013, 61, 7805-7809.	2.4	19
685	Genome Sequence of Xanthomonas campestris pv. campestris Strain Xca5. Genome Announcements, 2013, 1, .	0.8	17
686	Genome Sequence of the Vancomycin-Producing Amycolatopsis orientalis subsp. orientalis Strain KCTC 9412 T. Genome Announcements, 2013, 1, .	0.8	16
687	Genome Sequences of Three Atypical Xanthomonas campestris pv. campestris Strains, CN14, CN15, and CN16. Genome Announcements, 2013, 1, .	0.8	8
688	Genome Sequence of Rickettsia gravesii, Isolated from Western Australian Ticks. Genome Announcements, 2013, 1, .	0.8	6
689	EvolutionaryGenomics of Salmonellaenterica Subspecies. MBio, 2013, 4, .	1.8	106
690	Expression Divergence between Escherichia coli and Salmonella enterica serovar Typhimurium Reflects Their Lifestyles. Molecular Biology and Evolution, 2013, 30, 1302-1314.	3.5	27
691	Early Cone Setting in <i>Picea abies acrocona</i> Is Associated with Increased Transcriptional Activity of a MADS Box Transcription Factor Â Â. Plant Physiology, 2013, 161, 813-823.	2.3	46
692	CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species. Plant Physiology, 2013, 163, 354-362.	2.3	33
693	Piliation of Invasive Streptococcus pneumoniae Isolates in the Era before Pneumococcal Conjugate Vaccine Introduction in Malawi. Vaccine Journal, 2013, 20, 1729-1735.	3.2	12
694	Genome Sequence of an Environmental Isolate of the Bacterial Pathogen Legionella pneumophila. Genome Announcements, 2013, 1, .	0.8	10
695	Genome Sequencing of the Plant Pathogen <i>Taphrina deformans</i> , the Causal Agent of Peach Leaf Curl. MBio, 2013, 4, e00055-13.	1.8	81

#	ARTICLE	IF	CITATIONS
696	Comparative Genomics of Recent Shiga Toxin-Producing Escherichia coli O104:H4: Short-Term Evolution of an Emerging Pathogen. MBio, 2013, 4, e00452-12.	1.8	68
697	Identification of a Genetic Determinant in Clinical Enterococcus faecium Strains That Contributes to Intestinal Colonization During Antibiotic Treatment. Journal of Infectious Diseases, 2013, 207, 1780-1786.	1.9	79
698	Orthologous Gene Clusters and Taxon Signature Genes for Viruses of Prokaryotes. Journal of Bacteriology, 2013, 195, 941-950.	1.0	104
699	Comparative Analysis of Chlamydia psittaci Genomes Reveals the Recent Emergence of a Pathogenic Lineage with a Broad Host Range. MBio, 2013, 4, .	1.8	90
700	Chapter 15: Disease Gene Prioritization. PLoS Computational Biology, 2013, 9, e1002902.	1.5	65
701	Kinannote, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. Bioinformatics, 2013, 29, 2387-2394.	1.8	43
702	Comparative Genomics of Wolbachia and the Bacterial Species Concept. PLoS Genetics, 2013, 9, e1003381.	1.5	164
703	Genomic Mechanisms Accounting for the Adaptation to Parasitism in Nematode-Trapping Fungi. PLoS Genetics, 2013, 9, e1003909.	1.5	97
704	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers Â. Plant Cell, 2013, 25, 2813-2830.	3.1	95
705	Badgerâ€"an accessible genome exploration environment. Bioinformatics, 2013, 29, 2788-2789.	1.8	8
706	Comparative sequence analysis of nitrogen fixation-related genes in six legumes. Frontiers in Plant Science, 2013, 4, 300.	1.7	14
707	Comparative Genomics of<i>Cryptosporidium</i>. International Journal of Genomics, 2013, 2013, 1-8.	0.8	28
708	The Reference Genome of the Halophytic Plant Eutrema salsugineum. Frontiers in Plant Science, 2013, 4, 46.	1.7	198
709	A Gene Transfer Agent and a Dynamic Repertoire of Secretion Systems Hold the Keys to the Explosive Radiation of the Emerging Pathogen Bartonella. PLoS Genetics, 2013, 9, e1003393.	1.5	89
710	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. PLoS Genetics, 2013, 9, e1003323.	1.5	344
711	Identification of 526 Conserved Metazoan Genetic Innovations Exposes a New Role for Cofactor E-like in Neuronal Microtubule Homeostasis. PLoS Genetics, 2013, 9, e1003804.	1.5	16
712	Using Existing Drugs as Leads for Broad Spectrum Anthelmintics Targeting Protein Kinases. PLoS Pathogens, 2013, 9, e1003149.	2.1	36
713	Recruitment of EB1, a Master Regulator of Microtubule Dynamics, to the Surface of the Theileria annulata Schizont. PLoS Pathogens, 2013, 9, e1003346.	2.1	51

#	ARTICLE	IF	CITATIONS
714	Shared Protein Complex Subunits Contribute to Explaining Disrupted Co-occurrence. PLoS Computational Biology, 2013, 9, e1003124.	1.5	10
715	The Genome of Spraguea lophii and the Basis of Host-Microsporidian Interactions. PLoS Genetics, 2013, 9, e1003676.	1.5	66
716	Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining. PLoS Pathogens, 2013, 9, e1003745.	2.1	90
717	Minimum Core Genome Sequence Typing of Bacterial Pathogens: a Unified Approach for Clinical and Public Health Microbiology. Journal of Clinical Microbiology, 2013, 51, 2582-2591.	1.8	84
718	Repeat-Enriched Proteins Are Related to Host Cell Invasion and Immune Evasion in Parasitic Protozoa. Molecular Biology and Evolution, 2013, 30, 951-963.	3.5	38
719	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. Briefings in Functional Genomics, 2013, 12, 366-380.	1.3	57
720	HOMECAT: consensus homologs mapping for interspecific knowledge transfer and functional genomic data integration. Bioinformatics, 2013, 29, 1574-1576.	1.8	3
721	Large Scale Full-Length cDNA Sequencing Reveals a Unique Genomic Landscape in a Lepidopteran Model Insect, <i>Bombyx mori</i>. G3: Genes, Genomes, Genetics, 2013, 3, 1481-1492.	0.8	87
722	Phylogenetic Portrait of the Saccharomyces cerevisiae Functional Genome. G3: Genes, Genomes, Genetics, 2013, 3, 1335-1340.	0.8	4
723	Sequencing and Functional Annotation of Avian Pathogenic Escherichia coli Serogroup O78 Strains Reveal the Evolution of E. coli Lineages Pathogenic for Poultry via Distinct Mechanisms. Infection and Immunity, 2013, 81, 838-849.	1.0	82
724	Comparison of Metabolic Capacities and Inference of Gene Content Evolution in Mosquito-Associated Spiroplasma diminutum and S. taiwanense. Genome Biology and Evolution, 2013, 5, 1512-1523.	1.1	35
725	A guide to best practices for Gene Ontology (GO) manual annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat054-bat054.	1.4	135
726	Genetic circuitry of <i>Survival motor neuron</i> , the gene underlying spinal muscular atrophy. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2371-80.	3.3	37
727	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in Enterococcus faecium. Genome Biology and Evolution, 2013, 5, 1524-1535.	1.1	87
728	Genomic and Secretomic Analyses Reveal Unique Features of the Lignocellulolytic Enzyme System of Penicillium decumbens. PLoS ONE, 2013, 8, e55185.	1.1	159
729	Target Prediction for an Open Access Set of Compounds Active against Mycobacterium tuberculosis. PLoS Computational Biology, 2013, 9, e1003253.	1.5	51
730	Structural analyses of the tomato genome. Plant Biotechnology, 2013, 30, 257-263.	0.5	2
731	Complete Genomes of Two Dipteran-Associated Spiroplasmas Provided Insights into the Origin, Dynamics, and Impacts of Viral Invasion in Spiroplasma. Genome Biology and Evolution, 2013, 5, 1151-1164.	1.1	75

#	Article	IF	Citations
732	Origin and Evolution of Dishevelled. G3: Genes, Genomes, Genetics, 2013, 3, 251-262.	0.8	14
733	Genome Evolution and Phylogenomic Analysis of Candidatus Kinetoplastibacterium, the Betaproteobacterial Endosymbionts of Strigomonas and Angomonas. Genome Biology and Evolution, 2013, 5, 338-350.	1.1	47
734	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
735	<i>Toxoplasma gondii</i> Syntaxin 6 Is Required for Vesicular Transport Between Endosomalâ€Like Compartments and the Golgi Complex. Traffic, 2013, 14, 1166-1181.	1.3	29
736	Analysis of Synonymous Codon Usage Patterns in Seven Different<i>Citrus</i>Species. Evolutionary Bioinformatics, 2013, 9, EBO.S11930.	0.6	29
737	Unlocking Triticeae genomics to sustainably feed the future. Plant and Cell Physiology, 2013, 54, 1931-1950.	1.5	61
738	Fragmentation of an aflatoxinâ€like gene cluster in a forest pathogen. New Phytologist, 2013, 198, 525-535.	3.5	55
739	Modulation of potential respiratory pathogens by pH1N1 viral infection. Clinical Microbiology and Infection, 2013, 19, 930-935.	2.8	59
740	OrtholugeDB: a bacterial and archaeal orthology resource for improved comparative genomic analysis. Nucleic Acids Research, 2013, 41, D366-D376.	6.5	73
741	Draft genome of the kiwifruit Actinidia chinensis. Nature Communications, 2013, 4, 2640.	5.8	423
742	Evolution of Divergent Life History Strategies in Marine Alphaproteobacteria. MBio, 2013, 4, .	1.8	103
743	Genomics of Loa loa, a Wolbachia-free filarial parasite of humans. Nature Genetics, 2013, 45, 495-500.	9.4	173
744	Regional control of histone H3 lysine 27 methylation in <i>Neurospora</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6027-6032.	3.3	147
745	To Tree or Not to Tree? Genome-Wide Quantification of Recombination and Reticulate Evolution during the Diversification of Strict Intracellular Bacteria. Genome Biology and Evolution, 2013, 5, 2305-2317.	1.1	21
747	The Complete Genome Sequence of Methanobrevibacter sp. AbM4. Standards in Genomic Sciences, 2013, 8, 215-227.	1.5	42
748	Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in Anopheles gambiae. BMC Genomics, 2013, 14, 749.	1.2	94
749	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. Genome Biology, 2013, 14, r53.	3.8	225
750	Comparative Genomics of Multiple Strains of Pseudomonas cannabina pv. alisalensis, a Potential Model Pathogen of Both Monocots and Dicots. PLoS ONE, 2013, 8, e59366.	1.1	34

#	ARTICLE	IF	CITATIONS
751	A Review of Protein Function Prediction Under Machine Learning Perspective. Recent Patents on Biotechnology, 2013, 7, 122-141.	0.4	43
752	Conventional Simulation of Biological Sequences Leads to a Biased Assessment of Multi-Loci Phylogenetic Analysis. Evolutionary Bioinformatics, 2013, 9, EBO.S12483.	0.6	3
753	Abiotic and Biotic Stress Responses in <i>Solanum tuberosum</i> Group Phureja DM1â€•3 516 R44 as Measured through Whole Transcriptome Sequencing. Plant Genome, 2013, 6, plantgenome2013.05.0014.	1.6	40
754	PhyloTreePruner: A Phylogenetic Tree-Based Approach for selection of Orthologous sequences for phylogenomics. Evolutionary Bioinformatics, 2013, 9, EBO.S12813.	0.6	141
755	Searching Remote Homology with Spectral Clustering with Symmetry in Neighborhood Cluster Kernels. PLoS ONE, 2013, 8, e46468.	1.1	5
756	A Functional Bikaverin Biosynthesis Gene Cluster in Rare Strains of Botrytis cinerea Is Positively Controlled by VELVET. PLoS ONE, 2013, 8, e53729.	1.1	69
757	Combining Functional and Structural Genomics to Sample the Essential Burkholderia Structome. PLoS ONE, 2013, 8, e53851.	1.1	113
758	The Genome Sequences of Cellulomonas fimi and â€œCellvibrio gilvusâ€• Reveal the Cellulolytic Strategies of Two Facultative Anaerobes, Transfer of â€œCellvibrio gilvusâ€• to the Genus Cellulomonas, and Proposal of Cellulomonas gilvus sp. nov. PLoS ONE, 2013, 8, e53954.	1.1	56
759	Attachment and Invasion of Neisseria meningitidis to Host Cells Is Related to Surface Hydrophobicity, Bacterial Cell Size and Capsule. PLoS ONE, 2013, 8, e55798.	1.1	54
760	The Impact of Gene Duplication, Insertion, Deletion, Lateral Gene Transfer and Sequencing Error on Orthology Inference: A Simulation Study. PLoS ONE, 2013, 8, e56925.	1.1	34
761	Phenotypic Heterogeneity of Genomically-Diverse Isolates of Streptococcus mutans. PLoS ONE, 2013, 8, e61358.	1.1	87
762	ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes. PLoS ONE, 2013, 8, e62447.	1.1	9
763	Comparative Analysis of the Peanut Witches'-Broom Phytoplasma Genome Reveals Horizontal Transfer of Potential Mobile Units and Effectors. PLoS ONE, 2013, 8, e62770.	1.1	119
764	The Impact of Paralogy on Phylogenomic Studies â€“ A Case Study on Annelid Relationships. PLoS ONE, 2013, 8, e62892.	1.1	52
765	Transcriptome Analysis of Barbarea vulgaris Infested with Diamondback Moth (Plutella xylostella) Larvae. PLoS ONE, 2013, 8, e64481.	1.1	28
766	Evolutionary Dynamics of the Accessory Genome of Listeria monocytogenes. PLoS ONE, 2013, 8, e67511.	1.1	63
767	The Complete Plastid Genome Sequence of Madagascar Periwinkle Catharanthus roseus (L.) G. Don: Plastid Genome Evolution, Molecular Marker Identification, and Phylogenetic Implications in Asterids. PLoS ONE, 2013, 8, e68518.	1.1	53
768	TCW: Transcriptome Computational Workbench. PLoS ONE, 2013, 8, e69401.	1.1	17

#	Article	IF	Citations
769	Comparative Genomic Analysis of Brucella melitensis Vaccine Strain M5 Provides Insights into Virulence Attenuation. PLoS ONE, 2013, 8, e70852.	1.1	15
770	Comparative Genomics Reveals Insight into Virulence Strategies of Plant Pathogenic Oomycetes. PLoS ONE, 2013, 8, e75072.	1.1	164
771	The ComP-ComA Quorum System Is Essential For â€œTrojan horseâ€•Like Pathogenesis in Bacillus nematocida. PLoS ONE, 2013, 8, e76920.	1.1	17
772	Exploiting a Reference Genome in Terms of Duplications: The Network of Paralogs and Single Copy Genes in Arabidopsis thaliana. Biology, 2013, 2, 1465-1487.	1.3	6
773	Using the relation ontology Metarel for modelling Linked Data as multi-digraphs. Semantic Web, 2014, 5, 115-126.	1.1	3
774	Comparison of Potato and Asian Citrus Psyllid Adult and Nymph Transcriptomes Identified Vector Transcripts with Potential Involvement in Circulative, Propagative Liberibacter Transmission. Pathogens, 2014, 3, 875-907.	1.2	37
775	Genomics of Sponge-Associated Streptomyces spp. Closely Related to Streptomyces albus J1074: Insights into Marine Adaptation and Secondary Metabolite Biosynthesis Potential. PLoS ONE, 2014, 9, e96719.	1.1	51
776	Whole Genome and Global Gene Expression Analyses of the Model Mushroom Flammulina velutipes Reveal a High Capacity for Lignocellulose Degradation. PLoS ONE, 2014, 9, e93560.	1.1	107
777	Genomic Analysis of Xanthomonas translucens Pathogenic on Wheat and Barley Reveals Cross-Kingdom Gene Transfer Events and Diverse Protein Delivery Systems. PLoS ONE, 2014, 9, e84995.	1.1	39
778	Genomic Evidence Reveals the Extreme Diversity and Wide Distribution of the Arsenic-Related Genes in Burkholderiales. PLoS ONE, 2014, 9, e92236.	1.1	38
779	The Expanded Diversity of Methylophilaceae from Lake Washington through Cultivation and Genomic Sequencing of Novel Ecotypes. PLoS ONE, 2014, 9, e102458.	1.1	62
780	Drug Target Mining and Analysis of the Chinese Tree Shrew for Pharmacological Testing. PLoS ONE, 2014, 9, e104191.	1.1	17
781	Orthology Detection Combining Clustering and Synteny for Very Large Datasets. PLoS ONE, 2014, 9, e105015.	1.1	86
782	Genomic Analyses and Transcriptional Profiles of the Glycoside Hydrolase Family 18 Genes of the Entomopathogenic Fungus Metarhizium anisopliae. PLoS ONE, 2014, 9, e107864.	1.1	28
783	Molecular Evolution and Expansion Analysis of the NAC Transcription Factor in Zea mays. PLoS ONE, 2014, 9, e111837.	1.1	56
784	Identification of Transcription Factor Genes and Their Correlation with the High Diversity of Stramenopiles. PLoS ONE, 2014, 9, e111841.	1.1	12
785	Transcriptional responses of three model diatoms to nitrate limitation of growth. Frontiers in Marine Science, 2014, 1, .	1.2	111
786	DetecciÃ³n de blancos moleculares en la ruta de seÃ±alizaciÃ³n del fosfatidilinositol en Leishmania spp. a travÃ©s de herramientas bioinformÃ¡ticas y de modelado matemÃ¡tico. Biomedica, 2014, 35, .	0.3	1

#	Article	IF	Citations
787	Phylogenetics and Phylogenomics of the Fungal Tree of Life. , 0, , 36-49.		3
788	Biological process annotation of proteins across the plant kingdom. Current Plant Biology, 2014, 1, 73-82.	2.3	7
789	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
790	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. Nature Communications, 2014, 5, 5594.	5.8	135
791	Reconciliation Approaches to Determining HGT, Duplications, and Losses in Gene Trees. Methods in Microbiology, 2014, , 183-199.	0.4	12
792	The genome sequence of the Antarctic bullhead notothen reveals evolutionary adaptations to a cold environment. Genome Biology, 2014, 15, 468.	3.8	86
793	The genome of Eimeria falciformisv - reduction and specialization in a single host apicomplexan parasite. BMC Genomics, 2014, 15, 696.	1.2	44
794	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
795	Conserved syntenic clusters of protein coding genes are missing in birds. Genome Biology, 2014, 15, 565.	3.8	123
796	Genome sequencing of Sporisorium scitamineum provides insights into the pathogenic mechanisms of sugarcane smut. BMC Genomics, 2014, 15, 996.	1.2	112
797	In silico work flow for scaffold hopping in Leishmania. BMC Research Notes, 2014, 7, 802.	0.6	9
798	Finding gene regulatory network candidates using the gene expression knowledge base. BMC Bioinformatics, 2014, 15, 386.	1.2	8
799	Computational identification and analysis of orphan assembly-line polyketide synthases. Journal of Antibiotics, 2014, 67, 89-97.	1.0	59
800	TheCryptosporidium parvumApiAP2 gene family: insights into the evolution of apicomplexan AP2 regulatory systems. Nucleic Acids Research, 2014, 42, 8271-8284.	6.5	40
801	Genome Degeneration and Adaptation in a Nascent Stage of Symbiosis. Genome Biology and Evolution, 2014, 6, 76-93.	1.1	200
802	The Genome of Cardinium cBtQ1 Provides Insights into Genome Reduction, Symbiont Motility, and Its Settlement in Bemisia tabaci. Genome Biology and Evolution, 2014, 6, 1013-1030.	1.1	68
803	Transposable element-assisted evolution and adaptation to host plant within the Leptosphaeria maculans-Leptosphaeria biglobosa species complex of fungal pathogens. BMC Genomics, 2014, 15, 891.	1.2	189
804	Impact of analytic provenance in genome analysis. BMC Genomics, 2014, 15, S1.	1.2	13

#	ARTICLE	IF	CITATIONS
805	Comparative genome analysis of entomopathogenic fungi reveals a complex set of secreted proteins. BMC Genomics, 2014, 15, 822.	1.2	49
806	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
807	The evolutionary dynamics of variant antigen genes in Babesia reveal a history of genomic innovation underlying host-parasite interaction. Nucleic Acids Research, 2014, 42, 7113-7131.	6.5	90
808	GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. Nucleic Acids Research, 2014, 42, D1167-D1175.	6.5	108
809	Genome-scale data suggest reclassifications in the Leisingera-Phaeobacter cluster including proposals for Sedimentitalea gen. nov. and Pseudophaeobacter gen. nov.. Frontiers in Microbiology, 2014, 5, 416.	1.5	88
810	Annotation of a hybrid partial genome of the coffee rust (Hemileia vastatrix) contributes to the gene repertoire catalog of the Pucciniales. Frontiers in Plant Science, 2014, 5, 594.	1.7	34
811	Dissemination of Cephalosporin Resistance Genes between Escherichia coli Strains from Farm Animals and Humans by Specific Plasmid Lineages. PLoS Genetics, 2014, 10, e1004776.	1.5	276
812	The Transcriptomes of the Crucian Carp Complex (Carassius auratus) Provide Insights into the Distinction between Unisexual Triploids and Sexual Diploids. International Journal of Molecular Sciences, 2014, 15, 9386-9406.	1.8	12
813	Genome sequence of mungbean and insights into evolution within Vigna species. Nature Communications, 2014, 5, 5443.	5.8	453
814	Evolution of a Cellular Immune Response in Drosophila: A Phenotypic and Genomic Comparative Analysis. Genome Biology and Evolution, 2014, 6, 273-289.	1.1	51
815	Horizontal Transfers and Gene Losses in the Phospholipid Pathway of Bartonella Reveal Clues about Early Ecological Niches. Genome Biology and Evolution, 2014, 6, 2156-2169.	1.1	23
816	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. PLoS Genetics, 2014, 10, e1004078.	1.5	238
817	Palaeosymbiosis Revealed by Genomic Fossils of Wolbachia in a Strongyloidean Nematode. PLoS Genetics, 2014, 10, e1004397.	1.5	49
818	Duplications and losses in gene families of rust pathogens highlight putative effectors. Frontiers in Plant Science, 2014, 5, 299.	1.7	44
819	The Streamlined Genome of Phytomonas spp. Relative to Human Pathogenic Kinetoplastids Reveals a Parasite Tailored for Plants. PLoS Genetics, 2014, 10, e1004007.	1.5	66
820	The Genome of Spironucleus salmonicida Highlights a Fish Pathogen Adapted to Fluctuating Environments. PLoS Genetics, 2014, 10, e1004053.	1.5	63
821	Hidden Diversity in Honey Bee Gut Symbionts Detected by Single-Cell Genomics. PLoS Genetics, 2014, 10, e1004596.	1.5	131
822	Genome Update of the Dimorphic Human Pathogenic Fungi Causing Paracoccidioidomycosis. PLoS Neglected Tropical Diseases, 2014, 8, e3348.	1.3	38

#	ARTICLE	IF	CITATIONS
823	Comparative genomics defines the core genome of the growing N4-like phage genus and identifies N4-like Roseophage specific genes. Frontiers in Microbiology, 2014, 5, 506.	1.5	48
824	Phylogenetic Analyses. , 2014, , 93-110.		0
825	Elucidation of the molecular responses to waterlogging in Jatropha roots by transcriptome profiling. Frontiers in Plant Science, 2014, 5, 658.	1.7	51
826	PanGP: A tool for quickly analyzing bacterial pan-genome profile. Bioinformatics, 2014, 30, 1297-1299.	1.8	188
827	Analysis of the Genome and Transcriptome of Cryptococcus neoformans var. grubii Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	1.5	336
828	Widespread Genome Reorganization of an Obligate Virus Mutualist. PLoS Genetics, 2014, 10, e1004660.	1.5	83
829	Recurrent Loss of Specific Introns during Angiosperm Evolution. PLoS Genetics, 2014, 10, e1004843.	1.5	26
830	Nannochloropsis Genomes Reveal Evolution of Microalgal Oleaginous Traits. PLoS Genetics, 2014, 10, e1004094.	1.5	217
831	Whole-Genome Sequence of <i>Burkholderia</i> sp. Strain RPE67, a Bacterial Gut Symbiont of the Bean Bug <i>Riptortus pedestris</i>. Genome Announcements, 2014, 2, .	0.8	12
832	Draft Genome Sequence of Rickettsia aeschlimannii, Associated with Hyalomma marginatum Ticks. Genome Announcements, 2014, 2, .	0.8	4
833	Genome Sequence of Rickettsia tamurae, a Recently Detected Human Pathogen in Japan. Genome Announcements, 2014, 2, .	0.8	7
834	Complete Genome Sequence of Vibrio vulnificus 93U204, a Bacterium Isolated from Diseased Tilapia in Taiwan. Genome Announcements, 2014, 2, .	0.8	9
835	Complete Genome Sequence of Spiroplasma apis B31 T (ATCC 33834), a Bacterium Associated with May Disease of Honeybees (Apis mellifera). Genome Announcements, 2014, 2, .	0.8	23
836	Genome Sequence of Rickettsia hoogstraalii, a Geographically Widely Distributed Tick-Associated Bacterium. Genome Announcements, 2014, 2, .	0.8	4
837	Complete Genome Sequence of Mycobacterium tuberculosis Strain MtURU-001, Isolated from a Rapidly Progressing Outbreak in Uruguay. Genome Announcements, 2014, 2, .	0.8	1
838	Draft Genome Sequences of Streptococcus agalactiae Strains Isolated from Nile Tilapia (Oreochromis) Tj ETQq1 1 0.784314 rgBT /Ov	0.8	10
839	Comparison of gene expression of Paramecium bursaria with and without Chlorella variabilissymbionts. BMC Genomics, 2014, 15, 183.	1.2	57
840	Metagenome-Wide Association of Microbial Determinants of Host Phenotype in Drosophila melanogaster. MBio, 2014, 5, e01631-14.	1.8	112

#	ARTICLE	IF	CITATIONS
841	Sulfobacillus thermosulfidooxidans strain Cutipay enhances chalcopyrite bioleaching under moderate thermophilic conditions in the presence of chloride ion. AMB Express, 2014, 4, 84.	1.4	23
842	Literature-Based Gene Curation and Proposed Genetic Nomenclature for Cryptococcus. Eukaryotic Cell, 2014, 13, 878-883.	3.4	18
843	Insights into the Maize Pan-Genome and Pan-Transcriptome Â. Plant Cell, 2014, 26, 121-135.	3.1	498
844	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5135-5140.	3.3	674
845	The complex jujube genome provides insights into fruit tree biology. Nature Communications, 2014, 5, 5315.	5.8	251
846	Phylogenomics of â€œCandidatus Hepatoplasma crinochetorum,â€•a Lineage of Mollicutes Associated with Noninsect Arthropods. Genome Biology and Evolution, 2014, 6, 407-415.	1.1	35
847	A Proteomic Strategy for Global Analysis of Plant Protein Complexes. Plant Cell, 2014, 26, 3867-3882.	3.1	55
848	Identification of putative orthologous genes for the phylogenetic reconstruction of temperate woody bamboos (<scp>P</scp>oaceae: <scp>B</scp>ambusoideae). Molecular Ecology Resources, 2014, 14, 988-999.	2.2	8
849	Reversal of senescence by N resupply to N-starved Arabidopsis thaliana: transcriptomic and metabolomic consequences. Journal of Experimental Botany, 2014, 65, 3975-3992.	2.4	94
850	Highly parallelized inference of large genomeâ€based phylogenies. Concurrency Computation Practice and Experience, 2014, 26, 1715-1729.	1.4	63
851	Pathways and substrateâ€specific regulation of amino acid degradation in <i><scp>P</scp>haeobacter inhibens</i>â€…<scp>DSM</scp> 17395 (archetype of the marine <i><scp>R</scp>oseobacter</i> clade). Environmental Microbiology, 2014, 16, 218-238.	1.8	28
852	Conservation and divergence of gene expression plasticity following <i>c</i>. 140Âmillion years of evolution in lodgepole pine (<i><scp>P</scp>inus contorta</i>) and interior spruce (<i><scp>P</scp>icea glauca</i>ÂÃ—Â<i><scp>P</scp>icea engelmannii</i>). New Phytologist, 2014, 203, 578-591.	3.5	46
854	Comparative Genomics Provide Insights into Evolution of Trichoderma Nutrition Style. Genome Biology and Evolution, 2014, 6, 379-390.	1.1	57
855	Acetic Acid Bacteria Genomes Reveal Functional Traits for Adaptation to Life in Insect Guts. Genome Biology and Evolution, 2014, 6, 912-920.	1.1	66
856	P3DB 3.0: From plant phosphorylation sites to protein networks. Nucleic Acids Research, 2014, 42, D1206-D1213.	6.5	75
857	Comparative genomic analysis of clinical and environmental strains provides insight into the pathogenicity and evolution of Vibrio parahaemolyticus. BMC Genomics, 2014, 15, 1135.	1.2	19
858	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
859	The translation initiation complex eIF3 in trypanosomatids and other pathogenic excavates â€" identification of conserved and divergent features based on orthologue analysis. BMC Genomics, 2014, 15, 1175.	1.2	35

#	ARTICLE	IF	CITATIONS
860	From microbial gene essentiality to novel antimicrobial drug targets. BMC Genomics, 2014, 15, 958.	1.2	50
861	The temporal foliar transcriptome of the perennial C3 desert plant Rhazya stricta in its natural environment. BMC Plant Biology, 2014, 14, 2.	1.6	27
862	Phylogenetic analysis of pectin-related gene families in Physcomitrella patensand nine other plant species yields evolutionary insights into cell walls. BMC Plant Biology, 2014, 14, 79.	1.6	64
863	Mycobacteriophage-drived diversification of Mycobacterium abscessus. Biology Direct, 2014, 9, 19.	1.9	16
864	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. BMC Biology, 2014, 12, 86.	1.7	251
865	Molecular Evolution of the Substrate Utilization Strategies and Putative Virulence Factors in Mosquito-Associated Spiroplasma Species. Genome Biology and Evolution, 2014, 6, 500-509.	1.1	40
866	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
867	Massive Expansion of Ubiquitination-Related Gene Families within the Chlamydiae. Molecular Biology and Evolution, 2014, 31, 2890-2904.	3.5	43
868	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
869	DNA-Dependent RNA Polymerase Detects Hidden Giant Viruses in Published Databanks. Genome Biology and Evolution, 2014, 6, 1603-1610.	1.1	41
870	Dissecting Vancomycin-Intermediate Resistance in Staphylococcus aureus Using Genome-Wide Association. Genome Biology and Evolution, 2014, 6, 1174-1185.	1.1	132
871	Divergent and Conserved Elements Comprise the Chemoreceptive Repertoire of the Nonblood-Feeding Mosquito Toxorhynchites amboinensis. Genome Biology and Evolution, 2014, 6, 2883-2896.	1.1	31
872	The evolution of the ribosome biogenesis pathway from a yeast perspective. Nucleic Acids Research, 2014, 42, 1509-1523.	6.5	87
873	Orthology Inference in Nonmodel Organisms Using Transcriptomes and Low-Coverage Genomes: Improving Accuracy and Matrix Occupancy for Phylogenomics. Molecular Biology and Evolution, 2014, 31, 3081-3092.	3.5	299
874	Fifteen Million Years of Evolution in the Oryza Genus Shows Extensive Gene Family Expansion. Molecular Plant, 2014, 7, 642-656.	3.9	54
875	The Apicoplast and Mitochondrion ofÂToxoplasma gondii. , 2014, , 297-350.		5
876	Gene Loss Rather Than Gene Gain Is Associated with a Host Jump from Monocots to Dicots in the Smut Fungus Melanopsichium pennsylvanicum. Genome Biology and Evolution, 2014, 6, 2034-2049.	1.1	146
877	In vivo function and comparative genomic analyses of the Drosophila gut microbiota identify candidate symbiosis factors. Frontiers in Microbiology, 2014, 5, 576.	1.5	72

#	ARTICLE	IF	CITATIONS
878	Modularized Evolution in Archaeal Methanogens Phylogenetic Forest. Genome Biology and Evolution, 2014, 6, 3344-3359.	1.1	5
879	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau006-bau006.	1.4	64
880	Small but Powerful, the Primary Endosymbiont of Moss Bugs, Candidatus Evansia muelleri, Holds a Reduced Genome with Large Biosynthetic Capabilities. Genome Biology and Evolution, 2014, 6, 1875-1893.	1.1	42
881	A Pluralistic Account of Homology: Adapting the Models to the Data. Molecular Biology and Evolution, 2014, 31, 501-516.	3.5	37
882	Comparative genomics of Lactobacillus crispatus suggests novel mechanisms for the competitive exclusion of Gardnerella vaginalis. BMC Genomics, 2014, 15, 1070.	1.2	101
883	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. Genome Biology, 2014, 15, R39.	13.9	245
884	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. Nucleic Acids Research, 2014, 42, D1182-D1187.	6.5	800
885	MorusDB: a resource for mulberry genomics and genome biology. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau054-bau054.	1.4	40
886	Comparative Genomics of Taphrina Fungi Causing Varying Degrees of Tumorous Deformity in Plants. Genome Biology and Evolution, 2014, 6, 861-872.	1.1	33
887	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
888	Dissecting the cis and trans Elements That Regulate Adjacent-Gene Coregulation in Saccharomyces cerevisiae. Eukaryotic Cell, 2014, 13, 738-748.	3.4	14
889	Identification of tissue-specific gene clusters and orthologues of nodulation-related genes in Vigna angularis. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S21-S26.	0.4	2
890	A unified nomenclature of NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER family members in plants. Trends in Plant Science, 2014, 19, 5-9.	4.3	581
891	ToxoDB. , 2014, , 647-662.		0
892	Transcriptome and Gene Expression Analysis of an Oleaginous Diatom Under Different Salinity Conditions. Bioenergy Research, 2014, 7, 192-205.	2.2	55
893	ITEP: An integrated toolkit for exploration of microbial pan-genomes. BMC Genomics, 2014, 15, 8.	1.2	123
894	Genome of the human hookworm Necator americanus. Nature Genetics, 2014, 46, 261-269.	9.4	166
895	Population genomics of eusocial insects: the costs of a vertebrateâ€like effective population size. Journal of Evolutionary Biology, 2014, 27, 593-603.	0.8	89

#	ARTICLE	IF	CITATIONS
896	Comparative Analysis of the Full Genome of Helicobacter pylori Isolate Sahul64 Identifies Genes of High Divergence. Journal of Bacteriology, 2014, 196, 1073-1083.	1.0	25
897	Genomic analysis of NAC transcription factors in banana (Musa acuminata) and definition of NAC orthologous groups for monocots and dicots. Plant Molecular Biology, 2014, 85, 63-80.	2.0	91
898	Comparative genomics of unintrogressed Campylobacter coli clades 2 and 3. BMC Genomics, 2014, 15, 129.	1.2	36
899	ComPlEx: conservation and divergence of co-expression networks in A. thaliana, Populus and O. sativa. BMC Genomics, 2014, 15, 106.	1.2	69
900	Genome-wide analysis of the bHLH transcription factor family in Chinese cabbage (Brassica rapa ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	104
901	Genomic comparison of sporeforming bacilli isolated from milk. BMC Genomics, 2014, 15, 26.	1.2	27
902	Genomics in Coccidioides: Insights into evolution, ecology, and pathogenesis. Medical Mycology, 2014, 52, 149-155.	0.3	26
903	Comparative Phylogenomics and Evolution of the Brucellae Reveal a Path to Virulence. Journal of Bacteriology, 2014, 196, 920-930.	1.0	122
904	The tobacco genome sequence and its comparison with those of tomato and potato. Nature Communications, 2014, 5, 3833.	5.8	503
905	Comparing effective population sizes of dominant marine alphaproteobacteria lineages. Environmental Microbiology Reports, 2014, 6, 167-172.	1.0	27
906	Comparative genomics of closely related strains of Klebsiella pneumoniae reveals genes possibly involved in colistin resistance. Annals of Microbiology, 2014, 64, 887-890.	1.1	6
907	Analysis of Staphylococcus aureus clinical isolates with reduced susceptibility to ceftaroline: an epidemiological and structural perspective. Journal of Antimicrobial Chemotherapy, 2014, 69, 2065-2075.	1.3	105
908	Carbohydrate Catabolism in Phaeobacter inhibens DSM 17395, a Member of the Marine Roseobacter Clade. Applied and Environmental Microbiology, 2014, 80, 4725-4737.	1.4	35
909	The Genome of the Foraminiferan Reticulomyxa filosa. Current Biology, 2014, 24, 11-18.	1.8	73
910	Identification of Genetic Bases of Vibrio fluvialis Species-Specific Biochemical Pathways and Potential Virulence Factors by Comparative Genomic Analysis. Applied and Environmental Microbiology, 2014, 80, 2029-2037.	1.4	13
911	Genome assembly and annotation for red clover (<i>Trifolium pratense</i>; Fabaceae). American Journal of Botany, 2014, 101, 327-337.	0.8	69
912	Phylogenetic pinpointing of a paleopolyploidy event within the flax genus (Linum) using transcriptomics. Annals of Botany, 2014, 113, 753-761.	1.4	47
913	Detecting and Locating Whole Genome Duplications on a Phylogeny: A Probabilistic Approach. Molecular Biology and Evolution, 2014, 31, 750-762.	3.5	73

#	Article	IF	Citations
914	Enterococcus faecalis reconfigures its transcriptional regulatory network activation at different copper levels. Metallomics, 2014, 6, 572.	1.0	31
915	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
916	<scp>M</scp>ercator: a fast and simple web server for genome scale functional annotation of plant sequence data. Plant, Cell and Environment, 2014, 37, 1250-1258.	2.8	575
917	Chromosome Scale Genome Assembly and Transcriptome Profiling of Nannochloropsis gaditana in Nitrogen Depletion. Molecular Plant, 2014, 7, 323-335.	3.9	178
918	High-Resolution Transcript Profiling of the Atypical Biotrophic Interaction between<i>Theobroma cacao</i>and the Fungal Pathogen<i>Moniliophthora perniciosa</i>Â Â Â. Plant Cell, 2014, 26, 4245-4269.	3.1	99
919	Extensive transcriptional response associated with seasonal plasticity of butterfly wing patterns. Molecular Ecology, 2014, 23, 6123-6134.	2.0	37
920	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978.	5.8	532
921	Phylotranscriptomic analysis of the origin and early diversification of land plants. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4859-68.	3.3	1,123
922	Unencapsulated Streptococcus pneumoniae from conjunctivitis encode variant traits and belong to a distinct phylogenetic cluster. Nature Communications, 2014, 5, 5411.	5.8	45
923	An Orthology-Based Analysis of Pathogenic Protozoa Impacting Global Health: An Improved Comparative Genomics Approach with Prokaryotes and Model Eukaryote Orthologs. OMICS A Journal of Integrative Biology, 2014, 18, 524-538.	1.0	8
924	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. Nature Genetics, 2014, 46, 270-278.	9.4	867
925	The Tomato Kinome and the Tomato Kinase Library ORFeome: Novel Resources for the Study of Kinases and Signal Transduction in Tomato and <i>Solanaceae</i> Species. Molecular Plant-Microbe Interactions, 2014, 27, 7-17.	1.4	30
926	Genomics and host specialization of honey bee and bumble bee gut symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11509-11514.	3.3	305
927	Selective Constraint Dominates the Evolution of Genes Expressed in a Novel Reproductive Gland. Molecular Biology and Evolution, 2014, 31, 3266-3281.	3.5	12
928	Similar is not the same: Differences in the function of the (hemi-)cellulolytic regulator XlnR (Xlr1/Xyr1) in filamentous fungi. Fungal Genetics and Biology, 2014, 72, 73-81.	0.9	80
930	A Root-Expressed <scp>l</scp>-Phenylalanine:4-Hydroxyphenylpyruvate Aminotransferase Is Required for Tropane Alkaloid Biosynthesis in <i>Atropa belladonna</i> Â Â. Plant Cell, 2014, 26, 3745-3762.	3.1	69
931	Whole-genome sequencing reveals clonal expansion of multiresistant Staphylococcus haemolyticus in European hospitals. Journal of Antimicrobial Chemotherapy, 2014, 69, 2920-2927.	1.3	48
932	Comparative Genomic and Morphological Analyses of Listeria Phages Isolated from Farm Environments. Applied and Environmental Microbiology, 2014, 80, 4616-4625.	1.4	72

#	ARTICLE	IF	CITATIONS
933	Genome-wide evidence of positive selection in Bacteroides fragilis. Computational Biology and Chemistry, 2014, 52, 43-50.	1.1	7
934	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	6.0	520
935	Nucleotide polymorphism and copy number variant detection using exome capture and nextâ€generation sequencing in the polyploid grass P anicum virgatum. Plant Journal, 2014, 79, 993-1008.	2.8	39
936	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. Nature Biotechnology, 2014, 32, 1045-1052.	9.4	535
937	Compositional complexity of the mitochondrial proteome of a unicellular eukaryote (Acanthamoeba) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 2014, 109, 400-416.	1.2	68
938	Genomics and Proteomics Provide New Insight into the Commensal and Pathogenic Lifestyles of Bovine- and Human-Associated <i>Staphylococcus epidermidis</i> Strains. Journal of Proteome Research, 2014, 13, 3748-3762.	1.8	16
939	Genome Structures and Transcriptomes Signify Niche Adaptation for the Multiple-Ion-Tolerant Extremophyte <i>Schrenkiella parvula</i>. Plant Physiology, 2014, 164, 2123-2138.	2.3	77
940	A Transcriptomic Approach to Ribbon Worm Systematics (Nemertea): Resolving the Pilidiophora Problem. Molecular Biology and Evolution, 2014, 31, 3206-3215.	3.5	68
941	orthAgogue: an agile tool for the rapid prediction of orthology relations. Bioinformatics, 2014, 30, 734-736.	1.8	93
942	A new genome of Acidithiobacillus thiooxidans provides insights into adaptation to a bioleaching environment. Research in Microbiology, 2014, 165, 743-752.	1.0	48
943	Insights into Secondary Metabolism from a Global Analysis of Prokaryotic Biosynthetic Gene Clusters. Cell, 2014, 158, 412-421.	13.5	801
944	Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. Plant Cell, 2014, 26, 2792-2802.	3.1	220
945	Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. Nature Communications, 2014, 5, 4611.	5.8	128
946	morFeus: a web-based program to detect remotely conserved orthologs using symmetrical best hits and orthology network scoring. BMC Bioinformatics, 2014, 15, 263.	1.2	9
947	Differential gene expression between functionally specialized polyps of the colonial hydrozoan Hydractinia symbiolongicarpus (Phylum Cnidaria). BMC Genomics, 2014, 15, 406.	1.2	45
948	Whole-genome sequencing of Mesorhizobium huakuii 7653R provides molecular insights into host specificity and symbiosis island dynamics. BMC Genomics, 2014, 15, 440.	1.2	52
949	Comparative genomics of Riemerella anatipestifer reveals genetic diversity. BMC Genomics, 2014, 15, 479.	1.2	60
950	The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	1.2	91

#	ARTICLE	IF	CITATIONS
951	Genome sequencing of two Neorhizobium galegae strains reveals a noeT gene responsible for the unusual acetylation of the nodulation factors. BMC Genomics, 2014, 15, 500.	1.2	30
952	Analyses of Catharanthus roseus and Arabidopsis thaliana WRKY transcription factors reveal involvement in jasmonate signaling. BMC Genomics, 2014, 15, 502.	1.2	99
953	A genomic survey of proteases in Aspergilli. BMC Genomics, 2014, 15, 523.	1.2	36
954	Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef (Eragrostis) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	133
955	Comparative genome sequencing reveals chemotype-specific gene clusters in the toxigenic black mold Stachybotrys. BMC Genomics, 2014, 15, 590.	1.2	45
956	Gene Context Analysis Reveals Functional Divergence between Hypothetically Equivalent Enzymes of the Purineâ€“Ureide Pathway. Biochemistry, 2014, 53, 735-745.	1.2	7
957	Genome sequence and genetic diversity of the common carp, Cyprinus carpio. Nature Genetics, 2014, 46, 1212-1219.	9.4	576
958	Molecular Evolution of the Odorant and Gustatory Receptor Genes in Lepidopteran Insects: Implications for Their Adaptation and Speciation. Journal of Molecular Evolution, 2014, 79, 21-39.	0.8	122
959	A roadmap for natural product discovery based on large-scale genomics and metabolomics. Nature Chemical Biology, 2014, 10, 963-968.	3.9	416
960	Polyploidy-associated genome modifications during land plant evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130355.	1.8	90
961	Genome-wide identification, classification and expression analysis of the heat shock transcription factor family in Chinese cabbage. Molecular Genetics and Genomics, 2014, 289, 541-551.	1.0	59
962	Complete genome sequence of Tunisvirus, a new member of the proposed family Marseilleviridae. Archives of Virology, 2014, 159, 2349-2358.	0.9	69
963	Genome-Wide Analysis and Expression Patterns of NAC Transcription Factor Family Under Different Developmental Stages and Abiotic Stresses in Chinese Cabbage. Plant Molecular Biology Reporter, 2014, 32, 1041-1056.	1.0	55
964	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788.	6.0	1,479
965	Structural and functional partitioning of bread wheat chromosome 3B. Science, 2014, 345, 1249721.	6.0	542
966	Genome interplay in the grain transcriptome of hexaploid bread wheat. Science, 2014, 345, 1250091.	6.0	318
967	Ancient hybridizations among the ancestral genomes of bread wheat. Science, 2014, 345, 1250092.	6.0	629
968	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

#	Article	IF	Citations
969	Genome sequence of the cultivated cotton Gossypium arboreum. Nature Genetics, 2014, 46, 567-572.	9.4	883
970	Comparative Exoprotein Profiling of DifferentStaphylococcus epidermidisStrains Reveals Potential Link between Nonclassical Protein Export and Virulence. Journal of Proteome Research, 2014, 13, 3249-3261.	1.8	17
971	Nitrogen-Fixing Rhizobial Strains Isolated from Common Bean Seeds: Phylogeny, Physiology, and Genome Analysis. Applied and Environmental Microbiology, 2014, 80, 5644-5654.	1.4	48
972	Evolutionary analysis of a streamlined lineage of surface ocean Roseobacters. ISME Journal, 2014, 8, 1428-1439.	4.4	55
973	Genome-wide analysis of nucleotide-binding site disease resistance genes in Medicago truncatula. Science Bulletin, 2014, 59, 1129-1138.	1.7	16
974	Prevalence of transcription factors in ascomycete and basidiomycete fungi. BMC Genomics, 2014, 15, 214.	1.2	114
975	Genome sequence and transcriptome analyses of the thermophilic zygomycete fungus Rhizomucor miehei. BMC Genomics, 2014, 15, 294.	1.2	39
976	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
977	Proteomics and transcriptomics of the BABA-induced resistance response in potato using a novel functional annotation approach. BMC Genomics, 2014, 15, 315.	1.2	67
978	Genome analysis reveals three genomospecies in Mycobacterium abscessus. BMC Genomics, 2014, 15, 359.	1.2	79
979	Construction and verification of the transcriptional regulatory response network of Streptococcus mutansupon treatment with the biofilm inhibitor carolacton. BMC Genomics, 2014, 15, 362.	1.2	14
980	Transcriptomic analyses reveal the adaptive features and biological differences of guts from two invasive whitefly species. BMC Genomics, 2014, 15, 370.	1.2	37
981	Comparative genome analysis of pathogenic and non-pathogenic Clavibacter strains reveals adaptations to their lifestyle. BMC Genomics, 2014, 15, 392.	1.2	32
982	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
983	Comparative genomic analysis of the R2R3 MYB secondary cell wall regulators of Arabidopsis, poplar, rice, maize, and switchgrass. BMC Plant Biology, 2014, 14, 135.	1.6	74
984	Genes associated with agronomic traits in non-heading Chinese cabbage identified by expression profiling. BMC Plant Biology, 2014, 14, 71.	1.6	21
985	The complete genome of Blastobotrys (Arxula) adeninivorans LS3 - a yeast of biotechnological interest. Biotechnology for Biofuels, 2014, 7, 66.	6.2	57
986	Prediction of Potential Kinase Inhibitors in Leishmania spp. through a Machine Learning and Molecular Docking Approach. Advances in Intelligent Systems and Computing, 2014, , 63-70.	0.5	0

#	Article	IF	Citations
987	<scp>kdetrees</scp>: non-parametric estimation of phylogenetic tree distributions. Bioinformatics, 2014, 30, 2280-2287.	1.8	44
988	Inference of Transcriptional Networks in <i>Arabidopsis</i> through Conserved Noncoding Sequence Analysis. Plant Cell, 2014, 26, 2729-2745.	3.1	57
989	The genomeâ€scale metabolic network of <i>Ectocarpus siliculosus</i> (Ecto<scp>GEM</scp>): a resource to study brown algal physiology and beyond. Plant Journal, 2014, 80, 367-381.	2.8	39
990	Genomic analysis of the causative agents of coccidiosis in domestic chickens. Genome Research, 2014, 24, 1676-1685.	2.4	176
991	Data showing the compositional complexity of the mitochondrial proteome of a unicellular eukaryote (Acanthamoeba castellanii, supergroup Amoebozoa). Data in Brief, 2014, 1, 12-14.	0.5	4
992	Functional Genomic Characterization of Virulence Factors from Necrotizing Fasciitis-Causing Strains of Aeromonas hydrophila. Applied and Environmental Microbiology, 2014, 80, 4162-4183.	1.4	54
993	Genome-wide analysis of the GRAS gene family in Chinese cabbage (Brassica rapa ssp. pekinensis). Genomics, 2014, 103, 135-146.	1.3	114
994	DuctApe: A suite for the analysis and correlation of genomic and OmniLogâ„¢ Phenotype Microarray data. Genomics, 2014, 103, 1-10.	1.3	73
995	Genomic Analyses of Pneumococci from Children with Sickle Cell Disease Expose Host-Specific Bacterial Adaptations and Deficits in Current Interventions. Cell Host and Microbe, 2014, 15, 587-599.	5.1	57
996	Molecular evolution of the actin-like MreB protein gene family in wall-less bacteria. Biochemical and Biophysical Research Communications, 2014, 446, 927-932.	1.0	32
997	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	5.8	918
998	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. Nature Genetics, 2014, 46, 693-700.	9.4	139
999	Pseudozyma brasiliensis sp. nov., a xylanolytic, ustilaginomycetous yeast species isolated from an insect pest of sugarcane roots. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2159-2168.	0.8	17
1000	The Complete Genome Sequence of â€˜<i>Candidatus</i> Liberibacter americanusâ€™, Associated with Citrus Huanglongbing. Molecular Plant-Microbe Interactions, 2014, 27, 163-176.	1.4	97
1001	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
1002	The mitochondrial respiratory chain of the secondary green alga Euglena gracilis shares many additional subunits with parasitic Trypanosomatidae. Mitochondrion, 2014, 19, 338-349.	1.6	59
1003	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <i><scp>M</scp>agnetospira</i> sp. <scp>QH</scp>â€2 strain. Environmental Microbiology, 2014, 16, 525-544.	1.8	66
1004	A Real-Time PCR for Detection and Quantification of Mycoplasma ovipneumoniae. Journal of Veterinary Medical Science, 2014, 76, 1631-1634.	0.3	15

#	ARTICLE	IF	CITATIONS
1005	Phosphoproteomic analysis of the non-seed vascular plant model Selaginella moellendorffii. Proteome Science, 2014, 12, 16.	0.7	16
1006	Leptospiral Pathogenomics. Pathogens, 2014, 3, 280-308.	1.2	94
1007	A draft genome for the African crocodilian trypanosome Trypanosoma grayi. Scientific Data, 2014, 1, 140024.	2.4	39
1008	Gene Expression of Chicken Gonads Is Sex- and Side-Specific. Sexual Development, 2014, 8, 178-191.	1.1	11
1009	Identifying gene clusters by discovering common intervals in indeterminate strings. BMC Genomics, 2014, 15, S2.	1.2	4
1010	Complete genome sequence of Planctomyces brasiliensis type strain (DSM 5305T), phylogenomic analysis and reclassification of Planctomycetes including the descriptions of Gimesia gen. nov., Planctopirus gen. nov. and Rubinisphaera gen. nov. and emended descriptions of the order Planctomycetales and the family Planctomycetaceae. Standards in Genomic Sciences, 2014, 9, 10.	1.5	76
1011	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of Escherichia coli, and a proposal for delineating subspecies in microbial taxonomy. Standards in Genomic Sciences, 2014, 9, 2.	1.5	454
1012	Mapping genomic features to functional traits through microbial whole genome sequences. International Journal of Bioinformatics Research and Applications, 2014, 10, 461.	0.1	6
1013	The complete genome sequence of the rumen methanogen Methanobacterium formicicum BRM9. Standards in Genomic Sciences, 2014, 9, 15.	1.5	27
1014	TreSpExâ€“Detection of Misleading Signal in Phylogenetic Reconstructions Based on Tree Information. Evolutionary Bioinformatics, 2014, 10, EBO.S14239.	0.6	105
1015	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. Evolutionary Bioinformatics, 2014, 10, EBO.S13759.	0.6	23
1016	Genomic analysis of Agrobacterium radiobacter DSM 30147T and emended description of A. radiobacter (Beijerinck and van Delden 1902) Conn 1942 (Approved Lists 1980) emend. Sawada et al. 1993. Standards in Genomic Sciences, 2014, 9, 574-584.	1.5	12
1017	Complete genome sequence of the Phaeobacter gallaeciensis type strain CIP 105210T (= DSM 26640T =) Tj ETQq0 0 0 rgBT /Overlock 1	1.5	21
1018	Orthology and paralogy constraints: satisfiability and consistency. BMC Genomics, 2014, 15, S12.	1.2	35
1019	A meta-approach for improving the prediction and the functional annotation of ortholog groups. BMC Genomics, 2014, 15, S16.	1.2	20
1020	Whole genome sequence and analysis of the Marwari horse breed and its genetic origin. BMC Genomics, 2014, 15, S4.	1.2	30
1021	Evolutionary divergence of core and post-translational circadian clock genes in the pitcher-plant mosquito, Wyeomyia smithii. BMC Genomics, 2015, 16, 754.	1.2	12
1022	Angiosperms Are Unique among Land Plant Lineages in the Occurrence of Key Genes in the RNA-Directed DNA Methylation (RdDM) Pathway. Genome Biology and Evolution, 2015, 7, 2648-2662.	1.1	46

#	Article	IF	Citations
1023	Mining from transcriptomes: 315 singleâ€copy orthologous genes concatenated for the phylogenetic analyses of Orchidaceae. Ecology and Evolution, 2015, 5, 3800-3807.	0.8	21
1024	Supergroup C <i>Wolbachia</i> , mutualist symbionts of filarial nematodes, have a distinct genome structure. Open Biology, 2015, 5, 150099.	1.5	38
1025	Genomes of â€˜<i>Candidatus</i> Liberibacter solanacearumâ€™ Haplotype A from New Zealand and the United States Suggest Significant Genome Plasticity in the Species. Phytopathology, 2015, 105, 863-871.	1.1	35
1026	Whole-genome sequencing reveals the effect of vaccination on the evolution of Bordetella pertussis. Scientific Reports, 2015, 5, 12888.	1.6	44
1027	The Plasmodiophora brassicae genome reveals insights in its life cycle and ancestry of chitin synthases. Scientific Reports, 2015, 5, 11153.	1.6	202
1030	Donkey genome and insight into the imprinting of fast karyotype evolution. Scientific Reports, 2015, 5, 14106.	1.6	29
1031	Transcriptomes reveal the genetic mechanisms underlying ionic regulatory adaptations to salt in the crab-eating frog. Scientific Reports, 2015, 5, 17551.	1.6	14
1032	Candidate Gene Identification of Flowering Time Genes in Cotton. Plant Genome, 2015, 8, eplantgenome2014.12.0098.	1.6	14
1033	Comparative differential gene expression analysis of nucleus-encoded proteins for Rafflesia cantleyi against Arabidopsis thaliana. AIP Conference Proceedings, 2015, , .	0.3	0
1034	Genome-wide Annotation and Comparative Analysis of Long Terminal Repeat Retrotransposons between Pear Species of P. bretschneideri and P. Communis. Scientific Reports, 2015, 5, 17644.	1.6	16
1035	Comparative genomics Lactobacillus reuteri from sourdough reveals adaptation of an intestinal symbiont to food fermentations. Scientific Reports, 2015, 5, 18234.	1.6	65
1036	Exploring molecular variation in Schistosoma japonicum in China. Scientific Reports, 2015, 5, 17345.	1.6	33
1037	Insights into the Transcriptional Architecture of Behavioral Plasticity in the Honey Bee Apis mellifera. Scientific Reports, 2015, 5, 11136.	1.6	59
1038	Comparative genome analysis reveals the molecular basis of nicotine degradation and survival capacities of Arthrobacter. Scientific Reports, 2015, 5, 8642.	1.6	44
1039	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
1040	Comprehensive analysis of the flowering genes in Chinese cabbage and examination of evolutionary pattern of CO-like genes in plant kingdom. Scientific Reports, 2015, 5, 14631.	1.6	41
1041	Defining the Schistosoma haematobium kinome enables the prediction of essential kinases as anti-schistosome drug targets. Scientific Reports, 2015, 5, 17759.	1.6	37
1043	<i>De Novo</i> Assembly and Characterization of Four Anthozoan (Phylum Cnidaria) Transcriptomes. G3: Genes, Genomes, Genetics, 2015, 5, 2441-2452.	0.8	74

#	Article	IF	Citations
1044	Spatial differentiation of gene expression in Aspergillus niger colony grown for sugar beet pulp utilization. Scientific Reports, 2015, 5, 13592.	1.6	15
1045	Gene-pseudogene evolution: a probabilistic approach. BMC Genomics, 2015, 16, S12.	1.2	6
1046	Reconstructing a SuperGeneTree minimizing reconciliation. BMC Bioinformatics, 2015, 16, S4.	1.2	5
1047	Transcriptome sequencing of three Pseudo-nitzschia species reveals comparable gene sets and the presence of Nitric Oxide Synthase genes in diatoms. Scientific Reports, 2015, 5, 12329.	1.6	58
1048	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
1049	Transcriptome analysis of 20 taxonomically related benzylisoquinoline alkaloid-producing plants. BMC Plant Biology, 2015, 15, 227.	1.6	70
1050	Improved orthologous databases to ease protozoan targets inference. Parasites and Vectors, 2015, 8, 494.	1.0	2
1051	High quality draft genomic sequence of Flavobacterium enshiense DK69T and comparison among Flavobacterium genomes. Standards in Genomic Sciences, 2015, 10, 92.	1.5	2
1052	Genetic control of pear rootstock-induced dwarfing and precocity is linked to a chromosomal region syntenic to the apple Dw1 loci. BMC Plant Biology, 2015, 15, 230.	1.6	37
1053	Draft genome sequences of Chrysoporthe austroafricana, Diplodia scrobiculata, Fusarium nygamai, Leptographium lundbergii, Limonomyces culmigenus, Stagonosporopsis tanaceti, and Thielaviopsis punctulata. IMA Fungus, 2015, 6, 233-248.	1.7	46
1054	Following the Footsteps of Chlamydial Gene Regulation. Molecular Biology and Evolution, 2015, 32, msv193.	3.5	30
1055	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
1056	High quality draft genomic sequence of Arenimonas donghaensis DSM 18148T. Standards in Genomic Sciences, 2015, 10, 59.	1.5	6
1057	Draft genome sequence of Cellulomonas carbonis T26T and comparative analysis of six Cellulomonas genomes. Standards in Genomic Sciences, 2015, 10, 104.	1.5	5
1058	A host plant genome (<i>Zizania latifolia</i>) after a centuryâ€long endophyte infection. Plant Journal, 2015, 83, 600-609.	2.8	67
1059	Complete Genome Sequence of â€œCandidatus Sulcia muelleriâ€•ML, an Obligate Nutritional Symbiont of Maize Leafhopper (<i>Dalbulus maidis</i>). Genome Announcements, 2015, 3, .	0.8	20
1060	Analysis of 5â€™ gene regions reveals extraordinary conservation of novel non-coding sequences in a wide range of animals. BMC Evolutionary Biology, 2015, 15, 227.	3.2	7
1061	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

#	ARTICLE	IF	CITATIONS
1062	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
1063	Transcriptome-enabled marker discovery and mapping of plastochron-related genes in Petunia spp.. BMC Genomics, 2015, 16, 726.	1.2	23
1064	Comparative genome analysis of Weissella ceti, an emerging pathogen of farm-raised rainbow trout. BMC Genomics, 2015, 16, 1095.	1.2	12
1065	Positionally-conserved but sequence-diverged: identification of long non-coding RNAs in the Brassicaceae and Cleomaceae. BMC Plant Biology, 2015, 15, 217.	1.6	64
1066	OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. Genome Biology, 2015, 16, 157.	3.8	2,812
1067	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200.	3.8	77
1068	The first draft genome of the aquatic model plant Lemna minor opens the route for future stress physiology research and biotechnological applications. Biotechnology for Biofuels, 2015, 8, 188.	6.2	112
1069	Comparison of the protein-coding gene content of Chlamydia trachomatis and Protochlamydia amoebophila using a Raspberry Pi computer. BMC Research Notes, 2015, 8, 561.	0.6	4
1070	A comparison of the protein-coding genomes of two green sulphur bacteria, Chlorobium tepidum TLS and Pelodictyon phaeoclathratiforme BU-1. BMC Research Notes, 2015, 8, 565.	0.6	2
1071	Genomic information of the arsenic-resistant bacterium Lysobacter arseniciresistens type strain ZS79T and comparison of Lysobacter draft genomes. Standards in Genomic Sciences, 2015, 10, 88.	1.5	6
1072	High quality draft genome sequence of the moderately halophilic bacterium Pontibacillus yanchengensis Y32T and comparison among Pontibacillus genomes. Standards in Genomic Sciences, 2015, 10, 93.	1.5	5
1073	Complete Genome Sequence of Spiroplasma cantharicola CC-1 ^T (DSM 21588), a Bacterium Isolated from Soldier Beetle (<i>Cantharis carolinus</i>). Genome Announcements, 2015, 3, .	0.8	9
1074	BIR Pipeline for Preparation of Phylogenomic Data. Evolutionary Bioinformatics, 2015, 11, EBO.S10189.	0.6	8
1075	toxoMine: an integrated omics data warehouse forToxoplasma gondiisystems biology research. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav066.	1.4	7
1076	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. G3: Genes, Genomes, Genetics, 2015, 5, 629-638.	0.8	10
1077	Genome sequence of <i>Valsa</i> canker pathogens uncovers a potential adaptation of colonization of woody bark. New Phytologist, 2015, 208, 1202-1216.	3.5	158
1078	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
1079	Molecular evolution and speciesâ€specific expansion of the NAP members in plants. Journal of Integrative Plant Biology, 2015, 57, 673-687.	4.1	17

#	Article	IF	Citations
1080	PTGBase: an integrated database to study tandem duplicated genes in plants. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	46
1081	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav046.	1.4	62
1082	Fullâ€•length <i>de novo</i> assembly of RNAâ€•seq data in pea (<i><scp>P</scp>isum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. Plant Journal, 2015, 84, 1-19.	2.8	173
1083	Complete Genome Sequence of Spiroplasma litorale TN-1 ^T (DSM 21781), a Bacterium Isolated from a Green-Eyed Horsefly (<i>Tabanus nigrovittatus</i>). Genome Announcements, 2015, 3, .	0.8	12
1084	Genomic limitations to <scp>RNA</scp> sequencing expression profiling. Plant Journal, 2015, 84, 491-503.	2.8	34
1085	Draft Genome Sequence of a 16SrII-A Subgroup Phytoplasma Associated with Purple Coneflower () Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	21
1086	Comparative Genome Analysis Reveals Divergent Genome Size Evolution in a Carnivorous Plant Genus. Plant Genome, 2015, 8, eplantgenome2015.04.0021.	1.6	45
1087	Genome-Wide Identification of Evolutionarily Conserved Alternative Splicing Events in Flowering Plants. Frontiers in Bioengineering and Biotechnology, 2015, 3, 33.	2.0	138
1088	Full Genome Sequence Analysis of Two Isolates Reveals a Novel Xanthomonas Species Close to the Sugarcane Pathogen Xanthomonas albilineans. Genes, 2015, 6, 714-733.	1.0	19
1089	Genome-Wide Analysis of Sorbitol Dehydrogenase (SDH) Genes and Their Differential Expression in Two Sand Pear (Pyrus pyrifolia) Fruits. International Journal of Molecular Sciences, 2015, 16, 13065-13083.	1.8	16
1090	A predicted protein interactome identifies conserved global networks and disease resistance subnetworks in maize. Frontiers in Genetics, 2015, 6, 201.	1.1	35
1091	A taxonomic framework for emerging groups of ecologically important marine gammaproteobacteria based on the reconstruction of evolutionary relationships using genome-scale data. Frontiers in Microbiology, 2015, 6, 281.	1.5	168
1092	Whole-genome comparative analysis of virulence genes unveils similarities and differences between endophytes and other symbiotic bacteria. Frontiers in Microbiology, 2015, 6, 419.	1.5	31
1093	Welcome to pandoraviruses at the Ã¢â‚¬ËœFourth TRUCÃ¢â‚¬â„¢ club. Frontiers in Microbiology, 2015, 6, 423.	1.5	24
1094	Phylogenomics of Xanthomonas field strains infecting pepper and tomato reveals diversity in effector repertoires and identifies determinants of host specificity. Frontiers in Microbiology, 2015, 6, 535.	1.5	156
1095	Pithovirus sibericum, a new bona fide member of the â€œFourth TRUCâ€•club. Frontiers in Microbiology, 2015, 6, 722.	1.5	20
1096	Comparative genomic analysis of multiple strains of two unusual plant pathogens: Pseudomonas corrugata and Pseudomonas mediterranea. Frontiers in Microbiology, 2015, 6, 811.	1.5	50
1097	Genetic determinants of heat resistance in Escherichia coli. Frontiers in Microbiology, 2015, 6, 932.	1.5	105

#	ARTICLE	IF	CITATIONS
1098	Slow and Fast Evolving Endosymbiont Lineages: Positive Correlation between the Rates of Synonymous and Non-Synonymous Substitution. Frontiers in Microbiology, 2015, 6, 1279.	1.5	17
1099	Pan-Genome Analysis of Brazilian Lineage A Amoebal Mimiviruses. Viruses, 2015, 7, 3483-3499.	1.5	26
1100	Whole-Genome Optical Mapping and Finished Genome Sequence of Sphingobacterium deserti sp. nov., a New Species Isolated from the Western Desert of China. PLoS ONE, 2015, 10, e0122254.	1.1	6
1101	Extensive Identification of Bacterial Riboflavin Transporters and Their Distribution across Bacterial Species. PLoS ONE, 2015, 10, e0126124.	1.1	98
1102	Genome-Wide Transcriptional Profiling of Clostridium perfringens SM101 during Sporulation Extends the Core of Putative Sporulation Genes and Genes Determining Spore Properties and Germination Characteristics. PLoS ONE, 2015, 10, e0127036.	1.1	13
1103	Reproductive Mode and the Evolution of Genome Size and Structure in Caenorhabditis Nematodes. PLoS Genetics, 2015, 11, e1005323.	1.5	102
1104	The Dynamic Genome and Transcriptome of the Human Fungal Pathogen Blastomyces and Close Relative Emmonsia. PLoS Genetics, 2015, 11, e1005493.	1.5	57
1105	Targeting Lysine Deacetylases (KDACs) in Parasites. PLoS Neglected Tropical Diseases, 2015, 9, e0004026.	1.3	47
1106	Collembolan Transcriptomes Highlight Molecular Evolution of Hexapods and Provide Clues on the Adaptation to Terrestrial Life. PLoS ONE, 2015, 10, e0130600.	1.1	25
1107	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
1108	Genome Analysis of Pseudomonas fluorescens PCL1751: A Rhizobacterium that Controls Root Diseases and Alleviates Salt Stress for Its Plant Host. PLoS ONE, 2015, 10, e0140231.	1.1	70
1109	Pangenome Analysis of Burkholderia pseudomallei: Genome Evolution Preserves Gene Order despite High Recombination Rates. PLoS ONE, 2015, 10, e0140274.	1.1	37
1110	orthoFind Facilitates the Discovery of Homologous and Orthologous Proteins. PLoS ONE, 2015, 10, e0143906.	1.1	3
1111	Genomic Patterns of Positive Selection at the Origin of Rust Fungi. PLoS ONE, 2015, 10, e0143959.	1.1	20
1112	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
1113	Application of a Novel â€œPan-Genomeâ€•Based Strategy for Assigning RNAseq Transcript Reads to Staphylococcus aureus Strains. PLoS ONE, 2015, 10, e0145861.	1.1	9
1114	In Silico Comparative Transcriptome Analysis of Two Color Morphs of the Common Coral Trout (Plectropomus Leopardus). PLoS ONE, 2015, 10, e0145868.	1.1	20
1115	Leptomonas seymouri: Adaptations to the Dixenous Life Cycle Analyzed by Genome Sequencing, Transcriptome Profiling and Co-infection with Leishmania donovani. PLoS Pathogens, 2015, 11, e1005127.	2.1	96

#	ARTICLE	IF	CITATIONS
1116	Intraspecies Genomic Diversity and Long-Term Persistence of Bifidobacterium longum. PLoS ONE, 2015, 10, e0135658.	1.1	46
1117	A novel workflow correlating RNA-seq data to Phythophthora infestans resistance levels in wild Solanum species and potato clones. Frontiers in Plant Science, 2015, 6, 718.	1.7	21
1118	Transcriptome analysis reveals regulatory networks underlying differential susceptibility to Botrytis cinerea in response to nitrogen availability in Solanum lycopersicum. Frontiers in Plant Science, 2015, 6, 911.	1.7	41
1119	Comparative Genomics of Pathogenic and Nonpathogenic Strains of Xanthomonas arboricola Unveil Molecular and Evolutionary Events Linked to Pathoadaptation. Frontiers in Plant Science, 2015, 6, 1126.	1.7	68
1120	An Effective Big Data Supervised Imbalanced Classification Approach for Ortholog Detection in Related Yeast Species. BioMed Research International, 2015, 2015, 1-12.	0.9	17
1121	Genome-Wide Comparative Analysis of Flowering-Related Genes in Arabidopsis, Wheat, and Barley. International Journal of Plant Genomics, 2015, 2015, 1-17.	2.2	30
1122	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. ELife, 2015, 4, e06974.	2.8	198
1123	The<i>Glycine max</i>cv. Enrei Genome for Improvement of Japanese Soybean Cultivars. International Journal of Genomics, 2015, 2015, 1-8.	0.8	40
1124	Inside the Pan-genome - Methods and Software Overview. Current Genomics, 2015, 16, 245-252.	0.7	79
1125	Population structure of<i>Neisseria gonorrhoeae</i>based on whole genome data and its relationship with antibiotic resistance. PeerJ, 2015, 3, e806.	0.9	67
1126	Comparative genomic analysis of Helicobacter pylori from Malaysia identifies three distinct lineages suggestive of differential evolution. Nucleic Acids Research, 2015, 43, 324-335.	6.5	24
1127	The evolution of parasitism in Nematoda. Parasitology, 2015, 142, S26-S39.	0.7	199
1128	Employing Phylogenomics to Resolve the Relationships among Cnidarians, Ctenophores, Sponges, Placozoans, and Bilaterians. Integrative and Comparative Biology, 2015, 55, 1084-1095.	0.9	40
1129	Genomeâ€guided investigation of plant natural product biosynthesis. Plant Journal, 2015, 82, 680-692.	2.8	186
1130	Rapid molecular evolution across amniotes of the IIS/TOR network. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7055-7060.	3.3	59
1131	Phytomonas: Trypanosomatids Adapted to Plant Environments. PLoS Pathogens, 2015, 11, e1004484.	2.1	52
1132	Parallel Epidemics of Community-Associated Methicillin-Resistant<i>Staphylococcus aureus</i>USA300 Infection in North and South America. Journal of Infectious Diseases, 2015, 212, 1874-1882.	1.9	107
1133	The genomes of closely related Pantoea ananatis maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. Frontiers in Microbiology, 2015, 6, 440.	1.5	85

#	ARTICLE	IF	CITATIONS
1134	Genome-wide survey and expression analysis of the PUB family in Chinese cabbage (Brassica rapa ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.0	37
1135	High quality reference genome of drumstick tree (Moringa oleifera Lam.), a potential perennial crop. Science China Life Sciences, 2015, 58, 627-638.	2.3	53
1136	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
1137	Genome-wide analysis of AP2/ERF transcription factors in carrot (Daucus carota L.) reveals evolution and expression profiles under abiotic stress. Molecular Genetics and Genomics, 2015, 290, 2049-2061.	1.0	55
1138	Adapting simultaneous analysis phylogenomic techniques to study complex disease gene relationships. Journal of Biomedical Informatics, 2015, 54, 10-38.	2.5	3
1139	Genomic features separating ten strains of Neorhizobium galegae with different symbiotic phenotypes. BMC Genomics, 2015, 16, 348.	1.2	12
1140	Antigenicity and immunogenicity of PvRALP1, a novel Plasmodium vivax rhoptry neck protein. Malaria Journal, 2015, 14, 186.	0.8	8
1141	Genome sequences of the Shiga-like toxin-producing Escherichia coli NCCP15655 and NCCP15656. Gut Pathogens, 2015, 7, 13.	1.6	1
1142	OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species. Nucleic Acids Research, 2015, 43, W78-W84.	6.5	612
1143	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
1144	Wrangler's user environment: A software framework for management of data-intensive computing system. , 2015, , .		8
1145	Low Temperature Adaptation Is Not the Opposite Process of High Temperature Adaptation in Terms of Changes in Amino Acid Composition. Genome Biology and Evolution, 2015, 7, 3426-3433.	1.1	27
1146	Found and Lost: The Fates of Horizontally Acquired Genes in Arthropod-Symbiotic<i>Spiroplasma</i>. Genome Biology and Evolution, 2015, 7, 2458-2472.	1.1	51
1147	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. Genome Biology and Evolution, 2015, 7, evv172.	1.1	22
1148	Comparative Genomics of the Genus<i>Porphyromonas</i>Identifies Adaptations for Heme Synthesis within the Prevalent Canine Oral Species<i>Porphyromonas cangingivalis</i>. Genome Biology and Evolution, 2015, 7, 3397-3413.	1.1	23
1149	Phylotranscriptomic analyses in plants using Betulaceae as an example. Journal of Systematics and Evolution, 2015, 53, 403-410.	1.6	6
1150	Scrutinizing the immune defence inventory of Camponotus floridanus applying total transcriptome sequencing. BMC Genomics, 2015, 16, 540.	1.2	33
1151	Genome sequencing of herb Tulsi (Ocimum tenuiflorum) unravels key genes behind its strong medicinal properties. BMC Plant Biology, 2015, 15, 212.	1.6	80

#	Article	IF	Citations
1152	Phylogenomic Analysis of Oenococcus oeni Reveals Specific Domestication of Strains to Cider and Wines. Genome Biology and Evolution, 2015, 7, 1506-1518.	1.1	57
1153	Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two<i>Coxiella-</i>Like Endosymbionts in Ticks. Genome Biology and Evolution, 2015, 7, 1779-1796.	1.1	140
1154	SynFind: Compiling Syntenic Regions across Any Set of Genomes on Demand. Genome Biology and Evolution, 2015, 7, 3286-3298.	1.1	70
1155	Genome Sequences of Three Helicobacter pylori Strains from Patients with Gastric Mucosa-Associated Lymphoid Tissue Lymphoma. Genome Announcements, 2015, 3, .	0.8	10
1156	Complete Genome Sequence of Agrobacterium tumefaciens Ach5. Genome Announcements, 2015, 3, .	0.8	25
1157	Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. Nature, 2015, 527, 508-511.	13.7	291
1158	Hybrid de novo genome assembly of the Chinese herbal plant danshen (Salvia miltiorrhiza Bunge). GigaScience, 2015, 4, 62.	3.3	73
1159	A computational framework for integrative analysis of large microbial genomics data. , 2015, , .		1
1160	<i>Chlamydiaceae</i>Genomics Reveals Interspecies Admixture and the Recent Evolution of<i>Chlamydia abortus</i>Infecting Lower Mammalian Species and Humans. Genome Biology and Evolution, 2015, 7, 3070-3084.	1.1	30
1161	Comparative genomic analysis of Leishmania (Viannia) peruviana and Leishmania (Viannia) braziliensis. BMC Genomics, 2015, 16, 715.	1.2	54
1162	SpirPro: A Spirulina proteome database and web-based tools for the analysis of protein-protein interactions at the metabolic level in Spirulina (Arthrospira) platensis C1. BMC Bioinformatics, 2015, 16, 233.	1.2	14
1163	Deciphering Genome Content and Evolutionary Relationships of Isolates from the Fungus<i>Magnaporthe oryzae</i>Attacking Different Host Plants. Genome Biology and Evolution, 2015, 7, 2896-2912.	1.1	96
1164	Taxon-Rich Phylogenomic Analyses Resolve the Eukaryotic Tree of Life and Reveal the Power of Subsampling by Sites. Systematic Biology, 2015, 64, 406-415.	2.7	63
1165	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. Cell Reports, 2015, 10, 910-919.	2.9	77
1166	Comparative interrogation of the developing xylem transcriptomes of two woodâ€forming species: <i><scp>P</scp>opulus trichocarpa</i> and <i><scp>E</scp>ucalyptus grandis</i>. New Phytologist, 2015, 206, 1391-1405.	3.5	47
1167	Pantograph: A template-based method for genome-scale metabolic model reconstruction. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550006.	0.3	29
1168	Robust Identification of Orthologues and Paralogues for Microbial Pan-Genomics Using GET_HOMOLOGUES: A Case Study of pIncA/C Plasmids. Methods in Molecular Biology, 2015, 1231, 203-232.	0.4	54
1169	Biased Gene Conversion and GC-Content Evolution in the Coding Sequences of Reptiles and Vertebrates. Genome Biology and Evolution, 2015, 7, 240-250.	1.1	67

#	Article	IF	Citations
1170	Draft genome sequence of the intestinal parasite Blastocystis subtype 4-isolate WR1. Genomics Data, 2015, 4, 22-23.	1.3	27
1171	Insights on the Evolution of Mycoparasitism from the Genome of Clonostachys rosea. Genome Biology and Evolution, 2015, 7, 465-480.	1.1	150
1172	New Research Tools for Urogenital Schistosomiasis. Journal of Infectious Diseases, 2015, 211, 861-869.	1.9	24
1173	Functional and Phylogenetic Characterization of Proteins Detected in Various Nematode Intestinal Compartments*. Molecular and Cellular Proteomics, 2015, 14, 812-827.	2.5	23
1174	Genome-Wide Patterns of Genetic Polymorphism and Signatures of Selection in Plasmodium vivax. Genome Biology and Evolution, 2015, 7, 106-119.	1.1	44
1175	Draft genome sequence of adzuki bean, Vigna angularis. Scientific Reports, 2015, 5, 8069.	1.6	144
1176	Genome-Wide Analysis of Adaptive Molecular Evolution in the Carnivorous Plant Utricularia gibba. Genome Biology and Evolution, 2015, 7, 444-456.	1.1	33
1177	PLAZA 3.0: an access point for plant comparative genomics. Nucleic Acids Research, 2015, 43, D974-D981.	6.5	329
1178	The draft genome of Tibetan hulless barley reveals adaptive patterns to the high stressful Tibetan Plateau. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1095-1100.	3.3	147
1179	Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. Plant Journal, 2015, 81, 810-821.	2.8	149
1180	The Same or Not the Same: Lineage-Specific Gene Expansions and Homology Relationships in Multigene Families in Nematodes. Journal of Molecular Evolution, 2015, 80, 18-36.	0.8	23
1181	Genomic Diversification in Strains of Rickettsia felis Isolated from Different Arthropods. Genome Biology and Evolution, 2015, 7, 35-56.	1.1	66
1182	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
1183	Complete genome sequence and transcriptomics analyses reveal pigment biosynthesis and regulatory mechanisms in an industrial strain, Monascus purpureus YY-1. Scientific Reports, 2015, 5, 8331.	1.6	104
1184	The reverse evolution from multicellularity to unicellularity during carcinogenesis. Nature Communications, 2015, 6, 6367.	5.8	110
1185	The immediate global responses of Aliivibrio salmonicida to iron limitations. BMC Microbiology, 2015, 15, 9.	1.3	13
1186	Plasmids are vectors for redundant chromosomal genes in the Bacillus cereus group. BMC Genomics, 2015, 16, 6.	1.2	36
1187	High correlation between genotypes and phenotypes of environmental bacteria Comamonas testosteroni strains. BMC Genomics, 2015, 16, 110.	1.2	37

#	ARTICLE	IF	CITATIONS
1188	A framework to gauge the epidemic potential of plant pathogens in environmental reservoirs: the example of kiwifruit canker. Molecular Plant Pathology, 2015, 16, 137-149.	2.0	70
1189	The genome and transcriptome of the zoonotic hookworm Ancylostoma ceylanicum identify infection-specific gene families. Nature Genetics, 2015, 47, 416-422.	9.4	91
1190	Comparative genome and transcriptome analyses of the social amoeba Acytostelium subglobosum that accomplishes multicellular development without germ-soma differentiation. BMC Genomics, 2015, 16, 80.	1.2	23
1191	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
1192	Genetic blueprint of the zoonotic pathogen Toxocara canis. Nature Communications, 2015, 6, 6145.	5.8	103
1193	BMX: a tool for computing bacterial phyletic composition from orthologous maps. BMC Research Notes, 2015, 8, 51.	0.6	8
1194	Genome-wide analysis of bHLH transcription factor and involvement in the infection by yellow leaf curl virus in tomato (Solanum lycopersicum). BMC Genomics, 2015, 16, 39.	1.2	102
1195	A proposed new bacteriophage subfamily: â€œJerseyvirinaeâ€. Archives of Virology, 2015, 160, 1021-1033.	0.9	22
1196	Evidence of ancient genome reduction in red algae (Rhodophyta). Journal of Phycology, 2015, 51, 624-636.	1.0	71
1197	The Bimodal Distribution of Genic GC Content Is Ancestral to Monocot Species. Genome Biology and Evolution, 2015, 7, 336-348.	1.1	42
1198	Evolution of Gene Regulation during Transcription and Translation. Genome Biology and Evolution, 2015, 7, 1155-1167.	1.1	52
1199	Genomic Tools for the Study of Azospirillum and Other Plant Growth-Promoting Rhizobacteria. , 2015, , 83-97.		1
1200	A combinatorial approach of comprehensive QTL-based comparative genome mapping and transcript profiling identified a seed weight-regulating candidate gene in chickpea. Scientific Reports, 2015, 5, 9264.	1.6	61
1201	Articulating â€œArchiannelidsâ€. Phylogenomics and Annelid Relationships, with Emphasis on Meiofaunal Taxa. Molecular Biology and Evolution, 2015, 32, 2860-2875.	3.5	128
1202	GreedyPlus: An Algorithm for the Alignment of Interface Interaction Networks. Scientific Reports, 2015, 5, 12074.	1.6	0
1203	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. Biotechnology Advances, 2015, 33, 980-991.	6.0	21
1204	CceR and AkgR Regulate Central Carbon and Energy Metabolism in Alphaproteobacteria. MBio, 2015, 6, .	1.8	12
1205	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. MBio, 2015, 6, e00552-15.	1.8	25

#	Article	IF	Citations
1206	Draft Genome Sequences of Escherichia coli O157:H7 Strains Rafaela_II (Clade 8) and 7.1_Anguil (Clade) Tj ETQq0 0 0 rgBT /Overlock 1	0.8	0
1207	Application of RNAi to Genomic Drug Target Validation in Schistosomes. PLoS Neglected Tropical Diseases, 2015, 9, e0003801.	1.3	33
1208	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2015, 290, 18678-18698.	1.6	70
1209	Parasitic Plants &lt;i&gt;Striga&lt;/i&gt; and &lt;i&gt;Phelipanche&lt;/i&gt; Dependent upon Exogenous Strigolactones for Germination Have Retained Genes for Strigolactone Biosynthesis. American Journal of Plant Sciences, 2015, 06, 1151-1166.	0.3	12
1210	Global Genome and Transcriptome Analyses of Magnaporthe oryzae Epidemic Isolate 98-06 Uncover Novel Effectors and Pathogenicity-Related Genes, Revealing Gene Gain and Lose Dynamics in Genome Evolution. PLoS Pathogens, 2015, 11, e1004801.	2.1	148
1211	Selection Maintains Low Genomic GC Content in Marine SAR11 Lineages. Molecular Biology and Evolution, 2015, 32, 2738-2748.	3.5	47
1212	Genome dynamics and evolution of Salmonella Typhi strains from the typhoid-endemic zones. Scientific Reports, 2015, 4, 7457.	1.6	19
1213	Extraordinary Genetic Diversity in a Wood Decay Mushroom. Molecular Biology and Evolution, 2015, 32, 2775-2783.	3.5	42
1214	Chaos of Rearrangements in the Mating-Type Chromosomes of the Anther-Smut Fungus <i>Microbotryum lychnidis-dioicae</i>. Genetics, 2015, 200, 1275-1284.	1.2	78
1215	A draft network of ligandâ€“receptor-mediated multicellular signalling in human. Nature Communications, 2015, 6, 7866.	5.8	676
1216	Elevated levels of adaption in Helicobacter pylori genomes from Japan; a link to higher incidences of gastric cancer?. Evolution, Medicine and Public Health, 2015, 2015, 88-105.	1.1	6
1217	Phylogenetic study of clonal complex (CC)198 capsule null locus (cnl) genomes: A distinctive group within the species Neisseria meningitidis. Infection, Genetics and Evolution, 2015, 34, 372-377.	1.0	10
1218	Systematic analysis of maize class III peroxidase gene family reveals a conserved subfamily involved in abiotic stress response. Gene, 2015, 566, 95-108.	1.0	109
1219	The radish genome and comprehensive gene expression profile of tuberous root formation and development. Scientific Reports, 2015, 5, 10835.	1.6	154
1220	Regulators of Autophagosome Formation in Drosophila Muscles. PLoS Genetics, 2015, 11, e1005006.	1.5	46
1221	Comparative metagenomics reveals microbial community differentiation in a biological heap leaching system. Research in Microbiology, 2015, 166, 525-534.	1.0	21
1222	An Integrated Approach to Reconstructing Genome-Scale Transcriptional Regulatory Networks. PLoS Computational Biology, 2015, 11, e1004103.	1.5	23
1223	Genome Evolution in the Primary Endosymbiont of Whiteflies Sheds Light on Their Divergence. Genome Biology and Evolution, 2015, 7, 873-888.	1.1	61

#	Article	IF	Citations
1224	3-way Networks: Application of Hypergraphs for Modelling Increased Complexity in Comparative Genomics. PLoS Computational Biology, 2015, 11, e1004079.	1.5	29
1225	Elucidating evolutionary features and functional implications of orphan genes in Leishmania major. Infection, Genetics and Evolution, 2015, 32, 330-337.	1.0	14
1226	Comparative Genomics Reveals the Origins and Diversity of Arthropod Immune Systems. Molecular Biology and Evolution, 2015, 32, 2111-2129.	3.5	136
1227	The <i>Solanum commersonii</i> Genome Sequence Provides Insights into Adaptation to Stress Conditions and Genome Evolution of Wild Potato Relatives. Plant Cell, 2015, 27, 954-968.	3.1	149
1228	Genome-wide analysis of the family 1 glycosyltransferases in cotton. Molecular Genetics and Genomics, 2015, 290, 1805-1818.	1.0	47
1229	Faustovirus, an Asfarvirus-Related New Lineage of Giant Viruses Infecting Amoebae. Journal of Virology, 2015, 89, 6585-6594.	1.5	191
1230	Genomic and transcriptomic analysis of the endophytic fungus Pestalotiopsis fici reveals its lifestyle and high potential for synthesis of natural products. BMC Genomics, 2015, 16, 28.	1.2	102
1231	Genome-wide analysis of Dof family transcription factors and their responses to abiotic stresses in Chinese cabbage. BMC Genomics, 2015, 16, 33.	1.2	103
1232	Comparing Mycobacterium tuberculosis genomes using genome topology networks. BMC Genomics, 2015, 16, 85.	1.2	5
1233	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
1234	The Alternaria genomes database: a comprehensive resource for a fungal genus comprised of saprophytes, plant pathogens, and allergenic species. BMC Genomics, 2015, 16, 239.	1.2	105
1235	Comparative transcriptome analysis within the Lolium/Festuca species complex reveals high sequence conservation. BMC Genomics, 2015, 16, 249.	1.2	24
1236	The draft genome of Primula veris yields insights into the molecular basis of heterostyly. Genome Biology, 2015, 16, 12.	3.8	96
1238	Sequencing of the complete genome of an araphid pennate diatom Synedra acus subsp. radians from Lake Baikal. Doklady Biochemistry and Biophysics, 2015, 461, 84-88.	0.3	34
1239	The Genome of Dendrobium officinale Illuminates the Biology of the Important Traditional Chinese Orchid Herb. Molecular Plant, 2015, 8, 922-934.	3.9	228
1240	Diversity of Viruses Infecting the Green Microalga Ostreococcus lucimarinus. Journal of Virology, 2015, 89, 5812-5821.	1.5	35
1241	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
1242	Protocols and Methods for the in Silico Reconstruction of the Origin and Evolution of Metabolic Pathways. Springer Briefs in Molecular Science, 2015, , 67-75.	0.1	0

#	ARTICLE	IF	CITATIONS
1243	A Coxiella-Like Endosymbiont Is a Potential Vitamin Source for the Lone Star Tick. Genome Biology and Evolution, 2015, 7, 831-838.	1.1	204
1244	The red coral (<i>Corallium rubrum</i>) transcriptome: a new resource for population genetics and local adaptation studies. Molecular Ecology Resources, 2015, 15, 1205-1215.	2.2	47
1245	Genome Sequence and Transcriptome Analysis of Meat-Spoilage-Associated Lactic Acid Bacterium Lactococcus piscium MKFS47. Applied and Environmental Microbiology, 2015, 81, 3800-3811.	1.4	32
1246	Extracellular vesicle-mediated export of fungal RNA. Scientific Reports, 2015, 5, 7763.	1.6	185
1247	Plant Omics Data Center: An Integrated Web Repository for Interspecies Gene Expression Networks with NLP-Based Curation. Plant and Cell Physiology, 2015, 56, e9-e9.	1.5	55
1248	Streptococcus gallolyticus subsp. gallolyticus from Human and Animal Origins: Genetic Diversity, Antimicrobial Susceptibility, and Characterization of a Vancomycin-Resistant Calf Isolate Carrying a <i>vanA</i> -Tn <i>1546</i> -Like Element. Antimicrobial Agents and Chemotherapy, 2015, 59, 2006-2015.	1.4	15
1249	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing. MBio, 2015, 6, e00054.	1.8	97
1250	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. Biotechnology for Biofuels, 2015, 8, 107.	6.2	111
1251	Skipper genome sheds light on unique phenotypic traits and phylogeny. BMC Genomics, 2015, 16, 639.	1.2	38
1252	Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of Enterococcus faecium. Journal of Clinical Microbiology, 2015, 53, 3788-3797.	1.8	240
1253	Functionally Structured Genomes in Lactobacillus kunkeei Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. Genome Biology and Evolution, 2015, 7, 1455-1473.	1.1	50
1254	Homology-Independent Metrics for Comparative Genomics. Computational and Structural Biotechnology Journal, 2015, 13, 352-357.	1.9	12
1255	Bacillus thermoamylovorans Spores with Very-High-Level Heat Resistance Germinate Poorly in Rich Medium despite the Presence of <i>ger</i> Clusters but Efficiently upon Exposure to Calcium-Dipicolinic Acid. Applied and Environmental Microbiology, 2015, 81, 7791-7801.	1.4	24
1256	Are 100 enough? Inferring acanthomorph teleost phylogeny using Anchored Hybrid Enrichment. BMC Evolutionary Biology, 2015, 15, 113.	3.2	40
1257	Application of Subspace Clustering in DNA Sequence Analysis. Journal of Computational Biology, 2015, 22, 940-952.	0.8	4
1258	The <i>Symbiodinium kawagutii</i> genome illuminates dinoflagellate gene expression and coral symbiosis. Science, 2015, 350, 691-694.	6.0	430
1259	Domain similarity based orthology detection. BMC Bioinformatics, 2015, 16, 154.	1.2	11
1260	Extensive intra-phylotype diversity in lactobacilli and bifidobacteria from the honeybee gut. BMC Genomics, 2015, 16, 284.	1.2	111

#	ARTICLE	IF	CITATIONS
1261	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
1262	Evaluation of BLAST-based edge-weighting metrics used for homology inference with the Markov Clustering algorithm. BMC Bioinformatics, 2015, 16, 218.	1.2	18
1263	Novel genetic markers define a subgroup of pathogenicEscherichia colistrains belonging to the B2 phylogenetic group. FEMS Microbiology Letters, 2015, 362, fnv193.	0.7	15
1264	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. Plant Physiology, 2015, 169, 2444-2461.	2.3	111
1265	Comparative genomic and phenomic analysis of Clostridium difficile and Clostridium sordellii, two related pathogens with differing host tissue preference. BMC Genomics, 2015, 16, 448.	1.2	21
1266	Chromosomal copy number variation reveals differential levels of genomic plasticity in distinct Trypanosoma cruzi strains. BMC Genomics, 2015, 16, 499.	1.2	68
1267	The Genome and Methylome of a Beetle with Complex Social Behavior,<i>Nicrophorus vespilloides</i>(Coleoptera: Silphidae). Genome Biology and Evolution, 2015, 7, 3383-3396.	1.1	87
1268	Genomic signatures of human and animal disease in the zoonotic pathogen Streptococcus suis. Nature Communications, 2015, 6, 6740.	5.8	124
1269	Sexual Dimorphism and the Evolution of Sex-Biased Gene Expression in the Brown Alga Ectocarpus. Molecular Biology and Evolution, 2015, 32, 1581-1597.	3.5	111
1270	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
1271	A Genomic View of Lactobacilli and Pediococci Demonstrates that Phylogeny Matches Ecology and Physiology. Applied and Environmental Microbiology, 2015, 81, 7233-7243.	1.4	195
1272	The Dynamics of Genetic Interactions between<i>Vibrio metoecus</i>and<i>Vibrio cholerae</i>, Two Close Relatives Co-Occurring in the Environment. Genome Biology and Evolution, 2015, 7, 2941-2954.	1.1	33
1273	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed Alopecurus myosuroides (black-grass). BMC Genomics, 2015, 16, 590.	1.2	66
1274	Diversification of the ant odorant receptor gene family and positive selection on candidate cuticular hydrocarbon receptors. BMC Research Notes, 2015, 8, 380.	0.6	58
1275	The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332.	1.1	70
1276	Genomic comparison between pathogenic Streptococcus agalactiae isolated from Nile tilapia in Thailand and fish-derived ST7 strains. Infection, Genetics and Evolution, 2015, 36, 307-314.	1.0	18
1277	Contrasting hostâ€“pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. Nature Communications, 2015, 6, 7121.	5.8	90
1278	Identification of Thiotetronic Acid Antibiotic Biosynthetic Pathways by Target-directed Genome Mining. ACS Chemical Biology, 2015, 10, 2841-2849.	1.6	238

#	Article	IF	Citations
1279	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
1280	CNMS: The preferred genic markers for comparative genomic, molecular phylogenetic, functional genetic diversity and differential gene regulatory expression analyses in chickpea. Journal of Biosciences, 2015, 40, 579-592.	0.5	0
1281	Dissecting the fungal biology of Bipolaris papendorfii: from phylogenetic to comparative genomic analysis. DNA Research, 2015, 22, 219-232.	1.5	29
1282	Transcriptome of the egg parasitoid Fopius arisanus: an important biocontrol tool for Tephritid fruit fly suppression. GigaScience, 2015, 4, 36.	3.3	7
1283	Examining phylogenetic relationships of Erwinia and Pantoea species using whole genome sequence data. Antonie Van Leeuwenhoek, 2015, 108, 1037-1046.	0.7	35
1284	ProtPhylo: identification of proteinâ€“phenotype and proteinâ€“protein functional associations via phylogenetic profiling. Nucleic Acids Research, 2015, 43, W160-W168.	6.5	26
1285	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
1286	Recent events dominate interdomain lateral gene transfers between prokaryotes and eukaryotes and, with the exception of endosymbiotic gene transfers, few ancient transfer events persist. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140324.	1.8	19
1287	Phylogenetic Profiling for Probing the Modular Architecture of the Human Genome. Cell Systems, 2015, 1, 106-115.	2.9	24
1288	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. BMC Genomics, 2015, 16, 620.	1.2	107
1289	Early genome duplications in conifers and other seed plants. Science Advances, 2015, 1, e1501084.	4.7	236
1290	Evolutionarily Dynamic, but Robust, Targeting of Resistance Genes by the miR482/2118 Gene Family in the Solanaceae. Genome Biology and Evolution, 2015, 7, 3307-3321.	1.1	86
1291	Genome Evolution and Innovation across the Four Major Lineages of Cryptococcus gattii. MBio, 2015, 6, e00868-15.	1.8	101
1292	Draft genomic sequence of a selenite-reducing bacterium, Paenirhodobacter enshiensis DW2-9T. Standards in Genomic Sciences, 2015, 10, 38.	1.5	4
1293	Messenger RNA exchange between scions and rootstocks in grafted grapevines. BMC Plant Biology, 2015, 15, 251.	1.6	124
1294	Gut Symbionts from Distinct Hosts Exhibit Genotoxic Activity via Divergent Colibactin Biosynthesis Pathways. Applied and Environmental Microbiology, 2015, 81, 1502-1512.	1.4	65
1295	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
1296	Evolutionary origin of a streamlined marine bacterioplankton lineage. ISME Journal, 2015, 9, 1423-1433.	4.4	32

#	ARTICLE	IF	CITATIONS
1297	Comparative genomics in the Asteraceae reveals little evidence for parallel evolutionary change in invasive taxa. Molecular Ecology, 2015, 24, 2226-2240.	2.0	38
1298	Characterization of the <i>Campylobacter jejuni</i> Population in the Barnacle Geese Reservoir. Zoonoses and Public Health, 2015, 62, 209-221.	0.9	19
1299	Ten years of pan-genome analyses. Current Opinion in Microbiology, 2015, 23, 148-154.	2.3	498
1300	Ecophysiology of <i>Thioploca ingrica</i> as revealed by the complete genome sequence supplemented with proteomic evidence. ISME Journal, 2015, 9, 1166-1176.	4.4	35
1301	Genomic and transcriptome analyses reveal that MAPK- and phosphatidylinositol-signaling pathways mediate tolerance to 5-hydroxymethyl-2-furaldehyde for industrial yeast Saccharomyces cerevisiae. Scientific Reports, 2014, 4, 6556.	1.6	45
1302	Phytochemical genomics of the Madagascar periwinkle: Unravelling the last twists of the alkaloid engine. Phytochemistry, 2015, 113, 9-23.	1.4	92
1303	Deep sequencing reveals important roles of microRNAs in response to drought and salinity stress in cotton. Journal of Experimental Botany, 2015, 66, 789-804.	2.4	198
1304	Genome-wide analysis of the MADS-box gene family in Brassica rapa (Chinese cabbage). Molecular Genetics and Genomics, 2015, 290, 239-255.	1.0	80
1305	A guide for building biological pathways along with two case studies: hair and breast development. Methods, 2015, 74, 16-35.	1.9	5
1306	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
1307	Salmonella Phages and Prophages: Genomics, Taxonomy, and Applied Aspects. Methods in Molecular Biology, 2015, 1225, 237-287.	0.4	31
1308	Enabling comparative modeling of closely related genomes: example genus Brucella. 3 Biotech, 2015, 5, 101-105.	1.1	5
1309	A survey on prediction of specificity-determining sites in proteins. Briefings in Bioinformatics, 2015, 16, 71-88.	3.2	52
1310	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
1311	Comparative genome sequencing to assess the genetic diversity and virulence attributes of 15 <i><scp>V</scp>ibrio anguillarum</i> isolates. Journal of Fish Diseases, 2015, 38, 795-807.	0.9	18
1312	Bioinformatics Tools and Genomic Resources Available in Understanding the Structure and Function of Gossypium. , 2016, , .		4
1313	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
1314	Prediction and Analysis of the Protein-Protein Interaction Networks for Chickens, Cattle, Dogs, Horses and Rabbits. Current Bioinformatics, 2016, 11, 131-142.	0.7	5

#	ARTICLE	IF	CITATIONS
1315	OGS2: genome re-annotation of the jewel wasp Nasonia vitripennis. BMC Genomics, 2016, 17, 678.	1.2	35
1316	The genome of the emerging barley pathogen Ramularia collo-cygni. BMC Genomics, 2016, 17, 584.	1.2	36
1317	Draft Genome of the Scarab Beetle<i>Oryctes borbonicus</i>on La RÃ©union Island. Genome Biology and Evolution, 2016, 8, 2093-2105.	1.1	35
1318	RareDDB: An Integrated Catalog of Rare Disease Database. Clinical & Medical Biochemistry Open Access, 2016, , .	0.1	1
1319	Spider phylogenomics: untangling the Spider Tree of Life. PeerJ, 2016, 4, e1719.	0.9	253
1320	A Comparative <i>In Silico</i> Study of the Antioxidant Defense Gene Repertoire of Distinct Lifestyle Trypanosomatid Species. Evolutionary Bioinformatics, 2016, 12, EBO.S40648.	0.6	9
1321	Inferring Orthologs: Open Questions and Perspectives. Genomics Insights, 2016, 9, GEI.S37925.	3.0	50
1322	Genetic Characterization and Comparative Genome Analysis of<i>Brucella melitensis</i>Isolates from India. International Journal of Genomics, 2016, 2016, 1-13.	0.8	12
1323	Comparative Genomics ofH. pyloriand Non-PyloriHelicobacterSpecies to Identify New Regions Associated with Its Pathogenicity and Adaptability. BioMed Research International, 2016, 2016, 1-15.	0.9	20
1324	A set of genes conserved in sequence and expression traces back the establishment of multicellularity in social amoebae. BMC Genomics, 2016, 17, 871.	1.2	13
1325	Switches in Genomic GC Content Drive Shifts of Optimal Codons under Sustained Selection on Synonymous Sites. Genome Biology and Evolution, 2016, 9, evw201.	1.1	11
1326	Kaumoebavirus, a New Virus That Clusters with Faustoviruses and Asfarviridae. Viruses, 2016, 8, 278.	1.5	75
1327	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. ELife, 2016, 5, .	2.8	143
1328	DFAST and DAGA: web-based integrated genome annotation tools and resources. Bioscience of Microbiota, Food and Health, 2016, 35, 173-184.	0.8	194
1329	A transcriptional blueprint for a spiral-cleaving embryo. BMC Genomics, 2016, 17, 552.	1.2	20
1330	A Brazilian Marseillevirus Is the Founding Member of a Lineage in Family Marseilleviridae. Viruses, 2016, 8, 76.	1.5	74
1331	Clinical and Genomic Analysis of Liver Abscess-Causing Klebsiella pneumoniae Identifies New Liver Abscess-Associated Virulence Genes. Frontiers in Cellular and Infection Microbiology, 2016, 6, 165.	1.8	82
1332	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	1.5	153

#	Article	IF	Citations
1333	Genomic Insights into a New Citrobacter koseri Strain Revealed Gene Exchanges with the Virulence-Associated Yersinia pestis pPCP1 Plasmid. Frontiers in Microbiology, 2016, 7, 340.	1.5	13
1334	MG-Digger: An Automated Pipeline to Search for Giant Virus-Related Sequences in Metagenomes. Frontiers in Microbiology, 2016, 7, 428.	1.5	34
1335	The Geobacillus Pan-Genome: Implications for the Evolution of the Genus. Frontiers in Microbiology, 2016, 7, 723.	1.5	20
1336	Indole-3-Acetic Acid Is Produced by Emiliania huxleyi Coccolith-Bearing Cells and Triggers a Physiological Response in Bald Cells. Frontiers in Microbiology, 2016, 7, 828.	1.5	63
1337	A Comparison of 14 Erythrobacter Genomes Provides Insights into the Genomic Divergence and Scattered Distribution of Phototrophs. Frontiers in Microbiology, 2016, 7, 984.	1.5	35
1338	Genome Sequencing and Comparative Genomics Analysis Revealed Pathogenic Potential in Penicillium capsulatum as a Novel Fungal Pathogen Belonging to Eurotiales. Frontiers in Microbiology, 2016, 7, 1541.	1.5	11
1339	Temporal Metagenomic and Metabolomic Characterization of Fresh Perennial Ryegrass Degradation by Rumen Bacteria. Frontiers in Microbiology, 2016, 7, 1854.	1.5	69
1340	Genome Sequencing of Sulfolobus sp. A20 from Costa Rica and Comparative Analyses of the Putative Pathways of Carbon, Nitrogen, and Sulfur Metabolism in Various Sulfolobus Strains. Frontiers in Microbiology, 2016, 7, 1902.	1.5	26
1341	High-Level Heat Resistance of Spores of Bacillus amyloliquefaciens and Bacillus licheniformis Results from the Presence of a spoVA Operon in a Tn1546 Transposon. Frontiers in Microbiology, 2016, 7, 1912.	1.5	40
1342	Comparative Genomic Analysis of Bacillus amyloliquefaciens and Bacillus subtilis Reveals Evolutional Traits for Adaptation to Plant-Associated Habitats. Frontiers in Microbiology, 2016, 7, 2039.	1.5	54
1343	Systematic Identification of Anti-Fungal Drug Targets by a Metabolic Network Approach. Frontiers in Molecular Biosciences, 2016, 3, 22.	1.6	60
1344	Comprehensive Transcriptome Analysis Provides Evidence of Local Thermal Adaptation in Three Loaches (Genus: Misgurnus). International Journal of Molecular Sciences, 2016, 17, 1943.	1.8	8
1345	Distribution of Type I Restrictionâ€“Modification Systems in Streptococcus suis: An Outlook. Pathogens, 2016, 5, 62.	1.2	23
1346	IGDD: a database of intronless genes in dicots. BMC Bioinformatics, 2016, 17, 289.	1.2	23
1347	Pinpointing genes underlying annual/perennial transitions with comparative genomics. BMC Genomics, 2016, 17, 921.	1.2	16
1348	On the reversibility of parasitism: adaptation to a free-living lifestyle via gene acquisitions in the diplomonad Trepomonas sp. PC1. BMC Biology, 2016, 14, 62.	1.7	38
1349	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
1350	Genome Anatomy of Pyrenochaeta unguis-hominis UM 256, a Multidrug Resistant Strain Isolated from Skin Scraping. PLoS ONE, 2016, 11, e0162095.	1.1	9

#	ARTICLE	IF	CITATIONS
1351	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. PLoS Genetics, 2016, 12, e1005796.	1.5	25
1352	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. PLoS Genetics, 2016, 12, e1006433.	1.5	136
1353	WORMHOLE: Novel Least Diverged Ortholog Prediction through Machine Learning. PLoS Computational Biology, 2016, 12, e1005182.	1.5	21
1354	Comparative Genomics of the Sigatoka Disease Complex on Banana Suggests a Link between Parallel Evolutionary Changes in Pseudocercospora fijiensis and Pseudocercospora eumusae and Increased Virulence on the Banana Host. PLoS Genetics, 2016, 12, e1005904.	1.5	51
1355	Comparative Genomic Analysis of Sulfurospirillum cavolei MES Reconstructed from the Metagenome of an Electrosynthetic Microbiome. PLoS ONE, 2016, 11, e0151214.	1.1	20
1356	Genomic Characteristics of Chinese Borrelia burgdorferi Isolates. PLoS ONE, 2016, 11, e0153149.	1.1	3
1357	The Genomic Scrapheap Challenge; Extracting Relevant Data from Unmapped Whole Genome Sequencing Reads, Including Strain Specific Genomic Segments, in Rats. PLoS ONE, 2016, 11, e0160036.	1.1	5
1358	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
1359	Discovery of a Natural Microsporidian Pathogen with a Broad Tissue Tropism in Caenorhabditis elegans. PLoS Pathogens, 2016, 12, e1005724.	2.1	48
1360	The Genetic Analysis of an Acinetobacter johnsonii Clinical Strain Evidenced the Presence of Horizontal Genetic Transfer. PLoS ONE, 2016, 11, e0161528.	1.1	35
1361	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus Aspergillus cristatus. BMC Genomics, 2016, 17, 428.	1.2	55
1362	CoExpNetViz: Comparative Co-Expression Networks Construction and Visualization Tool. Frontiers in Plant Science, 2015, 6, 1194.	1.7	93
1363	Learning from Co-expression Networks: Possibilities and Challenges. Frontiers in Plant Science, 2016, 7, 444.	1.7	268
1364	Genetic Adaptation of Giant Lobelias (Lobelia aberdarica and Lobelia telekii) to Different Altitudes in East African Mountains. Frontiers in Plant Science, 2016, 7, 488.	1.7	9
1365	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
1366	RNA-seq of Ranunculus sceleratus and Identification of Orthologous Genes among Four Ranunculus Species. Frontiers in Plant Science, 2016, 7, 732.	1.7	5
1367	Nod Factor Effects on Root Hair-Specific Transcriptome of Medicago truncatula: Focus on Plasma Membrane Transport Systems and Reactive Oxygen Species Networks. Frontiers in Plant Science, 2016, 7, 794.	1.7	55
1368	Origination, Expansion, Evolutionary Trajectory, and Expression Bias of AP2/ERF Superfamily in Brassica napus. Frontiers in Plant Science, 2016, 7, 1186.	1.7	36

#	Article	IF	Citations
1369	Genome-Wide Comparative Analyses Reveal the Dynamic Evolution of Nucleotide-Binding Leucine-Rich Repeat Gene Family among Solanaceae Plants. Frontiers in Plant Science, 2016, 7, 1205.	1.7	75
1370	Genome-Wide Characterization of the MADS-Box Gene Family in Radish (Raphanus sativus L.) and Assessment of Its Roles in Flowering and Floral Organogenesis. Frontiers in Plant Science, 2016, 07, 1390.	1.7	41
1371	Comparative Transcriptome and Chloroplast Genome Analyses of Two Related Dipteronia Species. Frontiers in Plant Science, 2016, 7, 1512.	1.7	46
1372	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
1373	Comparative Transcriptomics of Strawberries (Fragaria spp.) Provides Insights into Evolutionary Patterns. Frontiers in Plant Science, 2016, 7, 1839.	1.7	33
1374	Splice Sites Seldom Slide: Intron Evolution in Oomycetes. Genome Biology and Evolution, 2016, 8, 2340-2350.	1.1	14
1375	Para-allopatry in hybridizing fire-bellied toads (<i>Bombina bombina</i>and<i>B. variegata</i>): Inference from transcriptome-wide coalescence analyses. Evolution; International Journal of Organic Evolution, 2016, 70, 1803-1818.	1.1	25
1376	Genomic approach to studying nutritional requirements of Clostridium tyrobutyricum and other Clostridia causing late blowing defects. Food Microbiology, 2016, 59, 213-223.	2.1	7
1377	Population genomics of sexual and asexual lineages in fissiparous ribbon worms (Lineus, Nemertea): hybridization, polyploidy and the Meselson effect. Molecular Ecology, 2016, 25, 3356-3369.	2.0	58
1378	A transposon present in specific strains of <i>Bacillus subtilis</i> negatively affects nutrientâ€•and dodecylamineâ€induced spore germination. Environmental Microbiology, 2016, 18, 4830-4846.	1.8	14
1379	A Small Number of Phylogenetically Distinct Clonal Complexes Dominate a Coastal Vibrio cholerae Population. Applied and Environmental Microbiology, 2016, 82, 5576-5586.	1.4	24
1380	Editorâ€™s Highlight: Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS): A Web-Based Tool for Addressing the Challenges of Cross-Species Extrapolation of Chemical Toxicity. Toxicological Sciences, 2016, 153, 228-245.	1.4	105
1381	Lower prevalence but similar fitness in a parasitic fungus at higher radiation levels near Chernobyl. Molecular Ecology, 2016, 25, 3370-3383.	2.0	9
1382	Traits of selected <i>Clostridium</i> strains for syngas fermentation to ethanol. Biotechnology and Bioengineering, 2016, 113, 531-539.	1.7	97
1383	The genome analysis of <scp><i>C</i></scp><i>andidatus</i>â€...<scp>B</scp>urkholderia crenata reveals that secondary metabolism may be a key function of the <scp><i>A</i></scp><i>rdisia crenata</i> leaf nodule symbiosis. Environmental Microbiology, 2016, 18, 2507-2522.	1.8	64
1384	The eukaryotic protein kinase superfamily of the necrotrophic fungal plant pathogen, <scp><i>S</i></scp><i>clerotinia sclerotiorum</i>. Molecular Plant Pathology, 2016, 17, 634-647.	2.0	8
1385	A novel <scp>l</scp>â€arabinoseâ€responsive regulator discovered in the riceâ€blast fungus <i>Pyricularia oryzae</i> (<i>Magnaporthe oryzae</i>). FEBS Letters, 2016, 590, 550-558.	1.3	22
1386	Trichinella spiralis : Adaptation and parasitism. Veterinary Parasitology, 2016, 231, 8-21.	0.7	14

#	ARTICLE	IF	CITATIONS
1387	Identification and qualification of 500 nuclear, singleâ€copy, orthologous genes for the Eupulmonata (Gastropoda) using transcriptome sequencing and exon capture. Molecular Ecology Resources, 2016, 16, 1107-1123.	2.2	40
1388	Characteristics of the draft genome of â€œ<i>Candidatus</i>Arsenophonus nilaparvataeâ€, a facultative endosymbiont of<i>Nilaparvata lugens</i>. Insect Science, 2016, 23, 478-486.	1.5	25
1389	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344
1390	Dioecy does not consistently accelerate or slow lineage diversification across multiple genera of angiosperms. New Phytologist, 2016, 209, 1290-1300.	3.5	37
1391	Complete Genome Sequence of <i>Streptococcus mitis</i> Strain SVGS_061 Isolated from a Neutropenic Patient with Viridans Group Streptococcal Shock Syndrome. Genome Announcements, 2016, 4, .	0.8	4
1392	Extensive horizontal gene transfers between plant pathogenic fungi. BMC Biology, 2016, 14, 41.	1.7	64
1393	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. Plant Physiology, 2016, 171, 2586-2598.	2.3	39
1394	Genome Sequences of Three Species of <i>Hanseniaspora</i> Isolated from Spontaneous Wine Fermentations. Genome Announcements, 2016, 4, .	0.8	39
1395	AP2/ERF Transcription Factors Involved in Response to Tomato Yellow Leaf Curly Virus in Tomato. Plant Genome, 2016, 9, plantgenome2015.09.0082.	1.6	43
1396	Annotation of the Tomato Genome. Compendium of Plant Genomes, 2016, , 159-171.	0.3	0
1397	Genomic evidence for plant-parasitic nematodes as the earliest Wolbachia hosts. Scientific Reports, 2016, 6, 34955.	1.6	54
1398	On the consistency of orthology relationships. BMC Bioinformatics, 2016, 17, 416.	1.2	3
1399	Do novel genes drive morphological novelty? An investigation of the nematosomes in the sea anemone Nematostella vectensis. BMC Evolutionary Biology, 2016, 16, 114.	3.2	56
1400	Screening lifespan-extending drugs in Caenorhabditis elegans via label propagation on drug-protein networks. BMC Systems Biology, 2016, 10, 131.	3.0	15
1401	Analysis of ethanol fermentation mechanism of ethanol producing white-rot fungus Phlebia sp. MG-60 by RNA-seq. BMC Genomics, 2016, 17, 616.	1.2	20
1402	Genome-guided Investigation of Antibiotic Substances produced by Allosalinactinospora lopnorensis CA15-2T from Lop Nor region, China. Scientific Reports, 2016, 6, 20667.	1.6	10
1403	Complete genomes of Hairstreak butterflies, their speciation and nucleo-mitochondrial incongruence. Scientific Reports, 2016, 6, 24863.	1.6	44
1404	Assessment of virulence potential of uncharacterized Enterococcus faecalis strains using pan genomic approach â€“ Identification of pathogenâ€“specific and habitat-specific genes. Scientific Reports, 2016, 6, 38648.	1.6	24

#	Article	IF	Citations
1405	Complete Genome Sequence of Spiroplasma helicoides TABS-2 ^T (DSM 22551), a Bacterium Isolated from a Horsefly (<i>Tabanus abactor</i>). Genome Announcements, 2016, 4, .	0.8	6
1406	Polymyxin Resistance in Acinetobacter baumannii: Genetic Mutations and Transcriptomic Changes in Response to Clinically Relevant Dosage Regimens. Scientific Reports, 2016, 6, 26233.	1.6	82
1407	Evolution of mitosome metabolism and invasion-related proteins in Cryptosporidium. BMC Genomics, 2016, 17, 1006.	1.2	63
1408	Genome analysis of<i>Hibiscus syriacus</i>provides insights of polyploidization and indeterminate flowering in woody plants. DNA Research, 2017, 24, dsw049.	1.5	38
1409	Structural Genomics of Angiosperm Trees: Genome Duplications, Ploidy, and Repeat Sequences. Plant Genetics and Genomics: Crops and Models, 2016, , 101-120.	0.3	0
1410	The genome of Rhizobiales bacteria in predatory ants reveals urease gene functions but no genes for nitrogen fixation. Scientific Reports, 2016, 6, 39197.	1.6	55
1411	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
1412	Characterization of the cytokinin-responsive transcriptome in rice. BMC Plant Biology, 2016, 16, 260.	1.6	38
1413	Genomic Identification and Comparative Expansion Analysis of the Non-Specific Lipid Transfer Protein Gene Family in Gossypium. Scientific Reports, 2016, 6, 38948.	1.6	34
1414	Complete Genome Sequence of Spiroplasma turonicum Tab4c ^T , a Bacterium Isolated from Horse Flies (<i>Haematopota</i> sp.). Genome Announcements, 2016, 4, .	0.8	7
1415	Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus Acrostichum. Scientific Reports, 2016, 6, 35634.	1.6	25
1416	Genome and methylome of the oleaginous diatom Cyclotella cryptica reveal genetic flexibility toward a high lipid phenotype. Biotechnology for Biofuels, 2016, 9, 258.	6.2	87
1417	Comparative genomics reveals Lysinibacillus sphaericus group comprises a novel species. BMC Genomics, 2016, 17, 709.	1.2	18
1418	Dictyocaulus viviparus genome, variome and transcriptome elucidate lungworm biology and support future intervention. Scientific Reports, 2016, 6, 20316.	1.6	23
1419	Analyses of Compact Trichinella Kinomes Reveal a MOS-Like Protein Kinase with a Unique N-Terminal Domain. G3: Genes, Genomes, Genetics, 2016, 6, 2847-2856.	0.8	6
1420	Genome-wide profiling of 24Âhr diel rhythmicity in the water flea, Daphnia pulex: network analysis reveals rhythmic gene expression and enhances functional gene annotation. BMC Genomics, 2016, 17, 653.	1.2	22
1421	The genome sequence of Sea-Island cotton (Gossypium barbadense) provides insights into the allopolyploidization and development of superior spinnable fibres. Scientific Reports, 2016, 5, 17662.	1.6	294
1422	Comparative genomics to explore phylogenetic relationship, cryptic sexual potential and host specificity of Rhynchosporium species on grasses. BMC Genomics, 2016, 17, 953.	1.2	33

#	Article	IF	Citations
1423	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
1424	Xenolog classification. Bioinformatics, 2017, 33, 640-649.	1.8	42
1425	The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. Scientific Reports, 2016, 6, 28594.	1.6	118
1426	From sequence reads to evolutionary inferences. , 0, , 305-335.		0
1427	Whole genome sequencing of a banana wild relative Musa itinerans provides insights into lineage-specific diversification of the Musa genus. Scientific Reports, 2016, 6, 31586.	1.6	51
1428	Network Metamodeling: Effect of Correlation Metric Choice on Phylogenomic and Transcriptomic Network Topology. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 143-183.	0.6	27
1429	Expansion and diversification of the MSDIN family of cyclic peptide genes in the poisonous agarics Amanita phalloides and A. bisporigera. BMC Genomics, 2016, 17, 1038.	1.2	37
1430	Gene Family Evolution Reflects Adaptation to Soil Environmental Stressors in the Genome of the Collembolan<i>Orchesella cincta</i>. Genome Biology and Evolution, 2016, 8, 2106-2117.	1.1	56
1431	The role of next generation sequencing technologies in shaping the future of insect molecular systematics. , 0, , 28-61.		0
1432	Cytokininâ€induced promotion of root meristem size in the fern <i>Azolla</i> supports a shootâ€like origin of euphyllophyte roots. New Phytologist, 2016, 209, 705-720.	3.5	59
1433	The Phylogeny of<i>Rickettsia</i>Using Different Evolutionary Signatures: How Tree-Like is Bacterial Evolution?. Systematic Biology, 2016, 65, 265-279.	2.7	64
1434	Multitasking of the piRNA Silencing Machinery: Targeting Transposable Elements and Foreign Genes in the Bdelloid Rotifer <i>Adineta vaga</i>. Genetics, 2016, 203, 255-268.	1.2	13
1435	Genomic resources and their influence on the detection of the signal of positive selection in genome scans. Molecular Ecology, 2016, 25, 170-184.	2.0	74
1436	Molecular phylogeny and dynamic evolution of disease resistance genes in the legume family. BMC Genomics, 2016, 17, 402.	1.2	47
1437	Sequencing and characterization of leaf transcriptomes of six diploid Nicotiana species. Journal of Biological Research, 2016, 23, 6.	2.2	13
1438	Gene expression characterizes different nutritional strategies among three mixotrophic protists. FEMS Microbiology Ecology, 2016, 92, fiw106.	1.3	45
1439	The Genome of<i>Haemoproteus tartakovskyi</i>and Its Relationship to Human Malaria Parasites. Genome Biology and Evolution, 2016, 8, 1361-1373.	1.1	58
1440	Nondegenerative Evolution in Ancient Heritable Bacterial Endosymbionts of Fungi. Molecular Biology and Evolution, 2016, 33, 2216-2231.	3.5	14

#	Article	IF	Citations
1441	Genome of Plant Maca (Lepidium meyenii) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Molecular Plant, 2016, 9, 1066-1077.	3.9	69
1442	<i>De Novo</i> Synthesis of Benzenoid Compounds by the Yeast <i>Hanseniaspora vineae</i> Increases the Flavor Diversity of Wines. Journal of Agricultural and Food Chemistry, 2016, 64, 4574-4583.	2.4	46
1443	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. BMC Genomics, 2016, 17, 267.	1.2	74
1444	Bivalve-specific gene expansion in the pearl oyster genome: implications of adaptation to a sessile lifestyle. Zoological Letters, 2016, 2, 3.	0.7	133
1445	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
1446	ANISEED 2015: a digital framework for the comparative developmental biology of ascidians. Nucleic Acids Research, 2016, 44, D808-D818.	6.5	68
1447	A mobile genetic element profoundly increases heat resistance of bacterial spores. ISME Journal, 2016, 10, 2633-2642.	4.4	75
1448	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. Nature Genetics, 2016, 48, 657-666.	9.4	432
1449	Genomes and virulence difference between two physiological races of Phytophthora nicotianae. GigaScience, 2016, 5, 3.	3.3	49
1450	A genomic comparison of 13 symbiotic <i>Vibrio fischeri</i> isolates from the perspective of their host source and colonization behavior. ISME Journal, 2016, 10, 2907-2917.	4.4	49
1451	Immunological evasion of immediate-early varicella zoster virus proteins. Immunogenetics, 2016, 68, 483-486.	1.2	8
1452	<i>Companion</i>: a web server for annotation and analysis of parasite genomes. Nucleic Acids Research, 2016, 44, W29-W34.	6.5	127
1453	A barrier to homologous recombination between sympatric strains of the cooperative soil bacterium <i>Myxococcus xanthus</i>. ISME Journal, 2016, 10, 2468-2477.	4.4	52
1454	A re-evaluation of the taxonomy of phytopathogenic genera Dickeya and Pectobacterium using whole-genome sequencing data. Systematic and Applied Microbiology, 2016, 39, 252-259.	1.2	97
1455	The draft genome of MD-2 pineapple using hybrid error correction of long reads. DNA Research, 2016, 23, 427-439.	1.5	35
1456	Evolution of a CAM anatomy predates the origins of Crassulacean acid metabolism in the Agavoideae (Asparagaceae). Molecular Phylogenetics and Evolution, 2016, 105, 102-113.	1.2	95
1457	A Primer on Infectious Disease Bacterial Genomics. Clinical Microbiology Reviews, 2016, 29, 881-913.	5.7	42
1458	High-Quality Genome Assembly and Annotation for Plasmodium coatneyi, Generated Using Single-Molecule Real-Time PacBio Technology. Genome Announcements, 2016, 4, .	0.8	33

#	Article	IF	Citations
1459	Correction of Weighted Orthology and Paralogy Relations - Complexity and Algorithmic Results. Lecture Notes in Computer Science, 2016, , 121-136.	1.0	8
1460	Comparative Metagenomic Analysis Reveals Mechanisms for Stress Response in Hypoliths from Extreme Hyperarid Deserts. Genome Biology and Evolution, 2016, 8, 2737-2747.	1.1	61
1461	The whole genome sequence of the Mediterranean fruit fly, Ceratitis capitata (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. Genome Biology, 2016, 17, 192.	3.8	130
1462	Rhodophyta. , 2016, , 1-45.		10
1463	Genome Diversity, Recombination, and Virulence across the Major Lineages of <i>Paracoccidioides</i>. MSphere, 2016, 1, .	1.3	109
1465	Comparative genomics and the diversity of life. Zoologica Scripta, 2016, 45, 5-13.	0.7	15
1466	Genomic Comparisons of Lactobacillus crispatus and Lactobacillus iners Reveal Potential Ecological Drivers of Community Composition in the Vagina. Applied and Environmental Microbiology, 2016, 82, 7063-7073.	1.4	114
1467	Functional and Evolutionary Characterization of a Gene Transfer Agentâ€™s Multilocus â€œGenomeâ€. Molecular Biology and Evolution, 2016, 33, 2530-2543.	3.5	58
1468	Allelic barley MLA immune receptors recognize sequence-unrelated avirulence effectors of the powdery mildew pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6486-E6495.	3.3	162
1469	Geographic Impact on Genomic Divergence as Revealed by Comparison of Nine Citromicrobial Genomes. Applied and Environmental Microbiology, 2016, 82, 7205-7216.	1.4	9
1470	Members of WRKY Group III transcription factors are important in TYLCV defense signaling pathway in tomato (Solanum lycopersicum). BMC Genomics, 2016, 17, 788.	1.2	90
1471	Convergent local adaptation to climate in distantly related conifers. Science, 2016, 353, 1431-1433.	6.0	303
1472	Phylogenomics of Lophotrochozoa with Consideration of Systematic Error. Systematic Biology, 2017, 66, syw079.	2.7	164
1473	Genomic studies of nitrogen-fixing rhizobial strains from Phaseolus vulgaris seeds and nodules. BMC Genomics, 2016, 17, 711.	1.2	17
1474	Horizontal Gene Transfer Contributes to the Evolution of Arthropod Herbivory. Genome Biology and Evolution, 2016, 8, 1785-1801.	1.1	155
1475	Phylogenetic evidence for cladogenetic polyploidization in land plants. American Journal of Botany, 2016, 103, 1252-1258.	0.8	39
1476	Evolutionary architecture of the infant-adapted group of Bifidobacterium species associated with the probiotic function. Systematic and Applied Microbiology, 2016, 39, 429-439.	1.2	23
1477	Genome sequence of <i>Candida versatilis</i> and comparative analysis with other yeast. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 1131-1138.	1.4	8

#	ARTICLE	IF	CITATIONS
1478	Pangolin genomes and the evolution of mammalian scales and immunity. Genome Research, 2016, 26, 1312-1322.	2.4	95
1479	Expression Pattern Similarities Support the Prediction of Orthologs Retaining Common Functions after Gene Duplication Events. Plant Physiology, 2016, 171, 2343-2357.	2.3	45
1480	Phylogenomics Using Transcriptome Data. Methods in Molecular Biology, 2016, 1452, 65-80.	0.4	2
1481	A modified two-stage Markov clustering algorithm for large and sparse networks. Computer Methods and Programs in Biomedicine, 2016, 135, 15-26.	2.6	4
1482	An antibiotic target ranking and prioritization pipeline combining sequence, structure and network-based approaches exemplified for Serratia marcescens. Gene, 2016, 591, 268-278.	1.0	17
1483	Repeated replacement of an intrabacterial symbiont in the tripartite nested mealybug symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5416-24.	3.3	222
1484	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). Plant Physiology, 2016, 172, 272-283.	2.3	88
1485	Intragenome Diversity of Gene Families Encoding Toxin-like Proteins in Venomous Animals. Integrative and Comparative Biology, 2016, 56, 938-949.	0.9	14
1486	The interplay between carbon availability and growth in different zones of the growing maize leaf. Plant Physiology, 2016, 172, pp.00994.2016.	2.3	24
1487	Tetracycline Selective Pressure and Homologous Recombination Shape the Evolution ofChlamydia suis: A Recently Identified Zoonotic Pathogen. Genome Biology and Evolution, 2016, 8, 2613-2623.	1.1	35
1489	Whole genome sequencing as a tool for phylogenetic analysis of clinical strains of Mitis group streptococci. European Journal of Clinical Microbiology and Infectious Diseases, 2016, 35, 1615-1625.	1.3	25
1490	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
1491	The Diversification of Plant<i>NBS-LRR</i>Defense Genes Directs the Evolution of MicroRNAs That Target Them. Molecular Biology and Evolution, 2016, 33, 2692-2705.	3.5	200
1492	The genome, transcriptome, and proteome of the nematode Steinernema carpocapsae: evolutionary signatures of a pathogenic lifestyle. Scientific Reports, 2016, 6, 37536.	1.6	25
1493	Reciprocal genomic evolution in the antâ€“fungus agricultural symbiosis. Nature Communications, 2016, 7, 12233.	5.8	106
1494	Genomic identification of WRKY transcription factors in carrot (Daucus carota) and analysis of evolution and homologous groups for plants. Scientific Reports, 2016, 6, 23101.	1.6	68
1495	Promiscuous Pathogenicity Islands and Phylogeny of Pathogenic Streptomyces spp.. Molecular Plant-Microbe Interactions, 2016, 29, 640-650.	1.4	48
1496	Draft genome of the living fossil Ginkgo biloba. GigaScience, 2016, 5, 49.	3.3	232

#	Article	IF	Citations
1497	Bioinformatic prediction of transcription factor binding sites at promoter regions of genes for photoperiod and vernalization responses in model and temperate cereal plants. BMC Genomics, 2016, 17, 573.	1.2	8
1498	From Sequence Data Including Orthologs, Paralogs, and Xenologs to Gene and Species Trees. , 2016, , 373-392.		16
1499	Multiple Polyploidization Events across Asteraceae with Two Nested Events in the Early History Revealed by Nuclear Phylogenomics. Molecular Biology and Evolution, 2016, 33, 2820-2835.	3.5	149
1500	What Signatures Dominantly Associate with Gene Age?. Genome Biology and Evolution, 2016, 8, 3083-3089.	1.1	39
1501	Comparative genome analysis of the oleaginous yeast Trichosporon fermentans reveals its potential applications in lipid accumulation. Microbiological Research, 2016, 192, 203-210.	2.5	15
1502	The<i>Ditylenchus destructor</i>genome provides new insights into the evolution of plant parasitic nematodes. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160942.	1.2	29
1503	Basidiomycete yeasts in the cortex of ascomycete macrolichens. Science, 2016, 353, 488-492.	6.0	409
1504	Nomadic lifestyle of <i>Lactobacillus plantarum</i> revealed by comparative genomics of 54 strains isolated from different habitats. Environmental Microbiology, 2016, 18, 4974-4989.	1.8	197
1505	Comparison of microsatellite distribution in genomes of Centruroides exilicauda and Mesobuthus martensii. Gene, 2016, 594, 41-46.	1.0	6
1506	Genome-scale comparison of expanded gene families in Plasmodium ovale wallikeri and Plasmodium ovale curtisi with Plasmodium malariae and with other Plasmodium species. International Journal for Parasitology, 2016, 46, 685-696.	1.3	59
1507	The pangenome of an agronomically important crop plant Brassica oleracea. Nature Communications, 2016, 7, 13390.	5.8	375
1508	Insights into long noncoding RNAs of naked mole rat (Heterocephalus glaber) and their potential association with cancer resistance. Epigenetics and Chromatin, 2016, 9, 51.	1.8	17
1509	Directional Selection from Host Plants Is a Major Force Driving Host Specificity in Magnaporthe Species. Scientific Reports, 2016, 6, 25591.	1.6	62
1510	Comparative genomics reveals convergent rates of evolution in antâ€“plant mutualisms. Nature Communications, 2016, 7, 12679.	5.8	47
1511	Comparative genomic and functional analyses: unearthing the diversity and specificity of nematicidal factors in Pseudomonas putida strain 1A00316. Scientific Reports, 2016, 6, 29211.	1.6	15
1512	The genome and transcriptome of Trichormus sp. NMC-1: insights into adaptation to extreme environments on the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 29404.	1.6	33
1513	Evolution of Rosaceae Fruit Types Based on Nuclear Phylogeny in the Context of Geological Times and Genome Duplication. Molecular Biology and Evolution, 2017, 34, msw242.	3.5	200
1514	Genomic resources for a unique, low-virulence Babesia taxon from China. Parasites and Vectors, 2016, 9, 564.	1.0	17

#	Article	IF	Citations
1515	Biofilm plasmids with a rhamnose operon are widely distributed determinants of the â€˜swim-or-stickâ€™ lifestyle in roseobacters. ISME Journal, 2016, 10, 2498-2513.	4.4	56
1516	The Gonium pectorale genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity. Nature Communications, 2016, 7, 11370.	5.8	125
1517	Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. Scientific Data, 2016, 3, 160030.	2.4	89
1518	The Dendrobium catenatum Lindl. genome sequence provides insights into polysaccharide synthase, floral development and adaptive evolution. Scientific Reports, 2016, 6, 19029.	1.6	255
1519	Genome sequence and analysis of the Japanese morning glory Ipomoea nil. Nature Communications, 2016, 7, 13295.	5.8	138
1520	From cholera to corals: Viruses as drivers of virulence in a major coral bacterial pathogen. Scientific Reports, 2016, 5, 17889.	1.6	70
1521	Estimation of Gene Insertion/Deletion Rates with Missing Data. Genetics, 2016, 204, 513-529.	1.2	3
1522	Are orphan genes protein-coding, prediction artifacts, or non-coding RNAs?. BMC Bioinformatics, 2016, 17, 226.	1.2	44
1523	BPGA- an ultra-fast pan-genome analysis pipeline. Scientific Reports, 2016, 6, 24373.	1.6	771
1524	The genome of the miiuy croaker reveals well-developed innate immune and sensory systems. Scientific Reports, 2016, 6, 21902.	1.6	67
1525	Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7010-E7019.	3.3	85
1526	Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. Nature Communications, 2016, 7, 12845.	5.8	43
1527	Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. Nature Communications, 2016, 7, 12997.	5.8	32
1528	Two flagellar BAR domain proteins in Trypanosoma brucei with stage-specific regulation. Scientific Reports, 2016, 6, 35826.	1.6	2
1529	A Survey of Computational Methods for Protein Function Prediction. , 2016, , 225-298.		42
1530	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. Genome Biology, 2016, 17, 211.	3.8	101
1531	Comprehensive analysis of the polygalacturonase and pectin methylesterase genes in Brassica rapa shed light on their different evolutionary patterns. Scientific Reports, 2016, 6, 25107.	1.6	34
1532	Genomic analysis of three Bifidobacterium species isolated from the calf gastrointestinal tract. Scientific Reports, 2016, 6, 30768.	1.6	20

#	ARTICLE	IF	CITATIONS
1533	A key genetic factor for fucosyllactose utilization affects infant gut microbiota development. Nature Communications, 2016, 7, 11939.	5.8	284
1534	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
1535	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
1536	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. Nature Communications, 2016, 7, 11362.	5.8	214
1537	Transcriptome sequencing of Crucihimalaya himalaica (Brassicaceae) reveals how Arabidopsis close relative adapt to the Qinghai-Tibet Plateau. Scientific Reports, 2016, 6, 21729.	1.6	47
1538	Dynamics of genome change among Legionella species. Scientific Reports, 2016, 6, 33442.	1.6	18
1539	Genomic survey of a hyperparasitic microsporidianAmphiamblyssp. (Metchnikovellidae). Genome Biology and Evolution, 2016, 9, evw235.	1.1	41
1540	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. Scientific Reports, 2016, 6, 28199.	1.6	16
1541	Comparative transcriptome analysis reveals insights into the streamlined genomes of haplosclerid demosponges. Scientific Reports, 2016, 6, 18774.	1.6	28
1542	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. Plant Cell, 2016, 28, 2700-2714.	3.1	183
1543	Systematic Search for Evidence of Interdomain Horizontal Gene Transfer from Prokaryotes to Oomycete Lineages. MSphere, 2016, 1, .	1.3	22
1544	Secondary metabolite gene clusters in the entomopathogen fungus Metarhizium anisopliae: genome identification and patterns of expression in a cuticle infection model. BMC Genomics, 2016, 17, 736.	1.2	36
1545	Comparative analysis of the terpenoid biosynthesis pathway in Azadirachta indica and Melia azedarach by RNA-seq. SpringerPlus, 2016, 5, 819.	1.2	9
1546	A De-Novo Genome Analysis Pipeline (DeNoGAP) for large-scale comparative prokaryotic genomics studies. BMC Bioinformatics, 2016, 17, 260.	1.2	17
1547	Genome and transcriptome sequencing characterises the gene space of Macadamia integrifolia (Proteaceae). BMC Genomics, 2016, 17, 937.	1.2	45
1548	Survey of Genes Involved in Biosynthesis, Transport, and Signaling of Phytohormones with Focus on<i>Solanum lycopersicum</i>. Bioinformatics and Biology Insights, 2016, 10, BBI.S38425.	1.0	21
1549	Using a Human Drug Network for generating novel hypotheses about drugs. Intelligent Data Analysis, 2016, 20, 183-197.	0.4	6
1550	An emerging zoonotic clone in the Netherlands provides clues to virulence and zoonotic potential of Streptococcus suis. Scientific Reports, 2016, 6, 28984.	1.6	41

#	ARTICLE	IF	CITATIONS
1551	Genomic content typifying a prevalent clade of bovine mastitis-associated Escherichia coli. Scientific Reports, 2016, 6, 30115.	1.6	51
1552	Snapshots of a shrinking partner: Genome reduction in Serratia symbiotica. Scientific Reports, 2016, 6, 32590.	1.6	68
1553	Evolutionary plasticity of restorer-of-fertility-like proteins in rice. Scientific Reports, 2016, 6, 35152.	1.6	46
1554	Reclassification of the taxonomic status of SEMIA3007 isolated in Mexico B-11A Mex as Rhizobium leguminosarum bv. viceae by bioinformatic tools. BMC Microbiology, 2016, 16, 260.	1.3	5
1555	Complete genome sequence of Leuconostoc gelidum subsp. gasicomitatum KG16-1, isolated from vacuum-packaged vegetable sausages. Standards in Genomic Sciences, 2016, 11, 40.	1.5	28
1556	Draft genomic sequence of a chromate- and sulfate-reducing Alishewanella strain with the ability to bioremediate Cr and Cd contamination. Standards in Genomic Sciences, 2016, 11, 48.	1.5	22
1557	The complete genome sequence of the rumen methanogen Methanobrevibacter millerae SM9. Standards in Genomic Sciences, 2016, 11, 49.	1.5	15
1558	Comparative genomics of Beauveria bassiana: uncovering signatures of virulence against mosquitoes. BMC Genomics, 2016, 17, 986.	1.2	38
1559	An evolutionary approach to identify potentially protective B cell epitopes involved in naturally acquired immunity to malaria and the role of EBA-175 in protection amongst denizens of Bolifamba, Cameroon. Malaria Journal, 2016, 15, 281.	0.8	1
1560	Genome Evolution in Three Species of Cactophilic<i>Drosophila</i>. G3: Genes, Genomes, Genetics, 2016, 6, 3097-3105.	0.8	30
1561	Genomic and transcriptomic analysis of the streptomycin-dependent Mycobacterium tuberculosis strain 18b. BMC Genomics, 2016, 17, 190.	1.2	18
1562	De novo genome assembly and annotation of rice sheath rot fungus Sarocladium oryzae reveals genes involved in Helvolic acid and Cerulenin biosynthesis pathways. BMC Genomics, 2016, 17, 271.	1.2	33
1563	Dissection of early transcriptional responses to water stress in Arundo donax L. by unigene-based RNA-seq. Biotechnology for Biofuels, 2016, 9, 54.	6.2	32
1564	Draft genome of the peanut A-genome progenitor (<i>Arachis duranensis</i>) provides insights into geocarpy, oil biosynthesis, and allergens. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6785-6790.	3.3	235
1565	Comparative genomics reveals Cyclospora cayetanensis possesses coccidia-like metabolism and invasion components but unique surface antigens. BMC Genomics, 2016, 17, 316.	1.2	42
1566	Complete genome sequence and genomic characterization of Microcystis panniformis FACHB 1757 by third-generation sequencing. Standards in Genomic Sciences, 2016, 11, 11.	1.5	19
1567	Heterogeneous molecular processes among the causes of how sequence similarity scores can fail to recapitulate phylogeny. Briefings in Bioinformatics, 2017, 18, bbw034.	3.2	17
1568	Effects of Gene Duplication, Positive Selection, and Shifts in Gene Expression on the Evolution of the Venom Gland Transcriptome in Widow Spiders. Genome Biology and Evolution, 2016, 8, 228-242.	1.1	54

#	Article	IF	Citations
1569	Evaluating and Characterizing Ancient Whole-Genome Duplications in Plants with Gene Count Data. Genome Biology and Evolution, 2016, 8, 1023-1037.	1.1	53
1570	Genus-Wide Comparative Genome Analyses of<i>Colletotrichum</i>Species Reveal Specific Gene Family Losses and Gains during Adaptation to Specific Infection Lifestyles. Genome Biology and Evolution, 2016, 8, 1467-1481.	1.1	69
1571	Transposons passively and actively contribute to evolution of the two-speed genome of a fungal pathogen. Genome Research, 2016, 26, 1091-1100.	2.4	308
1572	Salinity-induced changes in gene expression from anterior and posterior gills of Callinectes sapidus (Crustacea: Portunidae) with implications for crustacean ecological genomics. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 19, 34-44.	0.4	22
1573	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. Journal of Clinical Microbiology, 2016, 54, 2014-2022.	1.8	14
1574	Characterization of parasite-specific indels and their proposed relevance for selective anthelminthic drug targeting. Infection, Genetics and Evolution, 2016, 39, 201-211.	1.0	7
1575	EchinoDB, an application for comparative transcriptomics of deeply-sampled clades of echinoderms. BMC Bioinformatics, 2016, 17, 48.	1.2	26
1576	CDROM: Classification of Duplicate gene RetentiOn Mechanisms. BMC Evolutionary Biology, 2016, 16, 82.	3.2	11
1577	The genome of newly classified Ochroconis mirabilis: Insights into fungal adaptation to different living conditions. BMC Genomics, 2016, 17, 91.	1.2	26
1578	De novo transcriptome assembly of the grapevine phylloxera allows identification of genes differentially expressed between leaf- and root-feeding forms. BMC Genomics, 2016, 17, 219.	1.2	19
1579	The link between orthology relations and gene trees: a correction perspective. Algorithms for Molecular Biology, 2016, 11, 4.	0.3	26
1580	Genomic screens identify a new phytobacterial microbe-associated molecular pattern and the cognate Arabidopsis receptor-like kinase that mediates its immune elicitation. Genome Biology, 2016, 17, 98.	3.8	62
1581	Genome sequence of Escherichia coli NCCP15653, a group D strain isolated from a diarrhea patient. Gut Pathogens, 2016, 8, 7.	1.6	3
1582	Draft genome sequence of non-shiga toxin-producing Escherichia coli O157 NCCP15738. Gut Pathogens, 2016, 8, 13.	1.6	4
1583	Inverse correlation between salt tolerance and host-adaptation in mycobacteria. BMC Research Notes, 2016, 9, 249.	0.6	12
1584	Complete genome sequences of Francisella noatunensis subsp. orientalis strains FNO12, FNO24 and FNO190: a fish pathogen with genomic clonal behavior. Standards in Genomic Sciences, 2016, 11, 30.	1.5	13
1585	Understanding the Systems Biology of Pathogen Virulence Using Semantic Methodologies. , 2016, , .		0
1586	Horizontal Gene Acquisitions, Mobile Element Proliferation, and Genome Decay in the Host-Restricted Plant Pathogen<i>Erwinia Tracheiphila</i>. Genome Biology and Evolution, 2016, 8, 649-664.	1.1	34

#	Article	IF	Citations
1587	Reinventing the Wheel and Making It Round Again: Evolutionary Convergence in<i>Buchnera</i>â€"<i>Serratia</i>Symbiotic Consortia between the Distantly Related Lachninae Aphids<i>Tuberolachnus salignus</i>and<i>Cinara cedri</i>. Genome Biology and Evolution, 2016, 8, 1440-1458.	1.1	85
1588	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. G3: Genes, Genomes, Genetics, 2016, 6, 235-244.	0.8	38
1589	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
1590	Proteomics and metabolomics analyses reveal the cucurbit sieve tube system as a complex metabolic space. Plant Journal, 2016, 87, 442-454.	2.8	44
1591	Phylogenomic analysis supports a recent change in nitrate assimilation in the White-nose Syndrome pathogen, Pseudogymnoascus destructans. Fungal Ecology, 2016, 23, 20-29.	0.7	7
1592	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
1593	Polyploidy and sexual system in angiosperms: Is there an association?. American Journal of Botany, 2016, 103, 1223-1235.	0.8	39
1594	Complete genome sequence of the potato pathogen Ralstonia solanacearum UY031. Standards in Genomic Sciences, 2016, 11, 7.	1.5	26
1595	Orphan Crops Browser: a bridge between model and orphan crops. Molecular Breeding, 2016, 36, 9.	1.0	18
1596	The genome of the seagrass Zostera marina reveals angiosperm adaptation to the sea. Nature, 2016, 530, 331-335.	13.7	460
1597	Retention, Molecular Evolution, and Expression Divergence of the Auxin/Indole Acetic Acid and Auxin Response Factor Gene Families in<i>Brassica Rapa</i>Shed Light on Their Evolution Patterns in Plants. Genome Biology and Evolution, 2016, 8, 302-316.	1.1	35
1598	Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic Toxoplasma gondii genomes. Nature Communications, 2016, 7, 10147.	5.8	243
1599	Network-Thinking: Graphs to Analyze Microbial Complexity and Evolution. Trends in Microbiology, 2016, 24, 224-237.	3.5	110
1600	Immunoprotective potential of in silico predicted Acinetobacter baumannii outer membrane nuclease, NucAb. International Journal of Medical Microbiology, 2016, 306, 1-9.	1.5	51
1601	Draft genome sequence of the silver pomfret fish, <i>Pampus argenteus</i>. Genome, 2016, 59, 51-58.	0.9	14
1602	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. Nature Methods, 2016, 13, 435-438.	9.0	328
1603	Evolution of a heavy metal homeostasis/resistance island reflects increasing copper stress in Enterobacteria. Genome Biology and Evolution, 2016, 8, evw031.	1.1	68
1604	COLOMBOS v3.0: leveraging gene expression compendia for cross-species analyses: Table 1.. Nucleic Acids Research, 2016, 44, D620-D623.	6.5	69

#	Article	IF	Citations
1605	Profiles of low complexity regions in Apicomplexa. BMC Evolutionary Biology, 2016, 16, 47.	3.2	21
1606	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. Genome Biology and Evolution, 2016, 8, evw060.	1.1	117
1607	In-silicoidentification of candidate genes for fertility restoration in cytoplasmic male sterile perennial ryegrass (Lolium perenneL.). Genome Biology and Evolution, 2016, 9, evw047.	1.1	22
1608	Comparative genome analysis and genome evolution of members of the magnaporthaceae family of fungi. BMC Genomics, 2016, 17, 135.	1.2	27
1609	Towards plant pangenomics. Plant Biotechnology Journal, 2016, 14, 1099-1105.	4.1	203
1610	Genome-Wide Analysis Indicates Lineage-Specific Gene Loss during Papilionoideae Evolution. Genome Biology and Evolution, 2016, 8, 635-648.	1.1	11
1611	The de novo genome assembly and annotation of a female domestic dromedary of North African origin. Molecular Ecology Resources, 2016, 16, 314-324.	2.2	106
1612	The mid-developmental transition and the evolution of animal body plans. Nature, 2016, 531, 637-641.	13.7	231
1613	Ecological Genomics of the Uncultivated Marine Roseobacter Lineage CHAB-I-5. Applied and Environmental Microbiology, 2016, 82, 2100-2111.	1.4	50
1614	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i>. Plant Cell, 2016, 28, 388-405.	3.1	163
1615	Expression Divergence Is Correlated with Sequence Evolution but Not Positive Selection in Conifers. Molecular Biology and Evolution, 2016, 33, 1502-1516.	3.5	48
1616	Genome Content and Phylogenomics Reveal both Ancestral and Lateral Evolutionary Pathways in Plant-Pathogenic Streptomyces Species. Applied and Environmental Microbiology, 2016, 82, 2146-2155.	1.4	44
1617	Detecting false positive sequence homology: a machine learning approach. BMC Bioinformatics, 2016, 17, 101.	1.2	19
1618	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
1619	Evidence of horizontal gene transfer between obligate leaf nodule symbionts. ISME Journal, 2016, 10, 2092-2105.	4.4	63
1620	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. Biotechnology Advances, 2016, 34, 663-686.	6.0	30
1621	Life History Traits, Protein Evolution, and the Nearly Neutral Theory in Amniotes. Molecular Biology and Evolution, 2016, 33, 1517-1527.	3.5	75
1622	Ortholog-Finder: A Tool for Constructing an Ortholog Data Set. Genome Biology and Evolution, 2016, 8, 446-457.	1.1	18

#	ARTICLE	IF	CITATIONS
1623	A Fast and Exact Algorithm for the Exemplar Breakpoint Distance. Journal of Computational Biology, 2016, 23, 337-346.	0.8	35
1624	Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms. Plant Cell, 2016, 28, 326-344.	3.1	202
1625	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. Genome Biology and Evolution, 2016, 8, 915-931.	1.1	40
1626	Essential Genome of the Metabolically Versatile Alphaproteobacterium Rhodopseudomonas palustris. Journal of Bacteriology, 2016, 198, 867-876.	1.0	60
1627	Microbial Genomics of a Host-Associated Commensal Bacterium in Fragmented Populations of Endangered Takahe. Microbial Ecology, 2016, 71, 1020-1029.	1.4	7
1628	TheVignaGenome Server, â€˜VigGSâ€™: A Genomic Knowledge Base of the GenusVignaBased on High-Quality, Annotated Genome Sequence of the Azuki Bean,Vigna angularis(Willd.) Ohwi & Ohashi. Plant and Cell Physiology, 2016, 57, e2-e2.	1.5	49
1629	Comparison of Four Comamonas Catabolic Plasmids Reveals the Evolution of pBHB To Catabolize Haloaromatics. Applied and Environmental Microbiology, 2016, 82, 1401-1411.	1.4	24
1630	Genomic analysis of 38 Legionella species identifies large and diverse effector repertoires. Nature Genetics, 2016, 48, 167-175.	9.4	235
1631	Clonal spread and interspecies transmission of clinically relevant ESBL-producing<i>Escherichia coli</i>of ST410â€"another successful pandemic clone?. FEMS Microbiology Ecology, 2016, 92, fiv155.	1.3	120
1632	Abundance and Biogeography of Picoprasinophyte Ecotypes and Other Phytoplankton in the Eastern North Pacific Ocean. Applied and Environmental Microbiology, 2016, 82, 1693-1705.	1.4	53
1633	Kinetoplastid Phylogenomics Reveals the Evolutionary Innovations Associated with the Origins of Parasitism. Current Biology, 2016, 26, 161-172.	1.8	137
1634	Tomato Genome Sequence. Biotechnology in Agriculture and Forestry, 2016, , 1-13.	0.2	2
1635	Information Commons for Rice (IC4R). Nucleic Acids Research, 2016, 44, D1172-D1180.	6.5	41
1636	Computational prediction of secretion systems and secretomes of Brucella: identification of novel type IV effectors and their interaction with the host. Molecular BioSystems, 2016, 12, 178-190.	2.9	19
1637	Phylogenomic analysis of the genus Ralstonia based on 686 single-copy genes. Antonie Van Leeuwenhoek, 2016, 109, 71-82.	0.7	41
1638	PGSB/MIPS Plant Genome Information Resources and Concepts for the Analysis of Complex Grass Genomes. Methods in Molecular Biology, 2016, 1374, 165-186.	0.4	2
1639	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. Molecular Biology and Evolution, 2016, 33, 394-412.	3.5	259
1640	Protein function annotation using protein domain family resources. Methods, 2016, 93, 24-34.	1.9	32

#	Article	IF	Citations
1641	Microbial bioinformatics for food safety and production. Briefings in Bioinformatics, 2016, 17, 283-292.	3.2	53
1642	A <scp><i>R</i></scp><i>ickettsiales</i> symbiont of amoebae with ancient features. Environmental Microbiology, 2016, 18, 2326-2342.	1.8	73
1643	MTD: a mammalian transcriptomic database to explore gene expression and regulation. Briefings in Bioinformatics, 2017, 18, 28-36.	3.2	18
1644	Protein complex analysis: From raw protein lists to protein interaction networks. Mass Spectrometry Reviews, 2017, 36, 600-614.	2.8	22
1645	What constitutes an Arabian <i>Helicobacter pylori</i>? Lessons from comparative genomics. Helicobacter, 2017, 22, e12323.	1.6	9
1646	Genome Analysis of <i>Pseudoloma neurophilia</i>: A Microsporidian Parasite of Zebrafish (<i>Danio) Tj ETQq1 1 0.784314 rgBT /Ove	0.8	27
1647	Endozoicomonas genomes reveal functional adaptation and plasticity in bacterial strains symbiotically associated with diverse marine hosts. Scientific Reports, 2017, 7, 40579.	1.6	207
1648	Co-option and <i>de novo</i> gene evolution underlie molluscan shell diversity. Molecular Biology and Evolution, 2017, 34, msw294.	3.5	67
1649	ORCANâ€"a web-based meta-server for real-time detection and functional annotation of orthologs. Bioinformatics, 2017, 33, 1224-1226.	1.8	11
1650	An incoherent feedâ€forward loop mediates robustness and tunability in a plant immune network. EMBO Reports, 2017, 18, 464-476.	2.0	51
1651	Identification of microsporidia host-exposed proteins reveals a repertoire of rapidly evolving proteins. Nature Communications, 2017, 8, 14023.	5.8	88
1652	Safety and immunogenicity of mammalian cell derived and Modified Vaccinia Ankara vectored African swine fever subunit antigens in swine. Veterinary Immunology and Immunopathology, 2017, 185, 20-33.	0.5	64
1653	Paracoccidioides spp. catalases and their role in antioxidant defense against host defense responses. Fungal Genetics and Biology, 2017, 100, 22-32.	0.9	16
1654	Molecular Profiles of Contrasting Shade Response Strategies in Wild Plants: Differential Control of Immunity and Shoot Elongation. Plant Cell, 2017, 29, 331-344.	3.1	63
1655	Ecotype diversification of an abundant Roseobacter lineage. Environmental Microbiology, 2017, 19, 1625-1638.	1.8	17
1656	Designing an efficient multi-epitope oral vaccine against Helicobacter pylori using immunoinformatics and structural vaccinology approaches. Molecular BioSystems, 2017, 13, 699-713.	2.9	86
1657	Spore Heat Activation Requirements and Germination Responses Correlate with Sequences of Germinant Receptors and with the Presence of a Specific <i>spoVA</i> ^{2mob} Operon in Foodborne Strains of Bacillus subtilis. Applied and Environmental Microbiology, 2017, 83, .	1.4	27
1658	Domestication of rice has reduced the occurrence of transposable elements within gene coding regions. BMC Genomics, 2017, 18, 55.	1.2	30

#	ARTICLE	IF	CITATIONS
1659	Comparative Analysis Highlights Variable Genome Content of Wheat Rusts and Divergence of the Mating Loci. G3: Genes, Genomes, Genetics, 2017, 7, 361-376.	0.8	127
1660	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i>. Environmental Microbiology, 2017, 19, 2964-2983.	1.8	154
1661	Genome-Wide Convergence during Evolution of Mangroves from Woody Plants. Molecular Biology and Evolution, 2017, 34, msw277.	3.5	43
1662	A comparative genomic analysis of putative pathogenicity genes in the host-specific sibling species Colletotrichum graminicola and Colletotrichum sublineola. BMC Genomics, 2017, 18, 67.	1.2	53
1663	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	13.7	150
1664	Exploring the genomic diversity of black yeasts and relatives (<i>Chaetothyriales</i>,<i>Ascomycota</i>). Studies in Mycology, 2017, 86, 1-28.	4.5	144
1665	Comparative metabolite and genome analysis of tuber-bearing potato species. Phytochemistry, 2017, 137, 42-51.	1.4	41
1666	Convergent patterns in the evolution of mealybug symbioses involving different intrabacterial symbionts. ISME Journal, 2017, 11, 715-726.	4.4	49
1667	Transcriptomic analysis of common carp anterior kidney during Cyprinid herpesvirus 3 infection: Immunoglobulin repertoire and homologue functional divergence. Scientific Reports, 2017, 7, 41531.	1.6	26
1668	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
1669	Comparative analysis of the transcriptional responses to low and high temperatures in three rice planthopper species. Molecular Ecology, 2017, 26, 2726-2737.	2.0	68
1670	TipMT: Identification of PCR-based taxon-specific markers. BMC Bioinformatics, 2017, 18, 104.	1.2	2
1671	Genetic Adaptation of Schizothoracine Fish to the Phased Uplifting of the Qinghaiâ€“Tibetan Plateau. G3: Genes, Genomes, Genetics, 2017, 7, 1267-1276.	0.8	29
1672	Dissection of genomic features and variations of three pathotypes of Puccinia striiformis through whole genome sequencing. Scientific Reports, 2017, 7, 42419.	1.6	55
1673	Genome Report: Identification and Validation of Antigenic Proteins from <i>Pajaroellobacter abortibovis</i> Using <i>De Novo</i> Genome Sequence Assembly and Reverse Vaccinology. G3: Genes, Genomes, Genetics, 2017, 7, 321-331.	0.8	8
1674	A Guide to Computational Methods for Predicting Mitochondrial Localization. Methods in Molecular Biology, 2017, 1567, 1-14.	0.4	4
1675	Genomic changes associated with the evolutionary transition of an insect gut symbiont into a blood-borne pathogen. ISME Journal, 2017, 11, 1232-1244.	4.4	84
1676	In-silico screening, identification and validation of a novel vaccine candidate in the fight against Plasmodium falciparum. Parasitology Research, 2017, 116, 1293-1305.	0.6	13

#	ARTICLE	IF	CITATIONS
1677	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	3.4	99
1678	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in Hevea species. Scientific Reports, 2017, 7, 41457.	1.6	95
1679	The Genomics of Wood Formation in Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2017, , 205-225.	0.3	3
1680	Lineageâ€Specific and Highly Derived Gene Sequences Among Amoebozoa, Revealed by the Comparative Analysis of Transcriptomes from Twelve Amoebozoan Species. Journal of Eukaryotic Microbiology, 2017, 64, 622-631.	0.8	0
1682	The genome of Chenopodium quinoa. Nature, 2017, 542, 307-312.	13.7	569
1683	Novel taxa of thermally dimorphic systemic pathogens in the <i>Ajellomycetaceae</i> (<i>Onygenales</i>). Mycoses, 2017, 60, 296-309.	1.8	111
1684	The Echinococcus canadensis (G7) genome: a key knowledge of parasitic platyhelminth human diseases. BMC Genomics, 2017, 18, 204.	1.2	42
1685	The genome of Leishmania adleri from a mammalian host highlights chromosome fission in Sauroleishmania. Scientific Reports, 2017, 7, 43747.	1.6	34
1686	Divergence of annual and perennial species in the Brassicaceae and the contribution of cisâ€acting variation at <i><scp>FLC</scp></i> orthologues. Molecular Ecology, 2017, 26, 3437-3457.	2.0	63
1687	Multitarget Quantitative PCR Improves Detection and Predicts Cultivability of the Pathogen Burkholderia pseudomallei. Applied and Environmental Microbiology, 2017, 83, .	1.4	20
1688	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. G3: Genes, Genomes, Genetics, 2017, 7, 203-219.	0.8	43
1689	Structure-Based Targeting of Orthologous Pathogen Proteins Accelerates Antiparasitic Drug Discovery. ACS Infectious Diseases, 2017, 3, 281-292.	1.8	13
1690	Phylogenetic analysis of 25 plant species representing 19 angiosperm families and one gymnosperm family based on 390 orthologous genes. Plant Systematics and Evolution, 2017, 303, 413-417.	0.3	9
1691	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. Nature Genetics, 2017, 49, 765-772.	9.4	316
1692	Genomics and evolution of protein phosphatases. Science Signaling, 2017, 10, .	1.6	206
1693	The genome sequence of the wisent (Bison bonasus). GigaScience, 2017, 6, 1-5.	3.3	22
1694	Effect of methyl-Î²-cyclodextrin on gene expression in microbial conversion of phytosterol. Applied Microbiology and Biotechnology, 2017, 101, 4659-4667.	1.7	23
1695	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. Genome Research, 2017, 27, 885-896.	2.4	464

#	ARTICLE	IF	CITATIONS
1696	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
1697	Hybrid de novo genome assembly of the Chinese herbal fleabane Erigeron breviscapus. GigaScience, 2017, 6, 1-7.	3.3	22
1698	Sirtuins in the phylum Basidiomycota: A role in virulence in Cryptococcus neoformans. Scientific Reports, 2017, 7, 46567.	1.6	27
1699	Intrinsic protein disorder reduces small-scale gene duplicability. DNA Research, 2017, 24, 435-444.	1.5	10
1700	Genome characteristics of the proteorhodopsin-containing marine flavobacterium Polaribacter dokdonensis DSW-5. Journal of Microbiology, 2017, 55, 561-567.	1.3	7
1701	Insights into deepâ€•sea adaptations and hostâ€"symbiont interactions: A comparative transcriptome study on <i>Bathymodiolus</i> mussels and their coastal relatives. Molecular Ecology, 2017, 26, 5133-5148.	2.0	58
1702	Draft genomes of the corallimorpharians <i>Amplexidiscus fenestrafer</i> and <i>Discosoma</i> sp.. Molecular Ecology Resources, 2017, 17, e187-e195.	2.2	22
1703	A network perspective on the virus world. Communicative and Integrative Biology, 2017, 10, e1296614.	0.6	29
1704	Epidemiological and Molecular Characterization of an Invasive Group A Streptococcus <i>emm</i> 32.2 Outbreak. Journal of Clinical Microbiology, 2017, 55, 1837-1846.	1.8	12
1705	Genome sequence of Plasmopara viticola and insight into the pathogenic mechanism. Scientific Reports, 2017, 7, 46553.	1.6	81
1706	Genome-Wide Analysis Provides Evidence on the Genetic Relatedness of the Emergent <i>Xylella fastidiosa</i> Genotype in Italy to Isolates from Central America. Phytopathology, 2017, 107, 816-827.	1.1	61
1707	Genome-wide identification of physically clustered genes suggests chromatin-level co-regulation in male reproductive development in Arabidopsis thaliana. Nucleic Acids Research, 2017, 45, 3253-3265.	6.5	35
1708	Evolution, expression analysis, and functional verification of Catharanthus roseus RLK1-like kinase (CrRLK1L) family proteins in pear (Pyrus bretchneideri). Genomics, 2017, 109, 290-301.	1.3	25
1709	Bifidobacterium Bacteremia: Clinical Characteristics and a Genomic Approach To Assess Pathogenicity. Journal of Clinical Microbiology, 2017, 55, 2234-2248.	1.8	72
1710	Diversity and evolution of sex determination systems in terrestrial isopods. Scientific Reports, 2017, 7, 1084.	1.6	35
1711	Altered interactions between unicellular and multicellular genes drive hallmarks of transformation in a diverse range of solid tumors. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6406-6411.	3.3	159
1712	The Tea Tree Genome Provides Insights into Tea Flavor and Independent Evolution of Caffeine Biosynthesis. Molecular Plant, 2017, 10, 866-877.	3.9	563
1713	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. Genome Biology and Evolution, 2017, 9, 1130-1147.	1.1	75

#	ARTICLE	IF	CITATIONS
1714	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	13.7	1,365
1715	Comparative Genomics of Chrysochromulina Ericina Virus and Other Microalga-Infecting Large DNA Viruses Highlights Their Intricate Evolutionary Relationship with the Established Mimiviridae Family. Journal of Virology, 2017, 91, .	1.5	59
1716	Resolving interspecific relationships within evolutionarily young lineages using RNA-seq data: An example from Pedicularis section Cyathophora (Orobanchaceae). Molecular Phylogenetics and Evolution, 2017, 107, 345-355.	1.2	21
1717	The chimeric nature of the genomes of marine magnetotactic coccoidâ€ovoid bacteria defines a novel group of <scp><i>P</i></scp><i>roteobacteria</i>. Environmental Microbiology, 2017, 19, 1103-1119.	1.8	60
1718	Analysis of Germination Capacity and Germinant Receptor (Sub)clusters of Genome-Sequenced Bacillus cereus Environmental Isolates and Model Strains. Applied and Environmental Microbiology, 2017, 83, .	1.4	12
1719	Development of new methods for the quantitative detection and typing of Lactobacillus parabuchneri in dairy products. International Dairy Journal, 2017, 70, 65-71.	1.5	29
1720	Comparative pathogenomic characterization of a non-invasive serotype M71 strain Streptococcus pyogenes NS53 reveals incongruent phenotypic implications from distinct genotypic markers. Pathogens and Disease, 2017, 75, .	0.8	1
1721	Predicting Transcription Factor Binding Sites and Their Cognate Transcription Factors Using Gene Expression Data. Methods in Molecular Biology, 2017, 1629, 271-282.	0.4	3
1722	Regulators of plant biomass degradation in ascomycetous fungi. Biotechnology for Biofuels, 2017, 10, 152.	6.2	202
1723	Adaptation and evolution of deep-sea scale worms (Annelida: Polynoidae): insights from transcriptome comparison with a shallow-water species. Scientific Reports, 2017, 7, 46205.	1.6	31
1724	Transcriptomic Resources for an Endemic Neotropical Plant Lineage (Gesneriaceae). Applications in Plant Sciences, 2017, 5, 1600135.	0.8	4
1725	Genomic comparison of virulent and non-virulent serotype V ST1 Streptococcus agalactiae in fish. Veterinary Microbiology, 2017, 207, 164-169.	0.8	11
1726	Expansion of sesquiterpene biosynthetic gene clusters in pepper confers nonhost resistance to the Irish potato famine pathogen. New Phytologist, 2017, 215, 1132-1143.	3.5	37
1727	Genome and Transcriptome sequence of Finger millet (Eleusine coracana (L.) Gaertn.) provides insights into drought tolerance and nutraceutical properties. BMC Genomics, 2017, 18, 465.	1.2	165
1728	The Evolution of Venom by Co-option of Single-Copy Genes. Current Biology, 2017, 27, 2007-2013.e8.	1.8	99
1729	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. ISME Journal, 2017, 11, 2334-2344.	4.4	34
1730	The genome sequence of Barbarea vulgaris facilitates the study of ecological biochemistry. Scientific Reports, 2017, 7, 40728.	1.6	33
1731	Gene-enriched draft genome of the cattle tick Rhipicephalus microplus: assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. International Journal for Parasitology, 2017, 47, 569-583.	1.3	48

#	Article	IF	Citations
1732	â€œMycobacterium massilipolynesiensisâ€•sp. nov., a rapidly-growing mycobacterium of medical interest related to Mycobacterium phlei. Scientific Reports, 2017, 7, 40443.	1.6	6
1733	Genome Sequence of Acinetobacter lactucae OTEC-02, Isolated from Hydrocarbon-Contaminated Soil. Genome Announcements, 2017, 5, .	0.8	0
1734	Comparative analysis of the predicted secretomes of Rosaceae scab pathogens Venturia inaequalis and V. pirina reveals expanded effector families and putative determinants of host range. BMC Genomics, 2017, 18, 339.	1.2	68
1735	Phylogenomic Reconstruction of the Oomycete Phylogeny Derived from 37 Genomes. MSphere, 2017, 2, .	1.3	84
1736	Global analysis of transcriptome sequences highlights accelerated evolution of immune genes in Danio choprae and Danio albolineatus. Fish and Shellfish Immunology, 2017, 66, 390-397.	1.6	4
1737	The Genome of Medicinal Plant Macleaya cordata Provides New Insights into Benzylisoquinoline Alkaloids Metabolism. Molecular Plant, 2017, 10, 975-989.	3.9	116
1738	Draft genome of spinach and transcriptome diversity of 120 Spinacia accessions. Nature Communications, 2017, 8, 15275.	5.8	156
1739	Transcriptome-Wide Identification and Expression Analysis of DIVARICATA- and RADIALIS-Like Genes of the Mediterranean Orchid Orchis italica. Genome Biology and Evolution, 2017, 9, 1418-1431.	1.1	22
1740	Comparative transcriptomics provide insight into the morphogenesis and evolution of fistular leaves in Allium. BMC Genomics, 2017, 18, 60.	1.2	24
1741	The Evolutionary Basis of Translational Accuracy in Plants. G3: Genes, Genomes, Genetics, 2017, 7, 2363-2373.	0.8	5
1742	Genomics Perspectives on Metabolism, Survival Strategies, and Biotechnological Applications of <i>Brettanomyces bruxellensis</i> LAMAP2480. Journal of Molecular Microbiology and Biotechnology, 2017, 27, 147-158.	1.0	11
1743	Exploring structural variation and gene family architecture with De Novo assemblies of 15 Medicago genomes. BMC Genomics, 2017, 18, 261.	1.2	87
1744	An alternative pathway to eusociality: Exploring the molecular and functional basis of fortress defense. Evolution; International Journal of Organic Evolution, 2017, 71, 1986-1998.	1.1	8
1745	Whipworm kinomes reflect a unique biology and adaptation to the host animal. International Journal for Parasitology, 2017, 47, 857-866.	1.3	10
1746	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in Penicillium species. Nature Microbiology, 2017, 2, 17044.	5.9	198
1747	Niche partitioning of diverse sulfur-oxidizing bacteria at hydrothermal vents. ISME Journal, 2017, 11, 1545-1558.	4.4	168
1748	Scallop genome provides insights into evolution of bilaterian karyotype and development. Nature Ecology and Evolution, 2017, 1, 120.	3.4	353
1749	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. Nature Ecology and Evolution, 2017, 1, 121.	3.4	250

#	Article	IF	Citations
1750	Genome-wide sequencing of longan (Dimocarpus longan Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. GigaScience, 2017, 6, 1-14.	3.3	103
1751	Origin and Evolutionary Alteration of the Mitochondrial Import System in Eukaryotic Lineages. Molecular Biology and Evolution, 2017, 34, 1574-1586.	3.5	52
1752	Trade-off between Transcriptome Plasticity and Genome Evolution in Cephalopods. Cell, 2017, 169, 191-202.e11.	13.5	268
1753	Draft Genome Sequence of Citrobacter freundii Strain A47, Resistant to the Mycotoxin Deoxynivalenol. Genome Announcements, 2017, 5, .	0.8	6
1754	Complete genome sequence of Erythrobacter gangjinensis CGMCC 1.15024T with two chromosomes. Marine Genomics, 2017, 34, 15-18.	0.4	3
1755	Highly cited articles in malaria research: a bibliometric analysis. Collection Building, 2017, 36, 45-57.	0.5	8
1756	Comparative genomics of Vibrio campbellii strains and core species of the Vibrio Harveyi clade. Scientific Reports, 2017, 7, 41394.	1.6	42
1757	Decay of the glycolytic pathway and adaptation to intranuclear parasitism within Enterocytozoonidae microsporidia. Environmental Microbiology, 2017, 19, 2077-2089.	1.8	74
1758	Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. Nature Communications, 2017, 8, 14742.	5.8	96
1759	The crown-of-thorns starfish genome as a guide for biocontrol of this coral reef pest. Nature, 2017, 544, 231-234.	13.7	157
1760	Genome sequence of a rice pest, the white-backed planthopper (Sogatella furcifera). GigaScience, 2017, 6, 1-9.	3.3	43
1761	A Genome-Scale Model of <i>Shewanella piezotolerans</i> Simulates Mechanisms of Metabolic Diversity and Energy Conservation. MSystems, 2017, 2, .	1.7	14
1762	Draft genome of the Northern snakehead, Channa argus. GigaScience, 2017, 6, 1-5.	3.3	45
1763	Genome sequence of lung pathogenic Escherichia coli O78, a chimeric strain isolated from pneumonia forest musk deer. Genes and Genomics, 2017, 39, 805-815.	0.5	5
1764	Reconstructing the genome of the most recent common ancestor of flowering plants. Nature Genetics, 2017, 49, 490-496.	9.4	203
1765	Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. Nature Microbiology, 2017, 2, 17033.	5.9	17
1766	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. Current Biology, 2017, 27, 958-967.	1.8	423
1767	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
1768	Recurrent rewiring and emergence of RNA regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2816-E2825.	3.3	32
1769	The pangenome of the genus <scp><i>C</i></scp><i>lostridium</i>. Environmental Microbiology, 2017, 19, 2588-2603.	1.8	43
1770	The Bio-Analytic Resource for Plant Biology. Methods in Molecular Biology, 2017, 1533, 119-148.	0.4	36
1771	Genome sequence and genetic diversity of European ash trees. Nature, 2017, 541, 212-216.	13.7	166
1772	Draft genome and description of Orrella dioscoreae gen. nov. sp. nov., a new species of Alcaligenaceae isolated from leaf acumens of Dioscorea sansibarensis. Systematic and Applied Microbiology, 2017, 40, 11-21.	1.2	42
1773	Plant genome and transcriptome annotations: from misconceptions to simple solutions. Briefings in Bioinformatics, 2018, 19, bbw135.	3.2	62
1774	Origins of pandemic Vibrio cholerae from environmental gene pools. Nature Microbiology, 2017, 2, 16240.	5.9	42
1775	Evolution of floral diversity: genomics, genes and<i>gamma</i>. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20150509.	1.8	41
1776	Emergence of Novel Pathogenic Streptomyces Species by Site-Specific Accretion and cis-Mobilization of Pathogenicity Islands. Molecular Plant-Microbe Interactions, 2017, 30, 72-82.	1.4	20
1777	The genome draft of coconut (Cocos nucifera). GigaScience, 2017, 6, 1-11.	3.3	96
1778	Coordinated Functional Divergence of Genes after Genome Duplication in <i>Arabidopsis thaliana</i>. Plant Cell, 2017, 29, 2786-2800.	3.1	46
1779	A Chromosome-Scale Assembly of the<i>Bactrocera cucurbitae</i>Genome Provides Insight to the Genetic Basis of<i>white pupae</i>. G3: Genes, Genomes, Genetics, 2017, 7, 1927-1940.	0.8	33
1780	Comparative Transcriptomics of Steinernema and Caenorhabditis Single Embryos Reveals Orthologous Gene Expression Convergence during Late Embryogenesis. Genome Biology and Evolution, 2017, 9, 2681-2696.	1.1	21
1781	Genome sequencing of the winged midge, Parochlus steinenii, from the Antarctic Peninsula. GigaScience, 2017, 6, 1-8.	3.3	15
1782	Insights into Land Plant Evolution Garnered from the Marchantia polymorpha Genome. Cell, 2017, 171, 287-304.e15.	13.5	973
1784	The draft genome of tropical fruit durian (Durio zibethinus). Nature Genetics, 2017, 49, 1633-1641.	9.4	150
1785	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
1786	Genome of wild olive and the evolution of oil biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9413-E9422.	3.3	233

#	ARTICLE	IF	CITATIONS
1787	Identification and expression profiling analysis of TCP family genes involved in growth and development in maize. Physiology and Molecular Biology of Plants, 2017, 23, 779-791.	1.4	66
1788	Ctenophore relationships and their placement as the sister group to all other animals. Nature Ecology and Evolution, 2017, 1, 1737-1746.	3.4	202
1789	Comparative Genomics of Soybean and Other Legumes. Compendium of Plant Genomes, 2017, , 83-93.	0.3	1
1790	Constrained vertebrate evolution by pleiotropic genes. Nature Ecology and Evolution, 2017, 1, 1722-1730.	3.4	72
1791	Plasmodium falciparum specific helicase 3 is nucleocytoplasmic protein and unwinds DNA duplex in 3â€² to 5â€² direction. Scientific Reports, 2017, 7, 13146.	1.6	9
1792	Bioinformatic Identification and Analysis of Cell Wall Extensins in Three<i>Arabidopsis</i>Species. International Journal of Plant Sciences, 2017, 178, 724-739.	0.6	0
1793	Echinochloa crus-galli genome analysis provides insight into its adaptation and invasiveness as a weed. Nature Communications, 2017, 8, 1031.	5.8	138
1794	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
1795	Panax ginseng genome examination for ginsenoside biosynthesis. GigaScience, 2017, 6, 1-15.	3.3	150
1796	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	1.6	27
1797	Evolutionary strata on young mating-type chromosomes despite the lack of sexual antagonism. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7067-7072.	3.3	92
1798	New smut-specific primers for multilocus genotyping and phylogenetics of Ustilaginaceae. Mycological Progress, 2017, 16, 917-925.	0.5	10
1799	Draft genome of the Antarctic dragonfish, Parachaenichthys charcoti. GigaScience, 2017, 6, 1-6.	3.3	24
1800	Zygotic Genome Activation Occurs Shortly after Fertilization in Maize. Plant Cell, 2017, 29, 2106-2125.	3.1	127
1801	A-to-I RNA editing is developmentally regulated and generally adaptive for sexual reproduction in <i>Neurospora crassa</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7756-E7765.	3.3	73
1802	Comparative Genomics Reveals Two Major Bouts of Gene Retroposition Coinciding with Crucial Periods of Symbiodinium Evolution. Genome Biology and Evolution, 2017, 9, 2037-2047.	1.1	33
1803	The highâ€quality genome of <i>Brassica napus</i> cultivar â€˜<scp>ZS</scp>11â€™ reveals the introgression history in semiâ€winter morphotype. Plant Journal, 2017, 92, 452-468.	2.8	233
1804	The draft genome assembly of Rhododendron delavayi Franch. var. delavayi. GigaScience, 2017, 6, 1-11.	3.3	64

#	ARTICLE	IF	CITATIONS
1805	Metabolic Network Analysis and Metatranscriptomics Reveal Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acI. MSystems, 2017, 2, .	1.7	21
1806	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotechnology, 2017, 35, 969-976.	9.4	356
1807	Transcriptional response of the harmful raphidophyte Heterosigma akashiwo to nitrate and phosphate stress. Harmful Algae, 2017, 68, 258-270.	2.2	32
1808	Acidophilic green algal genome provides insights into adaptation to an acidic environment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8304-E8313.	3.3	93
1809	The Apostasia genome and the evolution of orchids. Nature, 2017, 549, 379-383.	13.7	305
1810	Genome-Enabled Insights into the Ecophysiology of the Comammox Bacterium â€œ <i>Candidatus</i> Nitrospira nitrosaâ€. MSystems, 2017, 2, .	1.7	119
1811	Identification and functional prediction of stress responsive AP2/ERF transcription factors in Brassica napus by genome-wide analysis. Computational Biology and Chemistry, 2017, 71, 32-56.	1.1	24
1812	The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies. Microbiology Spectrum, 2017, 5, .	1.2	169
1813	Genome Architecture and Evolution of a Unichromosomal Asexual Nematode. Current Biology, 2017, 27, 2928-2939.e6.	1.8	56
1814	KinFin: Software for Taxon-Aware Analysis of Clustered Protein Sequences. G3: Genes, Genomes, Genetics, 2017, 7, 3349-3357.	0.8	72
1815	Ancestral acquisitions, gene flow and multiple evolutionary trajectories of the type three secretion system and effectors in <i>Xanthomonas</i> plant pathogens. Molecular Ecology, 2017, 26, 5939-5952.	2.0	56
1816	Genome reconstruction in Cynara cardunculus taxa gains access to chromosome-scale DNA variation. Scientific Reports, 2017, 7, 5617.	1.6	30
1817	A genomic investigation of ecological differentiation between freeâ€living and <i>Drosophila</i>â€associated bacteria. Molecular Ecology, 2017, 26, 4536-4550.	2.0	52
1818	Seed desiccation mechanisms coâ€opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i>. Plant, Cell and Environment, 2017, 40, 2292-2306.	2.8	49
1819	Proteogenomic Analysis and Discovery of Immune Antigens in Mycobacterium vaccae. Molecular and Cellular Proteomics, 2017, 16, 1578-1590.	2.5	12
1820	Overcoming the loss of blue sensitivity through opsin duplication in the largest animal group, beetles. Scientific Reports, 2017, 7, 8.	1.6	178
1821	Temporal and spatial transcriptomic and micro<scp>RNA</scp> dynamics of <scp>CAM</scp> photosynthesis in pineapple. Plant Journal, 2017, 92, 19-30.	2.8	78
1822	A New Reference Genome Assembly for the Microcrustacean <i>Daphnia pulex</i>. G3: Genes, Genomes, Genetics, 2017, 7, 1405-1416.	0.8	95

#	Article	IF	Citations
1823	Orthology Correction for Gene Tree Reconstruction: Theoretical and Experimental Results. Procedia Computer Science, 2017, 108, 1115-1124.	1.2	17
1824	Inferring the shallow phylogeny of true salamanders (Salamandra) by multiple phylogenomic approaches. Molecular Phylogenetics and Evolution, 2017, 115, 16-26.	1.2	44
1825	The phylogeny of extant starfish (Asteroidea: Echinodermata) including Xyloplax, based on comparative transcriptomics. Molecular Phylogenetics and Evolution, 2017, 115, 161-170.	1.2	40
1826	An in silico strategy for identification of novel drug targets against Plasmodium falciparum. Parasitology Research, 2017, 116, 2539-2559.	0.6	7
1827	Comparative genomic analysis of Paenibacillus sp. SSG-1 and its closely related strains reveals the effect of glycometabolism on environmental adaptation. Scientific Reports, 2017, 7, 5720.	1.6	9
1828	Rhodophyta. , 2017, , 89-133.		14
1829	Polymorphisms in the LAC12 gene explain lactose utilisation variability in Kluyveromyces marxianus strains. FEMS Yeast Research, 2017, 17, .	1.1	46
1830	Genetic analysis of a PER-2-producing Shewanella sp. strain harbouring a variety of mobile genetic elements and antibiotic resistance determinants. Journal of Global Antimicrobial Resistance, 2017, 11, 81-86.	0.9	10
1831	The first complete genomes of Metalmarks and the classification of butterfly families. Genomics, 2017, 109, 485-493.	1.3	20
1832	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
1833	The draft genome sequence of a desert tree Populus pruinosa. GigaScience, 2017, 6, 1-7.	3.3	61
1834	The Conserved and Unique Genetic Architecture of Kernel Size and Weight in Maize and Rice. Plant Physiology, 2017, 175, 774-785.	2.3	114
1835	Basidiomyceteâ€specific <i>PsCaMKL1</i> encoding a CaMKâ€like protein kinase is required for full virulence of <i>Puccinia striiformis</i> f. sp. <i>tritici</i>. Environmental Microbiology, 2017, 19, 4177-4189.	1.8	7
1836	Parallel Evolution of Chromatin Structure Underlying Metabolic Adaptation. Molecular Biology and Evolution, 2017, 34, 2870-2878.	3.5	5
1837	Comparative Genomics of <i>Bacillus thuringiensis</i> Reveals a Path to Specialized Exploitation of Multiple Invertebrate Hosts. MBio, 2017, 8, .	1.8	43
1838	OrthoGNC: A Software for Accurate Identification of Orthologs Based on Gene Neighborhood Conservation. Genomics, Proteomics and Bioinformatics, 2017, 15, 361-370.	3.0	12
1839	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
1840	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

#	Article	IF	Citations
1841	Genomic assessment in Lactobacillus plantarum links the butyrogenic pathway with glutamine metabolism. Scientific Reports, 2017, 7, 15975.	1.6	25
1842	Identification and analysis of seven effector protein families with different adaptive and evolutionary histories in plant-associated members of the Xanthomonadaceae. Scientific Reports, 2017, 7, 16133.	1.6	35
1843	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. Nature Communications, 2017, 8, 1843.	5.8	85
1844	The Aegilops tauschii genome reveals multiple impacts of transposons. Nature Plants, 2017, 3, 946-955.	4.7	164
1845	Multiple Approaches to Phylogenomic Reconstruction of the Fungal Kingdom. Advances in Genetics, 2017, 100, 211-266.	0.8	19
1846	Genome sequence of the progenitor of the wheat D genome Aegilops tauschii. Nature, 2017, 551, 498-502.	13.7	563
1847	Ammoniaâ€oxidising archaea living at low pH: Insights from comparative genomics. Environmental Microbiology, 2017, 19, 4939-4952.	1.8	107
1848	Comparative Genomic Analysis of Globally Dominant ST131 Clone with Other Epidemiologically Successful Extraintestinal Pathogenic <i>Escherichia coli</i> (ExPEC) Lineages. MBio, 2017, 8, .	1.8	86
1849	Phylogenomic Insight into Salinispora (Bacteria, Actinobacteria) Species Designations. Scientific Reports, 2017, 7, 3564.	1.6	27
1850	Whole Genome Sequence of the Heterozygous Clinical Isolate <i>Candida krusei</i> 81-B-5. G3: Genes, Genomes, Genetics, 2017, 7, 2883-2889.	0.8	31
1851	Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. BMC Genomics, 2017, 18, 480.	1.2	12
1852	Genome-wide identification, evolution, and expression analysis of GATA transcription factors in apple (Malus Ã— domestica Borkh.). Gene, 2017, 627, 460-472.	1.0	26
1853	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
1854	Genomic Analysis of <i>Clavibacter michiganensis</i> Reveals Insight Into Virulence Strategies and Genetic Diversity of a Gram-Positive Bacterial Pathogen. Molecular Plant-Microbe Interactions, 2017, 30, 786-802.	1.4	56
1855	Contrasting Rates of Molecular Evolution and Patterns of Selection among Gymnosperms and Flowering Plants. Molecular Biology and Evolution, 2017, 34, 1363-1377.	3.5	164
1856	Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. Genetics, 2017, 207, 327-346.	1.2	105
1857	Transcriptome and metabolome analysis of Ferula gummosa Boiss. to reveal major biosynthetic pathways of galbanum compounds. Functional and Integrative Genomics, 2017, 17, 725-737.	1.4	17
1858	Transcriptional Analysis of Flowering Time in Switchgrass. Bioenergy Research, 2017, 10, 700-713.	2.2	19

#	Article	IF	Citations
1859	SparkBLAST: scalable BLAST processing using in-memory operations. BMC Bioinformatics, 2017, 18, 318.	1.2	27
1860	Comparative transcriptome analysis reveals different strategies for degradation of steam-exploded sugarcane bagasse by Aspergillus niger and Trichoderma reesei. BMC Genomics, 2017, 18, 501.	1.2	79
1861	Insights into the Geobacillus stearothermophilus species based on phylogenomic principles. BMC Microbiology, 2017, 17, 140.	1.3	41
1862	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. Plant Journal, 2017, 91, 1108-1128.	2.8	109
1863	Orthograph: a versatile tool for mapping coding nucleotide sequences to clusters of orthologous genes. BMC Bioinformatics, 2017, 18, 111.	1.2	146
1864	OrthoReD: a rapid and accurate orthology prediction tool with low computational requirement. BMC Bioinformatics, 2017, 18, 310.	1.2	27
1865	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
1866	Evolutionary origin and function of NOX4-art, an arthropod specific NADPH oxidase. BMC Evolutionary Biology, 2017, 17, 92.	3.2	14
1867	Divergent and convergent modes of interaction between wheat and Puccinia graminis f. sp. tritici isolates revealed by the comparative gene co-expression network and genome analyses. BMC Genomics, 2017, 18, 291.	1.2	20
1868	Pan genome and CRISPR analyses of the bacterial fish pathogen Moritella viscosa. BMC Genomics, 2017, 18, 313.	1.2	10
1869	A reference genome for Nicotiana tabacum enables map-based cloning of homeologous loci implicated in nitrogen utilization efficiency. BMC Genomics, 2017, 18, 448.	1.2	265
1870	Comparative transcriptomic analysis of the evolution and development of flower size in Saltugilia (Polemoniaceae). BMC Genomics, 2017, 18, 475.	1.2	18
1871	Evolutionary gradient of predicted nuclear localization signals (NLS)-bearing proteins in genomes of family Planctomycetaceae. BMC Microbiology, 2017, 17, 86.	1.3	2
1872	Approximating the correction of weighted and unweighted orthology and paralogy relations. Algorithms for Molecular Biology, 2017, 12, 4.	0.3	16
1873	Comparative genomic analysis of Shiga toxin-producing and non-Shiga toxin-producing Escherichia coli O157 isolated from outbreaks in Korea. Gut Pathogens, 2017, 9, 7.	1.6	3
1874	Ontology-based literature mining of E. coli vaccine-associated gene interaction networks. Journal of Biomedical Semantics, 2017, 8, 12.	0.9	13
1875	PorthoMCL: Parallel orthology prediction using MCL for the realm of massive genome availability. Big Data Analytics, 2017, 2, .	2.2	43
1876	Genome-wide comparative analysis of four Indian Drosophila species. Molecular Genetics and Genomics, 2017, 292, 1197-1208.	1.0	4

#	Article	IF	Citations
1877	AspWood: High-Spatial-Resolution Transcriptome Profiles Reveal Uncharacterized Modularity of Wood Formation in <i>Populus tremula</i>. Plant Cell, 2017, 29, 1585-1604.	3.1	219
1878	In silico search of inhibitors of Streptococcus mutans for the control of dental plaque. Archives of Oral Biology, 2017, 83, 68-75.	0.8	4
1879	Comparative analysis of the neurula transcriptomes of two species of flatfishes: Platichthys stellatus and Paralichthys olivaceus. Gene, 2017, 596, 147-153.	1.0	7
1880	The underlying mechanisms of genetic innovation and speciation in the family Corynebacteriaceae: A phylogenomics approach. Molecular Phylogenetics and Evolution, 2017, 107, 246-255.	1.2	38
1881	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
1882	Nuclear DNA content correlates with depth, body size, and diversification rate in amphipod crustaceans from ancient Lake Baikal, Russia. Genome, 2017, 60, 303-309.	0.9	22
1883	Architecture of a Species: Phylogenomics of Staphylococcus aureus. Trends in Microbiology, 2017, 25, 153-166.	3.5	91
1884	Opsins have evolved under the permanent heterozygote model: insights from phylotranscriptomics of Odonata. Molecular Ecology, 2017, 26, 1306-1322.	2.0	29
1885	Draft genome assembly and annotation of <i>Glycyrrhiza uralensis</i>, a medicinal legume. Plant Journal, 2017, 89, 181-194.	2.8	148
1886	Genomic study of the Type IVC secretion system in <i>Clostridium difficile</i>: understanding <i>C. difficile</i> evolution via horizontal gene transfer. Genome, 2017, 60, 8-16.	0.9	7
1887	Genome Dynamics and Molecular Infection Epidemiology of Multidrug-Resistant Helicobacter pullorum Isolates Obtained from Broiler and Free-Range Chickens in India. Applied and Environmental Microbiology, 2017, 83, .	1.4	28
1888	Convergent evolution of social hybridogenesis in <i>Messor</i> harvester ants. Molecular Ecology, 2017, 26, 1108-1117.	2.0	27
1889	Analysis of embryonic development in the unsequenced axolotl: Waves of transcriptomic upheaval and stability. Developmental Biology, 2017, 426, 143-154.	0.9	34
1890	A comprehensive draft genome sequence for lupin (<i>Lupinus angustifolius</i>), an emerging health food: insights into plantâ€“microbe interactions and legume evolution. Plant Biotechnology Journal, 2017, 15, 318-330.	4.1	153
1891	Monophyly of Anthozoa (Cnidaria): why do nuclear and mitochondrial phylogenies disagree?. Zoologica Scripta, 2017, 46, 363-371.	0.7	25
1892	Functional genomics provides insights into the role of Propionibacterium freudenreichii ssp. shermanii JS in cheese ripening. International Journal of Food Microbiology, 2017, 241, 39-48.	2.1	19
1893	Dissecting genome reduction and trait loss in insect endosymbionts. Annals of the New York Academy of Sciences, 2017, 1389, 52-75.	1.8	87
1894	The OGCleaner: filtering false-positive homology clusters. Bioinformatics, 2017, 33, 125-127.	1.8	5

#	ARTICLE	IF	CITATIONS
1895	The Complete Genome Sequence of the Phytopathogenic Fungus Sclerotinia sclerotiorum Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. Genome Biology and Evolution, 2017, 9, 593-618.	1.1	187
1896	Popmarker: Identifying Phylogenetic Markers at the Population Level. Evolutionary Bioinformatics, 2017, 13, 117693431772440.	0.6	2
1897	Comparative whole-genome analysis reveals artificial selection effects on Ustilago esculenta genome. DNA Research, 2017, 24, 635-648.	1.5	58
1898	Draft genome of the reindeer (Rangifer tarandus). GigaScience, 2017, 6, 1-5.	3.3	41
1899	Sequencing the Chickpea Genome. Compendium of Plant Genomes, 2017, , 117-123.	0.3	0
1900	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
1901	Draft genome of the lined seahorse, Hippocampus erectus. GigaScience, 2017, 6, 1-6.	3.3	38
1902	The origin, diversification and adaptation of a major mangrove clade (Rhizophoreae) revealed by whole-genome sequencing. National Science Review, 2017, 4, 721-734.	4.6	118
1903	A few sequence polymorphisms among isolates of Maize bushy stunt phytoplasma associate with organ proliferation symptoms of infected maize plants. Annals of Botany, 2017, 119, mcw213.	1.4	49
1904	Resequencing of the Leishmania infantum (strain JPCM5) genome and de novo assembly into 36 contigs. Scientific Reports, 2017, 7, 18050.	1.6	47
1905	Genomic, transcriptomic, and proteomic approaches towards understanding the molecular mechanisms of salt tolerance in Frankia strains isolated from Casuarina trees. BMC Genomics, 2017, 18, 633.	1.2	46
1906	Comparative transcriptome analysis and identification of candidate effectors in two related rust species (Gymnosporangium yamadae and Gymnosporangium asiaticum). BMC Genomics, 2017, 18, 651.	1.2	20
1907	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
1908	Rhodopsin gene copies in Japanese eel originated in a teleost-specific genome duplication. Zoological Letters, 2017, 3, 18.	0.7	15
1909	Evidence-based gene models for structural and functional annotations of the oil palm genome. Biology Direct, 2017, 12, 21.	1.9	24
1910	Genome-Based Analyses of Six Hexacorallian Species Reject the â€œNaked Coralâ€•Hypothesis. Genome Biology and Evolution, 2017, 9, 2626-2634.	1.1	8
1911	Insights into origin and evolution of Î±-proteobacterial gene transfer agents. Virus Evolution, 2017, 3, vex036.	2.2	53
1912	Complete Genome Sequence of Spiroplasma corruscae EC-1 ^T (DSM 19793), a Bacterium Isolated from a Lampyrid Beetle (Ellychnia corrusca). Genome Announcements, 2017, 5, .	0.8	2

#	ARTICLE	IF	CITATIONS
1913	Compensatory Evolution of Intrinsic Transcription Terminators in Bacillus Cereus. Genome Biology and Evolution, 2017, 9, 340-349.	1.1	1
1914	Orchidstra 2.0â€"A Transcriptomics Resource for the Orchid Family. Plant and Cell Physiology, 2017, 58, pcw220.	1.5	72
1915	Horizontal Acquisition and Transcriptional Integration of Novel Genes in Mosquito-Associated Spiroplasma. Genome Biology and Evolution, 2017, 9, 3246-3259.	1.1	27
1916	Comparative Genome Analysis Reveals Adaptation to the Ectophytic Lifestyle of Sooty Blotch and Flyspeck Fungi. Genome Biology and Evolution, 2017, 9, 3137-3151.	1.1	11
1917	Draft genome of the Marco Polo Sheep (Ovis ammon polii). GigaScience, 2017, 6, 1-7.	3.3	25
1918	SynAPhy and SynAVal: Mining a Synteny-Similarity Graph to Resolve Orthology of Proteins in Fungal Genomes. , 2017, , .		0
1919	Genome Polymorphism Detection Through Relaxed de Bruijn Graph Construction. , 2017, , .		0
1920	A molecular portrait of maternal sepsis from Byzantine Troy. ELife, 2017, 6, .	2.8	46
1921	The Fungal Tree of Life: From Molecular Systematics to Genome-Scale Phylogenies. , 2017, , 1-34.		25
1922	Comparative Genomics Integrated with Association Analysis Identifies Candidate Effector Genes Corresponding to Lr20 in Phenotype-Paired Puccinia triticina Isolates from Australia. Frontiers in Plant Science, 2017, 8, 148.	1.7	49
1923	Analysis of Plant Pan-Genomes and Transcriptomes with GET_HOMOLOGUES-EST, a Clustering Solution for Sequences of the Same Species. Frontiers in Plant Science, 2017, 8, 184.	1.7	63
1924	Transcriptome Comparison Reveals the Adaptive Evolution of Two Contrasting Ecotypes of Zn/Cd Hyperaccumulator Sedum alfredii Hance. Frontiers in Plant Science, 2017, 8, 425.	1.7	19
1925	Identification of MicroRNA Targets of Capsicum spp. Using MiRTransâ€"a Trans-Omics Approach. Frontiers in Plant Science, 2017, 8, 495.	1.7	5
1926	Evolutionary Analysis of DELLA-Associated Transcriptional Networks. Frontiers in Plant Science, 2017, 8, 626.	1.7	35
1927	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
1928	Identification of Putative Transmembrane Proteins Involved in Salinity Tolerance in Chenopodium quinoa by Integrating Physiological Data, RNAseq, and SNP Analyses. Frontiers in Plant Science, 2017, 8, 1023.	1.7	47
1929	RNA-Seq Analysis Provides the First Insights into the Phylogenetic Relationship and Interspecific Variation between Agropyron cristatum and Wheat. Frontiers in Plant Science, 2017, 8, 1644.	1.7	16
1930	Apophysomyces variabilis: draft genome sequence and comparison of predictive virulence determinants with other medically important Mucorales. BMC Genomics, 2017, 18, 736.	1.2	20

#	ARTICLE	IF	CITATIONS
1931	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
1932	Draft sequencing and assembly of the genome of the worldâ€™s largest fish, the whale shark: Rhincodon typus Smith 1828. BMC Genomics, 2017, 18, 532.	1.2	91
1933	Genome-Wide Organization and Expression Profiling of the SBP-Box Gene Family in Chinese Jujube (Ziziphus jujuba Mill.). International Journal of Molecular Sciences, 2017, 18, 1734.	1.8	25
1934	Coralsnake Venomics: Analyses of Venom Gland Transcriptomes and Proteomes of Six Brazilian Taxa. Toxins, 2017, 9, 187.	1.5	66
1935	MimiLook: A Phylogenetic Workflow for Detection of Gene Acquisition in Major Orthologous Groups of Megavirales. Viruses, 2017, 9, 72.	1.5	2
1936	Genome sequence of the ectophytic fungus Ramichloridium luteum reveals unique evolutionary adaptations to plant surface niche. BMC Genomics, 2017, 18, 729.	1.2	12
1937	Alienness: Rapid Detection of Candidate Horizontal Gene Transfers across the Tree of Life. Genes, 2017, 8, 248.	1.0	40
1938	Antibiotic Resistance Determinant-Focused Acinetobacter baumannii Vaccine Designed Using Reverse Vaccinology. International Journal of Molecular Sciences, 2017, 18, 458.	1.8	64
1939	The All-Rounder Sodalis: A New Bacteriome-Associated Endosymbiont of the Lygaeoid Bug Henestaris halophilus (Heteroptera: Henestarinae) and a Critical Examination of Its Evolution. Genome Biology and Evolution, 2017, 9, 2893-2910.	1.1	65
1940	The Bioinformatics Analysis of Comparative Genomics of Mycobacterium tuberculosis Complex (MTBC) Provides Insight into Dissimilarities between Intraspecific Groups Differing in Host Association, Virulence, and Epitope Diversity. Frontiers in Cellular and Infection Microbiology, 2017, 7, 88.	1.8	69
1941	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
1942	Comparative Pan-Genome Analysis of Piscirickettsia salmonis Reveals Genomic Divergences within Genogroups. Frontiers in Cellular and Infection Microbiology, 2017, 7, 459.	1.8	52
1943	RNA-Seq Analysis of the Distylous Plant Nymphoides peltata Identified Ortholog Genes between Long- and Short-Styled Flowers. Frontiers in Ecology and Evolution, 2017, 5, .	1.1	4
1944	Meta Analysis of Human AlzGene Database: Benefits and Limitations of Using C. elegans for the Study of Alzheimer's Disease and Co-morbid Conditions. Frontiers in Genetics, 2017, 8, 55.	1.1	17
1945	New Tools in Orthology Analysis: A Brief Review of Promising Perspectives. Frontiers in Genetics, 2017, 8, 165.	1.1	49
1946	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
1947	Classification of Isolates from the Pseudomonas fluorescens Complex into Phylogenomic Groups Based in Group-Specific Markers. Frontiers in Microbiology, 2017, 8, 413.	1.5	51
1948	Comparative Genome Analysis Provides Insights into Both the Lifestyle of Acidithiobacillus ferrivorans Strain CF27 and the Chimeric Nature of the Iron-Oxidizing Acidithiobacilli Genomes. Frontiers in Microbiology, 2017, 8, 1009.	1.5	8

#	ARTICLE	IF	CITATIONS
1949	Genome-Wide Analysis of Secondary Metabolite Gene Clusters in Ophiostoma ulmi and Ophiostoma novo-ulmi Reveals a Fujikurin-Like Gene Cluster with a Putative Role in Infection. Frontiers in Microbiology, 2017, 8, 1063.	1.5	22
1950	Genome-Wide Detection of Small Regulatory RNAs in Deep-Sea Bacterium Shewanella piezotolerans WP3. Frontiers in Microbiology, 2017, 8, 1093.	1.5	8
1951	Amplicon Sequencing of the slpH Locus Permits Culture-Independent Strain Typing of Lactobacillus helveticus in Dairy Products. Frontiers in Microbiology, 2017, 8, 1380.	1.5	9
1952	Comparative Genomics of Burkholderia singularis sp. nov., a Low G+C Content, Free-Living Bacterium That Defies Taxonomic Dissection of the Genus Burkholderia. Frontiers in Microbiology, 2017, 8, 1679.	1.5	36
1953	New Insights into the Diversity of the Genus Faecalibacterium. Frontiers in Microbiology, 2017, 8, 1790.	1.5	71
1954	Pathogenicity of Human ST23 Streptococcus agalactiae to Fish and Genomic Comparison of Pathogenic and Non-pathogenic Isolates. Frontiers in Microbiology, 2017, 8, 1933.	1.5	8
1955	Genomic Comparison among Lethal Invasive Strains of Streptococcus pyogenes Serotype M1. Frontiers in Microbiology, 2017, 8, 1993.	1.5	2
1956	Determinism and Contingency Shape Metabolic Complementation in an Endosymbiotic Consortium. Frontiers in Microbiology, 2017, 8, 2290.	1.5	5
1957	Complete Genome Sequencing of Mycobacterium bovis SP38 and Comparative Genomics of Mycobacterium bovis and M. tuberculosis Strains. Frontiers in Microbiology, 2017, 8, 2389.	1.5	40
1958	Strong Genomic and Phenotypic Heterogeneity in the Aeromonas sobria Species Complex. Frontiers in Microbiology, 2017, 8, 2434.	1.5	20
1959	Comprehensive Analysis Reveals Two Distinct Evolution Patterns of Salmonella Flagellin Gene Clusters. Frontiers in Microbiology, 2017, 8, 2604.	1.5	14
1960	Evolution of the Apicomplexan Sugar Transporter Gene Family Repertoire. International Journal of Genomics, 2017, 2017, 1-9.	0.8	4
1961	The genome of the Antarctic-endemic copepod, Tigriopus kingsejongensis. GigaScience, 2017, 6, 1-9.	3.3	12
1962	EUCANEXT: an integrated database for the exploration of genomic and transcriptomic data from Eucalyptus species. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	12
1963	Orthologous Matrix (OMA) algorithm 2.0: more robust to asymmetric evolutionary rates and more scalable hierarchical orthologous group inference. Bioinformatics, 2017, 33, i75-i82.	1.8	82
1964	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
1965	Whole-genome duplication and molecular evolution in Cornus L. (Cornaceae) â€“ Insights from transcriptome sequences. PLoS ONE, 2017, 12, e0171361.	1.1	17
1966	Analyses of the probiotic property and stress resistance-related genes of Lactococcus lactis subsp. lactis NCDO 2118 through comparative genomics and in vitro assays. PLoS ONE, 2017, 12, e0175116.	1.1	51

#	ARTICLE	IF	CITATIONS
1967	Genomic analyses of the ancestral Manila family of Mycobacterium tuberculosis. PLoS ONE, 2017, 12, e0175330.	1.1	8
1968	Myotis rufoniger genome sequence and analyses: M. rufonigerâ€™s genomic feature and the decreasing effective population size of Myotis bats. PLoS ONE, 2017, 12, e0180418.	1.1	10
1969	Characterization of the emerging zoonotic pathogen Arcobacter thereius by whole genome sequencing and comparative genomics. PLoS ONE, 2017, 12, e0180493.	1.1	21
1970	Patterns and Processes of Mycobacterium bovis Evolution Revealed by Phylogenomic Analyses. Genome Biology and Evolution, 2017, 9, 521-535.	1.1	31
1971	The sea cucumber genome provides insights into morphological evolution and visceral regeneration. PLoS Biology, 2017, 15, e2003790.	2.6	202
1972	Whole genome sequence of the Treponema pallidum subsp. pallidum strain Amoy: An Asian isolate highly similar to SS14. PLoS ONE, 2017, 12, e0182768.	1.1	47
1973	Genomics of parallel adaptation at two timescales in Drosophila. PLoS Genetics, 2017, 13, e1007016.	1.5	21
1974	Phylogenetics and Phylogenomics of Rust Fungi. Advances in Genetics, 2017, 100, 267-307.	0.8	68
1975	Species-specific genes under selection characterize the co-evolution of slavemaker and host lifestyles. BMC Evolutionary Biology, 2017, 17, 237.	3.2	12
1976	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive Helicoverpa pest species. BMC Biology, 2017, 15, 63.	1.7	238
1977	Single-molecule sequencing and Hi-C-based proximity-guided assembly of amaranth (Amaranthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	108
1978	Reconstruction of the microalga Nannochloropsis salina genome-scale metabolic model with applications to lipid production. BMC Systems Biology, 2017, 11, 66.	3.0	41
1979	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. Genome Biology, 2017, 18, 210.	3.8	255
1980	Transcriptomic characterization of Caecomyces churrovis: a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus. Biotechnology for Biofuels, 2017, 10, 305.	6.2	70
1981	TGTT and AACA: two transcriptionally active LTR retrotransposon subfamilies with a specific LTR structure and horizontal transfer in four Rosaceae species. Mobile DNA, 2017, 8, 14.	1.3	2
1982	Comparison of the protein-coding genomes of three deep-sea, sulfur-oxidising bacteria: â€œCandidatus Ruthia magnificaâ€; â€œCandidatus Vesicomyosocius okutaniiâ€•and Thiomicrospira crunogena. BMC Research Notes, 2017, 10, 296.	0.6	5
1983	Consideration of non-canonical splice sites improves gene prediction on the Arabidopsis thaliana Niederzenz-1 genome sequence. BMC Research Notes, 2017, 10, 667.	0.6	24
1984	High-quality-draft genomic sequence of Paenibacillus ferrarius CY1T with the potential to bioremediate Cd, Cr and Se contamination. Standards in Genomic Sciences, 2017, 12, 60.	1.5	4

#	ARTICLE	IF	CITATIONS
1985	Genome overview of eight Candida boidinii strains isolated from human activities and wild environments. Standards in Genomic Sciences, 2017, 12, 70.	1.5	13
1986	Synima: a Synteny imaging tool for annotated genome assemblies. BMC Bioinformatics, 2017, 18, 507.	1.2	38
1987	A modified GC-specific MAKER gene annotation method reveals improved and novel gene predictions of high and low GC content in Oryza sativa. BMC Bioinformatics, 2017, 18, 522.	1.2	17
1988	Complexity and specificity of the maize (Zea mays L.) root hair transcriptome. Journal of Experimental Botany, 2017, 68, 2175-2185.	2.4	19
1989	Evolutionary thrift: mycobacteria repurpose plasmid diversity during adaptation of type VII secretion systems. Genome Biology and Evolution, 2017, 9, 398-413.	1.1	33
1990	Duplications and Positive Selection Drive the Evolution of Parasitism-Associated Gene Families in the Nematode Strongyloides papillosus. Genome Biology and Evolution, 2017, 9, 790-801.	1.1	24
1991	Complete Genome Sequence of Spiroplasma sp. TU-14. Genome Announcements, 2017, 5, .	0.8	1
1992	The genomic sequence of<i>Exiguobacterium chiriqhucha</i>str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. PeerJ, 2017, 5, e3162.	0.9	27
1993	ProtozoaDB 2.0: A Trypanosoma Brucei Case Study. Pathogens, 2017, 6, 32.	1.2	1
1994	An In Silico Identification of Common Putative Vaccine Candidates against Treponema pallidum: A Reverse Vaccinology and Subtractive Genomics Based Approach. International Journal of Molecular Sciences, 2017, 18, 402.	1.8	37
1995	Lifestyle, gene gain and loss, and transcriptional remodeling cause divergence in the transcriptomes of Phytophthora infestans and Pythium ultimum during potato tuber colonization. BMC Genomics, 2017, 18, 764.	1.2	60
1996	Differentiation and Structure in Sulfolobus islandicus Rod-Shaped Virus Populations. Viruses, 2017, 9, 120.	1.5	26
1997	Preliminary comparative genomics revealed pathogenic potential and international spread of Staphylococcus argenteus. BMC Genomics, 2017, 18, 808.	1.2	44
1998	Comparative genomic analysis of Brevibacterium strains: insights into key genetic determinants involved in adaptation to the cheese habitat. BMC Genomics, 2017, 18, 955.	1.2	38
1999	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite Clonorchis sinensis: Biotechnological implications. Biotechnology Advances, 2018, 36, 894-904.	6.0	20
2000	Specialized plant biochemistry drives gene clustering in fungi. ISME Journal, 2018, 12, 1694-1705.	4.4	20
2001	Cooption of heat shock regulatory system for anhydrobiosis in the sleeping chironomid <i>Polypedilum vanderplanki</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2477-E2486.	3.3	25
2002	Trehalose 6-Phosphate Regulates Photosynthesis and Assimilate Partitioning in Reproductive Tissue. Plant Physiology, 2018, 176, 2623-2638.	2.3	121

#	ARTICLE	IF	CITATIONS
2003	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
2004	Comparative transcriptome analysis provides key insights into gene expression pattern during the formation of nodule-like structures in Brachypodium. Functional and Integrative Genomics, 2018, 18, 315-326.	1.4	13
2005	Genus-Wide Assessment of Lignocellulose Utilization in the Extremely Thermophilic Genus Caldicellulosiruptor by Genomic, Pangenomic, and Metagenomic Analyses. Applied and Environmental Microbiology, 2018, 84, .	1.4	33
2006	Whole-Genome Analysis Illustrates Global Clonal Population Structure of the Ubiquitous Dermatophyte Pathogen <i>Trichophyton rubrum</i>. Genetics, 2018, 208, 1657-1669.	1.2	48
2007	Horizontal gene cluster transfer increased hallucinogenic mushroom diversity. Evolution Letters, 2018, 2, 88-101.	1.6	73
2008	Single-molecule, full-length transcript sequencing provides insight into the extreme metabolism of the ruby-throated hummingbird Archilochus colubris. GigaScience, 2018, 7, 1-12.	3.3	67
2009	Draft genome of the protandrous Chinese black porgy, Acanthopagrus schlegelii. GigaScience, 2018, 7, 1-7.	3.3	70
2010	Phylogenomic analysis demonstrates a pattern of rare and long-lasting concerted evolution in prokaryotes. Communications Biology, 2018, 1, 12.	2.0	16
2011	Genome analysis of two novel <i>Pseudomonas</i> strains exhibiting differential hypersensitivity reactions on tobacco seedlings reveals differences in nonflagellar T3<scp>SS</scp> organization and predicted effector proteins. MicrobiologyOpen, 2018, 7, e00553.	1.2	10
2012	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. Genome Research, 2018, 28, 547-560.	2.4	78
2013	Comparative analysis of core genome MLST and SNP typing within a European Salmonella serovar Enteritidis outbreak. International Journal of Food Microbiology, 2018, 274, 1-11.	2.1	150
2014	Multiple large-scale gene and genome duplications during the evolution of hexapods. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4713-4718.	3.3	151
2015	Draft genome of the milu (Elaphurus davidianus). GigaScience, 2018, 7, .	3.3	22
2016	A Whole Genome Assembly of the Horn Fly, <i>Haematobia irritans</i>, and Prediction of Genes with Roles in Metabolism and Sex Determination. G3: Genes, Genomes, Genetics, 2018, 8, 1675-1686.	0.8	12
2017	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4151-E4158.	3.3	730
2018	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (Pyrus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 519-531.	1.4	21
2019	Genomic Inference of Recombination-Mediated Evolution in Xanthomonas euvesicatoria and X. perforans. Applied and Environmental Microbiology, 2018, 84, .	1.4	35
2020	Investigating the Central Metabolism of Clostridium thermosuccinogenes. Applied and Environmental Microbiology, 2018, 84, .	1.4	18

#	Article	IF	Citations
2021	Comparative qualitative phosphoproteomics analysis identifies shared phosphorylation motifs and associated biological processes in evolutionary divergent plants. Journal of Proteomics, 2018, 181, 152-159.	1.2	20
2022	Whole-Genome Analysis of an Extensively Drug-Resistance Empedobacter falsenii Strain Reveals Distinct Features and the Presence of a Novel Metallo-ÃŸ-Lactamase (EBR-2). Current Microbiology, 2018, 75, 1084-1089.	1.0	6
2023	The Genome of Artemisia annua Provides Insight into the Evolution of Asteraceae Family and Artemisinin Biosynthesis. Molecular Plant, 2018, 11, 776-788.	3.9	205
2024	The Gastrodia elata genome provides insights into plant adaptation to heterotrophy. Nature Communications, 2018, 9, 1615.	5.8	170
2025	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. Nature, 2018, 557, 43-49.	13.7	1,091
2026	<i>Leishmania naiffi</i>and<i>Leishmania guyanensis</i>reference genomes highlight genome structure and gene evolution in the<i>Viannia</i>subgenus. Royal Society Open Science, 2018, 5, 172212.	1.1	22
2027	Comparative transcriptome analysis of genes involved in anthocyanin synthesis in blueberry. Plant Physiology and Biochemistry, 2018, 127, 561-572.	2.8	76
2028	The Genome Sequence of â€œCandidatus Fokinia solitariaâ€ Insights on Reductive Evolution in Rickettsiales. Genome Biology and Evolution, 2018, 10, 1120-1126.	1.1	40
2029	Whole-genome sequence and genome annotation of Xanthomonas citri pv. mangiferaeindicae, causal agent of bacterial black spot on Mangifera indica. Archives of Microbiology, 2018, 200, 835-840.	1.0	4
2030	Genetic Variation of â€˜<i>Candidatus</i> Liberibacter solanacearumâ€™ Haplotype C and Identification of a Novel Haplotype from <i>Trioza urticae</i> and Stinging Nettle. Phytopathology, 2018, 108, 925-934.	1.1	65
2031	Phylogenomics of palearctic Formica species suggests a single origin of temporary parasitism and gives insights to the evolutionary pathway toward slave-making behaviour. BMC Evolutionary Biology, 2018, 18, 40.	3.2	15
2032	Genome and evolution of the shadeâ€requiring medicinal herb <i>Panax ginseng</i>. Plant Biotechnology Journal, 2018, 16, 1904-1917.	4.1	136
2033	De novo draft assembly of the Botrylloides leachii genome provides further insight into tunicate evolution. Scientific Reports, 2018, 8, 5518.	1.6	36
2034	Phylogenomic and comparative analysis of the distribution and regulatory patterns of TPP riboswitches in fungi. Scientific Reports, 2018, 8, 5563.	1.6	20
2035	The origins of the Psechridae: Web-building lycosoid spiders. Molecular Phylogenetics and Evolution, 2018, 125, 213-219.	1.2	17
2036	Draft genome of the Peruvian scallop Argopecten purpuratus. GigaScience, 2018, 7, .	3.3	60
2037	Comparative analysis of probiotic bacteria based on a new definition of core genome. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840012.	0.3	8
2038	The draft genome sequence of forest musk deer (Moschus berezovskii). GigaScience, 2018, 7, .	3.3	26

#	Article	IF	Citations
2039	HiMAP: Robust phylogenomics from highly multiplexed amplicon sequencing. Molecular Ecology Resources, 2018, 18, 1000-1019.	2.2	30
2040	The reduced genome of <i>Candidatus</i> Kinetoplastibacterium sorsogonicusi, the endosymbiont of <i>Kentomonas sorsogonicus</i> (Trypanosomatidae): loss of the haem-synthesis pathway. Parasitology, 2018, 145, 1287-1293.	0.7	20
2041	Comparative analysis of low complexity regions in Plasmodia. Scientific Reports, 2018, 8, 335.	1.6	20
2042	Chloroplast genomes of Byrsonima species (Malpighiaceae): comparative analysis and screening of high divergence sequences. Scientific Reports, 2018, 8, 2210.	1.6	108
2043	Comparative analyses of co-evolving host-parasite associations reveal unique gene expression patterns underlying slavemaker raiding and host defensive phenotypes. Scientific Reports, 2018, 8, 1951.	1.6	15
2044	A survey of metastasis suppressors in Metazoa. Laboratory Investigation, 2018, 98, 554-570.	1.7	7
2045	The genomes of two Eutrema species provide insight into plant adaptation to high altitudes. DNA Research, 2018, 25, 307-315.	1.5	38
2046	Hemimetabolous genomes reveal molecular basis of termite eusociality. Nature Ecology and Evolution, 2018, 2, 557-566.	3.4	223
2047	Diverse single-amino-acid repeat profiles in the genus Cryptosporidium. Parasitology, 2018, 145, 1151-1160.	0.7	3
2048	Updating the genomic taxonomy and epidemiology of Campylobacter hyointestinalis. Scientific Reports, 2018, 8, 2393.	1.6	42
2049	The systematic analysis of ultraconserved genomic regions in the budding yeast. Bioinformatics, 2018, 34, 361-366.	1.8	1
2051	Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. DNA Research, 2018, 25, 217-227.	1.5	33
2052	Multiple Roots of Fruiting Body Formation in Amoebozoa. Genome Biology and Evolution, 2018, 10, 591-606.	1.1	39
2053	Targeted Phenotypic Screening in Plasmodium falciparum and Toxoplasma gondii Reveals Novel Modes of Action of Medicines for Malaria Venture Malaria Box Molecules. MSphere, 2018, 3, .	1.3	30
2054	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. Nature Communications, 2018, 9, 448.	5.8	146
2055	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. Mycology, 2018, 9, 59-69.	2.0	12
2056	How the evolution of multicellularity set the stage for cancer. British Journal of Cancer, 2018, 118, 145-152.	2.9	89
2057	Draft genome sequence of ramie, <i>Boehmeria nivea</i> (L.) Gaudich. Molecular Ecology Resources, 2018, 18, 639-645.	2.2	46

#	Article	IF	Citations
2058	The mycobiota of the sand fly <i>Phlebotomus perniciosus</i>: Involvement of yeast symbionts in uric acid metabolism. Environmental Microbiology, 2018, 20, 1064-1077.	1.8	14
2059	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
2060	A hybrid-hierarchical genome assembly strategy to sequence the invasive golden mussel, Limnoperna fortunei. GigaScience, 2018, 7, .	3.3	60
2061	Systematic discovery of antiphage defense systems in the microbial pangenome. Science, 2018, 359, .	6.0	776
2062	The pomegranate (<i>Punica granatum</i> L.) genome provides insights into fruit quality and ovule developmental biology. Plant Biotechnology Journal, 2018, 16, 1363-1374.	4.1	115
2063	Slow evolution of sexâ€biased genes in the reproductive tissue of the dioecious plant <i>Salix viminalis</i>. Molecular Ecology, 2018, 27, 694-708.	2.0	37
2064	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. Genome, 2018, 61, 103-109.	0.9	7
2065	Gene Phylogenies and Orthologous Groups. Methods in Molecular Biology, 2018, 1704, 1-28.	0.4	11
2066	Comparative Genomics of Gene Loss and Gain in Caenorhabditis and Other Nematodes. Methods in Molecular Biology, 2018, 1704, 419-432.	0.4	22
2067	Comparative Genomics in Drosophila. Methods in Molecular Biology, 2018, 1704, 433-450.	0.4	1
2068	Pan-Genome Storage and Analysis Techniques. Methods in Molecular Biology, 2018, 1704, 29-53.	0.4	24
2069	Comparative Genomics for Prokaryotes. Methods in Molecular Biology, 2018, 1704, 55-78.	0.4	15
2070	Phylogenomics. Methods in Molecular Biology, 2018, 1704, 103-187.	0.4	15
2071	Characterization of the Theileria parva sporozoite proteome. International Journal for Parasitology, 2018, 48, 265-273.	1.3	24
2072	Widespread Whole Genome Duplications Contribute to Genome Complexity and Species Diversity in Angiosperms. Molecular Plant, 2018, 11, 414-428.	3.9	251
2073	Evolution within the fungal genus <i>Verticillium</i> is characterized by chromosomal rearrangement and gene loss. Environmental Microbiology, 2018, 20, 1362-1373.	1.8	70
2074	Preclinical efficacy and immunogenicity assessment to show that a chimeric <i>Plasmodium falciparum </i><scp>UB</scp>05â€09 antigen could be a malaria vaccine candidate. Parasite Immunology, 2018, 40, e12514.	0.7	3
2075	<scp>ARA</scp>1 regulates not only <scp>l</scp>â€arabinose but also <scp>d</scp>â€galactose catabolism in <i>Trichoderma reesei</i>. FEBS Letters, 2018, 592, 60-70.	1.3	37

#	Article	IF	Citations
2076	PLAZA 4.0: an integrative resource for functional, evolutionary and comparative plant genomics. Nucleic Acids Research, 2018, 46, D1190-D1196.	6.5	460
2077	MAGNAMWAR: an R package for genome-wide association studies of bacterial orthologs. Bioinformatics, 2018, 34, 1951-1952.	1.8	13
2078	Comparative genomic analyses reveal the features for adaptation to nematodes in fungi. DNA Research, 2018, 25, 245-256.	1.5	28
2079	The genome and microbiome of a dikaryotic fungus (<i>Inocybe terrigena</i>, Inocybaceae) revealed by metagenomics. Environmental Microbiology Reports, 2018, 10, 155-166.	1.0	17
2080	Genome sequence of the Japanese oak silk moth, Antheraea yamamai: the first draft genome in the family Saturniidae. GigaScience, 2018, 7, 1-11.	3.3	20
2081	Noncontiguous finished genome sequence of Megasphaera sp. ASD88, isolated from faeces of a child with autism spectrum disorder. New Microbes and New Infections, 2018, 22, 13-16.	0.8	5
2082	The fungus that came in from the cold: dry rotâ€™s pre-adapted ability to invade buildings. ISME Journal, 2018, 12, 791-801.	4.4	23
2083	The 4-Celled Tetrabaena socialis Nuclear Genome Reveals the Essential Components for Genetic Control of Cell Number at the Origin of Multicellularity in the Volvocine Lineage. Molecular Biology and Evolution, 2018, 35, 855-870.	3.5	43
2084	Recombinational DSBs-intersected genes converge on specific disease- and adaptability-related pathways. Bioinformatics, 2018, 34, 3421-3426.	1.8	1
2085	Convergent Acquisition of Nonembryonic Development in Styelid Ascidians. Molecular Biology and Evolution, 2018, 35, 1728-1743.	3.5	35
2086	Clustering of Pan- and Core-genome of Lactobacillus provides Novel Evolutionary Insights for Differentiation. BMC Genomics, 2018, 19, 284.	1.2	65
2087	Inter-genome comparison of the Quorn fungus Fusarium venenatum and the closely related plant infecting pathogen Fusarium graminearum. BMC Genomics, 2018, 19, 269.	1.2	28
2088	New insights into the phylogenetics and population structure of the prairie falcon (Falco mexicanus). BMC Genomics, 2018, 19, 233.	1.2	25
2089	SSR marker development and intraspecific genetic divergence exploration of Chrysanthemum indicum based on transcriptome analysis. BMC Genomics, 2018, 19, 291.	1.2	40
2090	Comparative transcriptome reveal the potential adaptive evolutionary genes in Andrias davidianus. Hereditas, 2018, 155, 18.	0.5	4
2091	The Phytophthora cactorum genome provides insights into the adaptation to host defense compounds and fungicides. Scientific Reports, 2018, 8, 6534.	1.6	52
2092	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	6.5	90
2093	Complete Genome Sequence of Agrobacterium tumefaciens 1D1609. Genome Announcements, 2018, 6, .	0.8	12

#	Article	IF	Citations
2094	Reconstruction of the ancestral metazoan genome reveals an increase in genomic novelty. Nature Communications, 2018, 9, 1730.	5.8	101
2095	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. Scientific Data, 2018, 5, 180079.	2.4	14
2096	Identification of General Patterns of Sex-Biased Expression in <i>Daphnia</i>, a Genus with Environmental Sex Determination. G3: Genes, Genomes, Genetics, 2018, 8, 1523-1533.	0.8	11
2097	Comparative genomics of 151 plant-associated bacteria reveal putative mechanisms underlying specific interactions between bacteria and plant hosts. Genes and Genomics, 2018, 40, 857-864.	0.5	10
2098	Identification of novel therapeutic candidates inCryptosporidium parvum: anin silicoapproach. Parasitology, 2018, 145, 1907-1916.	0.7	4
2099	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. Journal of Experimental Botany, 2018, 69, 3689-3702.	2.4	27
2100	Comparative Genomics Reveals Thousands of Novel Chemosensory Genes and Massive Changes in Chemoreceptor Repertories across Chelicerates. Genome Biology and Evolution, 2018, 10, 1221-1236.	1.1	35
2101	A New Database for Drug Discovery Through Application of Data-Integration and Semantics. , 2018, , .		1
2102	Practical considerations for plant phylogenomics. Applications in Plant Sciences, 2018, 6, e1038.	0.8	165
2103	Dispersal and speciation: The cross Atlantic relationship of two parasitic cnidarians. Molecular Phylogenetics and Evolution, 2018, 126, 346-355.	1.2	6
2104	Comparative genomic analysis of the â€˜pseudofungusâ€™<i>Hyphochytrium catenoides</i>. Open Biology, 2018, 8, 170184.	1.5	31
2105	Adhesive gland transcriptomics uncovers a diversity of genes involved in glue formation in marine tube-building polychaetes. Acta Biomaterialia, 2018, 72, 316-328.	4.1	21
2106	Virulence factors of Moraxella catarrhalis outer membrane vesicles are major targets for cross-reactive antibodies and have adapted during evolution. Scientific Reports, 2018, 8, 4955.	1.6	26
2107	Genome analysis reveals evolutionary mechanisms of adaptation in systemic dimorphic fungi. Scientific Reports, 2018, 8, 4473.	1.6	28
2108	Genomic Understanding of an Infectious Brain Disease from the Desert. G3: Genes, Genomes, Genetics, 2018, 8, 909-922.	0.8	39
2109	Molecular Footprints of Aquatic Adaptation Including Bone Mass Changes in Cetaceans. Genome Biology and Evolution, 2018, 10, 967-975.	1.1	23
2110	Gene Co-occurrence Networks Reflect Bacteriophage Ecology and Evolution. MBio, 2018, 9, .	1.8	41
2111	Genome-Wide Identification, Classification, and Expression Analysis of SNARE Genes in Chinese Cabbage (Brassica rapa ssp. pekinensis) Infected by Turnip mosaic virus. Plant Molecular Biology Reporter, 2018, 36, 210-224.	1.0	5

#	Article	IF	Citations
2112	Complete genome sequence of Erythrobacter seohaensis SW-135T sheds light on the ecological role of the genus Erythrobacter for phosphorus cycle in the marine environment. Marine Genomics, 2018, 40, 21-24.	0.4	8
2113	Advances in kinome research of parasitic worms - implications for fundamental research and applied biotechnological outcomes. Biotechnology Advances, 2018, 36, 915-934.	6.0	8
2114	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. Heliyon, 2018, 4, e00583.	1.4	12
2115	The genomic and functional landscapes of developmental plasticity in the American cockroach. Nature Communications, 2018, 9, 1008.	5.8	113
2116	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. Molecular Biology and Evolution, 2018, 35, 1160-1175.	3.5	54
2117	Step-wise evolution of complex chemical defenses in millipedes: a phylogenomic approach. Scientific Reports, 2018, 8, 3209.	1.6	31
2118	Draft genome analysis provides insights into the fiber yield, crude protein biosynthesis, and vegetative growth of domesticated ramie (Boehmeria nivea L. Gaud). DNA Research, 2018, 25, 173-181.	1.5	32
2119	Identifying selectively important amino acid positions associated with alternative habitat environments in fish mitochondrial genomes. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 511-524.	0.7	4
2120	Resolving Relationships among the Megadiverse Butterflies and Moths with a Novel Pipeline for Anchored Phylogenomics. Systematic Biology, 2018, 67, 78-93.	2.7	161
2121	Gene Tree Construction and Correction using SuperTree and Reconciliation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1-1.	1.9	6
2122	Early transcriptional response pathways in <i>Daphnia magna</i> are coordinated in networks of crustaceanâ€specific genes. Molecular Ecology, 2018, 27, 886-897.	2.0	38
2123	High throughput <i>in silico</i> identification and characterization of <i>Plasmodium falciparum</i> PRL phosphatase inhibitors. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3531-3540.	2.0	9
2124	Genomic Analysis of Bacillus sp. Strain B25, a Biocontrol Agent of Maize Pathogen Fusarium verticillioides. Current Microbiology, 2018, 75, 247-255.	1.0	40
2125	Genome structure of Rosa multiflora, a wild ancestor of cultivated roses. DNA Research, 2018, 25, 113-121.	1.5	70
2126	Know your farmer: Ancient origins and multiple independent domestications of ambrosia beetle fungal cultivars. Molecular Ecology, 2018, 27, 2077-2094.	2.0	67
2127	Aspartateâ€Î²â€semialdeyhyde dehydrogenase as a potential therapeutic target of <i>Mycobacterium tuberculosis</i> H37Rv: Evidence from in silico elementary mode analysis of biological network model. Journal of Cellular Biochemistry, 2018, 119, 2832-2842.	1.2	15
2128	Planctomycetes attached to algal surfaces: Insight into their genomes. Genomics, 2018, 110, 231-238.	1.3	39
2129	panX: pan-genome analysis and exploration. Nucleic Acids Research, 2018, 46, e5-e5.	6.5	241

#	ARTICLE	IF	CITATIONS
2130	Focusing the diversity of <i>Gardnerella vaginalis</i> through the lens of ecotypes. Evolutionary Applications, 2018, 11, 312-324.	1.5	34
2131	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. Molecular Plant, 2018, 11, 505-507.	3.9	33
2132	Assessing the utility of transcriptome data for inferring phylogenetic relationships among coleoid cephalopods. Molecular Phylogenetics and Evolution, 2018, 118, 330-342.	1.2	29
2133	Improved transcriptome sampling pinpoints 26 ancient and more recent polyploidy events in Caryophyllales, including two allopolyploidy events. New Phytologist, 2018, 217, 855-870.	3.5	85
2134	Oxygen-responsive transcriptional regulation of lipid homeostasis in fungi: Implications for anti-fungal drug development. Seminars in Cell and Developmental Biology, 2018, 81, 110-120.	2.3	12
2135	<i>Tremblaya phenacola</i> PPER: an evolutionary beta-gammaproteobacterium collage. ISME Journal, 2018, 12, 124-135.	4.4	14
2136	A genetic screen in rodent malaria parasites identifies five new apicoplast putative membrane transporters, one of which is essential in human malaria parasites. Cellular Microbiology, 2018, 20, e12789.	1.1	22
2137	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
2138	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. Plant Journal, 2018, 93, 460-471.	2.8	33
2139	Population transcriptomics in <i>Daphnia</i>: The role of thermal selection. Molecular Ecology, 2018, 27, 387-402.	2.0	22
2140	Genome-wide mining of perfect microsatellites and tetranucleotide orthologous microsatellites estimates in six primate species. Gene, 2018, 643, 124-132.	1.0	12
2141	The Hardy Rubber Tree Genome Provides Insights into the Evolution of Polyisoprene Biosynthesis. Molecular Plant, 2018, 11, 429-442.	3.9	62
2142	daTALbase: A Database for Genomic and Transcriptomic Data Related to TAL Effectors. Molecular Plant-Microbe Interactions, 2018, 31, 471-480.	1.4	22
2143	<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
2144	The complex pattern of codon usage evolution in the family Comamonadaceae. Ecological Genetics and Genomics, 2018, 6, 1-8.	0.3	5
2145	<i>De novo</i> assembly of the zucchini genome reveals a wholeâ€genome duplication associated with the origin of the <i>Cucurbita</i> genus. Plant Biotechnology Journal, 2018, 16, 1161-1171.	4.1	160
2146	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
2147	Phylogenomics of Bartheletia paradoxa reveals its basal position in Agaricomycotina and that the early evolutionary history of basidiomycetes was rapid and probably not strictly bifurcating. Mycological Progress, 2018, 17, 333-341.	0.5	11

#	Article	IF	Citations
2148	Whole-Genome Characterization of Bacillus cereus Associated with Specific Disease Manifestations. Infection and Immunity, 2018, 86, .	1.0	11
2149	Thermoacclimation and genome adaptation of the membrane lipidome in marine <i>Synechococcus</i>. Environmental Microbiology, 2018, 20, 612-631.	1.8	39
2150	Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes. Fungal Genetics and Biology, 2018, 112, 40-46.	0.9	42
2151	Transcriptional Profiles of Secondary Metabolite Biosynthesis Genes and Cytochromes in the Leaves of Four Papaver Species. Data, 2018, 3, 55.	1.2	7
2152	ViannaTopes: a database of predicted immunogenic peptides forLeishmania(Viannia) species. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1
2153	First complete genome sequence in Arborophila and comparative genomics reveals the evolutionary adaptation of Hainan Partridge (Arborophila ardens). Avian Research, 2018, 9, .	0.5	2
2154	Using Core Genome Alignments To Assign Bacterial Species. MSystems, 2018, 3, .	1.7	54
2155	High-quality-draft genome sequence of the heavy metal resistant and exopolysaccharides producing bacterium Mucilaginibacter pedocola TBZ30T. Standards in Genomic Sciences, 2018, 13, 34.	1.5	11
2156	Tracking a serial killer: Integrating phylogenetic relationships, epidemiology, and geography for two invasive meningococcal disease outbreaks. PLoS ONE, 2018, 13, e0202615.	1.1	8
2157	Transcriptome Analysis and Functional Identification of Xa13 and Piâ€ta Orthologs in Oryza granulata. Plant Genome, 2018, 11, 170097.	1.6	2
2158	Transcriptional Heterogeneity of <i>Cryptococcus gattii</i> VGII Compared with Non-VGII Lineages Underpins Key Pathogenicity Pathways. MSphere, 2018, 3, .	1.3	12
2159	Comprehensive transcriptome analysis of Sarcophaga peregrina, a forensically important fly species. Scientific Data, 2018, 5, 180220.	2.4	15
2160	Comparative genomics of Botryosphaeria dothidea and B. kuwatsukai, causal agents of apple ring rot, reveals both species expansion of pathogenicity-related genes and variations in virulence gene content during speciation. IMA Fungus, 2018, 9, 243-257.	1.7	37
2161	Rediscovery and analysis of Phytophthora carbohydrate esterase (CE) genes revealing their evolutionary diversity. Journal of Integrative Agriculture, 2018, 17, 878-891.	1.7	0
2162	Complete Genome Sequence of Spiroplasma monobiae MQ-1 T (ATCC 33825), a Bacterium Isolated from the Vespid Wasp (Monobia quadridens). Genome Announcements, 2018, 6, .	0.8	0
2163	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelersâ€™ diarrhea. Microbiome, 2018, 6, 201.	4.9	20
2164	Gene Co-expression Network Reveals Potential New Genes Related to Sugarcane Bagasse Degradation in Trichoderma reesei RUT-30. Frontiers in Bioengineering and Biotechnology, 2018, 6, 151.	2.0	36
2165	Genome sequence analysis of an extensively drug-resistant Acinetobacter baumannii indigo-pigmented strain depicts evidence of increase genome plasticity. Scientific Reports, 2018, 8, 16961.	1.6	28

#	Article	IF	Citations
2166	The genome of an underwater architect, the caddisfly<i>Stenopsyche tienmushanensis</i>Hwang (Insecta: Trichoptera). GigaScience, 2018, 7, .	3.3	41
2167	The Chrysanthemum nankingense Genome Provides Insights into the Evolution and Diversification of Chrysanthemum Flowers and Medicinal Traits. Molecular Plant, 2018, 11, 1482-1491.	3.9	148
2168	Patterns of Nucleotide Deletion and Insertion Inferred from Bacterial Pseudogenes. Genome Biology and Evolution, 2018, 10, 1792-1802.	1.1	12
2169	Comparative analysis of nucleus-encoded plastid-targeting proteins in Rafflesia cantleyi against photosynthetic and non-photosynthetic representatives reveals orthologous systems with potentially divergent functions. Scientific Reports, 2018, 8, 17258.	1.6	20
2170	Genomes of trombidid mites reveal novel predicted allergens and laterally transferred genes associated with secondary metabolism. GigaScience, 2018, 7, .	3.3	32
2171	The chromosome-level quality genome provides insights into the evolution of the biosynthesis genes for aroma compounds of Osmanthus fragrans. Horticulture Research, 2018, 5, 72.	2.9	77
2172	Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay. PLoS Genetics, 2018, 14, e1007807.	1.5	116
2173	Characterization of mitochondrial proteomes of nonbilaterian animals. IUBMB Life, 2018, 70, 1289-1301.	1.5	9
2174	High-quality-draft genome sequence of the multiple heavy metal resistant bacterium Pseudaminobacter manganicus JH-7T. Standards in Genomic Sciences, 2018, 13, 29.	1.5	8
2175	Aequatus: an open-source homology browser. GigaScience, 2018, 7, .	3.3	1
2176	Computational Tools for Population Genomics. Population Genomics, 2018, , 127-160.	0.2	2
2177	The genome of the oyster <i>Saccostrea</i> offers insight into the environmental resilience of bivalves. DNA Research, 2018, 25, 655-665.	1.5	92
2178	Conjugative Transposons and Their Cargo Genes Vary across Natural Populations of<i>Rickettsia buchneri</i>Infecting the Tick<i>Ixodes scapularis</i>. Genome Biology and Evolution, 2018, 10, 3218-3229.	1.1	36
2179	Presence of anAgrobacterium-Type Tumor-Inducing Plasmid inNeorhizobiumsp. NCHU2750 and the Link to Phytopathogenicity. Genome Biology and Evolution, 2018, 10, 3188-3195.	1.1	13
2180	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell, 2018, 175, 1533-1545.e20.	13.5	445
2181	<i>De novo</i> Short Read Assembly and Functional Annotation of <i>Eleocharis vivipara</i>, a C₃/C₄ Interconvertible Sedge Plant. Environmental Control in Biology, 2018, 56, 81-87.	0.3	2
2182	Genetic diversity of Escherichia coli in gut microbiota of patients with Crohnâ€™s disease discovered using metagenomic and genomic analyses. BMC Genomics, 2018, 19, 968.	1.2	26
2183	A comparative synteny analysis tool for target-gene SNP marker discovery: connecting genomics data to breeding in Solanaceae. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1

#	Article	IF	Citations
2184	Comparative analysis of Faecalibacterium prausnitzii genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. BMC Genomics, 2018, 19, 931.	1.2	78
2185	Ancestrality and Mosaicism of Giant Viruses Supporting the Definition of the Fourth TRUC of Microbes. Frontiers in Microbiology, 2018, 9, 2668.	1.5	44
2186	Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. Frontiers in Microbiology, 2018, 9, 3160.	1.5	45
2187	Genomic insights into multidrug-resistance, mating and virulence in Candida auris and related emerging species. Nature Communications, 2018, 9, 5346.	5.8	298
2188	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of Phoca largha, Callorhinus ursinus, and Eumetopias jubatus. Scientific Reports, 2018, 8, 16877.	1.6	7
2189	<i>In silico</i>prediction of proteinâ€"protein interaction between<i>Glossina m. morsitans</i>(Westwood, 1851) and<i>Trypanosoma brucei</i>(Kinetoplastida: Trypanosomatidae). Bioscience Horizons, 2018, 11, .	0.6	0
2190	Primula vulgaris (primrose) genome assembly, annotation and gene expression, with comparative genomics on the heterostyly supergene. Scientific Reports, 2018, 8, 17942.	1.6	40
2191	Complete Genome Sequencing of Lactobacillus plantarum ZLP001, a Potential Probiotic That Enhances Intestinal Epithelial Barrier Function and Defense Against Pathogens in Pigs. Frontiers in Physiology, 2018, 9, 1689.	1.3	46
2192	Genomic effects of population collapse in a critically endangered ironwood tree Ostrya rehderiana. Nature Communications, 2018, 9, 5449.	5.8	79
2193	Impact of Rearing Conditions on the Ambrosia Beetleâ€™s Microbiome. Life, 2018, 8, 63.	1.1	18
2194	Comparative transcriptomics identifies patterns of selection in roses. BMC Plant Biology, 2018, 18, 371.	1.6	13
2195	De novo transcriptome assembly of the Chinese pearl barley, adlay, by full-length isoform and short-read RNA sequencing. PLoS ONE, 2018, 13, e0208344.	1.1	12
2196	An integrated omics analysis reveals molecular mechanisms that are associated with differences in seed oil content between Glycine max and Brassica napus. BMC Plant Biology, 2018, 18, 328.	1.6	23
2197	Multilevel comparative bioinformatics to investigate evolutionary relationships and specificities in gene annotations: an example for tomato and grapevine. BMC Bioinformatics, 2018, 19, 435.	1.2	9
2198	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
2199	Comparative Genomics of Staphylococcus Reveals Determinants of Speciation and Diversification of Antimicrobial Defense. Frontiers in Microbiology, 2018, 9, 2753.	1.5	22
2200	Genome-wide analysis of horizontally acquired genes in the genus Mycobacterium. Scientific Reports, 2018, 8, 14817.	1.6	21
2201	Chromosomal-level assembly of yellow catfish genome using third-generation DNA sequencing and Hi-C analysis. GigaScience, 2018, 7, .	3.3	75

#	Article	IF	Citations
2202	Comparative Study on Alternative Splicing in Human Fungal Pathogens Suggests Its Involvement During Host Invasion. Frontiers in Microbiology, 2018, 9, 2313.	1.5	36
2203	Comparative genome analysis of jujube witchesâ€™-broom Phytoplasma, an obligate pathogen that causes jujube witchesâ€™-broom disease. BMC Genomics, 2018, 19, 689.	1.2	64
2204	Complete genome sequence of soil actinobacteria <i>Streptomyces cavourensis</i> TJ430. Journal of Basic Microbiology, 2018, 58, 1083-1090.	1.8	3
2205	Conserved Genes Underlie Phenotypic Plasticity in an Incipiently Social Bee. Genome Biology and Evolution, 2018, 10, 2749-2758.	1.1	24
2206	The genome of common long-arm octopus Octopus minor. GigaScience, 2018, 7, .	3.3	43
2207	Fast construction of a reference genome: challenges and opportunities using â€˜Royal Galaâ€™ apple as a case study. Acta Horticulturae, 2018, , 35-40.	0.1	0
2208	Phylogenetic, comparative genomic and structural analyses of human Streptococcus agalactiae ST485 in China. BMC Genomics, 2018, 19, 716.	1.2	7
2209	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. Genetics, 2018, 210, 883-894.	1.2	21
2210	Transcriptomic view of survival during early seedling growth of the extremophyte Haloxylon ammodendron. Plant Physiology and Biochemistry, 2018, 132, 475-489.	2.8	21
2211	Enhanced antibacterial effect of the novel T4-like bacteriophage KARL-1 in combination with antibiotics against multi-drug resistant Acinetobacter baumannii. Scientific Reports, 2018, 8, 14140.	1.6	79
2212	Deep taxon sampling reveals the evolutionary dynamics of novel gene families in <i>Pristionchus</i> nematodes. Genome Research, 2018, 28, 1664-1674.	2.4	53
2213	The genomic architecture and molecular evolution of ant odorant receptors. Genome Research, 2018, 28, 1757-1765.	2.4	59
2214	Genomic, expressional, protein-protein interactional analysis of Trihelix transcription factor genes in Setaria italia and inference of their evolutionary trajectory. BMC Genomics, 2018, 19, 665.	1.2	14
2215	Phylotranscriptomics of Pristionchus Nematodes Reveals Parallel Gene Loss in Six Hermaphroditic Lineages. Current Biology, 2018, 28, 3123-3127.e5.	1.8	33
2216	Codon usage bias reveals genomic adaptations to environmental conditions in an acidophilic consortium. PLoS ONE, 2018, 13, e0195869.	1.1	13
2217	Genome-wide identification and characterization of CONSTANS-like gene family in radish (Raphanus) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	23
2218	Characterisation of pathogen-specific regions and novel effector candidates in Fusarium oxysporum f. sp. cepae. Scientific Reports, 2018, 8, 13530.	1.6	77
2219	An Introduced Crop Plant Is Driving Diversification of the Virulent Bacterial Pathogen Erwinia tracheiphila. MBio, 2018, 9, .	1.8	28

#	ARTICLE	IF	CITATIONS
2220	Genes significantly associated with lineage II food isolates of Listeria monocytogenes. BMC Genomics, 2018, 19, 708.	1.2	43
2221	Environmental pH modulates transcriptomic responses in the fungus Fusarium sp. associated with KSHB Euwallacea sp. near fornicatus. BMC Genomics, 2018, 19, 721.	1.2	15
2222	Genome hypermobility by lateral transduction. Science, 2018, 362, 207-212.	6.0	187
2223	Whole-genome analysis and description of an outbreak due to carbapenem-resistant Ochrobactrum anthropi causing pseudo-bacteraemias. New Microbes and New Infections, 2018, 26, 100-106.	0.8	3
2224	Deciphering Genome Organization of the Polyploid Brassica napus. Compendium of Plant Genomes, 2018, , 87-97.	0.3	0
2225	Genome-wide identification of AP2/ERF superfamily genes and their expression during fruit ripening of Chinese jujube. Scientific Reports, 2018, 8, 15612.	1.6	67
2226	Bioinformatic characterisation of the effector repertoire of the strawberry pathogen Phytophthora cactorum. PLoS ONE, 2018, 13, e0202305.	1.1	40
2227	Conversion of Methionine to Cysteine in Lactobacillus paracasei Depends on the Highly Mobile cysK-ctl-cysE Gene Cluster. Frontiers in Microbiology, 2018, 9, 2415.	1.5	10
2228	Capsular Switching and ICE Transformation Occurred in Human Streptococcus agalactiae ST19 With High Pathogenicity to Fish. Frontiers in Veterinary Science, 2018, 5, 281.	0.9	3
2229	Genome-Wide Transcriptomic Analysis Reveals Insights into the Response to Citrus bark cracking viroid (CBCVd) in Hop (Humulus lupulus L.). Viruses, 2018, 10, 570.	1.5	23
2230	Genomic overview of closely related fungi with different Protea host ranges. Fungal Biology, 2018, 122, 1201-1214.	1.1	1
2231	Whole genome sequencing and microsatellite analysis of the Plasmodium falciparum E5 NF54 strain show that the var, rifin and stevor gene families follow Mendelian inheritance. Malaria Journal, 2018, 17, 376.	0.8	6
2232	Comparative Genomics of Wolbachiaâ€"Cardinium Dual Endosymbiosis in a Plant-Parasitic Nematode. Frontiers in Microbiology, 2018, 9, 2482.	1.5	36
2233	Biology and Taxonomy of crAss-like Bacteriophages, the Most Abundant Virus in the Human Gut. Cell Host and Microbe, 2018, 24, 653-664.e6.	5.1	233
2234	Overlapping Patterns of Gene Expression Between Gametophyte and Sporophyte Phases in the Fern Polypodium amorphum (Polypodiales). Frontiers in Plant Science, 2018, 9, 1450.	1.7	19
2235	Convergent evolution of complex genomic rearrangements in two fungal meiotic drive elements. Nature Communications, 2018, 9, 4242.	5.8	40
2236	Pseudocohnilembus persalinus genome database - the first genome database of facultative scuticociliatosis pathogens. BMC Genomics, 2018, 19, 676.	1.2	3
2237	Comparative Genomics of Degradative Novosphingobium Strains With Special Reference to Microcystin-Degrading Novosphingobium sp. THN1. Frontiers in Microbiology, 2018, 9, 2238.	1.5	43

#	ARTICLE	IF	CITATIONS
2238	To B or Not to B: Comparative Genomics Suggests Arsenophonus as a Source of B Vitamins in Whiteflies. Frontiers in Microbiology, 2018, 9, 2254.	1.5	49
2239	Comparative Genome-Wide Survey of Single Nucleotide Variation Uncovers the Genetic Diversity and Potential Biomedical Applications among Six Macaca Species. International Journal of Molecular Sciences, 2018, 19, 3123.	1.8	3
2240	The Roles of Introgression and Climate Change in the Rise to Dominance of Acropora Corals. Current Biology, 2018, 28, 3373-3382.e5.	1.8	65
2241	Growing and cultivating the forest genomics database, TreeGenes. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-11.	1.4	40
2242	Evidence of the Red-Queen Hypothesis from Accelerated Rates of Evolution of Genes Involved in Biotic Interactions in Pneumocystis. Genome Biology and Evolution, 2018, 10, 1596-1606.	1.1	9
2243	Genome sequence of the cauliflower mushroom Sparassis crispa (Hanabiratake) and its association with beneficial usage. Scientific Reports, 2018, 8, 16053.	1.6	32
2244	Genomic analysis of the Phalaenopsis pathogen Dickeya sp. PA1, representing the emerging species Dickeya fangzhongdai. BMC Genomics, 2018, 19, 782.	1.2	15
2245	Efficient inference of homologs in large eukaryotic pan-proteomes. BMC Bioinformatics, 2018, 19, 340.	1.2	10
2246	Regulation of Root Angle and Gravitropism. G3: Genes, Genomes, Genetics, 2018, 8, 3841-3855.	0.8	24
2247	Transcriptome Profiling of Two Ornamental and Medicinal Papaver Herbs. International Journal of Molecular Sciences, 2018, 19, 3192.	1.8	9
2248	GFDP: the gene family database in poplar. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	10
2249	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
2250	The Genome Sequence of the Wild Tomato Solanum pimpinellifolium Provides Insights Into Salinity Tolerance. Frontiers in Plant Science, 2018, 9, 1402.	1.7	69
2251	Comparison of diploid and triploid Carassius auratus provides insights into adaptation to environmental change. Science China Life Sciences, 2018, 61, 1407-1419.	2.3	9
2252	Comparative genome analysis reveals key genetic factors associated with probiotic property in Enterococcus faecium strains. BMC Genomics, 2018, 19, 652.	1.2	45
2253	A Gene-Based Positive Selection Detection Approach to Identify Vaccine Candidates Using Toxoplasma gondii as a Test Case Protozoan Pathogen. Frontiers in Genetics, 2018, 9, 332.	1.1	17
2254	Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Frontiers in Microbiology, 2018, 9, 2007.	1.5	2,599
2255	Transcriptome assembly of Modiolus modiolus and comparative analysis with Bathymodiolus platifrons. Acta Oceanologica Sinica, 2018, 37, 38-45.	0.4	1

#	Article	IF	Citations
2256	Genome Evolution of Bartonellaceae Symbionts of Ants at the Opposite Ends of the Trophic Scale. Genome Biology and Evolution, 2018, 10, 1687-1704.	1.1	26
2257	Insights into the Evolution of Multicellularity from the Sea Lettuce Genome. Current Biology, 2018, 28, 2921-2933.e5.	1.8	134
2258	Accurate prediction of orthologs in the presence of divergence after duplication. Bioinformatics, 2018, 34, i366-i375.	1.8	20
2259	Pleistocene diversification in an ancient lineage: a role for glacial cycles in the evolutionary history of <i>Dioon</i> Lindl. (Zamiaceae). American Journal of Botany, 2018, 105, 1512-1530.	0.8	18
2260	New insights into Phakopsora pachyrhizi infection based on transcriptome analysis in planta. Genetics and Molecular Biology, 2018, 41, 671-691.	0.6	4
2261	Complete genome of Gongronella sp. w5 provides insight into its relationship with plant. Journal of Biotechnology, 2018, 286, 1-4.	1.9	19
2262	Comparative Genomic Analysis of Vibrio diabolicus and Six Taxonomic Synonyms: A First Look at the Distribution and Diversity of the Expanded Species. Frontiers in Microbiology, 2018, 9, 1893.	1.5	24
2263	Genomic Analysis of Picochlorum Species Reveals How Microalgae May Adapt to Variable Environments. Molecular Biology and Evolution, 2018, 35, 2702-2711.	3.5	30
2264	Genome-wide analysis of purple acid phosphatase structure and expression in ten vegetable species. BMC Genomics, 2018, 19, 646.	1.2	16
2265	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
2266	The opium poppy genome and morphinan production. Science, 2018, 362, 343-347.	6.0	225
2267	Clues to an Evolutionary Mystery: The Genes for T-Toxin, Enabler of the Devastating 1970 Southern Corn Leaf Blight Epidemic, Are Present in Ancestral Species, Suggesting an Ancient Origin. Molecular Plant-Microbe Interactions, 2018, 31, 1154-1165.	1.4	12
2268	A comprehensive annotation for the root-knot nematode Meloidogyne incognita proteome data. Data in Brief, 2018, 19, 1073-1079.	0.5	6
2269	Global assessment of its network dynamics reveals that the kinase Plk1 inhibits the phosphatase PP6 to promote Aurora A activity. Science Signaling, 2018, 11, .	1.6	25
2270	Complete Genome Sequence of Spiroplasma floricola 23-6 ^T (ATCC 29989), a Bacterium Isolated from a Tulip Tree (Liriodendron tulipifera L.). Genome Announcements, 2018, 6, .	0.8	1
2271	Genome Analysis of the Ancient Tracheophyte Selaginella tamariscina Reveals Evolutionary Features Relevant to the Acquisition of Desiccation Tolerance. Molecular Plant, 2018, 11, 983-994.	3.9	122
2272	Genomic basis of recombination suppression in the hybrid between Caenorhabditis briggsae and C. nigoni. Nucleic Acids Research, 2018, 46, 1295-1307.	6.5	31
2273	Identification of Plant Virus Receptor Candidates in the Stylets of Their Aphid Vectors. Journal of Virology, 2018, 92, .	1.5	53

#	Article	IF	Citations
2274	Multiple convergent supergene evolution events in mating-type chromosomes. Nature Communications, 2018, 9, 2000.	5.8	81
2275	Genomes of all known members of a Plasmodium subgenus reveal paths to virulent human malaria. Nature Microbiology, 2018, 3, 687-697.	5.9	129
2276	Putative vaccine candidates and drug targets identified by reverse vaccinology and subtractive genomics approaches to control <i>Haemophilus ducreyi</i> , the causative agent of chancroid. Journal of the Royal Society Interface, 2018, 15, 20180032.	1.5	11
2278	Phylogeny and putative virulence gene analysis of <i>Bartonella bovis</i>. Journal of Veterinary Medical Science, 2018, 80, 653-661.	0.3	4
2279	The evolution of genomic and epigenomic features in two Pleurotus fungi. Scientific Reports, 2018, 8, 8313.	1.6	30
2280	Remodeling of the juvenile hormone pathway through casteâ€biased gene expression and positive selection along a gradient of termite eusociality. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 296-304.	0.6	17
2281	Cnidarian Cell Type Diversity and Regulation Revealed by Whole-Organism Single-Cell RNA-Seq. Cell, 2018, 173, 1520-1534.e20.	13.5	284
2282	De novo genome assembly of the red silk cotton tree (Bombax ceiba). GigaScience, 2018, 7, .	3.3	27
2283	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. Molecular Biology and Evolution, 2018, 35, 1840-1854.	3.5	43
2284	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
2285	A well-resolved fern nuclear phylogeny reveals the evolution history of numerous transcription factor families. Molecular Phylogenetics and Evolution, 2018, 127, 961-977.	1.2	80
2286	The Genome Sequences of 90 Mushrooms. Scientific Reports, 2018, 8, 9982.	1.6	73
2287	The kinetoplastid-infecting Bodo saltans virus (BsV), a window into the most abundant giant viruses in the sea. ELife, 2018, 7, .	2.8	71
2288	In Silico Characterization and Structural Modeling of<i> Dermacentor andersoni</i> p36 Immunosuppressive Protein. Advances in Bioinformatics, 2018, 2018, 1-12.	5.7	6
2289	Functional genomics of lipid metabolism in the oleaginous yeast Rhodosporidium toruloides. ELife, 2018, 7, .	2.8	98
2290	Adaptation and conservation insights from the koala genome. Nature Genetics, 2018, 50, 1102-1111.	9.4	163
2291	Genomic Variability among Field Isolates and Laboratory-Adapted Strains ofLeptospira borgpeterseniiSerovar Hardjo. International Journal of Microbiology, 2018, 2018, 1-12.	0.9	2
2292	Genome-wide identification and classification of MYB superfamily genes in peach. PLoS ONE, 2018, 13, e0199192.	1.1	46

#	ARTICLE	IF	CITATIONS
2293	Pan4Draft: A Computational Tool to Improve the Accuracy of Pan-Genomic Analysis Using Draft Genomes. Scientific Reports, 2018, 8, 9670.	1.6	14
2294	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
2295	De novo genome assembly of Oryza granulata reveals rapid genome expansion and adaptive evolution. Communications Biology, 2018, 1, 84.	2.0	24
2296	Patterns of Conservation and Diversification in the Fungal Polarization Network. Genome Biology and Evolution, 2018, 10, 1765-1782.	1.1	15
2297	Early metazoan cell type diversity and the evolution of multicellular gene regulation. Nature Ecology and Evolution, 2018, 2, 1176-1188.	3.4	226
2298	Landscape of the genome and host cell response of <i>Mycobacterium shigaense</i> reveals pathogenic features. Emerging Microbes and Infections, 2018, 7, 1-13.	3.0	3
2299	Gene family innovation, conservation and loss on the animal stem lineage. ELife, 2018, 7, .	2.8	149
2300	De Novo Sequencing of a <i>Sparassis latifolia</i> Genome and Its Associated Comparative Analyses. Canadian Journal of Infectious Diseases and Medical Microbiology, 2018, 2018, 1-12.	0.7	9
2301	High-quality assembly of the reference genome for scarlet sage, Salvia splendens, an economically important ornamental plant. GigaScience, 2018, 7, .	3.3	49
2302	Increased biofilm formation due to high-temperature adaptation in marine Roseobacter. Nature Microbiology, 2018, 3, 989-995.	5.9	29
2303	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. Nature Genetics, 2018, 50, 1289-1295.	9.4	335
2304	The genomic features of parasitism, Polyembryony and immune evasion in the endoparasitic wasp Macrocentrus cingulum. BMC Genomics, 2018, 19, 420.	1.2	53
2305	Draft Genome Sequence for the Tree PathogenPhytophthora plurivora. Genome Biology and Evolution, 2018, 10, 2432-2442.	1.1	19
2306	Distinctive characters of Nostoc genomes in cyanolichens. BMC Genomics, 2018, 19, 434.	1.2	30
2307	Discovery of Novel Genes and Other Lineage-Specific Features Through Comparative Genomics. , 2018, , 225-241.		2
2308	PanACEA: a bioinformatics tool for the exploration and visualization of bacterial pan-chromosomes. BMC Bioinformatics, 2018, 19, 246.	1.2	9
2309	An Updated Functional Annotation of Protein-Coding Genes in the Cucumber Genome. Frontiers in Plant Science, 2018, 9, 325.	1.7	2
2310	MorphDB: Prioritizing Genes for Specialized Metabolism Pathways and Gene Ontology Categories in Plants. Frontiers in Plant Science, 2018, 9, 352.	1.7	7

#	ARTICLE	IF	CITATIONS
2311	Genome Sequencing and Analysis of the Peanut B-Genome Progenitor (Arachis ipaensis). Frontiers in Plant Science, 2018, 9, 604.	1.7	38
2312	Horizontal Gene Transfer From Bacteria and Plants to the Arbuscular Mycorrhizal Fungus Rhizophagus irregularis. Frontiers in Plant Science, 2018, 9, 701.	1.7	77
2313	Comparative analysis of plant MKK gene family reveals novel expansion mechanism of the members and sheds new light on functional conservation. BMC Genomics, 2018, 19, 407.	1.2	29
2314	Biochemical characterization of <i>Plasmodium</i> complement factors binding protein for its role in immune modulation. Biochemical Journal, 2018, 475, 2877-2891.	1.7	3
2315	Comparative transcriptome analysis of Poncirus trifoliata identifies a core set of genes involved in arbuscular mycorrhizal symbiosis. Journal of Experimental Botany, 2018, 69, 5255-5264.	2.4	19
2316	Traceability, reproducibility and wiki-exploration for â€œÃ-la-carteâ€•reconstructions of genome-scale metabolic models. PLoS Computational Biology, 2018, 14, e1006146.	1.5	89
2317	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
2318	Integrative visual omics of the white-rot fungus Polyporus brumalis exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. Biotechnology for Biofuels, 2018, 11, 201.	6.2	45
2319	Pan-genome analyses of 24 Shewanella strains re-emphasize the diversification of their functions yet evolutionary dynamics of metal-reducing pathway. Biotechnology for Biofuels, 2018, 11, 193.	6.2	59
2320	In silico characterization and expression profiling of the diacylglycerol acyltransferase gene family (DGAT1, DGAT2, DGAT3 and WS/DGAT) from oil palm, Elaeis guineensis. Plant Science, 2018, 275, 84-96.	1.7	37
2321	Genomic study of a novel magnetotactic <i>Alphaproteobacteria</i> uncovers the multiple ancestry of magnetotaxis. Environmental Microbiology, 2018, 20, 4415-4430.	1.8	48
2322	Social regulation of insulin signaling and the evolution of eusociality in ants. Science, 2018, 361, 398-402.	6.0	125
2323	Genome-Wide Characterization and Expression Analyses of Pleurotus ostreatus MYB Transcription Factors during Developmental Stages and under Heat Stress Based on de novo Sequenced Genome. International Journal of Molecular Sciences, 2018, 19, 2052.	1.8	36
2324	Transcriptomic comparison reveals genetic variation potentially underlying seed developmental evolution of soybeans. Journal of Experimental Botany, 2018, 69, 5089-5104.	2.4	46
2325	De novo transcriptome assembly and positive selection analysis of an individual deep-sea fish. BMC Genomics, 2018, 19, 394.	1.2	49
2326	Genome-Wide Analysis of Corynespora cassiicola Leaf Fall Disease Putative Effectors. Frontiers in Microbiology, 2018, 9, 276.	1.5	58
2327	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. Frontiers in Microbiology, 2018, 9, 660.	1.5	33
2328	Comparative Genomic Analysis of Holospora spp., Intranuclear Symbionts of Paramecia. Frontiers in Microbiology, 2018, 9, 738.	1.5	29

#	Article	IF	Citations
2329	Thousands of Novel Endolysins Discovered in Uncultured Phage Genomes. Frontiers in Microbiology, 2018, 9, 1033.	1.5	50
2330	Comparative Genomics Reveals Evidence of Genome Reduction and High Extracellular Protein Degradation Potential in Kangiella. Frontiers in Microbiology, 2018, 9, 1224.	1.5	11
2331	Genome-Wide Identification and Characterization of the Potato bHLH Transcription Factor Family. Genes, 2018, 9, 54.	1.0	112
2332	A Possible Trifunctional Î²-Carotene Synthase Gene Identified in the Draft Genome of Aurantiochytrium sp. Strain KH105. Genes, 2018, 9, 200.	1.0	32
2333	Genome Sequence of the Freshwater Yangtze Finless Porpoise. Genes, 2018, 9, 213.	1.0	16
2334	Investigating the Molecular Genetic Basis of Cytoplasmic Sex Determination Caused by Wolbachia Endosymbionts in Terrestrial Isopods. Genes, 2018, 9, 290.	1.0	17
2335	Arsenic Reduces Gene Expression Response to Changing Salinity in Killifish. Environmental Science & Technology, 2018, 52, 8811-8821.	4.6	5
2336	Genomic signatures of mitonuclear coevolution across populations of Tigriopus californicus. Nature Ecology and Evolution, 2018, 2, 1250-1257.	3.4	154
2337	Comparative Analysis of 37 Acinetobacter Bacteriophages. Viruses, 2018, 10, 5.	1.5	37
2338	OneTwoTree: An online tool for phylogeny reconstruction. Molecular Ecology Resources, 2018, 18, 1492-1499.	2.2	29
2339	Cloning and characterization of BES1/BZR1 transcription factor genes in maize. Plant Growth Regulation, 2018, 86, 235-249.	1.8	62
2340	Genome of Wild Mandarin and Domestication History of Mandarin. Molecular Plant, 2018, 11, 1024-1037.	3.9	130
2341	Comprehensive analysis of NAC transcription factors and their expression during fruit spine development in cucumber (Cucumis sativus L.). Horticulture Research, 2018, 5, 31.	2.9	46
2342	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
2343	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
2344	Evaluation of Current and Emerging Antimalarial Medicines for Inhibition of <i>Toxoplasma gondii</i> Growth in Vitro. ACS Infectious Diseases, 2018, 4, 1264-1274.	1.8	41
2345	Genome comparison of different Zymomonas mobilis strains provides insights on conservation of the evolution. PLoS ONE, 2018, 13, e0195994.	1.1	6
2346	EOGD: the Euplotes octocarinatus genome database. BMC Genomics, 2018, 19, 63.	1.2	12

#	Article	IF	Citations
2347	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes Meloidogyne spp., with a focus on the asexuallyÂreproducing species. BMC Genomics, 2018, 19, 321.	1.2	18
2348	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
2349	Comparative genomics of the miniature wasp and pest control agent Trichogramma pretiosum. BMC Biology, 2018, 16, 54.	1.7	57
2350	Genomics analysis of Aphanomyces spp. identifies a new class of oomycete effector associated with host adaptation. BMC Biology, 2018, 16, 43.	1.7	62
2351	The aquatic animalsâ€™ transcriptome resource for comparative functional analysis. BMC Genomics, 2018, 19, 103.	1.2	5
2352	Comparison of the Chinese bamboo partridge and red Junglefowl genome sequences highlights the importance of demography in genome evolution. BMC Genomics, 2018, 19, 336.	1.2	17
2353	Comprehensive analyses of the BES1 gene family in Brassica napus and examination of their evolutionary pattern in representative species. BMC Genomics, 2018, 19, 346.	1.2	45
2354	Phylogenomics provides a robust topology of the major cnidarian lineages and insights on the origins of key organismal traits. BMC Evolutionary Biology, 2018, 18, .	3.2	182
2355	Identification, characterization and heparin binding capacity of a spore-wall, virulence protein from the shrimp microsporidian, Enterocytozoon hepatopenaei (EHP). Parasites and Vectors, 2018, 11, 177.	1.0	31
2356	Comparative genomic analysis reveals the evolution and environmental adaptation strategies of vibrios. BMC Genomics, 2018, 19, 135.	1.2	71
2357	Recent Asian origin of chytrid fungi causing global amphibian declines. Science, 2018, 360, 621-627.	6.0	389
2358	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. Scientific Reports, 2018, 8, 6808.	1.6	10
2359	Chromosomeâ€based survey sequencing reveals the genome organization of wild wheat progenitor <i>Triticum dicoccoides</i>. Plant Biotechnology Journal, 2018, 16, 2077-2087.	4.1	28
2360	Surveying alignment-free features for Ortholog detection in related yeast proteomes by using supervised big data classifiers. BMC Bioinformatics, 2018, 19, 166.	1.2	3
2361	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. GigaScience, 2018, 7, .	3.3	21
2362	Comparative genomics of <i>Pseudomonas syringae</i> reveals convergent gene gain and loss associated with specialization onto cherry (<i>Prunus avium</i>). New Phytologist, 2018, 219, 672-696.	3.5	52
2363	Genome sequence of the progenitor of wheat A subgenome Triticum urartu. Nature, 2018, 557, 424-428.	13.7	354
2364	Contrasting duplication patterns reflect functional diversities of <i>ubiquitin</i> and <i>ubiquitinâ€like protein modifiers</i> in plants. Plant Journal, 2018, 95, 296-311.	2.8	11

#	Article	IF	Citations
2365	Comparative transcriptomics provides insight into the molecular basis of species diversification of section Trigonopedia (Cypripedium) on the Qinghai-Tibetan Plateau. Scientific Reports, 2018, 8, 11640.	1.6	11
2366	Genome Analyses of the Microalga Picochlorum Provide Insights into the Evolution of Thermotolerance in the Green Lineage. Genome Biology and Evolution, 2018, 10, 2347-2365.	1.1	36
2367	PdumBase: a transcriptome database and research tool for Platynereis dumerilii and early development of other metazoans. BMC Genomics, 2018, 19, 618.	1.2	18
2368	OrthoList 2: A New Comparative Genomic Analysis of Human and <i>Caenorhabditis elegans</i> Genes. Genetics, 2018, 210, 445-461.	1.2	233
2369	Investigation of the thermophilic mechanism in the genus Porphyrobacter by comparative genomic analysis. BMC Genomics, 2018, 19, 385.	1.2	21
2370	Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics, 2018, 19, 588.	1.2	64
2371	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
2372	Whole-genome sequencing and comparative analysis of two plant-associated strains of Rhodopseudomonas palustris (PS3 and YSC3). Scientific Reports, 2018, 8, 12769.	1.6	32
2373	Plasmodium vivax-like genome sequences shed new insights into Plasmodium vivax biology and evolution. PLoS Biology, 2018, 16, e2006035.	2.6	32
2374	Convergent Evolution among Ruminant-Pathogenic Mycoplasma Involved Extensive Gene Content Changes. Genome Biology and Evolution, 2018, 10, 2130-2139.	1.1	48
2375	Comparison of three assembly strategies for a heterozygous seedless grapevine genome assembly. BMC Genomics, 2018, 19, 57.	1.2	15
2376	Horizontal gene transfer plays a major role in the pathological convergence of Xanthomonas lineages on common bean. BMC Genomics, 2018, 19, 606.	1.2	38
2377	A Freeloader? The Highly Eroded Yet Large Genome of the Serratia symbiotica Symbiont of Cinara strobi. Genome Biology and Evolution, 2018, 10, 2178-2189.	1.1	29
2378	Host- and Helminth-Derived Endocannabinoids That Have Effects on Host Immunity Are Generated during Infection. Infection and Immunity, 2018, 86, .	1.0	16
2379	Draft genome of Glyptosternon maculatum, an endemic fish from Tibet Plateau. GigaScience, 2018, 7, .	3.3	18
2380	Pathogenic adaptations of Colletotrichum fungi revealed by genome wide gene family evolutionary analyses. PLoS ONE, 2018, 13, e0196303.	1.1	46
2381	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
2382	In silico exploration of Red Sea Bacillus genomes for natural product biosynthetic gene clusters. BMC Genomics, 2018, 19, 382.	1.2	17

#	ARTICLE	IF	CITATIONS
2383	Homology Inference Based on a Reconciliation Approach for the Comparative Genomics of Protozoa. Evolutionary Bioinformatics, 2018, 14, 117693431878513.	0.6	1
2384	Tung Tree (Vernicia fordii, Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid Î²-Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. Plant and Cell Physiology, 2018, 59, 1990-2003.	1.5	45
2385	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. Scientific Reports, 2018, 8, 11168.	1.6	36
2386	Genomic Analysis of the Insect-Killing Fungus Beauveria bassiana JEF-007 as a Biopesticide. Scientific Reports, 2018, 8, 12388.	1.6	18
2387	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 2018, 9, 379.	1.0	25
2388	Assessment of an Organ-Specific <i>de Novo</i> Transcriptome of the Nematode Trap-Crop, <i>Solanum sisymbriifolium</i>. G3: Genes, Genomes, Genetics, 2018, 8, 2135-2143.	0.8	4
2389	Adaptations to marine versus terrestrial low temperature environments as revealed by comparative genomic analyses of the genus Psychrobacter. FEMS Microbiology Ecology, 2018, 94, .	1.3	17
2390	Horizontal Gene Acquisitions Contributed to Genome Expansion in Insect-Symbiotic Spiroplasma clarkii. Genome Biology and Evolution, 2018, 10, 1526-1532.	1.1	42
2391	Improved de novo genome assembly and analysis of the Chinese cucurbit Siraitia grosvenorii, also known as monk fruit or luo-han-guo. GigaScience, 2018, 7, .	3.3	32
2392	Proteins Potentially Involved in Immune Evasion Strategies in Sporothrix brasiliensis Elucidated by Ultra-High-Resolution Mass Spectrometry. MSphere, 2018, 3, .	1.3	30
2393	Comparative genomic analysis of the multispecies probiotic-marketed product VSL#3. PLoS ONE, 2018, 13, e0192452.	1.1	33
2394	Genomic insights into the broad antifungal activity, plant-probiotic properties, and their regulation, in Pseudomonas donghuensis strain SVBP6. PLoS ONE, 2018, 13, e0194088.	1.1	42
2395	Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus <i>Tolypocladium</i>. Mycologia, 2018, 110, 104-117.	0.8	12
2396	Fungal Genome Annotation. Methods in Molecular Biology, 2018, 1775, 171-184.	0.4	14
2397	Fungal Phylogenomics. Methods in Molecular Biology, 2018, 1775, 251-266.	0.4	4
2398	Anti-band 3 and anti-spectrin antibodies are increased in Plasmodium vivax infection and are associated with anemia. Scientific Reports, 2018, 8, 8762.	1.6	22
2399	Genome-wide analysis of maize CONSTANS-LIKE gene family and expression profiling under light/dark and abscisic acid treatment. Gene, 2018, 673, 1-11.	1.0	28
2400	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	4.7	303

#	Article	IF	Citations
2401	Clonorchis sinensis and Clonorchiasis: The Relevance of Exploring Genetic Variation. Advances in Parasitology, 2018, 100, 155-208.	1.4	18
2402	Genome sequence of <i>Jatropha curcas</i> L., a nonâ€edible biodiesel plant, provides a resource to improve seedâ€related traits. Plant Biotechnology Journal, 2019, 17, 517-530.	4.1	56
2403	JustOrthologs: a fast, accurate and user-friendly ortholog identification algorithm. Bioinformatics, 2019, 35, 546-552.	1.8	19
2404	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. Plant Biotechnology Journal, 2019, 17, 451-460.	4.1	89
2405	SonicParanoid: fast, accurate and easy orthology inference. Bioinformatics, 2019, 35, 149-151.	1.8	103
2406	Comparative and Evolutionary Genomics. , 2019, , 257-267.		5
2407	Bioinformatic analysis of the complete genome sequence of Pectobacterium carotovorum subsp. brasiliense BZA12 and candidate effector screening. Journal of Plant Pathology, 2019, 101, 39-49.	0.6	8
2408	Systematic discovery of novel and valuable plant gene modules by large-scale RNA-seq samples. Bioinformatics, 2019, 35, 361-364.	1.8	6
2409	The red bayberry genome and genetic basis of sex determination. Plant Biotechnology Journal, 2019, 17, 397-409.	4.1	61
2410	An improved genome assembly of the fluke Schistosoma japonicum. PLoS Neglected Tropical Diseases, 2019, 13, e0007612.	1.3	50
2411	Comparative genomics of Staphylococcus aureus associated with subclinical and clinical bovine mastitis. PLoS ONE, 2019, 14, e0220804.	1.1	27
2412	Genomic and physiological analyses reveal that extremely thermophilic <i>Caldicellulosiruptor changbaiensis</i> deploys uncommon cellulose attachment mechanisms. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1251-1263.	1.4	4
2413	Comparative genomic and functional analysis of Akkermansia muciniphila and closely related species. Genes and Genomics, 2019, 41, 1253-1264.	0.5	33
2414	Comparative Complete Chloroplast Genome Analyses and Contribution to the Understanding of Chloroplast Phylogeny and Adaptive Evolution in Subgenus Anguinum. Russian Journal of Genetics, 2019, 55, 872-884.	0.2	2
2415	Application of a high-resolution genetic map for chromosome-scale genome assembly and fine QTLs mapping of seed size and weight traits in castor bean. Scientific Reports, 2019, 9, 11950.	1.6	14
2416	Comparative Transcriptome Analyses Reveal the Role of Conserved Function in Electric Organ Convergence Across Electric Fishes. Frontiers in Genetics, 2019, 10, 664.	1.1	4
2417	Draft Genome and Complete Hox-Cluster Characterization of the Sterlet (Acipenser ruthenus). Frontiers in Genetics, 2019, 10, 776.	1.1	34
2418	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. Scientific Reports, 2019, 9, 11769.	1.6	179

#	ARTICLE	IF	CITATIONS
2419	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated <i>Thaumarchaeota</i>. MSystems, 2019, 4, .	1.7	59
2420	Identification and expression analysis of the GDSL esterase/lipase family genes, and the characterization of <i>SaGLIP8</i> in <i>Sedum alfredii</i> Hance under cadmium stress. PeerJ, 2019, 7, e6741.	0.9	18
2421	Population genomic evidence for radiative divergence of four Orychophragmus (Brassicaceae) species in eastern Asia. Botanical Journal of the Linnean Society, 2019, 191, 18-29.	0.8	8
2422	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. Science, 2019, 365, .	6.0	198
2423	Diversity, specificity and molecular evolution of the lytic arsenal of Pseudomonas phages: in silico perspective. Environmental Microbiology, 2019, 21, 4136-4150.	1.8	10
2424	Identifying miltefosine-resistant key genes in proteinâ€“protein interactions network and experimental verification in Iranian Leishmania major. Molecular Biology Reports, 2019, 46, 5371-5388.	1.0	4
2425	Genome Sequence Data of Six Isolates of <i>Phytophthora capsici</i> from Mexico. Molecular Plant-Microbe Interactions, 2019, 32, 1267-1269.	1.4	11
2426	Physiological and comparative genomic analysis of new isolated yeasts Spathaspora sp. JA1 and Meyerozyma caribbica JA9 reveal insights into xylitol production. FEMS Yeast Research, 2019, 19, .	1.1	22
2427	Nuclear loci developed from multiple transcriptomes yield high resolution in phylogeny of scaly tree ferns (Cyatheaceae) from China and Vietnam. Molecular Phylogenetics and Evolution, 2019, 139, 106567.	1.2	13
2428	geneHummus: an R package to define gene families and their expression in legumes and beyond. BMC Genomics, 2019, 20, 591.	1.2	3
2429	De novo European eel transcriptome provides insights into the evolutionary history of duplicated genes in teleost lineages. PLoS ONE, 2019, 14, e0218085.	1.1	41
2430	Musa balbisiana genome reveals subgenome evolution and functional divergence. Nature Plants, 2019, 5, 810-821.	4.7	132
2431	De novo genome assembly of the endangered Acer yangbiense, a plant species with extremely small populations endemic to Yunnan Province, China. GigaScience, 2019, 8, .	3.3	42
2432	The Methodology Behind Network Thinking: Graphs to Analyze Microbial Complexity and Evolution. Methods in Molecular Biology, 2019, 1910, 271-308.	0.4	4
2433	Diversifying Evolution of the Ubiquitin-26S Proteasome System in Brassicaceae and Poaceae. International Journal of Molecular Sciences, 2019, 20, 3226.	1.8	13
2434	Comparative transcriptomics reveals the selection patterns of domesticated ramie. Ecology and Evolution, 2019, 9, 7057-7068.	0.8	3
2435	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
2436	Shotgun proteomic analysis of Bordetella parapertussis provides insights into the physiological response to iron starvation and potential new virulence determinants absent in Bordetella pertussis. Journal of Proteomics, 2019, 206, 103448.	1.2	4

#	Article	IF	Citations
2437	Phased genome sequence of an interspecific hybrid flowering cherry, â€˜Somei-Yoshinoâ€™ (Cerasus Ã—) Tj ETQq0 0 0 rgBT /Overlock 1	1.5	59
2438	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
2439	Comparative transcriptomics suggest unique molecular adaptations within tardigrade lineages. BMC Genomics, 2019, 20, 607.	1.2	68
2440	Genomic and molecular characterisation of Escherichia marmotae from wild rodents in Qinghai-Tibet plateau as a potential pathogen. Scientific Reports, 2019, 9, 10619.	1.6	24
2441	Differentiations in Gene Content and Expression Response to Virulence Induction Between Two Agrobacterium Strains. Frontiers in Microbiology, 2019, 10, 1554.	1.5	25
2442	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
2443	The Parallel Molecular Adaptations to the Antarctic Cold Environment in Two Psychrophilic Green Algae. Genome Biology and Evolution, 2019, 11, 1897-1908.	1.1	19
2444	The genome assembly and annotation of yellowhorn (Xanthoceras sorbifolium Bunge). GigaScience, 2019, 8, .	3.3	37
2445	Cell Wall Enzymes in Zygnema circumcarinatum UTEX 1559 Respond to Osmotic Stress in a Plant-Like Fashion. Frontiers in Plant Science, 2019, 10, 732.	1.7	13
2446	Comparative Genomics of Wild Bee and Flower Isolated Lactobacillus Reveals Potential Adaptation to the Bee Host. Genome Biology and Evolution, 2019, 11, 2151-2161.	1.1	38
2447	Site-specific cleavage of bacterial MucD by secreted proteases mediates antibacterial resistance in Arabidopsis. Nature Communications, 2019, 10, 2853.	5.8	35
2448	Pseudomolecule-level assembly of the Chinese oil tree yellowhorn (Xanthoceras sorbifolium) genome. GigaScience, 2019, 8, .	3.3	47
2449	Identification and characterization of putative Aeromonas spp. T3SS effectors. PLoS ONE, 2019, 14, e0214035.	1.1	20
2450	Comparative Transcriptome Analysis Reveals Molecular Basis Underlying Fast Growth of the Selectively Bred Pacific Oyster, Crassostrea gigas. Frontiers in Genetics, 2019, 10, 610.	1.1	30
2451	Whole Genome Sequencing of the Blue Tilapia (Oreochromis aureus) Provides a Valuable Genetic Resource for Biomedical Research on Tilapias. Marine Drugs, 2019, 17, 386.	2.2	22
2452	Genome Sequences Provide Insights into the Reticulate Origin and Unique Traits of Woody Bamboos. Molecular Plant, 2019, 12, 1353-1365.	3.9	116
2453	OMA standalone: orthology inference among public and custom genomes and transcriptomes. Genome Research, 2019, 29, 1152-1163.	2.4	111
2454	Whole genome analysis of Aspergillus sojae SMF 134 supports its merits as a starter for soybean fermentation. Journal of Microbiology, 2019, 57, 874-883.	1.3	16

#	ARTICLE	IF	CITATIONS
2455	Evolutionary adaptation analysis of immune defense and hypoxia tolerance in two closely related Marsupenaeus species based on comparative transcriptomics. Fish and Shellfish Immunology, 2019, 92, 861-870.	1.6	13
2456	Draft genome sequence of cauliflower (Brassica oleracea L. var. botrytis) provides new insights into the C genome in Brassica species. Horticulture Research, 2019, 6, 82.	2.9	53
2457	Whole-Genome Sequencing of the Giant Devil Catfish, Bagarius yarrelli. Genome Biology and Evolution, 2019, 11, 2071-2077.	1.1	17
2458	The effect of Wolbachia on gene expression in Drosophila paulistorum and its implications for symbiont-induced host speciation. BMC Genomics, 2019, 20, 465.	1.2	21
2459	Analysis of 1,000 Type-Strain Genomes Improves Taxonomic Classification of Bacteroidetes. Frontiers in Microbiology, 2019, 10, 2083.	1.5	1,281
2460	A high-quality Actinidia chinensis (kiwifruit) genome. Horticulture Research, 2019, 6, 117.	2.9	109
2461	A chromosomal-level genome assembly for the giant African snail Achatina fulica. GigaScience, 2019, 8, .	3.3	42
2462	Chromosomeâ€level genome assembly of the razor clam <i>Sinonovacula constricta</i> (Lamarck, 1818). Molecular Ecology Resources, 2019, 19, 1647-1658.	2.2	45
2463	The draft genome of <i>Actinia tenebrosa</i> reveals insights into toxin evolution. Ecology and Evolution, 2019, 9, 11314-11328.	0.8	28
2464	Genomic Characterization of the Periwinkle Leaf Yellowing (PLY) Phytoplasmas in Taiwan. Frontiers in Microbiology, 2019, 10, 2194.	1.5	27
2465	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. Nature Communications, 2019, 10, 4702.	5.8	115
2466	Variable genome evolution in fungi after transposon-mediated amplification of a housekeeping gene. Mobile DNA, 2019, 10, 37.	1.3	1
2467	Genome-wide Identification and Characterization of a Superfamily of Bacterial Extracellular Contractile Injection Systems. Cell Reports, 2019, 29, 511-521.e2.	2.9	44
2468	The allotetraploid origin and asymmetrical genome evolution of theÂcommon carp Cyprinus carpio. Nature Communications, 2019, 10, 4625.	5.8	156
2469	Comparison of transcriptomes of an orthotospovirus vector and non-vector thrips species. PLoS ONE, 2019, 14, e0223438.	1.1	5
2470	Complex Evolutionary Origins of Specialized Metabolite Gene Cluster Diversity among the Plant Pathogenic Fungi of the Fusarium graminearum Species Complex. Genome Biology and Evolution, 2019, 11, 3106-3122.	1.1	24
2471	Biochemical characterization of PlasmodiumÂfalciparum parasite specific helicase 1 (PfPSH1). FEBS Open Bio, 2019, 9, 1909-1927.	1.0	3
2473	Genome Organization and Adaptive Potential of Archetypal Organophosphate Degrading Sphingobium fuliginis ATCC 27551. Genome Biology and Evolution, 2019, 11, 2557-2562.	1.1	12

#	Article	IF	Citations
2474	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. GigaScience, 2019, 8, .	3.3	152
2475	The wild sweetpotato (Ipomoea trifida) genome provides insights into storage root development. BMC Plant Biology, 2019, 19, 119.	1.6	33
2476	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
2477	Accelerated evolution and diversifying selection drove the adaptation of cetacean bone microstructure. BMC Evolutionary Biology, 2019, 19, 194.	3.2	5
2478	Analyses of Seven New Genomes of Xanthomonas citri pv. aurantifolii Strains, Causative Agents of Citrus Canker B and C, Show a Reduced Repertoire of Pathogenicity-Related Genes. Frontiers in Microbiology, 2019, 10, 2361.	1.5	14
2479	Isolation and Characterization of a Novel Pathogenic Strain of Ehrlichia minasensis. Microorganisms, 2019, 7, 528.	1.6	24
2480	Comparative Analysis of Intra- and Inter-Specific Genomic Variability in the Peach Potato Aphid, Myzus persicae. Insects, 2019, 10, 368.	1.0	3
2481	Chromosomal-level reference genome of Chinese peacock butterfly (Papilio bianor) based on third-generation DNA sequencing and Hi-C analysis. GigaScience, 2019, 8, .	3.3	26
2482	PacBio single-molecule long-read sequencing shed new light on the complexity of the Carex breviculmis transcriptome. BMC Genomics, 2019, 20, 789.	1.2	25
2483	Lignin degradation potential and draft genome sequence of Trametes trogii S0301. Biotechnology for Biofuels, 2019, 12, 256.	6.2	16
2484	The Impact of Type VI Secretion System, Bacteriocins and Antibiotics on Bacterial Competition of Pectobacterium carotovorum subsp. brasiliense and the Regulation of Carbapenem Biosynthesis by Iron and the Ferric-Uptake Regulator. Frontiers in Microbiology, 2019, 10, 2379.	1.5	23
2485	Scandinavium goeteborgense gen. nov., sp. nov., a New Member of the Family Enterobacteriaceae Isolated From a Wound Infection, Carries a Novel Quinolone Resistance Gene Variant. Frontiers in Microbiology, 2019, 10, 2511.	1.5	19
2486	Genome survey of resistance gene analogs in sugarcane: genomic features and differential expression of the innate immune system from a smut-resistant genotype. BMC Genomics, 2019, 20, 809.	1.2	22
2487	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
2488	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. Nature Communications, 2019, 10, 5158.	5.8	94
2489	Pleurotus eryngii Genomes Reveal Evolution and Adaptation to the Gobi Desert Environment. Frontiers in Microbiology, 2019, 10, 2024.	1.5	19
2490	Genomic characteristics and comparative genomics analysis of the endophytic fungus Sarocladium brachiariae. BMC Genomics, 2019, 20, 782.	1.2	23
2491	Genome-wide characterization and evolutionary analysis of heat shock transcription factors (HSFs) to reveal their potential role under abiotic stresses in radish (Raphanus sativus L.). BMC Genomics, 2019, 20, 772.	1.2	23

#	Article	IF	Citations
2492	The genome of the migratoryÂnematode, Radopholus similis, reveals signatures of close associationÂto the sedentary cyst nematodes. PLoS ONE, 2019, 14, e0224391.	1.1	13
2493	Genomic and metabolic differences between Pseudomonas putida populations inhabiting sugarcane rhizosphere or bulk soil. PLoS ONE, 2019, 14, e0223269.	1.1	9
2494	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of Auricularia Species. Frontiers in Microbiology, 2019, 10, 2255.	1.5	12
2495	How to build distylous flowers: comparative floral development and evolution of distylous species across the angiosperms. American Journal of Botany, 2019, 106, 1285-1299.	0.8	1
2496	Origin and diversification of Xanthomonas citri subsp. citri pathotypes revealed by inclusive phylogenomic, dating, and biogeographic analyses. BMC Genomics, 2019, 20, 700.	1.2	33
2497	Biological process activity transformation of single cell gene expression for cross-species alignment. Nature Communications, 2019, 10, 4899.	5.8	29
2498	Comprehensive analysis of bZIP transcription factors uncovers their roles during dimorphic floret differentiation and stress response in Cleistogenes songorica. BMC Genomics, 2019, 20, 760.	1.2	15
2499	Insight into adaptation mechanisms of marine bacterioplankton from comparative genomic analysis of the genus Pseudohongiella. Deep-Sea Research Part II: Topical Studies in Oceanography, 2019, 167, 62-69.	0.6	5
2500	Multilocus Analysis Resolves the European Finch Epidemic Strain of Trichomonas gallinae and Suggests Introgression from Divergent Trichomonads. Genome Biology and Evolution, 2019, 11, 2391-2402.	1.1	17
2501	Raptor genomes reveal evolutionary signatures of predatory and nocturnal lifestyles. Genome Biology, 2019, 20, 181.	3.8	11
2502	Negative regulators of plant immunity derived from cinnamyl alcohol dehydrogenases are targeted by multiple <i>Phytophthora</i> Avr3aâ€like effectors. New Phytologist, 2019, , .	3.5	46
2503	TreeCluster: Clustering biological sequences using phylogenetic trees. PLoS ONE, 2019, 14, e0221068.	1.1	99
2504	Reconstruction of the full-length transcriptome atlas using PacBio Iso-Seq provides insight into the alternative splicing in Gossypium australe. BMC Plant Biology, 2019, 19, 365.	1.6	43
2505	A chromosome-level draft genome of the grain aphid Sitobion miscanthi. GigaScience, 2019, 8, .	3.3	41
2506	Marine-freshwater prokaryotic transitions require extensive changes in the predicted proteome. Microbiome, 2019, 7, 117.	4.9	56
2507	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	3.8	71
2508	Plant evolution and environmental adaptation unveiled by long-read whole-genome sequencing of<i>Spirodela</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18893-18899.	3.3	76
2509	Elevated Heterozygosity in Adults Relative to Juveniles Provides Evidence of Viability Selection on Eagles and Falcons. Journal of Heredity, 2019, 110, 696-706.	1.0	6

#	Article	IF	Citations
2510	Characterization of an Environmental Multidrug-Resistant Acinetobacter seifertii and Comparative Genomic Analysis Reveals Co-occurrence of Antimicrobial Resistance and Metal Tolerance Determinants. Frontiers in Microbiology, 2019, 10, 2151.	1.5	16
2511	Maintenance of High Genome Integrity over Vegetative Growth in the Fairy-Ring Mushroom Marasmius oreades. Current Biology, 2019, 29, 2758-2765.e6.	1.8	28
2512	High-quality Schistosoma haematobium genome achieved by single-molecule and long-range sequencing. GigaScience, 2019, 8, .	3.3	41
2513	Gene Tags Assessment by Comparative Genomics (GTACG): A User-Friendly Framework for Bacterial Comparative Genomics. Frontiers in Genetics, 2019, 10, 725.	1.1	4
2514	Assembly and Annotation of a Draft Genome of the Medicinal Plant Polygonum cuspidatum. Frontiers in Plant Science, 2019, 10, 1274.	1.7	36
2515	Genome sequence of the Chinese white wax scale insect Ericerus pela: the first draft genome for the Coccidae family of scale insects. GigaScience, 2019, 8, .	3.3	15
2516	A chromosome-level genome assembly of Cydia pomonella provides insights into chemical ecology and insecticide resistance. Nature Communications, 2019, 10, 4237.	5.8	102
2517	The Draft Genome of the Endangered Sichuan Partridge (Arborophila rufipectus) with Evolutionary Implications. Genes, 2019, 10, 677.	1.0	8
2518	De novo transcriptome assembly and analysis of the freshwater araphid diatom Fragilaria radians, Lake Baikal. Scientific Data, 2019, 6, 183.	2.4	14
2519	Draft genome sequence of Solanum aethiopicum provides insights into disease resistance, drought tolerance, and the evolution of the genome. GigaScience, 2019, 8, .	3.3	38
2520	The sequence and de novo assembly of Takifugu bimaculatus genome using PacBio and Hi-C technologies. Scientific Data, 2019, 6, 187.	2.4	29
2521	Genetics of Adaptation of the Ascomycetous Fungus Podospora anserina to Submerged Cultivation. Genome Biology and Evolution, 2019, 11, 2807-2817.	1.1	1
2522	Complete Genome Sequencing and Comparative Genome Characterization of Lactobacillus johnsonii ZLJ010, a Potential Probiotic With Health-Promoting Properties. Frontiers in Genetics, 2019, 10, 812.	1.1	38
2523	A Survey of Gene Prioritization Tools for Mendelian and Complex Human Diseases. Journal of Integrative Bioinformatics, 2019, 16, .	1.0	25
2524	Molecular Targets for Coevolutionary Interactions Between Pacific Oyster Larvae and Their Sympatric Vibrios. Frontiers in Microbiology, 2019, 10, 2067.	1.5	10
2525	Comparative Genome Analyses Reveal the Genomic Traits and Host Plant Adaptations of Flavobacterium akiainvivens IK-1T. International Journal of Molecular Sciences, 2019, 20, 4910.	1.8	1
2526	Haplotype-resolved genomes of geminivirus-resistant and geminivirus-susceptible African cassava cultivars. BMC Biology, 2019, 17, 75.	1.7	42
2527	Transcriptome analyses reveal alterations in muscle metabolism, immune responses and reproductive behavior of Japanese mantis shrimp (Oratosquilla oratoria) at different cold temperature. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 32, 100615.	0.4	9

#	ARTICLE	IF	CITATIONS
2528	Analysis of Orthologous SECONDARY WALL-ASSOCIATED NAC DOMAIN1 (SND1) Promotor Activity in Herbaceous and Woody Angiosperms. International Journal of Molecular Sciences, 2019, 20, 4623.	1.8	2
2529	Chromosome-level assembly of the mustache toad genome using third-generation DNA sequencing and Hi-C analysis. GigaScience, 2019, 8, .	3.3	25
2530	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in Streptomycetes. Applied and Environmental Microbiology, 2019, 85, .	1.4	16
2531	Dataset on evolution analysis of splenic transcriptome in bighead carp and silver carp. Data in Brief, 2019, 22, 812-814.	0.5	1
2532	Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. Nature Communications, 2019, 10, 356.	5.8	328
2533	Genome sequence of<i>Malania oleifera</i>, a tree with great value for nervonic acid production. GigaScience, 2019, 8, .	3.3	36
2534	Genome structure and evolution of Antirrhinum majus L. Nature Plants, 2019, 5, 174-183.	4.7	85
2535	The Role of Homology and Orthology in the Phylogenomic Analysis of Metazoan Gene Content. Molecular Biology and Evolution, 2019, 36, 643-649.	3.5	44
2536	Genomic analysis of <i>Lactobacillus reuteri </i><scp>WHH</scp>1689 reveals its probiotic properties and stress resistance. Food Science and Nutrition, 2019, 7, 844-857.	1.5	30
2537	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
2538	Chromosome conformation capture resolved near complete genome assembly of broomcorn millet. Nature Communications, 2019, 10, 464.	5.8	81
2539	Highly Resolved Phylogenetic Relationships within Order Acipenseriformes According to Novel Nuclear Markers. Genes, 2019, 10, 38.	1.0	18
2540	Nearâ€complete genome assembly and annotation of the yellow drum (<i>Nibea albiflora</i>) provide insights into population and evolutionary characteristics of this species. Ecology and Evolution, 2019, 9, 568-575.	0.8	11
2541	Genomic Signals of Adaptation towards Mutualism and Sociality in Two Ambrosia Beetle Complexes. Life, 2019, 9, 2.	1.1	5
2542	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
2543	Comparison of Open-Source Reverse Vaccinology Programs for Bacterial Vaccine Antigen Discovery. Frontiers in Immunology, 2019, 10, 113.	2.2	107
2544	Genomic evidence of the illumination response mechanism and evolutionary history of magnetotactic bacteria within the Rhodospirillaceae family. BMC Genomics, 2019, 20, 407.	1.2	8
2545	Comparative analysis reveals conservation in genome organization among intestinal Cryptosporidium species and sequence divergence in potential secreted pathogenesis determinants among major human-infecting species. BMC Genomics, 2019, 20, 406.	1.2	37

#	ARTICLE	IF	CITATIONS
2546	Heterozygous diploid structure of Amorphotheca resinae ZN1 contributes efficient biodetoxification on solid pretreated corn stover. Biotechnology for Biofuels, 2019, 12, 126.	6.2	24
2547	The transcriptome of Cryptosporidium oocysts and intracellular stages. Scientific Reports, 2019, 9, 7856.	1.6	21
2548	Horizontal Gene Transfer as an Indispensable Driver for Evolution of Neocallimastigomycota into a Distinct Gut-Dwelling Fungal Lineage. Applied and Environmental Microbiology, 2019, 85, .	1.4	61
2549	Genetic and Phenotypic Features of a Novel Acinetobacter Species, Strain A47, Isolated From the Clinical Setting. Frontiers in Microbiology, 2019, 10, 1375.	1.5	4
2550	A chromosome-scale genome assembly of cucumber (Cucumis sativus L.). GigaScience, 2019, 8, .	3.3	138
2551	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
2552	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. Frontiers in Genetics, 2019, 10, 654.	1.1	8
2553	Transcriptome Changes during Major Developmental Transitions Accompanied with Little Alteration of DNA Methylome in Two Pleurotus Species. Genes, 2019, 10, 465.	1.0	8
2554	RedoxiBase: A database for ROS homeostasis regulated proteins. Redox Biology, 2019, 26, 101247.	3.9	73
2555	Psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens. Fungal Ecology, 2019, 41, 147-164.	0.7	55
2556	Serotype-specific evolutionary patterns of antimicrobial-resistant Salmonella enterica. BMC Evolutionary Biology, 2019, 19, 132.	3.2	20
2557	Comparative genome analysis indicates high evolutionary potential of pathogenicity genes in Colletotrichum tanaceti. PLoS ONE, 2019, 14, e0212248.	1.1	19
2558	Developmental dynamics of lncRNAs across mammalian organs and species. Nature, 2019, 571, 510-514.	13.7	219
2559	Comparing time series transcriptome data between plants using a network module finding algorithm. Plant Methods, 2019, 15, 61.	1.9	7
2560	Comparative Genomics and Transcriptomics During Sexual Development Gives Insight Into the Life History of the Cosmopolitan Fungus Fusarium neocosmosporiellum. Frontiers in Microbiology, 2019, 10, 1247.	1.5	15
2561	Genome sequencing provides insights into the evolution and antioxidant activity of Chinese bayberry. BMC Genomics, 2019, 20, 458.	1.2	31
2562	Integrating natural history collections and comparative genomics to study the genetic architecture of convergent evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180248.	1.8	32
2563	Evolutionary Analyses Reveal Diverged Patterns of SQUAMOSA Promoter Binding Protein-Like (SPL) Gene Family in Oryza Genus. Frontiers in Plant Science, 2019, 10, 565.	1.7	37

#	ARTICLE	IF	CITATIONS
2564	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
2565	Detection of Ralstonia solanacearum phylotype II, race 2 causing Moko disease and validation of genetic resistance observed in the hybrid plantain FHIA-21. Tropical Plant Pathology, 2019, 44, 371-379.	0.8	5
2566	Comparative transcriptomic analysis reveals genetic divergence and domestication genes in Diospyros. BMC Plant Biology, 2019, 19, 227.	1.6	16
2567	Chromulinavorax destructans, a pathogen of microzooplankton that provides a window into the enigmatic candidate phylum Dependentiae. PLoS Pathogens, 2019, 15, e1007801.	2.1	59
2568	Genome Analysis of Hypomyces perniciosus, the Causal Agent of Wet Bubble Disease of Button Mushroom (Agaricus bisporus). Genes, 2019, 10, 417.	1.0	17
2569	Metagenomic analysis exhibited the co-metabolism of polycyclic aromatic hydrocarbons by bacterial community from estuarine sediment. Environment International, 2019, 129, 308-319.	4.8	93
2570	Genome Annotation. Compendium of Plant Genomes, 2019, , 71-80.	0.3	0
2571	Loss of Wood Formation Genes in Monocot Genomes. Genome Biology and Evolution, 2019, 11, 1986-1996.	1.1	20
2572	Comparative analysis of B-BOX genes and their expression pattern analysis under various treatments in Dendrobium officinale. BMC Plant Biology, 2019, 19, 245.	1.6	31
2573	Pluripotency and the origin of animal multicellularity. Nature, 2019, 570, 519-522.	13.7	106
2574	Genomic erosion and extensive horizontal gene transfer in gut-associated Acetobacteraceae. BMC Genomics, 2019, 20, 472.	1.2	32
2575	Evolution and comparative genomics of the most common Trichoderma species. BMC Genomics, 2019, 20, 485.	1.2	181
2576	Hidden genomic evolution in a morphospeciesâ€"The landscape of rapidly evolving genes in Tetrahymena. PLoS Biology, 2019, 17, e3000294.	2.6	31
2577	Genome Resequencing. Compendium of Plant Genomes, 2019, , 205-218.	0.3	0
2578	Characterization of internalin genes in Listeria monocytogenes from food and humans, and their association with the invasion of Caco-2 cells. Gut Pathogens, 2019, 11, 30.	1.6	30
2579	The olfactory subgenome and specific odor recognition in forest musk deer. Animal Genetics, 2019, 50, 358-366.	0.6	7
2580	Transcriptomic analysis reveals insights into deep-sea adaptations of the dominant species, Shinkaia crosnieri (Crustacea: Decapoda: Anomura), inhabiting both hydrothermal vents and cold seeps. BMC Genomics, 2019, 20, 388.	1.2	23
2581	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. PLoS Biology, 2019, 17, e3000255.	2.6	116

#	ARTICLE	IF	CITATIONS
2582	M1CR0B1AL1Z3Râ€"a user-friendly web server for the analysis of large-scale microbial genomics data. Nucleic Acids Research, 2019, 47, W88-W92.	6.5	86
2583	PhyloToL: A Taxon/Gene-Rich Phylogenomic Pipeline to Explore Genome Evolution of Diverse Eukaryotes. Molecular Biology and Evolution, 2019, 36, 1831-1842.	3.5	23
2584	Positive Selection Evidence in Xylose-Related Genes Suggests Methylglyoxal Reductase as a Target for the Improvement of Yeastsâ€™ Fermentation in Industry. Genome Biology and Evolution, 2019, 11, 1923-1938.	1.1	11
2585	Comparative Transcriptome Analysis Shows Conserved Metabolic Regulation during Production of Secondary Metabolites in Filamentous Fungi. MSystems, 2019, 4, .	1.7	12
2586	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
2587	Fungal acetylome comparative analysis identifies an essential role of acetylation in human fungal pathogen virulence. Communications Biology, 2019, 2, 154.	2.0	38
2588	Chimeric dihydrofolate reductases display properties of modularity and biophysical diversity. Protein Science, 2019, 28, 1359-1367.	3.1	3
2589	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
2590	Genome-wide comparison reveals divergence of cassava and rubber aquaporin family genes after the recent whole-genome duplication. BMC Genomics, 2019, 20, 380.	1.2	18
2591	Modified recipe to inhibit fruiting body formation for living fungal biomaterial manufacture. PLoS ONE, 2019, 14, e0209812.	1.1	22
2592	Comparative genomics of Bifidobacterium species isolated from marmosets and humans. American Journal of Primatology, 2019, 81, e983.	0.8	12
2593	Expanding dynamics of the virulence-related gene variations in the toxigenic Vibrio cholerae serogroup O1. BMC Genomics, 2019, 20, 360.	1.2	9
2594	Comparative Transcriptome Analysis in Eggplant Reveals Selection Trends during Eggplant Domestication. International Journal of Genomics, 2019, 2019, 1-12.	0.8	5
2595	Complete Genome Sequence of Spiroplasma alleghenense PLHS-1 T (ATCC 51752), a Bacterium Isolated from Scorpion Fly (Panorpa helena). Microbiology Resource Announcements, 2019, 8, .	0.3	0
2596	Comparative transcriptome analysis reveals potential evolutionary differences in adaptation of temperature and body shape among four Percidae species. PLoS ONE, 2019, 14, e0215933.	1.1	6
2597	A universal transcriptomic signature of age reveals the temporal scaling of Caenorhabditis elegans aging trajectories. Scientific Reports, 2019, 9, 7368.	1.6	39
2598	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
2599	Modeling Protein Destiny in Developing Fruit. Plant Physiology, 2019, 180, 1709-1724.	2.3	33

#	Article	IF	Citations
2600	Fullâ€length <scp>mRNA</scp> sequencing and gene expression profiling reveal broad involvement of natural antisense transcript gene pairs in pepper development and response to stresses. Plant Journal, 2019, 99, 763-783.	2.8	9
2601	Evaluation of Phage Therapy in the Context of Enterococcus faecalis and Its Associated Diseases. Viruses, 2019, 11, 366.	1.5	55
2602	Complete assembly of the Leishmania donovani (HU3 strain) genome and transcriptome annotation. Scientific Reports, 2019, 9, 6127.	1.6	18
2603	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	3.8	81
2604	Genes Associated With Psychrotolerant Bacillus cereus Group Isolates. Frontiers in Microbiology, 2019, 10, 662.	1.5	6
2605	Sequencing of Cultivated Peanut, Arachis hypogaea, Yields Insights into Genome Evolution and Oil Improvement. Molecular Plant, 2019, 12, 920-934.	3.9	185
2606	Evolution of Complex Thallus Alga: Genome Sequencing of Saccharina japonica. Frontiers in Genetics, 2019, 10, 378.	1.1	20
2607	Genomic Plasticity Mediated by Transposable Elements in the Plant Pathogenic Fungus Colletotrichum higginsianum. Genome Biology and Evolution, 2019, 11, 1487-1500.	1.1	47
2608	OrthoVenn2: a web server for whole-genome comparison and annotation of orthologous clusters across multiple species. Nucleic Acids Research, 2019, 47, W52-W58.	6.5	661
2609	Novel lineageâ€specific transmembrane Î²â€barrel proteins in the endoplasmic reticulum of <i>EntamoebaÂhistolytica</i>. FEBS Journal, 2019, 286, 3416-3432.	2.2	4
2610	The genomes of pecan and Chinese hickory provide insights into Carya evolution and nut nutrition. GigaScience, 2019, 8, .	3.3	88
2611	Rapid functional divergence after small-scale gene duplication in grasses. BMC Evolutionary Biology, 2019, 19, 97.	3.2	23
2612	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
2613	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. Nature Genetics, 2019, 51, 865-876.	9.4	398
2614	Molecular convergence and positive selection associated with the evolution of symbiont transmission mode in stony corals. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190111.	1.2	5
2615	In-depth transcriptome characterization uncovers distinct gene family expansions for Cupressus gigantea important to this long-lived speciesâ€™ adaptability to environmental cues. BMC Genomics, 2019, 20, 213.	1.2	12
2616	Infection mechanisms and putative effector repertoire of the mosquito pathogenic oomycete Pythium guiyangense uncovered by genomic analysis. PLoS Genetics, 2019, 15, e1008116.	1.5	38
2617	The Significance of Comparative Genomics in Modern Evolutionary Venomics. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	26

#	Article	IF	Citations
2618	Chromosome-Level Assembly of the Chinese Seabass (Lateolabrax maculatus) Genome. Frontiers in Genetics, 2019, 10, 275.	1.1	33
2619	Genomic Analyses of Bifidobacterium moukalabense Reveal Adaptations to Frugivore/Folivore Feeding Behavior. Microorganisms, 2019, 7, 99.	1.6	6
2620	Complete genome sequence of bile-isolated Enterococcus avium strain 352. Gut Pathogens, 2019, 11, 16.	1.6	12
2621	Mitotic Recombination and Rapid Genome Evolution in the Invasive Forest Pathogen <i>Phytophthora ramorum</i>. MBio, 2019, 10, .	1.8	50
2622	Rapid genetic and phenotypic changes in Pseudomonas aeruginosa clinical strains during ventilator-associated pneumonia. Scientific Reports, 2019, 9, 4720.	1.6	24
2623	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
2624	Inadvertent Paralog Inclusion Drives Artifactual Topologies and Timetree Estimates in Phylogenomics. Molecular Biology and Evolution, 2019, 36, 1344-1356.	3.5	56
2625	New insights into the origin and evolution of Î±-amylase genes in green plants. Scientific Reports, 2019, 9, 4929.	1.6	14
2626	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
2627	Adaptations and evolution of a heritable leaf nodule symbiosis between <i>Dioscorea sansibarensis</i> and <i>Orrella dioscoreae</i>. ISME Journal, 2019, 13, 1831-1844.	4.4	17
2628	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7137-7146.	3.3	108
2629	Plant-Pathogenic <i>Agrobacterium tumefaciens</i> Strains Have Diverse Type VI Effector-Immunity Pairs and Vary in In-Planta Competitiveness. Molecular Plant-Microbe Interactions, 2019, 32, 961-971.	1.4	36
2630	Systematic Identification of Pathogenic <i>Streptomyces</i> sp. AMCC400023 That Causes Common Scab and Genomic Analysis of Its Pathogenicity Island. Phytopathology, 2019, 109, 1115-1128.	1.1	11
2631	Genome-wide analysis reveals the genomic features of the turkey vulture (Cathartes aura) as a scavenger. Molecular Genetics and Genomics, 2019, 294, 679-692.	1.0	10
2632	PamulDB: a comprehensive genomic resource for the study of human- and animal-pathogenic <i>Pasteurella multocida</i>. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	1
2633	Comparative Genome Analysis of Lactococcus lactis Indicates Niche Adaptation and Resolves Genotype/Phenotype Disparity. Frontiers in Microbiology, 2019, 10, 4.	1.5	50
2634	Genome and secretome of Chondrostereum purpureum correspond to saprotrophic and phytopathogenic life styles. PLoS ONE, 2019, 14, e0212769.	1.1	11
2635	Comparative genomics sheds light on the predatory lifestyle of accipitrids and owls. Scientific Reports, 2019, 9, 2249.	1.6	14

#	ARTICLE	IF	CITATIONS
2636	The Draft Genome of an Octocoral, <i>Dendronephthya gigantea</i>. Genome Biology and Evolution, 2019, 11, 949-953.	1.1	44
2637	Contrasting patterns of divergence at the regulatory and sequence level in European <i>Daphnia galeata</i> natural populations. Ecology and Evolution, 2019, 9, 2487-2504.	0.8	6
2638	Water impacts nutrient dose responses genome-wide to affect crop production. Nature Communications, 2019, 10, 1374.	5.8	19
2639	Paternally Expressed Imprinted Genes under Positive Darwinian Selection in Arabidopsis thaliana. Molecular Biology and Evolution, 2019, 36, 1239-1253.	3.5	18
2640	A process of convergent amplification and tissueâ€specific expression dominates the evolution of toxin and toxinâ€like genes in sea anemones. Molecular Ecology, 2019, 28, 2272-2289.	2.0	48
2641	Tea Plant Information Archive: a comprehensive genomics and bioinformatics platform for tea plant. Plant Biotechnology Journal, 2019, 17, 1938-1953.	4.1	220
2642	Structural organization and functional divergence of high isoelectric point Î±-amylase genes in bread wheat (Triticum aestivum L.) and barley (Hordeum vulgare L.). BMC Genetics, 2019, 20, 25.	2.7	19
2643	An Experimental Human Blood-Stage Model for Studying Plasmodium malariae Infection. Journal of Infectious Diseases, 2020, 221, 948-955.	1.9	18
2644	Genome-wide analyses reveal genes subject to positive selection in Toxoplasma gondii. Gene, 2019, 699, 73-79.	1.0	1
2645	Acquisition and Loss of Secondary Metabolites Shaped the Evolutionary Path of Three Emerging Phytopathogens of Wheat. Genome Biology and Evolution, 2019, 11, 890-905.	1.1	22
2647	Evolution of Cold Acclimation and Its Role in Niche Transition in the Temperate Grass Subfamily Pooideae. Plant Physiology, 2019, 180, 404-419.	2.3	45
2648	Genomic changes underlying host specialization in the bee gut symbiont <i>Lactobacillus</i> Firm5. Molecular Ecology, 2019, 28, 2224-2237.	2.0	45
2649	Bioinformatics applied to biotechnology: A review towards bioenergy research. Biomass and Bioenergy, 2019, 123, 195-224.	2.9	17
2650	Whole-genome resequencing of 472 Vitis accessions for grapevine diversity and demographic history analyses. Nature Communications, 2019, 10, 1190.	5.8	155
2651	Computational identification of co-evolving multi-gene modules in microbial biosynthetic gene clusters. Communications Biology, 2019, 2, 83.	2.0	20
2652	Draft Genome Sequence of Trypanosoma equiperdum Strain IVM-t1. Microbiology Resource Announcements, 2019, 8, .	0.3	12
2653	In silico characterization of multiple genes encoding the GP63 virulence protein from Leishmania braziliensis: identification of sources of variation and putative roles in immune evasion. BMC Genomics, 2019, 20, 118.	1.2	15
2654	Comparative genomics of plant pathogenic Botrytis species with distinct host specificity. BMC Genomics, 2019, 20, 203.	1.2	53

#	Article	IF	Citations
2655	Genome-enhanced detection and identification of fungal pathogens responsible for pine and poplar rust diseases. PLoS ONE, 2019, 14, e0210952.	1.1	14
2657	Draft Genome Sequencing of the Pathogenic Fungus <i>Cladosporium phlei</i> ATCC 36193 Identifies Candidates of Novel Polyketide Synthase Genes Involved in Perylenequinone-Group Pigment Production. Evolutionary Bioinformatics, 2019, 15, 117693431983130.	0.6	6
2658	Multispecies genome-wide analysis defines the MAP3K gene family in Gossypium hirsutum and reveals conserved family expansions. BMC Bioinformatics, 2019, 20, 99.	1.2	5
2659	Phylogenomic analyses and divergence time estimation of Elateroidea (Coleoptera) based on RNA-Seq data. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 30, 283-289.	0.4	10
2660	Genome sequence of the corn leaf aphid (<i>Rhopalosiphum maidis</i>Fitch). GigaScience, 2019, 8, .	3.3	60
2661	Gene Family Evolutionâ€"An Algorithmic Framework. Computational Biology, 2019, , 87-119.	0.1	9
2662	Identification and evolution of GRAS transcription factor family in four Brassica species. AIP Conference Proceedings, 2019, , .	0.3	3
2663	The First Transcriptome Assembly of Yenyuan Stream Salamander (Batrachuperus yenyuanensis) Provides Novel Insights into Its Molecular Evolution. International Journal of Molecular Sciences, 2019, 20, 1529.	1.8	7
2664	Quantitative Proteomic Analysis of the Response of Probiotic Putative Lactococcus lactis NCDO 2118 Strain to Different Oxygen Availability Under Temperature Variation. Frontiers in Microbiology, 2019, 10, 759.	1.5	12
2665	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. Nature Ecology and Evolution, 2019, 3, 823-833.	3.4	99
2666	The genome of the giant Nomuraâ€™s jellyfish sheds light on the early evolution of active predation. BMC Biology, 2019, 17, 28.	1.7	38
2667	Comparative genomics and transcriptomics analysis reveals evolution patterns of selection in the Salix phylogeny. BMC Genomics, 2019, 20, 253.	1.2	9
2668	A high-quality apple genome assembly reveals the association of a retrotransposon and red fruit colour. Nature Communications, 2019, 10, 1494.	5.8	254
2669	Rhodnius prolixus: Identification of missing components of the IMD immune signaling pathway and functional characterization of its role in eliminating bacteria. PLoS ONE, 2019, 14, e0214794.	1.1	37
2670	Comparative Genomics Reveals the Genetic Mechanisms of Musk Secretion and Adaptive Immunity in Chinese Forest Musk Deer. Genome Biology and Evolution, 2019, 11, 1019-1032.	1.1	17
2671	Variation of gene expression in plants is influenced by gene architecture and structural properties of promoters. PLoS ONE, 2019, 14, e0212678.	1.1	29
2672	<i>De novo</i> genome assembly of the white-spotted flower chafer (<i>Protaetia brevitarsis</i>). GigaScience, 2019, 8, .	3.3	28
2673	Gene duplication and evolution in recurring polyploidizationâ€"diploidization cycles in plants. Genome Biology, 2019, 20, 38.	3.8	542

#	Article	IF	Citations
2674	Haplotype-Phased Genome Assembly of Virulent <i>Phytophthora ramorum</i> Isolate ND886 Facilitated by Long-Read Sequencing Reveals Effector Polymorphisms and Copy Number Variation. Molecular Plant-Microbe Interactions, 2019, 32, 1047-1060.	1.4	24
2675	A Chromosome-Scale Genome Assembly of Paper Mulberry (Broussonetia papyrifera) Provides New Insights into Its Forage and Papermaking Usage. Molecular Plant, 2019, 12, 661-677.	3.9	83
2676	GeM-Pro: a tool for genome functional mining and microbial profiling. Applied Microbiology and Biotechnology, 2019, 103, 3123-3134.	1.7	13
2677	The genomic basis for colonizing the freezing Southern Ocean revealed by Antarctic toothfish and Patagonian robalo genomes. GigaScience, 2019, 8, .	3.3	47
2678	Transcriptomics Identifies Modules of Differentially Expressed Genes and Novel Cyclotides in Viola pubescens. Frontiers in Plant Science, 2019, 10, 156.	1.7	12
2679	A Cluster of MYB Transcription Factors Regulates Anthocyanin Biosynthesis in Carrot (Daucus carota) Tj ETQq1 1 0.784314 rgBT /Overl	1.7	64
2680	Rapid turnover of life-cycle-related genes in the brown algae. Genome Biology, 2019, 20, 35.	3.8	36
2681	Contrasting Patterns of Rapid Molecular Evolution within the<i>p53</i>Network across Mammal and Sauropsid Lineages. Genome Biology and Evolution, 2019, 11, 629-643.	1.1	7
2682	Molecular evidence for distinct modes of nutrient acquisition between visceral and neurotropic schistosomes of birds. Scientific Reports, 2019, 9, 1347.	1.6	17
2683	Unveiling the Kinomes of Leishmania infantum and L. braziliensis Empowers the Discovery of New Kinase Targets and Antileishmanial Compounds. Computational and Structural Biotechnology Journal, 2019, 17, 352-361.	1.9	16
2684	Evolutionary dynamics of linc RNA transcription in nine citrus species. Plant Journal, 2019, 98, 912-927.	2.8	43
2685	Complex population evolutionary history of four cold-tolerant Notopterygium herb species in the Qinghai-Tibetan Plateau and adjacent areas. Heredity, 2019, 123, 242-263.	1.2	14
2686	Plasmodium falciparum specific helicase 2 is a dual, bipolar helicase and is crucial for parasite growth. Scientific Reports, 2019, 9, 1519.	1.6	5
2687	Antarctic blackfin icefish genome reveals adaptations to extreme environments. Nature Ecology and Evolution, 2019, 3, 469-478.	3.4	115
2688	The Galleria mellonella Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. Cell Reports, 2019, 26, 2451-2464.e5.	2.9	103
2689	Genome Sequencing of Cladobotryum protrusum Provides Insights into the Evolution and Pathogenic Mechanisms of the Cobweb Disease Pathogen on Cultivated Mushroom. Genes, 2019, 10, 124.	1.0	25
2690	Carbohydrate catabolic capability of a Flavobacteriia bacterium isolated from hadal water. Systematic and Applied Microbiology, 2019, 42, 263-274.	1.2	25
2691	Unraveling the complex genome of Saccharum spontaneum using Polyploid Gene Assembler. DNA Research, 2019, 26, 205-216.	1.5	8

#	ARTICLE	IF	CITATIONS
2692	Wnt Signaling Pathway Linked to Intestinal Regeneration via Evolutionary Patterns and Gene Expression in the Sea Cucumber Apostichopus japonicus. Frontiers in Genetics, 2019, 10, 112.	1.1	27
2693	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. Communications Biology, 2019, 2, 56.	2.0	75
2694	Evolutionary Origins of Pseudogenes and Their Association with Regulatory Sequences in Plants. Plant Cell, 2019, 31, 563-578.	3.1	47
2695	Developing a High-Quality Linkage Map for the Atlantic Killifish<i>Fundulus heteroclitus</i>. G3: Genes, Genomes, Genetics, 2019, 9, 2851-2862.	0.8	11
2696	Draft Genome of Busseola fusca, the Maize Stalk Borer, a Major Crop Pest in Sub-Saharan Africa. Genome Biology and Evolution, 2019, 11, 2203-2207.	1.1	5
2697	Identifying molecularly defined antigens for a Histoplasma capsulatum-specific interferon gamma release assay. Revista Iberoamericana De Micologia, 2019, 36, 186-191.	0.4	2
2698	A partial genome assembly of the miniature parasitoid wasp, Megaphragma amalphitanum. PLoS ONE, 2019, 14, e0226485.	1.1	10
2699	Gene Regulation Shifts Shed Light on Fungal Adaption in Plant Biomass Decomposers. MBio, 2019, 10, .	1.8	47
2700	Redox Regulation of a Light-Harvesting Antenna Complex in an Anoxygenic Phototroph. MBio, 2019, 10, .	1.8	14
2701	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. MSystems, 2019, 4, .	1.7	36
2702	Tung Tree (Vernicia fordii) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. Genomics, Proteomics and Bioinformatics, 2019, 17, 558-575.	3.0	43
2703	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. Plant Cell, 2019, 31, 2430-2455.	3.1	198
2704	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. MBio, 2019, 10, .	1.8	37
2705	Recapitulation-like developmental transitions of chromatin accessibility in vertebrates. Zoological Letters, 2019, 5, 33.	0.7	24
2706	<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
2707	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
2708	Genome Sequencing of <i>Pleurozium schreberi</i>: The Assembled and Annotated Draft Genome of a Pleurocarpous Feather Moss. G3: Genes, Genomes, Genetics, 2019, 9, 2791-2797.	0.8	35
2709	<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

#	Article	IF	Citations
2710	The genome of a subterrestrial nematode reveals adaptations to heat. Nature Communications, 2019, 10, 5268.	5.8	22
2711	OrthoFinder: phylogenetic orthology inference for comparative genomics. Genome Biology, 2019, 20, 238.	3.8	3,367
2712	Genomeâ€"Scale Metabolic Networks Shed Light on the Carotenoid Biosynthesis Pathway in the Brown Algae Saccharina japonica and Cladosiphon okamuranus. Antioxidants, 2019, 8, 564.	2.2	19
2713	A High-quality Draft Genome Assembly of the Black-necked Crane (Grus nigricollis) Based on Nanopore Sequencing. Genome Biology and Evolution, 2019, 11, 3332-3340.	1.1	5
2714	Resolution of deep divergence of club fungi (phylum Basidiomycota). Synthetic and Systems Biotechnology, 2019, 4, 225-231.	1.8	6
2715	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
2716	Convergent degeneration of olfactory receptor gene repertoires in marine mammals. BMC Genomics, 2019, 20, 977.	1.2	31
2717	Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of Croton draco (Euphorbiaceae). BMC Plant Biology, 2019, 19, 560.	1.6	7
2718	A Phylogenomic Analysis of the Floral Transcriptomes of Sexually Deceptive and Rewarding European Orchids, Ophrys and Gymnadenia. Frontiers in Plant Science, 2019, 10, 1553.	1.7	26
2719	The genetic basis of adaptive evolution in parasitic environment from the Angiostrongylus cantonensis genome. PLoS Neglected Tropical Diseases, 2019, 13, e0007846.	1.3	9
2720	Broad-Spectrum Amino Acid Transporters ClAAP3 and ClAAP6 Expressed in Watermelon Fruits. International Journal of Molecular Sciences, 2019, 20, 5855.	1.8	2
2721	Signatures of the Evolution of Parthenogenesis and Cryptobiosis in the Genomes of Panagrolaimid Nematodes. IScience, 2019, 21, 587-602.	1.9	27
2722	Hostâ€"Symbiont Interactions in Deep-Sea Chemosymbiotic Vesicomyid Clams: Insights From Transcriptome Sequencing. Frontiers in Marine Science, 2019, 6, .	1.2	17
2723	Trochodendron aralioides, the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. GigaScience, 2019, 8, .	3.3	20
2724	A Mesophilic Aeromonas salmonicida Strain Isolated from an Unsuspected Host, the Migratory Bird Pied Avocet. Microorganisms, 2019, 7, 592.	1.6	16
2725	A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. Scientific Data, 2019, 6, 281.	2.4	28
2726	Phylogenomics investigation of sparids (Teleostei: Spariformes) using high-quality proteomes highlights the importance of taxon sampling. Communications Biology, 2019, 2, 400.	2.0	7
2727	Development and Application of a Software Tool/Package for Pan-Genomic Analysis. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
2728	First Draft Genome Assembly of Redlip Mullet (Liza haematocheila) From Family Mugilidae. Frontiers in Genetics, 2019, 10, 1246.	1.1	7
2729	RNA-seq, de novo transcriptome assembly and flavonoid gene analysis in 13 wild and cultivated berry fruit species with high content of phenolics. BMC Genomics, 2019, 20, 995.	1.2	27
2730	Genome sequencing of Mycobacterium pinnipedii strains: genetic characterization and evidence of superinfection in a South American sea lion (Otaria flavescens). BMC Genomics, 2019, 20, 1030.	1.2	21
2731	Charting the diversity of uncultured viruses of Archaea and Bacteria. BMC Biology, 2019, 17, 109.	1.7	26
2732	Genomic and transcriptomic insights into molecular basis of sexually dimorphic nuptial spines in Leptobrachium leishanense. Nature Communications, 2019, 10, 5551.	5.8	52
2733	SimSpliceEvol: alternative splicing-aware simulation of biological sequence evolution. BMC Bioinformatics, 2019, 20, 640.	1.2	3
2734	ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. BMC Genomics, 2019, 20, 981.	1.2	18
2735	Crowdsourcing and the feasibility of manual gene annotation: A pilot study in the nematode Pristionchus pacificus. Scientific Reports, 2019, 9, 18789.	1.6	22
2736	Genomic insights into mite phylogeny, fitness, development, and reproduction. BMC Genomics, 2019, 20, 954.	1.2	25
2737	A whole genome assembly of <i>Leptospermum scoparium</i> (Myrtaceae) for mÄnuka research. New Zealand Journal of Crop and Horticultural Science, 2019, 47, 233-260.	0.7	31
2738	Basal Rot of Narcissus: Understanding Pathogenicity in Fusarium oxysporum f. sp. narcissi. Frontiers in Microbiology, 2019, 10, 2905.	1.5	8
2739	Enzymatic Adaptation of Podospora anserina to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. Biotechnology Journal, 2019, 14, 1800185.	1.8	11
2740	Computational determination of gene age and characterization of evolutionary dynamics in human. Briefings in Bioinformatics, 2019, 20, 2141-2149.	3.2	1
2741	Secretome Analysis and In Planta Expression of Salivary Proteins Identify Candidate Effectors from the Brown Planthopper <i>Nilaparvata lugens</i>. Molecular Plant-Microbe Interactions, 2019, 32, 227-239.	1.4	57
2742	Draft genome of the cotton aphid Aphis gossypii. Insect Biochemistry and Molecular Biology, 2019, 105, 25-32.	1.2	55
2743	Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant <i>Balanophora</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 934-943.	3.3	66
2744	Chromosomal level reference genome of <i>Tachypleus tridentatus</i> provides insights into evolution and adaptation of horseshoe crabs. Molecular Ecology Resources, 2019, 19, 744-756.	2.2	25
2745	Understanding the transition from water to land: Insights from multi-omic analyses of the perivitelline fluid of apple snail eggs. Journal of Proteomics, 2019, 194, 79-88.	1.2	11

#	Article	IF	Citations
2746	VFDB 2019: a comparative pathogenomic platform with an interactive web interface. Nucleic Acids Research, 2019, 47, D687-D692.	6.5	1,286
2747	Lineage-Specific Expression Divergence in Grasses Is Associated with Male Reproduction, Host-Pathogen Defense, and Domestication. Genome Biology and Evolution, 2019, 11, 207-219.	1.1	6
2748	Pelagiphages in the <i>Podoviridae</i> family integrate into host genomes. Environmental Microbiology, 2019, 21, 1989-2001.	1.8	50
2749	Genome-wide identification, characterization, and expression analysis of the expansin gene family in Chinese jujube (Ziziphus jujuba Mill.). Planta, 2019, 249, 815-829.	1.6	32
2750	Long-Read Annotation: Automated Eukaryotic Genome Annotation Based on Long-Read cDNA Sequencing. Plant Physiology, 2019, 179, 38-54.	2.3	45
2751	Transâ€lineage polymorphism and nonbifurcating diversification of the genus <i>Picea</i>. New Phytologist, 2019, 222, 576-587.	3.5	29
2752	Transcriptome and Comparative Genomics Analyses Reveal New Functional Insights on Key Determinants of Pathogenesis and Interbacterial Competition in <i>Pectobacterium</i> and <i>Dickeya</i> spp. Applied and Environmental Microbiology, 2019, 85, .	1.4	61
2753	The genome of the medicinal plant <i>Andrographis paniculata</i> provides insight into the biosynthesis of the bioactive diterpenoid neoandrographolide. Plant Journal, 2019, 97, 841-857.	2.8	75
2754	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
2755	Pan-genomic analysis provides novel insights into the association of <i>E.coli</i> with human host and its minimal genome. Bioinformatics, 2019, 35, 1987-1991.	1.8	22
2756	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
2757	The genome of â€˜Candidatus Phytoplasma solaniâ€™ strain SA-1 is highly dynamic and prone to adopting foreign sequences. Systematic and Applied Microbiology, 2019, 42, 117-127.	1.2	53
2758	Phylogenetic analysis of upland cotton MATE gene family reveals a conserved subfamily involved in transport of proanthocyanidins. Molecular Biology Reports, 2019, 46, 161-175.	1.0	17
2759	Molecular docking and in silico studies of the physicochemical properties of potential inhibitors for the phosphotransferase system of Streptococcus mutans. Archives of Oral Biology, 2019, 98, 164-175.	0.8	5
2760	Species-specific genes account for the differences in floral transition between continuous-flowering and once-flowering roses. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 312-319.	0.9	1
2761	The Evolutionary Traceability of a Protein. Genome Biology and Evolution, 2019, 11, 531-545.	1.1	23
2762	Gene duplication and genetic innovation in cereal genomes. Genome Research, 2019, 29, 261-269.	2.4	29
2763	Genome Sequence of<i>Jaltomata</i>Addresses Rapid Reproductive Trait Evolution and Enhances Comparative Genomics in the Hyper-Diverse Solanaceae. Genome Biology and Evolution, 2019, 11, 335-349.	1.1	17

#	Article	IF	Citations
2764	Plant-specific ribosome biogenesis factors in <i>Arabidopsis thaliana</i> with essential function in rRNA processing. Nucleic Acids Research, 2019, 47, 1880-1895.	6.5	47
2765	Conserved transcriptomic profiles underpin monogamy across vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1331-1336.	3.3	75
2766	Delineation of the pan-proteome of fish-pathogenic Streptococcus agalactiae strains using a label-free shotgun approach. BMC Genomics, 2019, 20, 11.	1.2	23
2767	Comparative bioinformatic analysis suggests that specific dauer-like signalling pathway components regulate Toxocara canis development and migration in the mammalian host. Parasites and Vectors, 2019, 12, 32.	1.0	15
2768	Complete and de novo assembly of the Leishmania braziliensis (M2904) genome. Memorias Do Instituto Oswaldo Cruz, 2019, 114, e180438.	0.8	17
2769	Genomic Characterization Provides New Insights Into the Biosynthesis of the Secondary Metabolite Huperzine a in the Endophyte Colletotrichum gloeosporioides Cg01. Frontiers in Microbiology, 2018, 9, 3237.	1.5	23
2770	Innate immunity in the simplest animals â€“ placozoans. BMC Genomics, 2019, 20, 5.	1.2	28
2771	Putative antibiotic resistance genes present in extant Bacillus licheniformis and Bacillus paralicheniformis strains are probably intrinsic and part of the ancient resistome. PLoS ONE, 2019, 14, e0210363.	1.1	30
2772	Genome-wide identification and comparative analysis of alternative splicing across four legume species. Planta, 2019, 249, 1133-1142.	1.6	16
2773	Pedobacter paludis sp. nov., isolated from wetland soil. Archives of Microbiology, 2019, 201, 349-355.	1.0	4
2774	A unique life-strategy of an endophytic yeast Rhodotorula mucilaginosa JGTA-S1â€”a comparative genomics viewpoint. DNA Research, 2019, 26, 131-146.	1.5	25
2775	Landscape of gene transpositionâ€“duplication within the Brassicaceae family. DNA Research, 2019, 26, 21-36.	1.5	19
2776	Identification of Phytocyanin Gene Family in Legume Plants and their Involvement in Nodulation of<i>Medicago truncatula</i>. Plant and Cell Physiology, 2019, 60, 900-915.	1.5	12
2777	Differential co-expression networks of long non-coding RNAs and mRNAs in Cleistogenes songorica under water stress and during recovery. BMC Plant Biology, 2019, 19, 23.	1.6	70
2778	Comparative proteomic analysis of four biotechnological strains <i>Lactococcus lactis</i> through labelâ€free quantitative proteomics. Microbial Biotechnology, 2019, 12, 265-274.	2.0	19
2779	Independent losses and duplications of autophagyâ€related genes in fungal tree of life. Environmental Microbiology, 2019, 21, 226-243.	1.8	11
2780	Genomic and Transcriptomic Basis of Hanseniaspora vineae's Impact on Flavor Diversity and Wine Quality. Applied and Environmental Microbiology, 2019, 85, .	1.4	51
2781	Revising the taxonomy of the Acinetobacter lwoffii group: The description of Acinetobacter pseudolwoffii sp. nov. and emended description of Acinetobacter lwoffii. Systematic and Applied Microbiology, 2019, 42, 159-167.	1.2	45

#	Article	IF	Citations
2782	Computational analysis of alternative splicing in plant genomes. Gene, 2019, 685, 186-195.	1.0	9
2783	Insight into the evolution and functional characteristics of the panâ€genome assembly from sesame landraces and modern cultivars. Plant Biotechnology Journal, 2019, 17, 881-892.	4.1	79
2784	Fall webworm genomes yield insights into rapid adaptation of invasive species. Nature Ecology and Evolution, 2019, 3, 105-115.	3.4	82
2785	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	3.3	108
2786	First assembly of the geneâ€space of <i>Lolium multiflorum</i> and comparison to other Poaceae genomes. Grassland Science, 2019, 65, 125-134.	0.6	20
2787	ORTHOSCOPE: An Automatic Web Tool for Phylogenetically Inferring Bilaterian Orthogroups with User-Selected Taxa. Molecular Biology and Evolution, 2019, 36, 621-631.	3.5	21
2788	Draft genomes and genomic divergence of two <i>Lepidurus</i> tadpole shrimp species (Crustacea,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.2	14
2789	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. Molecular Genetics and Genomics, 2019, 294, 211-226.	1.0	10
2790	High intraspecific diversity of <i>Restorerâ€ofâ€fertilityâ€like</i> genes in barley. Plant Journal, 2019, 97, 281-295.	2.8	24
2791	Comparative analysis of spleen transcriptome detects differences in evolutionary adaptation of immune defense functions in bighead carp and silver carp. Fish and Shellfish Immunology, 2019, 84, 148-157.	1.6	12
2792	A comparative in silico linear B-cell epitope prediction and characterization for South American and African Trypanosoma vivax strains. Genomics, 2019, 111, 407-417.	1.3	16
2793	CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 981-989.	1.9	2
2794	OBSOLETE: Bioinformatic Platforms for Metagenomics. , 2020, , .		0
2795	Network-based methods for predicting essential genes or proteins: a survey. Briefings in Bioinformatics, 2020, 21, 566-583.	3.2	90
2796	Whole genome sequencing and genome annotation of the wild edible mushroom, Russula griseocarnosa. Genomics, 2020, 112, 603-614.	1.3	30
2797	Comprehensive Analysis of Wall-Associated Kinase Genes and Their Expression Under Abiotic and Biotic Stress in Chinese Cabbage (Brassica rapa ssp. pekinensis). Journal of Plant Growth Regulation, 2020, 39, 72-86.	2.8	13
2798	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (Moringa oleifera). Genomics, 2020, 112, 621-628.	1.3	22
2799	Comparative genomics reveals differences in algal galactan biosynthesis and related pathways in early and late diverging red algae. Genomics, 2020, 112, 1536-1544.	1.3	6

#	ARTICLE	IF	CITATIONS
2800	Serial horizontal transfer of vitamin-biosynthetic genes enables the establishment of new nutritional symbionts in aphidsâ€™ di-symbiotic systems. ISME Journal, 2020, 14, 259-273.	4.4	79
2801	A chromosomeâ€level genome assembly reveals the genetic basis of cold tolerance in a notorious rice insect pest, <i>Chilo suppressalis</i>. Molecular Ecology Resources, 2020, 20, 268-282.	2.2	51
2802	A chromosomeâ€level genome assembly of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). Molecular Ecology Resources, 2020, 20, 216-227.	2.2	37
2803	Comparative genome/transcriptome analysis probes Boraginales' phylogenetic position, WGDs in Boraginales, and key enzyme genes in the alkannin/shikonin core pathway. Molecular Ecology Resources, 2020, 20, 228-241.	2.2	24
2804	Genome sequencing of the Australian wild diploid species <i>Gossypium australe</i> highlights disease resistance and delayed gland morphogenesis. Plant Biotechnology Journal, 2020, 18, 814-828.	4.1	61
2805	Recurrent genome duplication events likely contributed to both the ancient and recent rise of ferns. Journal of Integrative Plant Biology, 2020, 62, 433-455.	4.1	43
2806	Whole-genome sequencing and analysis of the Chinese herbal plant Gelsemium elegans. Acta Pharmaceutica Sinica B, 2020, 10, 374-382.	5.7	29
2807	Genome-wide analysis sheds light on the high-altitude adaptation of the buff-throated partridge (Tetraophasis szechenyii). Molecular Genetics and Genomics, 2020, 295, 31-46.	1.0	11
2808	The draft genome of a wild barley genotype reveals its enrichment in genes related to biotic and abiotic stresses compared to cultivated barley. Plant Biotechnology Journal, 2020, 18, 443-456.	4.1	45
2809	Exploring the evolutionary dynamics of <i>Rhizobium</i> plasmids through bipartite network analysis. Environmental Microbiology, 2020, 22, 934-951.	1.8	7
2810	Comparative transcriptomics enables the identification of functional orthologous genes involved in early leaf growth. Plant Biotechnology Journal, 2020, 18, 553-567.	4.1	24
2811	Accessing Cryptosporidium Omic and Isolate Data via CryptoDB.org. Methods in Molecular Biology, 2020, 2052, 139-192.	0.4	10
2812	Genomic evidence sheds light on the genetic mechanisms of musk secretion in muskrats. International Journal of Biological Macromolecules, 2020, 145, 1189-1198.	3.6	3
2813	Phylogenetic analysis revealed that Salmonella Typhimurium ST313 isolated from humans and food in Brazil presented a high genomic similarity. Brazilian Journal of Microbiology, 2020, 51, 53-64.	0.8	4
2814	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
2815	Phylogenomics of the genus <i>Populus</i> reveals extensive interspecific gene flow and balancing selection. New Phytologist, 2020, 225, 1370-1382.	3.5	93
2816	Genetic Contribution of Paleopolyploidy to Adaptive Evolution in Angiosperms. Molecular Plant, 2020, 13, 59-71.	3.9	178
2817	<i>Mesostigma viride</i> Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. Advanced Science, 2020, 7, 1901850.	5.6	40

#	ARTICLE	IF	CITATIONS
2818	Metatranscriptomics yields new genomic resources and sensitive detection of infections for diverse blood parasites. Molecular Ecology Resources, 2020, 20, 14-28.	2.2	25
2819	The improved assembly of 7DL chromosome provides insight into the structure and evolution of bread wheat. Plant Biotechnology Journal, 2020, 18, 732-742.	4.1	6
2820	Egg perivitelline fluid proteome of a freshwater snail: Insight into the transition from aquatic to terrestrial egg deposition. Rapid Communications in Mass Spectrometry, 2020, 34, e8605.	0.7	5
2821	Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of Brassica napus. Nature Plants, 2020, 6, 34-45.	4.7	449
2822	Domestication and breeding changed tomato fruit transcriptome. Journal of Integrative Agriculture, 2020, 19, 120-132.	1.7	18
2823	Chromosome-level genome assembly reveals the unique genome evolution of the swimming crab (Portunus trituberculatus). GigaScience, 2020, 9, .	3.3	44
2824	Comparative Genomics Analysis of Lactobacillus ruminis from Different Niches. Genes, 2020, 11, 70.	1.0	27
2825	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
2826	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
2827	A Sequential Multidimensional Analysis Algorithm for Aptamer Identification based on Structure Analysis and Machine Learning. Analytical Chemistry, 2020, 92, 3307-3314.	3.2	45
2828	Phylogenomics â€" principles, opportunities and pitfalls of bigâ€data phylogenetics. Systematic Entomology, 2020, 45, 225-247.	1.7	118
2829	The phylogeny of insects in the dataâ€driven era. Systematic Entomology, 2020, 45, 540-551.	1.7	18
2831	Characterization and expression analysis of seven putative JHBPs in the mud crab Scylla paramamosain: Putative relationship with methyl farnesoate. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2020, 241, 110390.	0.7	6
2832	Corynebacterium sanguinis sp. nov., a clinical and environmental associated corynebacterium. Systematic and Applied Microbiology, 2020, 43, 126039.	1.2	20
2833	Molecular evidence for adaptive evolution of olfactory-related genes in cervids. Genes and Genomics, 2020, 42, 355-360.	0.5	2
2834	Genomic mosaicism underlies the adaptation of marine <i>Synechococcus</i> ecotypes to distinct oceanic iron niches. Environmental Microbiology, 2020, 22, 1801-1815.	1.8	32
2835	The water lily genome and the early evolution of flowering plants. Nature, 2020, 577, 79-84.	13.7	238
2836	Functional Genomics of a Symbiotic Community: Shared Traits in the Olive Fruit Fly Gut Microbiota. Genome Biology and Evolution, 2020, 12, 3778-3791.	1.1	16

#	ARTICLE	IF	CITATIONS
2837	The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis. Molecular Plant, 2020, 13, 336-350.	3.9	73
2838	Early Stage Adaptation of a Mesophilic Green Alga to Antarctica: Systematic Increases in Abundance of Enzymes and LEA Proteins. Molecular Biology and Evolution, 2020, 37, 849-863.	3.5	12
2839	Comparative Genomics to Develop a Specific Multiplex PCR Assay for Detection of <i>Clavibacter michiganensis</i>. Phytopathology, 2020, 110, 556-566.	1.1	11
2840	Structure and genetics of<i>Escherichia coli</i>O antigens. FEMS Microbiology Reviews, 2020, 44, 655-683.	3.9	143
2841	A Tripartite Interaction among the Basidiomycete <i>Rhodotorula mucilaginosa</i>, N₂-Fixing Endobacteria, and Rice Improves Plant Nitrogen Nutrition. Plant Cell, 2020, 32, 486-507.	3.1	29
2842	The Coix Genome Provides Insights into Panicoideae Evolution and Papery Hull Domestication. Molecular Plant, 2020, 13, 309-320.	3.9	28
2843	Genomic landscape and genetic manipulation of the black soldier fly Hermetia illucens, a natural waste recycler. Cell Research, 2020, 30, 50-60.	5.7	136
2844	Comparison of <i>Arachis monticola</i> with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced Science, 2020, 7, 1901672.	5.6	43
2845	Longâ€read sequencing and de novo assembly of the <i>Luffa cylindrica</i> (L.) Roem. genome. Molecular Ecology Resources, 2020, 20, 511-519.	2.2	27
2846	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
2847	Expression of Heat Shock Proteins in Thermally Challenged Pacific Abalone Haliotis discus hannai. Genes, 2020, 11, 22.	1.0	17
2848	Draft Genomes of Two Artocarpus Plants, Jackfruit (A. heterophyllus) and Breadfruit (A. altilis). Genes, 2020, 11, 27.	1.0	30
2849	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
2850	First Steps in the Analysis of Prokaryotic Pan-Genomes. Bioinformatics and Biology Insights, 2020, 14, 117793222093806.	1.0	48
2851	Genome Sequence of the Human Opportunistic Fungus Arthrocladium fulminans (CBS 136243). G3: Genes, Genomes, Genetics, 2020, 10, 1817-1821.	0.8	3
2852	No Evidence That Homologs of Key Circadian Clock Genes Direct Circadian Programs of Development or mRNA Abundance in Verticillium dahliae. Frontiers in Microbiology, 2020, 11, 1977.	1.5	6
2853	A Pan-Genome Guided Metabolic Network Reconstruction of Five Propionibacterium Species Reveals Extensive Metabolic Diversity. Genes, 2020, 11, 1115.	1.0	18
2854	Conserved Patterns in Developmental Processes and Phases, Rather than Genes, Unite the Highly Divergent Bilateria. Life, 2020, 10, 182.	1.1	2

#	ARTICLE	IF	CITATIONS
2855	Integrated analysis of co-expression, conserved genes and gene families reveal core regulatory network of heat stress response in Cleistogenes songorica, a xerophyte perennial desert plant. BMC Genomics, 2020, 21, 715.	1.2	9
2856	Operon Prediction Using Broad Learning System. , 2020, , .		2
2857	Expanded genome-wide comparisons give novel insights into population structure and genetic heterogeneity of Leishmania tropica complex. PLoS Neglected Tropical Diseases, 2020, 14, e0008684.	1.3	14
2858	Genomic and experimental data provide new insights into luciferin biosynthesis and bioluminescence evolution in fireflies. Scientific Reports, 2020, 10, 15882.	1.6	14
2859	The genome of Chinese flowering cherry (Cerasus serrulata) provides new insights into Cerasus species. Horticulture Research, 2020, 7, 165.	2.9	22
2860	Genomic divergence between Dickeya zeae strain EC2 isolated from rice and previously identified strains, suggests a different rice foot rot strain. PLoS ONE, 2020, 15, e0240908.	1.1	5
2861	From Orphan Phage to a Proposed New Familyâ€"The Diversity of N4-Like Viruses. Antibiotics, 2020, 9, 663.	1.5	39
2862	Origin and adaptation to high altitude of Tibetan semi-wild wheat. Nature Communications, 2020, 11, 5085.	5.8	104
2863	Phylogenomics from transcriptomic â€œbycatchâ€•clarify the origins and diversity of avian trypanosomes in North America. PLoS ONE, 2020, 15, e0240062.	1.1	8
2864	Phylogenomics of the Epigenetic Toolkit Reveals Punctate Retention of Genes across Eukaryotes. Genome Biology and Evolution, 2020, 12, 2196-2210.	1.1	12
2865	Dynamics in Secondary Metabolite Gene Clusters in Otherwise Highly Syntenic and Stable Genomes in the Fungal Genus<i>Botrytis</i>. Genome Biology and Evolution, 2020, 12, 2491-2507.	1.1	22
2866	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 2020, 30, 5018-5025.e5.	1.8	34
2867	Historical isolation facilitates species radiation by sexual selection: Insights from <i>Chorthippus</i> grasshoppers. Molecular Ecology, 2020, 29, 4985-5002.	2.0	18
2868	Large-Scale Comparative Analyses of Tick Genomes Elucidate Their Genetic Diversity and Vector Capacities. Cell, 2020, 182, 1328-1340.e13.	13.5	145
2869	Genomic Analyses Reveal Genetic Adaptations to Tropical Climates in Chickens. IScience, 2020, 23, 101644.	1.9	28
2870	Positive Selection and Gene Expression Analyses from Salivary Glands Reveal Discrete Adaptations within the Ecologically Diverse Bat Family Phyllostomidae. Genome Biology and Evolution, 2020, 12, 1419-1428.	1.1	7
2871	Plasmids Related to the Symbiotic Nitrogen Fixation Are Not Only Cooperated Functionally but Also May Have Evolved over a Time Span in Family <i>Rhizobiaceae</i>. Genome Biology and Evolution, 2020, 12, 2002-2014.	1.1	14
2872	<i>Cercospora beticola</i>: The intoxicating lifestyle of the leaf spot pathogen of sugar beet. Molecular Plant Pathology, 2020, 21, 1020-1041.	2.0	39

#	Article	IF	Citations
2873	Illegitimate Recombination Between Homeologous Genes in Wheat Genome. Frontiers in Plant Science, 2020, 11, 1076.	1.7	11
2874	Genomic insights of body plan transitions from bilateral to pentameral symmetry in Echinoderms. Communications Biology, 2020, 3, 371.	2.0	34
2875	Excessive Parallelism in Protein Evolution of Lake Baikal Amphipod Species Flock. Genome Biology and Evolution, 2020, 12, 1493-1503.	1.1	1
2876	Is Phylotranscriptomics as Reliable as Phylogenomics?. Molecular Biology and Evolution, 2020, 37, 3672-3683.	3.5	52
2877	A newly recorded Rickettsia of the Torix group is a recent intruder and an endosymbiont in the whitefly Bemisia tabaci. Environmental Microbiology, 2020, 22, 1207-1221.	1.8	20
2878	Genomic insights on the contribution of balancing selection and local adaptation to the longâ€term survival of a widespread living fossil tree, <i>Cercidiphyllum japonicum</i>. New Phytologist, 2020, 228, 1674-1689.	3.5	22
2879	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
2880	ShadowCaster: Compositional Methods under the Shadow of Phylogenetic Models to Detect Horizontal Gene Transfers in Prokaryotes. Genes, 2020, 11, 756.	1.0	11
2881	Genomic characterization of Parengyodontium americanum sp. nov. Fungal Genetics and Biology, 2020, 138, 103351.	0.9	4
2882	Transcriptome and complete chloroplast genome of Glycyrrhiza inflata and comparative analyses with the other two licorice species. Genomics, 2020, 112, 4179-4188.	1.3	8
2883	Cestode strobilation: predictionÂof developmental genes and pathways. BMC Genomics, 2020, 21, 487.	1.2	5
2884	Speciation through chromosomal fusion and fission in Lepidoptera. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190539.	1.8	76
2885	Comparative genomics of rice false smut fungi Ustilaginoidea virens Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. 3 Biotech, 2020, 10, 342.	1.1	10
2886	Genome-wide analysis on the maize genome reveals weak selection on synonymous mutations. BMC Genomics, 2020, 21, 333.	1.2	12
2887	Genome-Scale Characterization of Predicted Plastid-Targeted Proteomes in Higher Plants. Scientific Reports, 2020, 10, 8281.	1.6	7
2888	Species Boundaries and Molecular Markers for the Classification of 16SrI Phytoplasmas Inferred by Genome Analysis. Frontiers in Microbiology, 2020, 11, 1531.	1.5	25
2889	Genome-enabled discovery of anthraquinone biosynthesis in Senna tora. Nature Communications, 2020, 11, 5875.	5.8	57
2890	Draft Genome of the European Mouflon (Ovis orientalis musimon). Frontiers in Genetics, 2020, 11, 533611.	1.1	3

#	Article	IF	Citations
2891	Genomic analysis of two Acinetobacter baumannii strains belonging to two different sequence types (ST172 and ST25). Journal of Global Antimicrobial Resistance, 2020, 23, 154-161.	0.9	6
2892	Evolution of Oxidative Phosphorylation (OXPHOS) Genes Reflecting the Evolutionary and Life Histories of Fig Wasps (Hymenoptera, Chalcidoidea). Genes, 2020, 11, 1353.	1.0	4
2893	A highâ€quality reference genome sequence of <i>Salvia miltiorrhiza</i> provides insights into tanshinone synthesis in its red rhizomes. Plant Genome, 2020, 13, e20041.	1.6	45
2894	Improved de novo Assembly of the Achlorophyllous Orchid Gastrodia elata. Frontiers in Genetics, 2020, 11, 580568.	1.1	11
2895	CAPRIB: a user-friendly tool to study amino acid changes and selection for the exploration of intra-genus evolution. BMC Genomics, 2020, 21, 832.	1.2	2
2896	Genomics and lipidomics analysis of the biotechnologically important oleaginous red yeast Rhodotorula glutinis ZHK provides new insights into its lipid and carotenoid metabolism. BMC Genomics, 2020, 21, 834.	1.2	16
2897	High-quality de novo assembly of the Eucommia ulmoides haploid genome provides new insights into evolution and rubber biosynthesis. Horticulture Research, 2020, 7, 183.	2.9	28
2898	Speciation and adaptive evolution reshape antioxidant enzymatic system diversity across the phylum Nematoda. BMC Biology, 2020, 18, 181.	1.7	10
2899	Whole Genome Sequencing and Tn5-Insertion Mutagenesis of Pseudomonas taiwanensis CMS to Probe Its Antagonistic Activity Against Rice Bacterial Blight Disease. International Journal of Molecular Sciences, 2020, 21, 8639.	1.8	2
2900	Bacteria-Derived Hemolysis-Related Genes Widely Exist in Scuticociliates. Microorganisms, 2020, 8, 1838.	1.6	4
2901	The de novo genome assembly of Tapiscia sinensis and the transcriptomic and developmental bases of androdioecy. Horticulture Research, 2020, 7, 191.	2.9	3
2902	Distribution and Evolution of the Bacteriophage WO and Its Antagonism With Wolbachia. Frontiers in Microbiology, 2020, 11, 595629.	1.5	12
2903	Miocene Diversification and High-Altitude Adaptation of Parnassius Butterflies (Lepidoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 267 754.	1.0	10
2904	Electrolocation? The evidence for redoxâ€mediated taxis in Shewanella oneidensis. Molecular Microbiology, 2020, 115, 1069-1079.	1.2	13
2905	The complete chloroplast genome of Isochrysis galbana and comparison with related haptophyte species. Algal Research, 2020, 50, 101989.	2.4	14
2906	A high-quality sponge gourd (Luffa cylindrica) genome. Horticulture Research, 2020, 7, 128.	2.9	35
2907	Dataset for homologous proteins in Drosophila melanogaster for SARS-CoV-2/human interactome. Data in Brief, 2020, 32, 106082.	0.5	7
2908	Genome sequence of Acremonium strictum AAJ6 strain isolated from the Cerrado biome in Brazil and CAZymes expression in thermotolerant industrial yeast for ethanol production. Process Biochemistry, 2020, 98, 139-150.	1.8	5

#	Article	IF	Citations
2909	Dissection of the domesticationâ€shaped genetic architecture of lettuce primary metabolism. Plant Journal, 2020, 104, 613-630.	2.8	24
2910	The Genome Sequence of Alpine Megacarpaea delavayi Identifies Species-Specific Whole-Genome Duplication. Frontiers in Genetics, 2020, 11, 812.	1.1	10
2911	The chromosome-level wintersweet (Chimonanthus praecox) genome provides insights into floral scent biosynthesis and flowering in winter. Genome Biology, 2020, 21, 200.	3.8	69
2912	Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biology, 2020, 21, 180.	3.8	419
2913	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
2914	A chromosomeâ€level genome assembly provides new insights into paternal genome elimination in the cotton mealybug <i>Phenacoccus solenopsis</i>. Molecular Ecology Resources, 2020, 20, 1733-1747.	2.2	12
2915	Analysis of the Antifungal Properties of Bacillus velezensis B-4 Through a Bioassay and Complete-Genome Sequencing. Frontiers in Genetics, 2020, 11, 703.	1.1	11
2916	Transcriptomic variation of the flowerâ€“fruit transition in Physalis and Solanum. Planta, 2020, 252, 28.	1.6	7
2917	Genomic Variation and Arsenic Tolerance Emerged as Niche Specific Adaptations by Different Exiguobacterium Strains Isolated From the Extreme Salar de Huasco Environment in Chilean â€“ Altiplano. Frontiers in Microbiology, 2020, 11, 1632.	1.5	14
2918	The whale shark genome reveals how genomic and physiological properties scale with body size. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20662-20671.	3.3	32
2919	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys. PLoS Pathogens, 2020, 16, e1008717.	2.1	18
2920	Enterococci from Wild Magellanic Penguins (Spheniscus magellanicus) as an Indicator of Marine Ecosystem Health and Human Impact. Applied and Environmental Microbiology, 2020, 86, .	1.4	5
2921	Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus Friedmanniomyces endolithicus. Fungal Biology, 2020, 124, 458-467.	1.1	23
2922	Evol2Circos: A Web-Based Tool for Genome Synteny and Collinearity Analysis and its Visualization in Fishes. Journal of Heredity, 2020, 111, 486-490.	1.0	4
2923	Life in hot acid: a genomeâ€based reassessment of the archaeal order <i>Sulfolobales</i>. Environmental Microbiology, 2021, 23, 3568-3584.	1.8	20
2924	Evolutionary Remodeling of the Cell Envelope in Bacteria of the Planctomycetes Phylum. Genome Biology and Evolution, 2020, 12, 1528-1548.	1.1	13
2925	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
2926	Genome of the four-finger threadfin Eleutheronema tetradactylum (Perciforms: Polynemidae). BMC Genomics, 2020, 21, 726.	1.2	4

#	ARTICLE	IF	CITATIONS
2927	Triticum population sequencing provides insights into wheat adaptation. Nature Genetics, 2020, 52, 1412-1422.	9.4	178
2928	Accurate reconstruction of bacterial pan- and core genomes with PEPPAN. Genome Research, 2020, 30, 1667-1679.	2.4	56
2929	Gene duplication and stress genomics in Brassicas: Current understanding and future prospects. Journal of Plant Physiology, 2020, 255, 153293.	1.6	18
2930	The Untapped Australasian Diversity of Astaxanthin-Producing Yeasts with Biotechnological Potentialâ€"Phaffia australis sp. nov. and Phaffia tasmanica sp. nov.. Microorganisms, 2020, 8, 1651.	1.6	9
2931	The Phoebe genome sheds light on the evolution of magnoliids. Horticulture Research, 2020, 7, 146.	2.9	41
2932	Comparative genomic analysis of Vibrios yields insights into genes associated with virulence towards C. gigas larvae. BMC Genomics, 2020, 21, 599.	1.2	11
2933	Genetic Adaptations of an Island Pit-Viper to a Unique Sedentary Life with Extreme Seasonal Food Availability. G3: Genes, Genomes, Genetics, 2020, 10, 1639-1646.	0.8	3
2934	Molecular Evolutionary and Expression Pattern Analysis of AKR Genes Shed New Light on GalUR Functional Characteristics in Brassica rapa. International Journal of Molecular Sciences, 2020, 21, 5987.	1.8	3
2935	Comparative Genomics of Spatholobus suberectus and Insight Into Flavonoid Biosynthesis. Frontiers in Plant Science, 2020, 11, 528108.	1.7	6
2936	Complete Genome and Comparative Genome Analysis of Lactobacillus reuteri YSJL-12, a Potential Probiotics Strain Isolated From Healthy Sow Fresh Feces. Evolutionary Bioinformatics, 2020, 16, 117693432094219.	0.6	4
2937	Construction of Pseudomolecules for the Chinese Chestnut (<i>Castanea mollissima</i>) Genome. G3: Genes, Genomes, Genetics, 2020, 10, 3565-3574.	0.8	25
2938	Origin and Evolution of Fusidane-Type Antibiotics Biosynthetic Pathway through Multiple Horizontal Gene Transfers. Genome Biology and Evolution, 2020, 12, 1830-1840.	1.1	7
2939	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
2940	Long-read sequencing and de novo genome assembly of marine medaka (Oryzias melastigma). BMC Genomics, 2020, 21, 640.	1.2	7
2941	Chromosome duplication causing geneâ€dosageâ€based effects on the gene expression level inGossypium hirsutumâ€Gossypium australeaddition lines. Plant Direct, 2020, 4, e00247.	0.8	1
2942	Panâ€genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. Environmental Microbiology, 2021, 23, 3599-3613.	1.8	4
2943	Transcriptomic analysis at organ and time scale reveals gene regulatory networks controlling the sulfate starvation response of Solanum lycopersicum. BMC Plant Biology, 2020, 20, 385.	1.6	13
2944	A high-quality reference genome for cabbage obtained with SMRT reveals novel genomic features and evolutionary characteristics. Scientific Reports, 2020, 10, 12394.	1.6	29

#	ARTICLE	IF	CITATIONS
2945	Adaptation and molecular evidence for convergence in decapod crustaceans from deepâ€sea hydrothermal vent environments. Molecular Ecology, 2020, 29, 3954-3969.	2.0	13
2946	Circadian clock mechanism driving mammalian photoperiodism. Nature Communications, 2020, 11, 4291.	5.8	42
2947	Exploring the Diversity Within the Genus Francisella â€" An Integrated Pan-Genome and Genome-Mining Approach. Frontiers in Microbiology, 2020, 11, 1928.	1.5	14
2948	Chromosome-level genome assembly of the female western mosquitofish (Gambusia affinis). GigaScience, 2020, 9, .	3.3	5
2949	Complete Genome Sequence of â€œ <i>Candidatus</i> Phytoplasma asterisâ€•RP166, a Plant Pathogen Associated with Rapeseed Phyllody Disease in Poland. Microbiology Resource Announcements, 2020, 9, .	0.3	15
2950	Regional sequence expansion or collapse in heterozygous genome assemblies. PLoS Computational Biology, 2020, 16, e1008104.	1.5	31
2951	Panâ€genome: A promising resource for noncoding RNA discovery in plants. Plant Genome, 2020, 13, e20046.	1.6	15
2952	An Overview of Duplicated Gene Detection Methods: Why the Duplication Mechanism Has to Be Accounted for in Their Choice. Genes, 2020, 11, 1046.	1.0	65
2953	De Novo Gene Birth, Horizontal Gene Transfer, and Gene Duplication as Sources of New Gene Families Associated with the Origin of Symbiosis in<i>Amanita</i>. Genome Biology and Evolution, 2020, 12, 2168-2182.	1.1	5
2954	Echolocation call frequency variation in horseshoe bats: molecular basis revealed by comparative transcriptomics. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20200875.	1.2	6
2955	Molecular Dialogues between Early Divergent Fungi and Bacteria in an Antagonism versus a Mutualism. MBio, 2020, 11, .	1.8	19
2956	Evolutionary Mechanisms of Long-Term Genome Diversification Associated With Niche Partitioning in Marine Picocyanobacteria. Frontiers in Microbiology, 2020, 11, 567431.	1.5	37
2957	Genomic Signatures of Honey Bee Association in an Acetic Acid Symbiont. Genome Biology and Evolution, 2020, 12, 1882-1894.	1.1	18
2958	Comparative Analysis of the Secretome and Interactome of Trypanosoma cruzi and Trypanosoma rangeli Reveals Species Specific Immune Response Modulating Proteins. Frontiers in Immunology, 2020, 11, 1774.	2.2	7
2959	Genomic Characteristics Distinguish Geographically Distributed Dehalococcoidia. Frontiers in Microbiology, 2020, 11, 546063.	1.5	18
2960	Reconstruction of time-consistent species trees. Algorithms for Molecular Biology, 2020, 15, 16.	0.3	5
2961	The chromosome-level draft genome of Dalbergia odorifera. GigaScience, 2020, 9, .	3.3	21
2962	Cross-reactivity between tumor MHC class Iâ€"restricted antigens and an enterococcal bacteriophage. Science, 2020, 369, 936-942.	6.0	217

#	Article	IF	Citations
2963	Comparative analysis of diet-associated responses in two rice planthopper species. BMC Genomics, 2020, 21, 565.	1.2	9
2964	Novel xylose transporter Cs4130 expands the sugar uptake repertoire in recombinant Saccharomyces cerevisiae strains at high xylose concentrations. Biotechnology for Biofuels, 2020, 13, 145.	6.2	19
2965	Pan-genome analysis of Paenibacillus polymyxa strains reveals the mechanism of plant growth promotion and biocontrol. Antonie Van Leeuwenhoek, 2020, 113, 1539-1558.	0.7	17
2966	Comparative Genomic and Secretomic Analysis Provide Insights Into Unique Agar Degradation Function of Marine Bacterium Vibrio fluvialis A8 Through Horizontal Gene Transfer. Frontiers in Microbiology, 2020, 11, 1934.	1.5	7
2967	Pan-genome analysis and ancestral state reconstruction of class halobacteria: probability of a new super-order. Scientific Reports, 2020, 10, 21205.	1.6	13
2968	Mutation of hilD in a Salmonella Derby lineage linked to swine adaptation and reduced risk to human health. Scientific Reports, 2020, 10, 21539.	1.6	7
2969	A Chromosome-Level Genome Assembly of the Anglerfish Lophius litulon. Frontiers in Genetics, 2020, 11, 581161.	1.1	2
2970	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite Schistosoma mansoni. Nature Communications, 2020, 11, 6411.	5.8	51
2971	Unconventional Secretion of Nigerolysins A from Aspergillus Species. Microorganisms, 2020, 8, 1973.	1.6	5
2972	First Draft Genome Assembly of the Malaysian Stingless Bee, Heterotrigona itama (Apidae, Meliponinae). Data, 2020, 5, 112.	1.2	0
2973	An Overview of Genomics, Phylogenomics and Proteomics Approaches in Ascomycota. Life, 2020, 10, 356.	1.1	12
2974	A Novel Family of Acinetobacter Mega-Plasmids Are Disseminating Multi-Drug Resistance Across the Globe While Acquiring Location-Specific Accessory Genes. Frontiers in Microbiology, 2020, 11, 605952.	1.5	18
2975	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. Genome Biology and Evolution, 2020, 12, 2258-2266.	1.1	23
2976	Genomic and physiological mechanisms underlying skin plasticity during water to air transition in an amphibious fish. Journal of Experimental Biology, 2021, 224, .	0.8	10
2977	Comparative genomics of Sporothrix species and identification of putative pathogenic-gene determinants. Future Microbiology, 2020, 15, 1465-1481.	1.0	4
2978	Phylogenetic supertree reveals detailed evolution of SARS-CoV-2. Scientific Reports, 2020, 10, 22366.	1.6	39
2979	Simultaneous Quantification of Vibrio metoecus and Vibrio cholerae with Its O1 Serogroup and Toxigenic Subpopulations in Environmental Reservoirs. Pathogens, 2020, 9, 1053.	1.2	8
2980	Insights into the genetic basis of predatorâ€induced response in Daphnia galeata. Ecology and Evolution, 2020, 10, 13095-13108.	0.8	9

#	ARTICLE	IF	CITATIONS
2981	MAGUS: Multiple sequence Alignment using Graph clUStering. Bioinformatics, 2021, 37, 1666-1672.	1.8	39
2982	Genome sequencing and phylogenetic analysis of allotetraploid Salix matsudana Koidz. Horticulture Research, 2020, 7, 201.	2.9	30
2983	Transcriptome profiles of sturgeon lateral line electroreceptor and mechanoreceptor during regeneration. BMC Genomics, 2020, 21, 875.	1.2	4
2984	Integrated Analysis of the Transcriptome and Metabolome of Cecropia obtusifolia: A Plant with High Chlorogenic Acid Content Traditionally Used to Treat Diabetes Mellitus. International Journal of Molecular Sciences, 2020, 21, 7572.	1.8	10
2985	The Draft Genome of Red Lechwe, Kobus leche leche. Frontiers in Genetics, 2020, 11, 582638.	1.1	0
2986	The draft genome of the blood pheasant (<i>Ithaginis cruentus</i>): Phylogeny and highâ€altitude adaptation. Ecology and Evolution, 2020, 10, 11440-11452.	0.8	1
2987	Complete representation of a tapeworm genome reveals chromosomes capped by centromeres, necessitating a dual role in segregation and protection. BMC Biology, 2020, 18, 165.	1.7	19
2988	Comparative Genomics of Pathogenic Clavibacter michiganensis subsp. michiganensis Strains from Chile Reveals Potential Virulence Features for Tomato Plants. Microorganisms, 2020, 8, 1679.	1.6	14
2989	Population Genomic Analysis of Mycoplasma bovis Elucidates Geographical Variations and Genes associated with Host-Types. Microorganisms, 2020, 8, 1561.	1.6	13
2990	Genome Sequence Resource for Pathogen <i>Bipolaris sorokiniana</i> Shoemaker GN1 Causing Spot Blotch of Barley (<i>Hordeum vulgare</i> L.). Plant Disease, 2020, 104, 1574-1577.	0.7	7
2991	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
2992	Dynamic Expression of Long Non-Coding RNAs Throughout Parasite Sexual and Neural Maturation in Schistosoma Japonicum. Non-coding RNA, 2020, 6, 15.	1.3	7
2993	Comparative Genomic Analysis Provides Insights into the Phylogeny, Resistome, Virulome, and Host Adaptation in the Genus Ewingella. Pathogens, 2020, 9, 330.	1.2	7
2994	Noncoding regions underpin avian bill shape diversification at macroevolutionary scales. Genome Research, 2020, 30, 553-565.	2.4	24
2995	Phylogenomic Analyses of Members of the Widespread Marine Heterotrophic Genus Pseudovibrio Suggest Distinct Evolutionary Trajectories and a Novel Genus, Polycladidibacter gen. nov. Applied and Environmental Microbiology, 2020, 86, .	1.4	6
2996	Horizontally Acquired Quorum-Sensing Regulators Recruited by the PhoP Regulatory Network Expand the Host Adaptation Repertoire in the Phytopathogen <i>Pectobacterium brasiliense</i>. MSystems, 2020, 5, .	1.7	11
2997	Divergent Evolution of <i>Legionella</i> RCC1 Repeat Effectors Defines the Range of Ran GTPase Cycle Targets. MBio, 2020, 11, .	1.8	11
2998	A high-quality reference genome of wild Cannabis sativa. Horticulture Research, 2020, 7, 73.	2.9	73

#	Article	IF	Citations
2999	Comparative genomics of whole-cell pertussis vaccine strains from India. BMC Genomics, 2020, 21, 345.	1.2	6
3000	Phylogenetic tree building in the genomic age. Nature Reviews Genetics, 2020, 21, 428-444.	7.7	226
3001	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
3002	Metabolic strategies of marine subseafloor Chloroflexi inferred from genome reconstructions. Environmental Microbiology, 2020, 22, 3188-3204.	1.8	49
3003	Chromosome-level reference genome of the jellyfish Rhopilema esculentum. GigaScience, 2020, 9, .	3.3	20
3004	Phylogenetic Reconstruction Based on Synteny Block and Gene Adjacencies. Molecular Biology and Evolution, 2020, 37, 2747-2762.	3.5	29
3005	Chromosomeâ€level reference genome assembly and gene editing of the deadâ€leaf butterfly <i>Kallima inachus</i>. Molecular Ecology Resources, 2020, 20, 1080-1092.	2.2	22
3006	Chromosomeâ€level genome assembly of the greenfin horseâ€faced filefish (<i>Thamnaconus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Ecology Resources, 2020, 20, 1069-1079.	2.2	27
3007	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
3008	The genome sequence of star fruit (Averrhoa carambola). Horticulture Research, 2020, 7, 95.	2.9	18
3009	Similitudes and differences between two closely related Ficus species in the synthesis by the ostiole of odors attracting their host-specific pollinators: A transcriptomic based investigation. Acta Oecologica, 2020, 105, 103554.	0.5	9
3010	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i>. Ecology and Evolution, 2020, 10, 4518-4530.	0.8	34
3011	Pan-Genome Analyses of Geobacillus spp. Reveal Genetic Characteristics and Composting Potential. International Journal of Molecular Sciences, 2020, 21, 3393.	1.8	7
3012	The Protector within: Comparative Genomics of APSE Phages across Aphids Reveals Rampant Recombination and Diverse Toxin Arsenals. Genome Biology and Evolution, 2020, 12, 878-889.	1.1	22
3013	PhyloMCL: Accurate clustering of hierarchical orthogroups guided by phylogenetic relationship and inference of polyploidy events. Methods in Ecology and Evolution, 2020, 11, 943-954.	2.2	9
3014	Convergent Loss of an EDS1/PAD4 Signaling Pathway in Several Plant Lineages Reveals Coevolved Components of Plant Immunity and Drought Response. Plant Cell, 2020, 32, 2158-2177.	3.1	66
3015	Towards Unraveling Macroecological Patterns in Rhizosphere Microbiomes. Trends in Plant Science, 2020, 25, 1017-1029.	4.3	42
3016	Genome and single-cell RNA-sequencing of the earthworm Eisenia andrei identifies cellular mechanisms underlying regeneration. Nature Communications, 2020, 11, 2656.	5.8	43

#	ARTICLE	IF	CITATIONS
3017	Whole-genome sequence of Phellinus gilvus (mulberry Sanghuang) reveals its unique medicinal values. Journal of Advanced Research, 2020, 24, 325-335.	4.4	24
3018	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. Science Advances, 2020, 6, eaaz7677.	4.7	59
3019	Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter gourd (Momordica spp.). Horticulture Research, 2020, 7, 85.	2.9	41
3020	Bacterial symbionts support larval sap feeding and adult folivory in (semi-)aquatic reed beetles. Nature Communications, 2020, 11, 2964.	5.8	42
3021	Revealing the key point of the temperature stress response of Arthrospira platensis C1 at the interconnection of C- and N- metabolism by proteome analyses and PPI networking. BMC Molecular and Cell Biology, 2020, 21, 43.	1.0	4
3022	Genomic insights into the phylogeny of Bacillus strains and elucidation of their secondary metabolic potential. Genomics, 2020, 112, 3191-3200.	1.3	15
3023	Dissecting the genome of star fruit (Averrhoa carambola L.). Horticulture Research, 2020, 7, 94.	2.9	16
3024	Draft genomes of two outcrossing wild rice, Oryza rufipogon and O. longistaminata , reveal genomic features associated with matingâ€system evolution. Plant Direct, 2020, 4, e00232.	0.8	9
3025	Genomes of major fishes in world fisheries and aquaculture: Status, application and perspective. Aquaculture and Fisheries, 2020, 5, 163-173.	1.2	30
3026	Origin and evolution of jasmonate signaling. Plant Science, 2020, 298, 110542.	1.7	14
3027	Reprogramming of Stem Cell Activity to Convert Thorns into Branches. Current Biology, 2020, 30, 2951-2961.e5.	1.8	30
3028	Identification and characterization of male reproduction-related genes in pig (Sus scrofa) using transcriptome analysis. BMC Genomics, 2020, 21, 381.	1.2	7
3029	Genome-Wide Characterization and Comparative Analysis of MYB Transcription Factors in <i>Ganoderma</i> Species. G3: Genes, Genomes, Genetics, 2020, 10, 2653-2660.	0.8	12
3030	Molecular footprints of selection effects and whole genome duplication (WGD) events in three blueberry species: detected by transcriptome dataset. BMC Plant Biology, 2020, 20, 250.	1.6	15
3031	Defining Critical Genes During Spherule Remodeling and Endospore Development in the Fungal Pathogen, Coccidioides posadasii. Frontiers in Genetics, 2020, 11, 483.	1.1	23
3032	Comparative genomics shows niche-specific variations of Lactobacillus plantarum strains isolated from human, Drosophila melanogaster, vegetable and dairy sources. Food Bioscience, 2020, 35, 100581.	2.0	27
3033	High-Quality Genome Assembly of Chrysaora quinquecirrha Provides Insights Into the Adaptive Evolution of Jellyfish. Frontiers in Genetics, 2020, 11, 535.	1.1	6
3034	Comparative Genomics of Acinetobacter baumannii Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. Frontiers in Microbiology, 2020, 11, 1176.	1.5	24

#	Article	IF	Citations
3035	Insights into the Evolution of Neoteny from the Genome of the Asian Icefish Protosalanx chinensis. IScience, 2020, 23, 101267.	1.9	7
3036	Pan-Genome of Wild and Cultivated Soybeans. Cell, 2020, 182, 162-176.e13.	13.5	508
3037	Genome Assembly and Pathway Analysis of Edible Mushroom Agrocybe cylindracea. Genomics, Proteomics and Bioinformatics, 2020, 18, 341-351.	3.0	18
3038	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
3039	Tandem gene duplications drive divergent evolution of caffeine and crocin biosynthetic pathways in plants. BMC Biology, 2020, 18, 63.	1.7	94
3040	A chromosomeâ€level genome assembly of the parasitoid wasp <i>Pteromalus puparum</i>. Molecular Ecology Resources, 2020, 20, 1384-1402.	2.2	35
3041	Evolutionary Patterns of Sex-Biased Genes in Three Species of Haplodiploid Insects. Insects, 2020, 11, 326.	1.0	1
3042	Effector Repertoire of Phytophthora betacei: In Search of Possible Virulence Factors Responsible for Its Host Specificity. Frontiers in Genetics, 2020, 11, 579.	1.1	4
3043	Chromosome Level Genome Assembly of Andrographis paniculata. Frontiers in Genetics, 2020, 11, 701.	1.1	14
3044	Complete Genome of Lactobacillus iners KY Using Flongle Provides Insight Into the Genetic Background of Optimal Adaption to Vaginal Econiche. Frontiers in Microbiology, 2020, 11, 1048.	1.5	16
3045	Comparative Genomics Unveils Regionalized Evolution of the Faustovirus Genomes. Viruses, 2020, 12, 577.	1.5	7
3046	New bacterial and archaeal lineages discovered in organic rich sediments of a large tropical Bay. Marine Genomics, 2020, 54, 100789.	0.4	22
3047	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. Nature Communications, 2020, 11, 3051.	5.8	47
3048	A chromosome-level assembly of the cat flea genome uncovers rampant gene duplication and genome size plasticity. BMC Biology, 2020, 18, 70.	1.7	29
3049	Convergent adaptation of the genomes of woody plants at the landâ€"sea interface. National Science Review, 2020, 7, 978-993.	4.6	44
3050	Comparative Genomics of Pediococcus pentosaceus Isolated From Different Niches Reveals Genetic Diversity in Carbohydrate Metabolism and Immune System. Frontiers in Microbiology, 2020, 11, 253.	1.5	36
3051	The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. New Phytologist, 2020, 227, 930-943.	3.5	68
3052	Comparative transcriptomic analysis of deep- and shallow-water barnacle species (Cirripedia,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2020, 21, 240.	1.2	18

#	Article	IF	Citations
3053	Whole genome phylogeny of Gallus: introgression and data-type effects. Avian Research, 2020, 11, .	0.5	17
3054	Phylogenetic Relationship Among Brackishwater <i>Vibrio</i> Species. Evolutionary Bioinformatics, 2020, 16, 117693432090328.	0.6	9
3055	Best match graphs and reconciliation of gene trees with species trees. Journal of Mathematical Biology, 2020, 80, 1459-1495.	0.8	14
3056	The genome evolution and domestication of tropical fruit mango. Genome Biology, 2020, 21, 60.	3.8	104
3057	Chromosome-level genome assembly and annotation of the loquat (Eriobotrya japonica) genome. GigaScience, 2020, 9, .	3.3	43
3059	Chromosome-level genome assembly of Aldrichina grahami, a forensically important blowfly. GigaScience, 2020, 9, .	3.3	4
3060	Improved hybrid <i>de novo</i> genome assembly and annotation of African wild rice, <i>Oryza longistaminata</i>, from Illumina and PacBio sequencing reads. Plant Genome, 2020, 13, e20001.	1.6	15
3061	First draft genome for the sand-hopper Trinorchestia longiramus. Scientific Data, 2020, 7, 85.	2.4	8
3062	Chromosomeâ€level analysis of the <i>Crassostrea hongkongensis</i> genome reveals extensive duplication of immuneâ€related genes in bivalves. Molecular Ecology Resources, 2020, 20, 980-994.	2.2	45
3063	Highâ€quality genome assembly and transcriptome of <i>Ancherythroculter nigrocauda</i>, an endemic Chinese cyprinid species. Molecular Ecology Resources, 2020, 20, 882-891.	2.2	11
3064	The genome of jojoba (<i>Simmondsia chinensis</i>): A taxonomically isolated species that directs wax ester accumulation in its seeds. Science Advances, 2020, 6, eaay3240.	4.7	53
3065	Wheat genomics and genome editing. , 2020, , 331-346.		2
3066	A megaplasmid family driving dissemination of multidrug resistance in Pseudomonas. Nature Communications, 2020, 11, 1370.	5.8	90
3067	Survival in the Tropics despite isolation, inbreeding and asexual reproduction: insights from the genome of the worldâ€™s southernmost poplar (<i>Populus ilicifolia</i>). Plant Journal, 2020, 103, 430-442.	2.8	23
3068	Genome-Wide Identification of the MdKNOX Gene Family and Characterization of Its Transcriptional Regulation in Malus domestica. Frontiers in Plant Science, 2020, 11, 128.	1.7	24
3069	The molecular basis of venom resistance in a rattlesnakeâ€squirrel predatorâ€prey system. Molecular Ecology, 2020, 29, 2871-2888.	2.0	23
3070	COVID-19 Coronavirus Vaccine Design Using Reverse Vaccinology and Machine Learning. Frontiers in Immunology, 2020, 11, 1581.	2.2	301
3071	Network analysis of synonymous codon usage. Bioinformatics, 2020, 36, 4876-4884.	1.8	6

#	ARTICLE	IF	CITATIONS
3072	Comparative Genomics Uncovers the Genetic Diversity and Characters of Veillonella atypica and Provides Insights Into Its Potential Applications. Frontiers in Microbiology, 2020, 11, 1219.	1.5	10
3073	Evolution of Plant Architecture in Oryza Driven by the PROG1 Locus. Frontiers in Plant Science, 2020, 11, 876.	1.7	5
3074	Adaptation to Extreme Antarctic Environments Revealed by the Genome of a Sea Ice Green Alga. Current Biology, 2020, 30, 3330-3341.e7.	1.8	48
3075	The Chromosome-Level Genome Assembly and Comprehensive Transcriptomes of the Razor Clam (Sinonovacula constricta). Frontiers in Genetics, 2020, 11, 664.	1.1	18
3076	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in Platycodon grandiflorus, a medicinal plant. Horticulture Research, 2020, 7, 112.	2.9	38
3077	Broccoli: Combining Phylogenetic and Network Analyses for Orthology Assignment. Molecular Biology and Evolution, 2020, 37, 3389-3396.	3.5	65
3078	Molecular adaptation and convergent evolution of frugivory in Old World and neotropical fruit bats. Molecular Ecology, 2020, 29, 4366-4381.	2.0	32
3079	The Gut Microbiota in Prediabetes and Diabetes: A Population-Based Cross-Sectional Study. Cell Metabolism, 2020, 32, 379-390.e3.	7.2	233
3080	The genome, transcriptome, and proteome of the fish parasite Pomphorhynchus laevis (Acanthocephala). PLoS ONE, 2020, 15, e0232973.	1.1	19
3081	CCPRD: A Novel Analytical Framework for the Comprehensive Proteomic Reference Database Construction of NonModel Organisms. ACS Omega, 2020, 5, 15370-15384.	1.6	7
3082	Comparative study of the SBP-box gene family in rice siblings. Journal of Biosciences, 2020, 45, 1.	0.5	2
3083	Comparative analysis of long noncoding RNAs in long-lived mammals provides insights into natural cancer-resistance. RNA Biology, 2020, 17, 1657-1665.	1.5	8
3084	Casein Kinase 1 Regulates Cytorhabdovirus Replication and Transcription by Phosphorylating a Phosphoprotein Serine-Rich Motif. Plant Cell, 2020, 32, 2878-2897.	3.1	17
3085	Detecting bracoviral orthologs distribution in five tsetse fly species and the housefly genomes. BMC Research Notes, 2020, 13, 318.	0.6	1
3086	Pathogenic Allodiploid Hybrids of Aspergillus Fungi. Current Biology, 2020, 30, 2495-2507.e7.	1.8	39
3087	New genomic resources for three exploited Mediterranean fishes. Genomics, 2020, 112, 4297-4303.	1.3	8
3088	Is Lactobacillus Gram-Positive? A Case Study of Lactobacillus iners. Microorganisms, 2020, 8, 969.	1.6	12
3089	Transcriptome analysis of Eucalyptus grandis genotypes reveals constitutive overexpression of genes related to rust (Austropuccinia psidii) resistance. Plant Molecular Biology, 2020, 104, 339-357.	2.0	29

#	Article	IF	Citations
3090	High-Quality Genome Assembly of Eriocheir japonica sinensis Reveals Its Unique Genome Evolution. Frontiers in Genetics, 2019, 10, 1340.	1.1	32
3091	Genomic and ecological attributes of marine bacteriophages encoding bacterial virulence genes. BMC Genomics, 2020, 21, 126.	1.2	26
3092	Taxonomic Organization of the Family Brucellaceae Based on a Phylogenomic Approach. Frontiers in Microbiology, 2019, 10, 3083.	1.5	33
3093	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
3094	The hornwort genome and early land plant evolution. Nature Plants, 2020, 6, 107-118.	4.7	203
3095	Gene family expansion of pinewood nematode to detoxify its host defence chemicals. Molecular Ecology, 2020, 29, 940-955.	2.0	23
3096	Identification and Comparative Analysis of Venom Proteins in a Pupal Ectoparasitoid, Pachycrepoideus vindemmiae. Frontiers in Physiology, 2020, 11, 9.	1.3	21
3097	Identification of an SCPL Gene Controlling Anthocyanin Acylation in Carrot (Daucus carota L.) Root. Frontiers in Plant Science, 2020, 10, 1770.	1.7	21
3098	Fine-Scale Population Genetic Structure and Parapatric Cryptic Species of Kuruma Shrimp (Marsupenaeus japonicus), Along the Northwestern Pacific Coast of China. Frontiers in Genetics, 2020, 11, 118.	1.1	8
3099	Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. Nature Plants, 2020, 6, 215-222.	4.7	88
3100	Chromosomal-level assembly of Juglans sigillata genome using Nanopore, BioNano, and Hi-C analysis. GigaScience, 2020, 9, .	3.3	33
3101	Extracting novel hypotheses and findings from RNA-seq data. FEMS Yeast Research, 2020, 20, .	1.1	6
3102	Whole genome sequencing and comparative genomic analysis of oleaginous red yeast Sporobolomyces pararoseus NGR identifies candidate genes for biotechnological potential and ballistospores-shooting. BMC Genomics, 2020, 21, 181.	1.2	9
3103	Genomeâ€wide analyses of <i>Liberibacter</i> species provides insights into evolution, phylogenetic relationships, and virulence factors. Molecular Plant Pathology, 2020, 21, 716-731.	2.0	62
3104	Comparative Genomics Uncovers the Genetic Diversity and Synthetic Biology of Secondary Metabolite Production of Trametes. Mycobiology, 2020, 48, 104-114.	0.6	5
3105	Ab Initio Construction and Evolutionary Analysis of Protein-Coding Gene Families with Partially Homologous Relationships: Closely Related Drosophila Genomes as a Case Study. Genome Biology and Evolution, 2020, 12, 185-202.	1.1	2
3106	Genome sequence of the agarwood tree Aquilaria sinensis (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeceae family. GigaScience, 2020, 9, .	3.3	34
3107	Functional Genomics Insights Into the Pathogenicity, Habitat Fitness, and Mechanisms Modifying Plant Development of Rhodococcus sp. PBTS1 and PBTS2. Frontiers in Microbiology, 2020, 11, 14.	1.5	20

#	ARTICLE	IF	CITATIONS
3108	Differential Gene Expression between Fungal Mating Types Is Associated with Sequence Degeneration. Genome Biology and Evolution, 2020, 12, 243-258.	1.1	11
3109	Substantially adaptive potential in polyploid cyprinid fishes: evidence from biogeographic, phylogenetic and genomic studies. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20193008.	1.2	30
3110	Transcriptional response of Emiliania huxleyi under changing nutrient environments in the North Pacific Subtropical Gyre. Environmental Microbiology, 2020, 22, 1847-1860.	1.8	13
3111	Genome-wide identification and analyses of the AHL gene family in cotton (Gossypium). BMC Genomics, 2020, 21, 69.	1.2	23
3112	First Draft Genome of the Sable, Martes zibellina. Genome Biology and Evolution, 2020, 12, 59-65.	1.1	5
3113	Deciphering Patterns of Adaptation and Acclimation in the Transcriptome of <i>Phaeocystis antarctica</i> to Changing Iron Conditions¹. Journal of Phycology, 2020, 56, 747-760.	1.0	10
3114	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
3115	Understanding divergent domestication traits from the whole-genome sequencing of swamp- and river-buffalo populations. National Science Review, 2020, 7, 686-701.	4.6	43
3116	The persimmon genome reveals clues to the evolution of a lineage-specific sex determination system in plants. PLoS Genetics, 2020, 16, e1008566.	1.5	54
3117	Extreme Genome and Nervous System Streamlining in the Invertebrate Parasite Intoshia variabili. Current Biology, 2020, 30, 1292-1298.e3.	1.8	35
3118	Comparative Genomic Analysis of a Novel Strain of Taiwan Hot-Spring Cyanobacterium Thermosynechococcus sp. CL-1. Frontiers in Microbiology, 2020, 11, 82.	1.5	38
3119	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
3120	Phylogenetic analysis and transcriptional profiling of WRKY genes in sunflower (Helianthus annuus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Products, 2020, 148, 112268.	2.5	27
3121	The draft genome of horseshoe crab Tachypleus tridentatus reveals its evolutionary scenario and well-developed innate immunity. BMC Genomics, 2020, 21, 137.	1.2	22
3122	Comparative genome characterization of the periodontal pathogen Tannerella forsythia. BMC Genomics, 2020, 21, 150.	1.2	9
3123	Genomics Evolutionary History and Diagnostics of the Alternaria alternata Species Group Including Apple and Asian Pear Pathotypes. Frontiers in Microbiology, 2019, 10, 3124.	1.5	41
3124	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
3125	Cultureâ€independent tracking of Vibrio cholerae lineages reveals complex spatiotemporal dynamics in a natural population. Environmental Microbiology, 2020, 22, 4244-4256.	1.8	15

#	ARTICLE	IF	CITATIONS
3126	The <i>Ficus erecta</i> genome aids <i>Ceratocystis</i> canker resistance breeding in common fig (<i>F. carica</i>). Plant Journal, 2020, 102, 1313-1322.	2.8	15
3127	Top-Down and Bottom-Up Controls on Microeukaryotic Diversity (i.e., Amplicon Analyses of SAR) Tj ETQq1 1 0.784314 rgBT /Overlock 1 Frontiers in Marine Science, 2020, 6, .	1.2	5
3128	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. Cell, 2020, 180, 263-277.e20.	13.5	87
3129	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of Morchella crassipes. International Journal of Molecular Sciences, 2020, 21, 483.	1.8	27
3130	Gene gain and loss across the metazoan tree of life. Nature Ecology and Evolution, 2020, 4, 524-533.	3.4	116
3131	Genomic features of the fall armyworm (Spodoptera frugiperda) (J.E. Smith) yield insights into its defense system and flight capability. Entomological Research, 2020, 50, 100-112.	0.6	10
3132	Genomic analyses of a â€œliving fossilâ€: The endangered doveâ€tree. Molecular Ecology Resources, 2020, 20, 756-769.	2.2	26
3133	Characterization of Venom Components and Their Phylogenetic Properties in Some Aculeate Bumblebees and Wasps. Toxins, 2020, 12, 47.	1.5	16
3134	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
3135	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Studies in Mycology, 2020, 96, 141-153.	4.5	135
3136	Comparative Genomics Analysis of Lactobacillus mucosae from Different Niches. Genes, 2020, 11, 95.	1.0	15
3137	Redundancy and Specificity of Type VI Secretion vgrG Loci in Antibacterial Activity of Agrobacterium tumefaciens 1D1609 Strain. Frontiers in Microbiology, 2019, 10, 3004.	1.5	18
3138	Comparative Transcriptome Analysis of Different Dendrobium Species Reveals Active Ingredients-Related Genes and Pathways. International Journal of Molecular Sciences, 2020, 21, 861.	1.8	23
3139	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
3140	A draft genome assembly of spotted hyena, Crocuta crocuta. Scientific Data, 2020, 7, 126.	2.4	6
3141	MetaPhOrs 2.0: integrative, phylogeny-based inference of orthology and paralogy across the tree of life. Nucleic Acids Research, 2020, 48, W553-W557.	6.5	27
3142	Comparative Genomic and Transcriptomic Analyses of Mycobacterium kansasii Subtypes Provide New Insights Into Their Pathogenicity and Taxonomy. Frontiers in Cellular and Infection Microbiology, 2020, 10, 122.	1.8	10
3143	A Major QTL Located in Chromosome 8 of Cucurbita moschata Is Responsible for Resistance to Tomato Leaf Curl New Delhi Virus. Frontiers in Plant Science, 2020, 11, 207.	1.7	30

#	Article	IF	Citations
3144	Genomic Features of Cladobotryum dendroides, Which Causes Cobweb Disease in Edible Mushrooms, and Identification of Genes Related to Pathogenicity and Mycoparasitism. Pathogens, 2020, 9, 232.	1.2	15
3145	Bioinformatics approaches applied in pan-genomics and their challenges. , 2020, , 43-64.		1
3146	Re-annotation of the Theileria parva genome refines 53% of the proteome and uncovers essential components of N-glycosylation, a conserved pathway in many organisms. BMC Genomics, 2020, 21, 279.	1.2	17
3147	Evolutionary pan-genomics and applications. , 2020, , 65-80.		0
3148	TMEM70 functions in the assembly of complexes I and V. Biochimica Et Biophysica Acta - Bioenergetics, 2020, 1861, 148202.	0.5	31
3149	Chromosome-level genome assembly, annotation and evolutionary analysis of the ornamental plant Asparagus setaceus. Horticulture Research, 2020, 7, 48.	2.9	27
3150	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. Nature Communications, 2020, 11, 1657.	5.8	64
3151	Genome sequence of Gossypium herbaceum and genome updates of Gossypium arboreum and Gossypium hirsutum provide insights into cotton A-genome evolution. Nature Genetics, 2020, 52, 516-524.	9.4	240
3152	Draft genomes of two Atlantic bay scallop subspecies Argopecten irradians irradians and A. i. concentricus. Scientific Data, 2020, 7, 99.	2.4	37
3153	SMRT sequencing of the Oryza rufipogon genome reveals the genomic basis of rice adaptation. Communications Biology, 2020, 3, 167.	2.0	20
3154	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
3155	Cultivable, Host-Specific <i>Bacteroidetes</i> Symbionts Exhibit Diverse Polysaccharolytic Strategies. Applied and Environmental Microbiology, 2020, 86, .	1.4	30
3156	From the Inside Out: an Epibiotic <i>Bdellovibrio</i> Predator with an Expanded Genomic Complement. Journal of Bacteriology, 2020, 202, .	1.0	14
3157	Paenibacillus odorifer, the Predominant <i>Paenibacillus</i> Species Isolated from Milk in the United States, Demonstrates Genetic and Phenotypic Conservation of Psychrotolerance but Clade-Associated Differences in Nitrogen Metabolic Pathways. MSphere, 2020, 5, .	1.3	9
3158	Comparative Genomics of Lactobacillus crispatus from the Gut and Vagina Reveals Genetic Diversity and Lifestyle Adaptation. Genes, 2020, 11, 360.	1.0	27
3159	First Whole Genome Sequence of Anaplasma platys, an Obligate Intracellular Rickettsial Pathogen of Dogs. Pathogens, 2020, 9, 277.	1.2	10
3160	Comparative Genomic Analysis of Closely Related Acetobacter pasteurianus Strains Provides Evidence of Horizontal Gene Transfer and Reveals Factors Necessary for Thermotolerance. Journal of Bacteriology, 2020, 202, .	1.0	17
3161	Analysis of 1,000+ Type-Strain Genomes Substantially Improves Taxonomic Classification of Alphaproteobacteria. Frontiers in Microbiology, 2020, 11, 468.	1.5	1,537

#	Article	IF	Citations
3162	Identification, evolution and expression analyses of whole genome-wide TLP gene family in Brassica napus. BMC Genomics, 2020, 21, 264.	1.2	19
3163	Using Colonization Assays and Comparative Genomics To Discover Symbiosis Behaviors and Factors in Vibrio fischeri. MBio, 2020, 11, .	1.8	17
3164	Molecular adaptation to salinity fluctuation in tropical intertidal environments of a mangrove tree Sonneratia alba. BMC Plant Biology, 2020, 20, 178.	1.6	24
3165	Chromosomeâ€level genome assembly of an important pine defoliator, <i>Dendrolimus punctatus</i> (Lepidoptera; Lasiocampidae). Molecular Ecology Resources, 2020, 20, 1023-1037.	2.2	34
3166	ToxoDB: the functional genomic resource for Toxoplasma and related organisms. , 2020, , 1021-1041.		2
3167	Gcluster: a simple-to-use tool for visualizing and comparing genome contexts for numerous genomes. Bioinformatics, 2020, 36, 3871-3873.	1.8	11
3168	The Aphid X Chromosome Is a Dangerous Place for Functionally Important Genes: Diverse Evolution of Hemipteran Genomes Based on Chromosome-Level Assemblies. Molecular Biology and Evolution, 2020, 37, 2357-2368.	3.5	41
3169	Comparative genomics reveals different population structures associated with host and geographic origin in antimicrobialâ€resistant <scp><i>Salmonella enterica</i></scp>. Environmental Microbiology, 2020, 22, 2811-2828.	1.8	12
3170	Comprehensive transcriptome analyses of two <i>Oocystis</i> algae provide insights into the adaptation to Qinghaiâ€“Tibet Plateau. Journal of Systematics and Evolution, 2021, 59, 1209-1219.	1.6	9
3171	The lasting after-effects of an ancient polyploidy on the genomes of teleosts. PLoS ONE, 2020, 15, e0231356.	1.1	27
3172	Genome Insights of the Plant-Growth Promoting Bacterium Cronobacter muytjensii JZ38 With Volatile-Mediated Antagonistic Activity Against Phytophthora infestans. Frontiers in Microbiology, 2020, 11, 369.	1.5	39
3173	Revisiting Parameter Estimation in Biological Networks: Influence of Symmetries. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 836-849.	1.9	6
3174	Genome-wide identification and expression analysis of the VQ gene family in sunflower (Helianthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	6
3175	Chromosomalâ€level genomes of three rice planthoppers provide new insights into sex chromosome evolution. Molecular Ecology Resources, 2021, 21, 226-237.	2.2	44
3176	A highâ€quality genome of taro (<i>Colocasia esculenta</i> (L.) Schott), one of the world's oldest crops. Molecular Ecology Resources, 2021, 21, 68-77.	2.2	28
3177	A chromosomeâ€scale reference genome and genomeâ€wide genetic variations elucidate adaptation in yak. Molecular Ecology Resources, 2021, 21, 201-211.	2.2	14
3178	Panâ€genomic analysis reveals that the evolution of <i>Dietzia</i> species depends on their living habitats. Environmental Microbiology, 2021, 23, 861-877.	1.8	14
3179	A chromosome-level genome assembly of the wild rice Oryza rufipogon facilitates tracing the origins of Asian cultivated rice. Science China Life Sciences, 2021, 64, 282-293.	2.3	24

#	Article	IF	Citations
3180	Panâ€genome analysis of <i>Streptococcus suis</i> serotype 2 revealed genomic diversity among strains of different virulence. Transboundary and Emerging Diseases, 2021, 68, 637-647.	1.3	19
3181	Phylogenomic analysis reveals a twoâ€stage process of the evolutionary transition of <i>Shewanella</i> from the upper ocean to the hadal zone. Environmental Microbiology, 2021, 23, 744-756.	1.8	17
3182	New Approaches for Inferring Phylogenies in the Presence of Paralogs. Trends in Genetics, 2021, 37, 174-187.	2.9	53
3183	High quality genome of <i>Erigeron breviscapus</i> provides a reference for herbal plants in Asteraceae. Molecular Ecology Resources, 2021, 21, 153-169.	2.2	21
3184	Chromosomeâ€level genome assembly of <i>Paralithodes platypus</i> provides insights into evolution and adaptation of king crabs. Molecular Ecology Resources, 2021, 21, 511-525.	2.2	14
3185	One stem cell program to rule them all?. FEBS Journal, 2021, 288, 3394-3406.	2.2	8
3186	A chromosomeâ€level genome assembly of rice leaffolder, <i>Cnaphalocrocis medinalis</i>. Molecular Ecology Resources, 2021, 21, 561-572.	2.2	15
3187	A comparative whole genome analysis of <i>Helicobacter pylori</i> from a human dense South Asian setting. Helicobacter, 2021, 26, e12766.	1.6	11
3188	A Chromosomal-scale Reference Genome of the Kelp Grouper Epinephelus moara. Marine Biotechnology, 2021, 23, 12-16.	1.1	7
3189	Comprehensive identification and analyses of the Hsf gene family in the whole-genome of three Apiaceae species. Horticultural Plant Journal, 2021, 7, 457-468.	2.3	15
3190	Chromosomeâ€level genome assembly of <i>Lethenteron reissneri</i> provides insights into lamprey evolution. Molecular Ecology Resources, 2021, 21, 448-463.	2.2	25
3191	Increased WD40 motifs in Planctomycete bacteria and their evolutionary relevance. Molecular Phylogenetics and Evolution, 2021, 155, 107018.	1.2	4
3192	Comparative Genomic Analyses Reveal Functional Insights Into Key Determinants of the Pathogenesis of Pectobacterium actinidiae in Kiwifruit. Phytopathology, 2021, 111, PHYTO-07-20-028.	1.1	3
3193	Wholeâ€genome assembly and resequencing reveal genomic imprint and key genes of rapid domestication in narrowâ€leafed lupin. Plant Journal, 2021, 105, 1192-1210.	2.8	12
3194	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
3195	Physiological and Proteomic Signatures Reveal Mechanisms of Superior Drought Resilience in Pearl Millet Compared to Wheat. Frontiers in Plant Science, 2020, 11, 600278.	1.7	44
3196	Hybrid speciation via inheritance of alternate alleles of parental isolating genes. Molecular Plant, 2021, 14, 208-222.	3.9	68
3197	Fâ€box protein CFK1 interacts with and degrades <i>de novo</i> DNA methyltransferase in Arabidopsis. New Phytologist, 2021, 229, 3303-3317.	3.5	13

#	Article	IF	Citations
3198	Chemogenomics and bioinformatics approaches for prioritizing kinases as drug targets for neglected tropical diseases. Advances in Protein Chemistry and Structural Biology, 2021, 124, 187-223.	1.0	2
3199	Eukaryote-conserved histone post-translational modification landscape in Giardia duodenalis revealed by mass spectrometry. International Journal for Parasitology, 2021, 51, 225-239.	1.3	8
3200	Recent advances in constraint and machine learning-based metabolic modeling by leveraging stoichiometric balances, thermodynamic feasibility and kinetic law formalisms. Metabolic Engineering, 2021, 63, 13-33.	3.6	26
3201	The genome of Shanputao (<i>Vitis amurensis</i>) provides a new insight into cold tolerance of grapevine. Plant Journal, 2021, 105, 1495-1506.	2.8	52
3202	Chromosomeâ€level genome assembly of the aphid parasitoid <i>Aphidius gifuensis</i> using Oxford Nanopore sequencing and Hiâ€C technology. Molecular Ecology Resources, 2021, 21, 941-954.	2.2	10
3203	Wholeâ€genome sequence data of <i>Hypericum perforatum</i> and functional characterization of melatonin biosynthesis by Nâ€acetylserotonin Oâ€methyltransferase. Journal of Pineal Research, 2021, 70, e12709.	3.4	30
3204	The American Paddlefish Genome Provides Novel Insights into Chromosomal Evolution and Bone Mineralization in Early Vertebrates. Molecular Biology and Evolution, 2021, 38, 1595-1607.	3.5	44
3205	PlacentaCellEnrich: A tool to characterize gene sets using placenta cell-specific gene enrichment analysis. Placenta, 2021, 103, 164-171.	0.7	24
3206	Cyanorak v2.1: a scalable information system dedicated to the visualization and expert curation of marine and brackish picocyanobacteria genomes. Nucleic Acids Research, 2021, 49, D667-D676.	6.5	38
3207	High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. Molecular Phylogenetics and Evolution, 2021, 154, 106965.	1.2	5
3208	MolluscDB: an integrated functional and evolutionary genomics database for the hyper-diverse animal phylum Mollusca. Nucleic Acids Research, 2021, 49, D988-D997.	6.5	54
3209	Niche differentiation and evolution of the wood decay machinery in the invasive fungus <i>Serpula lacrymans</i>. ISME Journal, 2021, 15, 592-604.	4.4	16
3210	Dioecy Is Associated with High Genetic Diversity and Adaptation Rates in the Plant Genus<i>Silene</i>. Molecular Biology and Evolution, 2021, 38, 805-818.	3.5	31
3211	Polyphenism of a Novel Trait Integrated Rapidly Evolving Genes into Ancestrally Plastic Networks. Molecular Biology and Evolution, 2021, 38, 331-343.	3.5	19
3212	<i>CoreCruncher</i>: Fast and Robust Construction of Core Genomes in Large Prokaryotic Data Sets. Molecular Biology and Evolution, 2021, 38, 727-734.	3.5	17
3213	The genome of <i>Cleistogenes songorica</i> provides a blueprint for functional dissection of dimorphic flower differentiation and drought adaptability. Plant Biotechnology Journal, 2021, 19, 532-547.	4.1	21
3214	Genomic Signatures of Coevolution between Nonmodel Mammals and Parasitic Roundworms. Molecular Biology and Evolution, 2021, 38, 531-544.	3.5	10
3215	Challenges in gene-oriented approaches for pangenome content discovery. Briefings in Bioinformatics, 2021, 22, .	3.2	8

#	Article	IF	Citations
3216	Reverse vaccinology and subtractive genomics approaches for identifying common therapeutics against Mycobacterium leprae and Mycobacterium lepromatosis. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2021, 27, e20200027.	0.8	3
3217	Revising transcriptome assemblies with phylogenetic information. PLoS ONE, 2021, 16, e0244202.	1.1	11
3218	Sinbase 2.0: An Updated Database to Study Multi-Omics in Sesamum indicum. Plants, 2021, 10, 272.	1.6	6
3222	Genome Assembly and Analyses of the Macrofungus Macrocybe gigantea. BioMed Research International, 2021, 2021, 1-14.	0.9	4
3223	Phytoactinopolyspora limicolaâ€,sp. nov., an alkaliphilic actinomycete isolated from a soda alkali-saline soil. Archives of Microbiology, 2021, 203, 1367-1374.	1.0	5
3224	Integration of 1:1 orthology maps and updated datasets into Echinobase. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	10
3225	Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in Hypsizygus marmoreus. Journal of Genetics and Genomics, 2021, 48, 75-87.	1.7	14
3226	De novo genome assembly of the potent medicinal plant Rehmannia glutinosa using nanopore technology. Computational and Structural Biotechnology Journal, 2021, 19, 3954-3963.	1.9	26
3227	Mucoromycotina Fungi Possess the Ability to Utilize Plant Sucrose as a Carbon Source: Evidence From Gongronella sp. w5. Frontiers in Microbiology, 2020, 11, 591697.	1.5	3
3229	Insight into different host range of three planthoppers by transcriptomic and microbiomic analysis. Insect Molecular Biology, 2021, 30, 287-296.	1.0	2
3230	A chromosome-level genome assembly of the oriental river prawn, <i>Macrobrachium nipponense</i>. GigaScience, 2021, 10, .	3.3	28
3231	Long read sequencing of <i>Toona sinensis</i> (A. Juss) Roem: A chromosomeâ€level reference genome for the family Meliaceae. Molecular Ecology Resources, 2021, 21, 1243-1255.	2.2	20
3232	Genomics Insights into Pseudomonas sp. CG01: An Antarctic Cadmium-Resistant Strain Capable of Biosynthesizing CdS Nanoparticles Using Methionine as S-Source. Genes, 2021, 12, 187.	1.0	5
3233	Genome Annotation and Gene Families in Sesame. Compendium of Plant Genomes, 2021, , 255-266.	0.3	2
3234	Paraflavitalea devenefica sp. nov., isolated from urban soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
3235	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0
3236	The type VI secretion system of Xanthomonas phaseoli pv. manihotis is involved in virulence and in vitro motility. BMC Microbiology, 2021, 21, 14.	1.3	16
3237	Transcription Profiling of Cultured<i>Acropora digitifera</i>Adult Cells Reveals the Existence of Ancestral Genome Regulatory Modules Underlying Pluripotency and Cell Differentiation in Cnidaria. Genome Biology and Evolution, 2021, 13, .	1.1	6

#	Article	IF	Citations
3238	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
3239	<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
3240	Design of a diagnostic system based on molecular markers derived from the ascomycetes pan-genome analysis: The case of Fusarium dieback disease. PLoS ONE, 2021, 16, e0246079.	1.1	3
3241	Positive selection analysis reveals the deep-sea adaptation of a hadal sea cucumber (Paelopatides sp.) to the Mariana Trench. Journal of Oceanology and Limnology, 2021, 39, 266-281.	0.6	9
3242	Phylogenomic fingerprinting of tempo and functions of horizontal gene transfer within ochrophytes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	37
3243	Multi-Omics Driven Metabolic Network Reconstruction and Analysis of Lignocellulosic Carbon Utilization in Rhodosporidium toruloides. Frontiers in Bioengineering and Biotechnology, 2020, 8, 612832.	2.0	25
3244	Chromosome-scale genome assembly of brown-spotted flathead <i>Platycephalus</i> sp.1 provides insights into demersal adaptation in flathead fish. Zoological Research, 2021, 42, 660-665.	0.9	2
3245	NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2021, , 47-90.		0
3246	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. Methods in Molecular Biology, 2021, 2242, 91-112.	0.4	0
3247	The repertoire of ABC proteins in Clostridioides difficile. Computational and Structural Biotechnology Journal, 2021, 19, 2905-2920.	1.9	5
3248	Analysis of Rice Transcriptome Reveals the LncRNA/CircRNA Regulation in Tissue Development. Rice, 2021, 14, 14.	1.7	26
3249	Diverse Evolution in 111 Plant Genomes Reveals Purifying and Dosage Balancing Selection Models for F-Box Genes. International Journal of Molecular Sciences, 2021, 22, 871.	1.8	7
3250	Popularity-Based Hierarchical Caching for Next Generation Content Delivery Networks. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2021, , 73-87.	0.2	0
3251	Genome and population evolution and environmental adaptation of <i>Glyptosternon maculatum</i> on the Qinghai-Tibet Plateau. Zoological Research, 2021, 42, 502-513.	0.9	7
3252	Chromosome-level genome assembly of the Chinese longsnout catfish <i>Leiocassis longirostris</i>. Zoological Research, 2021, 42, 417-422.	0.9	14
3253	Bioinformatics Tools and Moringa Genomics. Compendium of Plant Genomes, 2021, , 145-156.	0.3	0
3254	Chromosome-scale genome assembly provides insights into the evolution and flavor synthesis of passion fruit (Passiflora edulis Sims). Horticulture Research, 2021, 8, 14.	2.9	62
3255	Evolution of regulatory networks associated with traits under selection in cichlids. Genome Biology, 2021, 22, 25.	3.8	17

#	ARTICLE	IF	CITATIONS
3256	Bioinformatic Platforms for Metagenomics. , 2021, , 91-112.		0
3257	Inferring the Phylogenetic Positions of Two Fig Wasp Subfamilies of Epichrysomallinae and Sycophaginae Using Transcriptomes and Mitochondrial Data. Life, 2021, 11, 40.	1.1	4
3258	Genome Assembly and Transcriptome Analysis of the Fungus Coniella diplodiella During Infection on Grapevine (Vitis vinifera L.). Frontiers in Microbiology, 2020, 11, 599150.	1.5	7
3259	Pathogenomic analyses of Mycobacterium microti, an ESX-1-deleted member of the Mycobacterium tuberculosis complex causing disease in various hosts. Microbial Genomics, 2021, 7, .	1.0	11
3261	Chromosome-Level Genome Assembly and Annotation of a Sciaenid Fish, Argyrosomus japonicus. Genome Biology and Evolution, 2021, 13, .	1.1	6
3265	A chromosomeâ€level genome assembly for the tertiary relict plant <i>Tetracentron sinense</i> oliv. (trochodendraceae). Molecular Ecology Resources, 2021, 21, 1186-1199.	2.2	12
3266	Evolutionary and genomic comparisons of hybrid uninucleate and nonhybrid Rhizoctonia fungi. Communications Biology, 2021, 4, 201.	2.0	16
3267	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. Nature Communications, 2021, 12, 1227.	5.8	37
3268	Analyses of transcriptomes and the first complete genome of Leucocalocybe mongolica provide new insights into phylogenetic relationships and conservation. Scientific Reports, 2021, 11, 2930.	1.6	7
3269	Orthology and synteny analysis of receptor-like kinases â€œRLKâ€•and receptor-like proteins â€œRLPâ€•in legumes. BMC Genomics, 2021, 22, 113.	1.2	4
3270	Behavioral and Genomic Sensory Adaptations Underlying the Pest Activity of<i>Drosophila suzukii</i>. Molecular Biology and Evolution, 2021, 38, 2532-2546.	3.5	31
3271	Comparative genomics of a novel clade shed light on the evolution of the genus Erysipelothrix and characterise an emerging species. Scientific Reports, 2021, 11, 3383.	1.6	10
3272	A highâ€quality genome assembly of the eggplant provides insights into the molecular basis of disease resistance and chlorogenic acid synthesis. Molecular Ecology Resources, 2021, 21, 1274-1286.	2.2	39
3273	The genetic basis of cytoplasmic male sterility and fertility restoration in wheat. Nature Communications, 2021, 12, 1036.	5.8	58
3274	The genome of Tripterygium wilfordii and characterization of the celastrol biosynthesis pathway. GigaByte, 0, 2021, 1-32.	0.0	3
3275	Plant NLR diversity: the known unknowns of pan-NLRomes. Plant Cell, 2021, 33, 814-831.	3.1	99
3276	Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp. Communications Biology, 2021, 4, 186.	2.0	37
3278	Genome sequence and evolution of<i>Betula platyphylla</i>. Horticulture Research, 2021, 8, 37.	2.9	53

#	Article	IF	Citations
3279	Comparative Genomic and Transcriptomic Analysis Reveals Specific Features of Gene Regulation in Kluyveromyces marxianus. Frontiers in Microbiology, 2021, 12, 598060.	1.5	8
3281	Genomic characterization and probiotic potential of <i>Lactobacillus casei</i> IDCC 3451 isolated from infant faeces. Letters in Applied Microbiology, 2021, 72, 578-588.	1.0	7
3283	Comparative Analyses of Euonymus Chloroplast Genomes: Genetic Structure, Screening for Loci With Suitable Polymorphism, Positive Selection Genes, and Phylogenetic Relationships Within Celastrineae. Frontiers in Plant Science, 2020, 11, 593984.	1.7	25
3284	A chromosomeâ€level assembly of the harlequin ladybird <i>Harmonia axyridis</i> as a genomic resource to study beetle and invasion biology. Molecular Ecology Resources, 2021, 21, 1318-1332.	2.2	17
3285	Regulation of a Trehalose-Specific Facilitated Transporter (TRET) by Insulin and Adipokinetic Hormone in Rhodnius prolixus, a Vector of Chagas Disease. Frontiers in Physiology, 2021, 12, 624165.	1.3	18
3286	Genome annotation of disease-causing microorganisms. Briefings in Bioinformatics, 2021, 22, 845-854.	3.2	13
3287	Whole-genome comparative analysis of Malaysian Burkholderia pseudomallei clinical isolates. Microbial Genomics, 2021, 7, .	1.0	7
3288	Multiple Pathways to Homothallism in Closely Related Yeast Lineages in the Basidiomycota. MBio, 2021, 12, .	1.8	5
3289	Novel Two-Component System-Like Elements Reveal Functional Domains Associated with Restrictionâ€"Modification Systems and paraMORC ATPases in Bacteria. Genome Biology and Evolution, 2021, 13, .	1.1	4
3290	Genomic Insights into the Origin and Evolution of Molluscan Red-Bloodedness in the Blood Clam<i>Tegillarca granosa</i>. Molecular Biology and Evolution, 2021, 38, 2351-2365.	3.5	28
3291	Total Ortholog Median Matrix as an alternative unsupervised approach for phylogenomics based on evolutionary distance between protein coding genes. Scientific Reports, 2021, 11, 3791.	1.6	2
3294	Resources in the Genome Database for Rosaceae for peach research. Acta Horticulturae, 2021, , 99-106.	0.1	4
3295	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of Akebia trifoliata subsp. australis. Horticulture Research, 2021, 8, 33.	2.9	23
3296	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
3297	Salmonella enterica Serovars Dublin and Enteritidis Comparative Proteomics Reveals Differential Expression of Proteins Involved in Stress Resistance, Virulence, and Anaerobic Metabolism. Infection and Immunity, 2021, 89, .	1.0	6
3299	Mutanofactin promotes adhesion and biofilm formation of cariogenic Streptococcus mutans. Nature Chemical Biology, 2021, 17, 576-584.	3.9	28
3300	Deep-sea microbes as tools to refine the rules of innate immune pattern recognition. Science Immunology, 2021, 6, .	5.6	21
3301	Clade-specific chromosomal rearrangements and loss of subtelomeric adhesins in <i>Candida auris</i>. Genetics, 2021, 218, .	1.2	54

#	ARTICLE	IF	CITATIONS
3302	A towering genome: Experimentally validated adaptations to high blood pressure and extreme stature in the giraffe. Science Advances, 2021, 7, .	4.7	31
3303	OMAmer: tree-driven and alignment-free protein assignment to subfamilies outperforms closest sequence approaches. Bioinformatics, 2021, 37, 2866-2873.	1.8	5
3304	Genomic analysis of <i>Medicago ruthenica</i> provides insights into its tolerance to abiotic stress and demographic history. Molecular Ecology Resources, 2021, 21, 1641-1657.	2.2	17
3305	Genome-scale metabolic model of the diatom Thalassiosira pseudonana highlights the importance of nitrogen and sulfur metabolism in redox balance. PLoS ONE, 2021, 16, e0241960.	1.1	17
3306	Genome assembly and annotation at the chromosomal level of first Pleuronectidae: Verasper variegatus provides a basis for phylogenetic study of Pleuronectiformes. Genomics, 2021, 113, 717-726.	1.3	8
3307	Transcriptomic Responses of Four Pelagophytes to Nutrient (N, P) and Light Stress. Frontiers in Marine Science, 2021, 8, .	1.2	3
3308	Regulation of mating genes during arbuscular mycorrhizal isolate co-existenceâ€"where is the evidence?. ISME Journal, 2021, 15, 2173-2179.	4.4	4
3312	Fine-scale metabolic discontinuity in a stratified prokaryote microbiome of a Red Sea deep halocline. ISME Journal, 2021, 15, 2351-2365.	4.4	11
3313	Long-insert clone experimental evidence for assembly improvement and chimeric chromosomes detection in an allopentaploid beer yeast. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
3314	Genomes of 12 fig wasps provide insights into the adaptation of pollinators to fig syconia. Journal of Genetics and Genomics, 2021, 48, 225-236.	1.7	6
3315	A route to de novo domestication of wild allotetraploid rice. Cell, 2021, 184, 1156-1170.e14.	13.5	259
3316	Measuring potential effects of the developmental burden associated with the vertebrate notochord. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2022, 338, 129-136.	0.6	4
3318	Predicting transcriptional responses to cold stress across plant species. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	46
3319	Genome-wide identification of CLE gene family and their potential roles in bolting and fruit bearing in cucumber (Cucumis sativus L.). BMC Plant Biology, 2021, 21, 143.	1.6	15
3320	Tracing the genetic footprints of vertebrate landing in non-teleost ray-finned fishes. Cell, 2021, 184, 1377-1391.e14.	13.5	66
3321	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
3322	Loquat (Eriobotrya japonica (Thunb.) Lindl) population genomics suggests a twoâ€staged domestication and identifies genes showing convergence/parallel selective sweeps with apple or peach. Plant Journal, 2021, 106, 942-952.	2.8	2
3323	The<i>Corylus mandshurica</i>genome provides insights into the evolution of Betulaceae genomes and hazelnut breeding. Horticulture Research, 2021, 8, 54.	2.9	20

#	Article	IF	Citations
3325	Genome Sequence and Characterization of<i>Acinetobacter</i>Phage DMU1. Phage, 2021, 2, 50-56.	0.8	2
3326	Pelagibacterium limicola sp. nov., isolated from a soda alkali-saline soil. Archives of Microbiology, 2021, 203, 2681-2687.	1.0	3
3327	Evolutionary Contribution of Duplicated Genes to Genome Evolution in the Ginseng Species Complex. Genome Biology and Evolution, 2021, 13, .	1.1	4
3329	The genome of Magnolia biondii Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. Horticulture Research, 2021, 8, 38.	2.9	32
3330	Exploring Antibiotic Susceptibility, Resistome and Mobilome Structure of Planctomycetes from Gemmataceae Family. Sustainability, 2021, 13, 5031.	1.6	5
3331	The chromosome-level Hemerocallis citrina Borani genome provides new insights into the rutin biosynthesis and the lack of colchicine. Horticulture Research, 2021, 8, 89.	2.9	25
3332	Phylogenomics Reveals that<i>Asaia</i>Symbionts from Insects Underwent Convergent Genome Reduction, Preserving an Insecticide-Degrading Gene. MBio, 2021, 12, .	1.8	10
3333	Comparative genomics of the gut commensal Bifidobacterium bifidum reveals adaptation to carbohydrate utilization. Biochemical and Biophysical Research Communications, 2021, 547, 155-161.	1.0	17
3334	A Chromosomeâ€"Level Genome Assembly of the Spotted Scat (<i>Scatophagus argus</i>). Genome Biology and Evolution, 2021, 13, .	1.1	17
3335	Antarctic Rahnella inusitata: A Producer of Cold-Stable Î²-Galactosidase Enzymes. International Journal of Molecular Sciences, 2021, 22, 4144.	1.8	8
3336	The Evolution of Calcification in Reef-Building Corals. Molecular Biology and Evolution, 2021, 38, 3543-3555.	3.5	19
3337	Plasmodium vinckei genomes provide insights into the pan-genome and evolution of rodent malaria parasites. BMC Biology, 2021, 19, 69.	1.7	10
3338	Context-dependent and -independent selection on synonymous mutations revealed by 1,135 genomes of Arabidopsis thaliana. Bmc Ecology and Evolution, 2021, 21, 68.	0.7	9
3340	Chromosomeâ€level genome assembly of the Arctic fox (<i>Vulpes lagopus</i>) using PacBio sequencing and Hiâ€C technology. Molecular Ecology Resources, 2021, 21, 2093-2108.	2.2	15
3341	Genome of a citrus rootstock and global DNA demethylation caused by heterografting. Horticulture Research, 2021, 8, 69.	2.9	45
3342	Genomic features underlying the evolutionary transitions of <i>Apibacter</i> to honey bee gut symbionts. Insect Science, 2022, 29, 259-275.	1.5	13
3343	Root Exudates Alter the Expression of Diverse Metabolic, Transport, Regulatory, and Stress Response Genes in Rhizosphere Pseudomonas. Frontiers in Microbiology, 2021, 12, 651282.	1.5	58
3344	Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. Nature Genetics, 2021, 53, 752-760.	9.4	64

#	ARTICLE	IF	CITATIONS
3345	Comparative Genomics and Transcriptomics of the Extreme Halophyte Puccinellia tenuiflora Provides Insights Into Salinity Tolerance Differentiation Between Halophytes and Glycophytes. Frontiers in Plant Science, 2021, 12, 649001.	1.7	14
3346	Genome sequencing and comparative genomic analysis of highly and weakly aggressive strains of Sclerotium rolfsii, the causal agent of peanut stem rot. BMC Genomics, 2021, 22, 276.	1.2	20
3347	Halosimplex halophilum sp. nov. and Halosimplex salinum sp. nov., isolated from saline soil and a salt mine. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	8
3348	A family of pathogen-induced cysteine-rich transmembrane proteins is involved in plant disease resistance. Planta, 2021, 253, 102.	1.6	8
3349	Protein Serine/Threonine Phosphatase Type 2C of Leishmania mexicana. Frontiers in Cellular and Infection Microbiology, 2021, 11, 641356.	1.8	3
3350	Chromosomeâ€level genome reference and genome editing of the tea geometrid. Molecular Ecology Resources, 2021, 21, 2034-2049.	2.2	8
3351	Large-Scale Annotation and Evolution Analysis of MiRNA in Insects. Genome Biology and Evolution, 2021, 13, .	1.1	15
3352	Lytic Bacteriophages Facilitate Antibiotic Sensitization of Enterococcus faecium. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	30
3353	Functional genomics of a Spiroplasma associated with the carmine cochineals Dactylopius coccus and Dactylopius opuntiae. BMC Genomics, 2021, 22, 240.	1.2	7
3354	Genomic-, phenotypic-, and toxicity-based safety assessment and probiotic potency of <i>Bacillus coagulans</i> IDCC 1201 isolated from green malt. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	1.4	14
3355	Host-Diet Effect on the Metabolism of Bifidobacterium. Genes, 2021, 12, 609.	1.0	17
3356	Large-scale sequencing of flatfish genomes provides insights into the polyphyletic origin of their specialized body plan. Nature Genetics, 2021, 53, 742-751.	9.4	30
3357	Single-cell transcriptome atlas and chromatin accessibility landscape reveal differentiation trajectories in the rice root. Nature Communications, 2021, 12, 2053.	5.8	107
3358	Draft Genomes and Comparative Analysis of Seven Mangrove Rhizosphere-Associated Fungi Isolated From Kandelia obovata and Acanthus ilicifolius. Frontiers in Fungal Biology, 2021, 2, .	0.9	2
3360	Complete genome sequence analysis of the peanut pathogen Ralstonia solanacearum strain Rs-P.362200. BMC Microbiology, 2021, 21, 118.	1.3	5
3363	Temporal Ordered Clustering in Dynamic Networks: Unsupervised and Semi-Supervised Learning Algorithms. IEEE Transactions on Network Science and Engineering, 2021, 8, 1426-1442.	4.1	1
3364	Insight into the denitrification mechanism of Bacillus subtilis JD-014 and its application potential in bioremediation of nitrogen wastewater. Process Biochemistry, 2021, 103, 78-86.	1.8	23
3365	Molecular evidence of the avocado defense response to Fusarium kuroshium infection: a deep transcriptome analysis using RNA-Seq. PeerJ, 2021, 9, e11215.	0.9	10

#	Article	IF	Citations
3366	The Meishan pig genome reveals structural variationâ€mediated gene expression and phenotypic divergence underlying Asian pig domestication. Molecular Ecology Resources, 2021, 21, 2077-2092.	2.2	20
3367	A chromosome-level reference genome of the hazelnut, <i>Corylus heterophylla</i> Fisch. GigaScience, 2021, 10, .	3.3	13
3368	Chromosome-level genome assembly of the hard-shelled mussel <i>Mytilus coruscus</i>, a widely distributed species from the temperate areas of East Asia. GigaScience, 2021, 10, .	3.3	45
3369	A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes. F1000Research, 2021, 10, 286.	0.8	5
3371	Genome-Wide Analysis of nsLTP Gene Family and Identification of SiLTPs Contributing to High Oil Accumulation in Sesame (Sesamum indicum L.). International Journal of Molecular Sciences, 2021, 22, 5291.	1.8	20
3372	Chromosomal-Level Reference Genome of the Neotropical Tree Jacaranda mimosifolia D. Don. Genome Biology and Evolution, 2021, 13, .	1.1	7
3373	Large Phylogenomic Data sets Reveal Deep Relationships and Trait Evolution in Chlorophyte Green Algae. Genome Biology and Evolution, 2021, 13, .	1.1	14
3374	Functional and Comparative Analysis of Centromeres Reveals Clade-Specific Genome Rearrangements in <i>Candida auris</i> and a Chromosome Number Change in Related Species. MBio, 2021, 12, .	1.8	11
3375	Extensive variation within the pan-genome of cultivated and wild sorghum. Nature Plants, 2021, 7, 766-773.	4.7	94
3376	Adaptive Proteome Diversification by Nonsynonymous A-to-I RNA Editing in Coleoid Cephalopods. Molecular Biology and Evolution, 2021, 38, 3775-3788.	3.5	22
3377	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. Molecular Biology and Evolution, 2021, 38, 3621-3636.	3.5	41
3378	Genome of the butterfly hillstream loach provides insights into adaptations to torrential mountain stream life. Molecular Ecology Resources, 2021, 21, 1922-1935.	2.2	1
3379	Updates to HCOP: the HGNC comparison of orthology predictions tool. Briefings in Bioinformatics, 2021, 22, .	3.2	20
3380	Sporulation is dispensable for the vegetableâ€associated life cycle of the human pathogen <i>BacillusÂcereus</i>. Microbial Biotechnology, 2021, 14, 1550-1565.	2.0	13
3381	The genome of the warm-season turfgrass African bermudagrass (<i>Cynodon transvaalensis</i>). Horticulture Research, 2021, 8, 93.	2.9	19
3384	pSONIC: Ploidy-aware Syntenic Orthologous Networks Identified via Collinearity. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	8
3385	The Vaginal Microbial Signatures of Preterm Birth Delivery in Indian Women. Frontiers in Cellular and Infection Microbiology, 2021, 11, 622474.	1.8	23
3386	An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related <i>Aspergillus</i> fungi. Genetics, 2021, 218, .	1.2	18

#	Article	IF	Citations
3387	Rampant Genome-Wide Admixture across the<i>Heliconius</i>Radiation. Genome Biology and Evolution, 2021, 13, .	1.1	31
3388	Physiological and Genomic Analysis of Bacillus pumilus UAMX Isolated from the Gastrointestinal Tract of Overweight Individuals. Microorganisms, 2021, 9, 1076.	1.6	2
3389	Genome analysis of Spiroplasma citri strains from different host plants and its leafhopper vectors. BMC Genomics, 2021, 22, 373.	1.2	8
3390	Chromosome-scale assembly of the <i>Sparassis latifolia</i> genome obtained using long-read and Hi-C sequencing. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	4
3391	The genome of Nautilus pompilius illuminates eye evolution and biomineralization. Nature Ecology and Evolution, 2021, 5, 927-938.	3.4	40
3392	Analysis of Paralogs in Target Enrichment Data Pinpoints Multiple Ancient Polyploidy Events in <i>Alchemilla</i> s.l. (Rosaceae). Systematic Biology, 2021, 71, 190-207.	2.7	26
3393	Proteomic Identification of Bombyx mori Organelles Using the Engineered Ascorbate Peroxidase APEX and Development of Silkworm Organelle Proteome Database (SilkOrganPDB). International Journal of Molecular Sciences, 2021, 22, 5051.	1.8	0
3394	Whole-genome resequencing of Osmanthus fragrans provides insights into flower color evolution. Horticulture Research, 2021, 8, 98.	2.9	35
3395	Molecular mechanisms of mutualistic and antagonistic interactions in a plantâ€“pollinator association. Nature Ecology and Evolution, 2021, 5, 974-986.	3.4	30
3396	The genome of a wild Medicago species provides insights into the tolerant mechanisms of legume forage to environmental stress. BMC Biology, 2021, 19, 96.	1.7	39
3397	Computational Design of Novel Allosteric Inhibitors for Plasmodium falciparum DegP. Molecules, 2021, 26, 2742.	1.7	5
3398	Comprehensive phylogeny of Konosirus punctatus (Clupeiformes: Clupeidae) based on transcriptomic data. Bioscience Reports, 2021, 41, .	1.1	2
3399	Inhibition of a nutritional endosymbiont by glyphosate abolishes mutualistic benefit on cuticle synthesis in Oryzaephilus surinamensis. Communications Biology, 2021, 4, 554.	2.0	21
3400	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
3401	Bacillus pumilus Group Comparative Genomics: Toward Pangenome Features, Diversity, and Marine Environmental Adaptation. Frontiers in Microbiology, 2021, 12, 571212.	1.5	9
3402	Transcriptional Analysis of Coccidioides immitis Mycelia and Spherules by RNA Sequencing. Journal of Fungi (Basel, Switzerland), 2021, 7, 366.	1.5	13
3404	Complete Genome Sequence of Xylella taiwanensis and Comparative Analysis of Virulence Gene Content With Xylella fastidiosa. Frontiers in Microbiology, 2021, 12, 684092.	1.5	6
3406	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

#	Article	IF	Citations
3407	PHROG: families of prokaryotic virus proteins clustered using remote homology. NAR Genomics and Bioinformatics, 2021, 3, lqab067.	1.5	134
3408	The Chromosome-Level Genome of <i>Triplophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. Genome Biology and Evolution, 2021, 13, .	1.1	7
3409	Heterotrophic euglenid Rhabdomonas costata resembles its phototrophic relatives in many aspects of molecular and cell biology. Scientific Reports, 2021, 11, 13070.	1.6	5
3410	The chromosome-level reference genome of Coptis chinensis provides insights into genomic evolution and berberine biosynthesis. Horticulture Research, 2021, 8, 121.	2.9	25
3411	Insights into the ancestry evolution of the<i>Mycobacterium tuberculosis</i>complex from analysis of<i>Mycobacterium riyadhense</i>. NAR Genomics and Bioinformatics, 2021, 3, lqab070.	1.5	3
3412	Large-scale phylogenomic analysis provides new insights into the phylogeny of the class Oligohymenophorea (Protista, Ciliophora) with establishment of a new subclass Urocentria nov. subcl. Molecular Phylogenetics and Evolution, 2021, 159, 107112.	1.2	23
3413	The American lobster genome reveals insights on longevity, neural, and immune adaptations. Science Advances, 2021, 7, .	4.7	27
3414	Innovation, conservation, and repurposing of gene function in root cell type development. Cell, 2021, 184, 3333-3348.e19.	13.5	48
3415	A chromosome-level Camptotheca acuminata genome assembly provides insights into the evolutionary origin of camptothecin biosynthesis. Nature Communications, 2021, 12, 3531.	5.8	66
3416	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
3417	Cotton D genome assemblies built with long-read data unveil mechanisms of centromere evolution and stress tolerance divergence. BMC Biology, 2021, 19, 115.	1.7	14
3418	Wolfberry genomes and the evolution of LyciumÂ(Solanaceae). Communications Biology, 2021, 4, 671.	2.0	40
3419	Cytoplasmic incompatibility between Old and New World populations of a tramp ant. Evolution; International Journal of Organic Evolution, 2021, 75, 1775-1791.	1.1	13
3420	Comparative Genomics and Molecular Analysis of Epidermophyton floccosum. Mycopathologia, 2021, 186, 487-497.	1.3	5
3421	Analysis of the Coptis chinensis genome reveals the diversification of protoberberine-type alkaloids. Nature Communications, 2021, 12, 3276.	5.8	68
3422	Comparative Genomic Insights Into the Taxonomic Classification, Diversity, and Secondary Metabolic Potentials of Kitasatospora, a Genus Closely Related to Streptomyces. Frontiers in Microbiology, 2021, 12, 683814.	1.5	11
3424	A Chromosome-Level Genome Assembly of the Mandarin Fish (Siniperca chuatsi). Frontiers in Genetics, 2021, 12, 671650.	1.1	8
3425	The chromosome-level Stevia genome provides insights into steviol glycoside biosynthesis. Horticulture Research, 2021, 8, 129.	2.9	35

#	ARTICLE	IF	CITATIONS
3426	Genomic Characteristics and Comparative Genomics Analysis of Two Chinese Corynespora cassiicola Strains Causing Corynespora Leaf Fall (CLF) Disease. Journal of Fungi (Basel, Switzerland), 2021, 7, 485.	1.5	5
3427	A high-quality genome assembly of <i>Morinda officinalis</i>, a famous native southern herb in the Lingnan region of southern China. Horticulture Research, 2021, 8, 135.	2.9	17
3428	Chromosome-Scale Genome Assembly of the Resurrection Plant <i>Acanthochlamys bracteata</i> (Velloziaceae). Genome Biology and Evolution, 2021, 13, .	1.1	6
3429	Two gap-free reference genomes and a global view of the centromere architecture in rice. Molecular Plant, 2021, 14, 1757-1767.	3.9	133
3430	Genomic insights into the fast growth of paulownias and the formation of Paulownia witches' broom. Molecular Plant, 2021, 14, 1668-1682.	3.9	39
3431	Genomic insights into the adaptation and evolution of the nautilus, an ancient but evolving â€œliving fossilâ€ Molecular Ecology Resources, 2022, 22, 15-27.	2.2	15
3432	Interplay of Various Evolutionary Modes in Genome Diversification and Adaptive Evolution of the Family Sulfolobaceae. Frontiers in Microbiology, 2021, 12, 639995.	1.5	2
3433	Chromosomeâ€level genome assembly of the bean bug <i>Riptortus pedestris</i>. Molecular Ecology Resources, 2021, 21, 2423-2436.	2.2	24
3434	Chromosomeâ€scale genome assembly of areca palm (<i>Areca catechu</i>). Molecular Ecology Resources, 2021, 21, 2504-2519.	2.2	20
3436	Chromosome-level genome assembly of a regenerable maize inbred line A188. Genome Biology, 2021, 22, 175.	3.8	32
3437	A chromosome-level genome assembly of the blackspotted croaker (Protonibea diacanthus). Aquaculture and Fisheries, 2022, 7, 616-622.	1.2	1
3438	Linking a Gene Cluster to Atranorin, a Major Cortical Substance of Lichens, through Genetic Dereplication and Heterologous Expression. MBio, 2021, 12, e0111121.	1.8	33
3439	Comparison of whole genome sequences of three Bacillus cereus strains reveals the food safety risks of Apostichopus japonicus in China. Aquaculture Reports, 2021, 20, 100649.	0.7	2
3440	Dissecting the chromosome-level genome of the Asian Clam (Corbicula fluminea). Scientific Reports, 2021, 11, 15021.	1.6	5
3441	Physiological, Genomic and Transcriptomic Analyses Reveal the Adaptation Mechanisms of Acidiella bohemica to Extreme Acid Mine Drainage Environments. Frontiers in Microbiology, 2021, 12, 705839.	1.5	11
3442	High-Quality Genome Assembly and Comprehensive Transcriptome of the Painted Lady Butterfly<i>Vanessa cardui</i>. Genome Biology and Evolution, 2021, 13, .	1.1	10
3443	Integrated miRNA-mRNA analysis provides potential biomarkers for selective breeding in bay scallop (Argopecten irradians). Genomics, 2021, 113, 2744-2755.	1.3	3
3444	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

#	Article	IF	Citations
3445	Genome assembly of the popular Korean soybean cultivar Hwangkeum. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
3446	Improved genome assembly of Chinese shrimp (<i>Fenneropenaeus chinensis</i>) suggests adaptation to the environment during evolution and domestication. Molecular Ecology Resources, 2022, 22, 334-344.	2.2	14
3447	Pangenome analysis and virulence profiling of Streptococcus intermedius. BMC Genomics, 2021, 22, 522.	1.2	7
3448	Comparative Transcriptome and Endophytic Bacterial Community Analysis of Morchella conica SH. Frontiers in Microbiology, 2021, 12, 682356.	1.5	3
3449	Genomic Analysis of Sarcomyxa edulis Reveals the Basis of Its Medicinal Properties and Evolutionary Relationships. Frontiers in Microbiology, 2021, 12, 652324.	1.5	6
3450	Evolution of Toll, Spatzle and MyD88 in insects: the problem of the Diptera bias. BMC Genomics, 2021, 22, 562.	1.2	13
3451	De novo chromosome-level assembly of the Centella asiatica genome. Genomics, 2021, 113, 2221-2228.	1.3	14
3452	Physiological and genomic features of Henriciella with the description of Henriciella mobilis sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	6
3453	Comparative Transcriptomics Reveals Distinct Patterns of Gene Expression Conservation through Vertebrate Embryogenesis. Genome Biology and Evolution, 2021, 13, .	1.1	2
3454	Integrated Phenotypicâ€"Genotypic Analysis of LatilactobacillusÂsakei from Different Niches. Foods, 2021, 10, 1717.	1.9	10
3455	The Welwitschia genome reveals aÂunique biology underpinning extreme longevity in deserts. Nature Communications, 2021, 12, 4247.	5.8	51
3456	Gulosibacter sediminis sp. nov., isolated from Indian Ocean marine sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
3457	Chromosomalâ€scale genome assembly of Eleutherococcus senticosus provides insights into chromosome evolution in Araliaceae. Molecular Ecology Resources, 2021, 21, 2204-2220.	2.2	10
3458	Species Tree Inference Methods Intended to Deal with Incomplete Lineage Sorting Are Robust to the Presence of Paralogs. Systematic Biology, 2022, 71, 367-381.	2.7	26
3459	Genome sequence of Apostasia ramifera provides insights into the adaptive evolution in orchids. BMC Genomics, 2021, 22, 536.	1.2	9
3460	Comparative Genomics of Clinical Isolates of the Emerging Tick-Borne Pathogen Neoehrlichia mikurensis. Microorganisms, 2021, 9, 1488.	1.6	9
3461	A chromosome-level genome assembly of the miiuy croaker (Miichthys miiuy) using nanopore sequencing and Hi-C. Aquaculture and Fisheries, 2024, 9, 218-225.	1.2	4
3462	The chromosome-level reference genome assembly for Dendrobium officinale and its utility of functional genomics research and molecular breeding study. Acta Pharmaceutica Sinica B, 2021, 11, 2080-2092.	5.7	54

#	ARTICLE	IF	CITATIONS
3464	Comparative analyses of the Hymenoscyphus fraxineus and Hymenoscyphus albidus genomes reveals potentially adaptive differences in secondary metabolite and transposable element repertoires. BMC Genomics, 2021, 22, 503.	1.2	6
3465	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
3466	De Novo Sequencing and High-Contiguity Genome Assembly of Moniezia expansa Reveals Its Specific Fatty Acid Metabolism and Reproductive Stem Cell Regulatory Network. Frontiers in Cellular and Infection Microbiology, 2021, 11, 693914.	1.8	3
3467	Comparative transcriptome analysis and identification of candidate adaptive evolution genes of Miscanthus lutarioriparius and Miscanthus sacchariflorus. Physiology and Molecular Biology of Plants, 2021, 27, 1499-1512.	1.4	2
3468	Genomics and transcriptomics yields a system-level view of the biology of the pathogen Naegleria fowleri. BMC Biology, 2021, 19, 142.	1.7	18
3469	Effects of Bacillus coagulans as an adjunct starter culture on yogurt quality and storage. Journal of Dairy Science, 2021, 104, 7466-7479.	1.4	11
3470	orthofisher: a broadly applicable tool for automated gene identification and retrieval. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	12
3471	A Chromosome-level Genome Assembly of Wild Castor Provides New Insights into its Adaptive Evolution in Tropical Desert. Genomics, Proteomics and Bioinformatics, 2022, 20, 42-59.	3.0	18
3472	The Evolutionary Origins of Extreme Halophilic Archaeal Lineages. Genome Biology and Evolution, 2021, 13, .	1.1	20
3473	Genome-Wide Analysis and Functional Characterization of the UDP-Glycosyltransferase Family in Grapes. Horticulturae, 2021, 7, 204.	1.2	11
3475	Genomic diversity, life strategies and ecology of marine HTVC010P-type pelagiphages. Microbial Genomics, 2021, 7, .	1.0	6
3476	Genomic and transcriptomic analyses reveal metabolic complementarity between whiteflies and their symbionts. Insect Science, 2022, 29, 539-549.	1.5	9
3477	Halobaculum halophilum sp. nov. and Halobaculum salinum sp. nov., isolated from salt lake and saline soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
3478	Pyricularia sp. jiangsuensis , a new cryptic rice panicle blast pathogen from rice fields in Jiangsu Province, China. Environmental Microbiology, 2021, 23, 5463-5480.	1.8	1
3479	Evolution of Benincasa hispida in the Cucurbitaceae family and phylogenetic relationships of the phenylalanine ammonia-lyase gene family in six Cucurbitaceae species. Plant Growth Regulation, 2021, 95, 157.	1.8	1
3480	Evolutionarily recent dual obligatory symbiosis among adelgids indicates a transition between fungus- and insect-associated lifestyles. ISME Journal, 2022, 16, 247-256.	4.4	16
3481	Draft Genome Assembly and Transcriptome Dataset for European Turnip (Brassica rapa L. ssp. rapifera), ECD4 Carrying Clubroot Resistance. Frontiers in Genetics, 2021, 12, 651298.	1.1	5
3482	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. Systematic Biology, 2022, 71, 526-546.	2.7	32

#	ARTICLE	IF	CITATIONS
3483	Reconstruction of ancestral karyotype illuminates chromosome evolution in the genus <i>Cucumis</i>. Plant Journal, 2021, 107, 1243-1259.	2.8	23
3484	Draft genome assembly of the Aral barbell <i>Luciobarbus brachycephalus</i> using PacBio sequencing. Genome Biology and Evolution, 2021, 13, .	1.1	0
3485	Chromosome-level genome of Himalayan yew provides insights into the origin and evolution of the paclitaxel biosynthetic pathway. Molecular Plant, 2021, 14, 1199-1209.	3.9	46
3486	A comparative genomic analysis of Xanthomonas arboricola pv. juglandis strains reveal hallmarks of mobile genetic elements in the adaptation and accelerated evolution of virulence. Genomics, 2021, 113, 2513-2525.	1.3	9
3487	Mobilization of the nonconjugative virulence plasmid from hypervirulent Klebsiella pneumoniae. Genome Medicine, 2021, 13, 119.	3.6	60
3488	New Histoplasma Diagnostic Assays Designed via Whole Genome Comparisons. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Ov	1.5	7
3489	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
3490	Chromosomeâ€level genome assembly of the endangered humphead wrasse <i>CheilinusÂundulat</i><i>u</i><i>s</i>: Insight into the expansion of opsin genes in fishes. Molecular Ecology Resources, 2021, 21, 2388-2406.	2.2	11
3491	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. Plant Biotechnology Journal, 2021, 19, 2206-2220.	4.1	23
3492	Genetic and biological characterisation of three cryptic Eimeria operational taxonomic units that infect chickens (Gallus gallus domesticus). International Journal for Parasitology, 2021, 51, 621-634.	1.3	24
3493	Chromosomeâ€level genome assembly of <i>Welwitschia mirabilis</i>, a unique Namib Desert species. Molecular Ecology Resources, 2022, 22, 391-403.	2.2	1
3494	Genomic and Phenotypic Biology of Novel Strains of Dickeya zeae Isolated From Pineapple and Taro in Hawaii: Insights Into Genome Plasticity, Pathogenicity, and Virulence Determinants. Frontiers in Plant Science, 2021, 12, 663851.	1.7	15
3495	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
3496	Haplotype-resolved genome of diploid ginger (<i>Zingiber officinale</i>) and its unique gingerol biosynthetic pathway. Horticulture Research, 2021, 8, 189.	2.9	53
3497	The genome of the thin-necked bladder worm Taenia hydatigena reveals evolutionary strategies for helminth survival. Communications Biology, 2021, 4, 1004.	2.0	2
3498	Comparative transcriptome provides insights into the selection adaptation between wild and farmed foxes. Ecology and Evolution, 2021, 11, 13475-13486.	0.8	2
3499	Comparative transcriptomics provides a strategy for phylogenetic analysis and SSR marker development in Chaenomeles. Scientific Reports, 2021, 11, 16441.	1.6	2
3500	Crossâ€species analysis between the maize smut fungi <i>Ustilago maydis</i> and <i>Sporisorium reilianum</i> highlights the role of transcriptional change of effector orthologs for virulence and disease. New Phytologist, 2021, 232, 719-733.	3.5	13

#	Article	IF	Citations
3501	High-quality genome assembly and resequencing of modern cotton cultivars provide resources for crop improvement. Nature Genetics, 2021, 53, 1385-1391.	9.4	76
3502	Complete Genomic Characterization and Identification of Saccharomycopsisphalluae sp. nov., a Novel Pathogen Causes Yellow Rot Disease on Phallus rubrovolvatus. Journal of Fungi (Basel, Switzerland), 2021, 7, 707.	1.5	8
3503	ExOrthist: a tool to infer exon orthologies at any evolutionary distance. Genome Biology, 2021, 22, 239.	3.8	11
3504	Quest for Novel Preventive and Therapeutic Options Against Multidrug-Resistant Pseudomonas aeruginosa. International Journal of Peptide Research and Therapeutics, 2021, 27, 2313-2331.	0.9	2
3505	Gene Annotation and Transcriptome Delineation on a De Novo Genome Assembly for the Reference Leishmania major Friedlin Strain. Genes, 2021, 12, 1359.	1.0	7
3506	The Cardamine enshiensis genome reveals whole genome duplication and insight into selenium hyperaccumulation and tolerance. Cell Discovery, 2021, 7, 62.	3.1	15
3507	An improved draft genome assembly of Meloidogyne graminicola IARI strain using long-read sequencing. Gene, 2021, 793, 145748.	1.0	8
3508	Genome-wide identification and characterization of <i>WOX</i> genes in <i>Cucumis sativus</i>. Genome, 2021, 64, 761-776.	0.9	18
3509	Comparative Genomic and Transcriptomic Analysis of Naegleria fowleri Clinical and Environmental Isolates. MSphere, 2021, 6, e0063721.	1.3	8
3511	New highâ€quality peach (<i>Prunus persica</i> L. Batsch) genome assembly to analyze the molecular evolutionary mechanism of volatile compounds in peach fruits. Plant Journal, 2021, 108, 281-295.	2.8	31
3513	Genus-level evolutionary relationships of FAR proteins reflect the diversity of lifestyles of free-living and parasitic nematodes. BMC Biology, 2021, 19, 178.	1.7	4
3514	Evolutionary and functional relationships in the ribosome biogenesis SBDS and EFL1 protein families. Molecular Genetics and Genomics, 2021, 296, 1263-1278.	1.0	0
3515	Genome Analysis of Phytophthora nicotianae JM01 Provides Insights into Its Pathogenicity Mechanisms. Plants, 2021, 10, 1620.	1.6	4
3516	Legionella pneumophila CRISPR-Cas Suggests Recurrent Encounters with One or More Phages in the Family <i>Microviridae</i>. Applied and Environmental Microbiology, 2021, 87, e0046721.	1.4	6
3518	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
3519	Comparative Genomics of <i>Exiguobacterium</i> Reveals What Makes a Cosmopolitan Bacterium. MSystems, 2021, 6, e0038321.	1.7	13
3520	Distinct mutations in importin-Î² family nucleocytoplasmic transport receptors transportin-SR and importin-13 affect specific cargo binding. Scientific Reports, 2021, 11, 15649.	1.6	4
3521	Concerted genomic and epigenomic changes accompany stabilization of Arabidopsis allopolyploids. Nature Ecology and Evolution, 2021, 5, 1382-1393.	3.4	41

#	ARTICLE	IF	CITATIONS
3522	Population Genomics Reveals Gene Flow and Adaptive Signature in Invasive Weed Mikania micrantha. Genes, 2021, 12, 1279.	1.0	2
3523	Pan-genome of Raphanus highlights genetic variation and introgression among domesticated, wild, and weedy radishes. Molecular Plant, 2021, 14, 2032-2055.	3.9	56
3524	The genome of <i>Cymbidium sinense</i> revealed the evolution of orchid traits. Plant Biotechnology Journal, 2021, 19, 2501-2516.	4.1	46
3525	An Efficient, Nonphylogenetic Method for Detecting Genes Sharing Evolutionary Signals in Phylogenomic Data Sets. Genome Biology and Evolution, 2021, 13, .	1.1	1
3526	A chromosome-level genome assembly of the striped catfish (Pangasianodon hypophthalmus). Genomics, 2021, 113, 3349-3356.	1.3	18
3527	A Prioritized and Validated Resource of Mitochondrial Proteins in <i>Plasmodium</i> Identifies Unique Biology. MSphere, 2021, 6, e0061421.	1.3	16
3528	Isolation and Characterization of High-Efficiency Rhizobia From Western Kenya Nodulating With Common Bean. Frontiers in Microbiology, 2021, 12, 697567.	1.5	12
3529	Chromosomeâ€•scale genome assembly and population genomics provide insights into the adaptation, domestication, and flavonoid metabolism of Chinese plum. Plant Journal, 2021, 108, 1174-1192.	2.8	16
3530	Gene Body Methylation Confers Transcription Robustness in Mangroves During Long-Term Stress Adaptation. Frontiers in Plant Science, 2021, 12, 733846.	1.7	2
3531	Incipient diploidization of the medicinal plant Perilla within 10,000 years. Nature Communications, 2021, 12, 5508.	5.8	35
3532	Comparative transcriptome analysis revealed omnivorous adaptation of the small intestine of Melinae. Scientific Reports, 2021, 11, 19162.	1.6	1
3533	In-depth Phylogenomic Analysis of Arbuscular Mycorrhizal Fungi Based on a Comprehensive Set of de novo Genome Assemblies. Frontiers in Fungal Biology, 2021, 2, .	0.9	15
3534	Haploid Genome Analysis Reveals a Tandem Cluster of Four HSP20 Genes Involved in the High-Temperature Adaptation of Coriolopsis trogii. Microbiology Spectrum, 2021, 9, e0028721.	1.2	7
3535	Chromosomeâ€•level genome assembly of the mirid predator <i>Cyrtorhinus lividipennis</i> Reuter (Hemiptera: Miridae), an important natural enemy in the rice ecosystem. Molecular Ecology Resources, 2022, 22, 1086-1099.	2.2	7
3536	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
3537	Single-genome sequencing reveals within-host evolution of human malaria parasites. Cell Host and Microbe, 2021, 29, 1496-1506.e3.	5.1	11
3538	Genome of Ganoderma Species Provides Insights Into the Evolution, Conifers Substrate Utilization, and Terpene Synthesis for Ganoderma tsugae. Frontiers in Microbiology, 2021, 12, 724451.	1.5	13
3542	Genomic Stability and Genetic Defense Systems in<i>Dolosigranulum pigrum</i>, a Candidate Beneficial Bacterium from the Human Microbiome. MSystems, 2021, 6, e0042521.	1.7	11

#	Article	IF	Citations
3544	Comparative Genomics and Specific Functional Characteristics Analysis of Lactobacillus acidophilus. Microorganisms, 2021, 9, 1992.	1.6	22
3545	The <i>Euscaphis japonica</i> genome and the evolution of malvids. Plant Journal, 2021, 108, 1382-1399.	2.8	6
3546	Genomic anatomy of male-specific microchromosomes in a gynogenetic fish. PLoS Genetics, 2021, 17, e1009760.	1.5	17
3547	Colonized Niche, Evolution and Function Signatures of Bifidobacterium pseudolongum within Bifidobacterial Genus. Foods, 2021, 10, 2284.	1.9	6
3548	Chromosome-level genome assembly of <i>Gynostemma pentaphyllum</i> provides insights into gypenoside biosynthesis. DNA Research, 2021, 28, .	1.5	14
3549	OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. Life Science Alliance, 2021, 4, e202101167.	1.3	4
3550	Characterization of toxigenic Corynebacterium diphtheriae strains isolated in Russia. Russian Journal of Infection and Immunity, 2021, 11, 683-691.	0.2	1
3551	<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
3553	High-Quality de novo Chromosome-Level Genome Assembly of a Single Bombyx mori With BmNPV Resistance by a Combination of PacBio Long-Read Sequencing, Illumina Short-Read Sequencing, and Hi-C Sequencing. Frontiers in Genetics, 2021, 12, 718266.	1.1	5
3554	A high-quality chromosome-level genome of wild <i>Rosa rugosa</i>. DNA Research, 2021, 28, .	1.5	10
3555	Flavobacterium erciyesense sp. nov., a putative non-pathogenic fish symbiont. Archives of Microbiology, 2021, 203, 5783-5792.	1.0	10
3556	Comparative Genomic Analysis of Bifidobacterium bifidum Strains Isolated from Different Niches. Genes, 2021, 12, 1504.	1.0	6
3557	A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes. F1000Research, 2021, 10, 286.	0.8	3
3558	Avian Neo-Sex Chromosomes Reveal Dynamics of Recombination Suppression and W Degeneration. Molecular Biology and Evolution, 2021, 38, 5275-5291.	3.5	25
3559	Genome Evolution of Filamentous Cyanobacterium Nostoc Species: From Facultative Symbiosis to Free Living. Microorganisms, 2021, 9, 2015.	1.6	4
3560	Evolutionary origin of a tetraploid <i>Allium</i> species on the Qinghaiâ€“Tibet Plateau. Molecular Ecology, 2021, 30, 5780-5795.	2.0	11
3561	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
3562	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

#	ARTICLE	IF	CITATIONS
3563	The genomes of nucleocytoplasmic large DNA viruses: viral evolution writ large. Microbial Genomics, 2021, 7, .	1.0	13
3564	Insights into angiosperm evolution, floral development and chemical biosynthesis from the Aristolochia fimbriata genome. Nature Plants, 2021, 7, 1239-1253.	4.7	51
3565	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
3566	Comparative genetic analyses provide clues about capsule switching in Streptococcus suis 2 strains with different virulence levels and genetic backgrounds. Microbiological Research, 2021, 250, 126814.	2.5	8
3567	Characterization of mitogenomes from four <i>Mucorales</i> species and insights into pathogenicity. Mycoses, 2022, 65, 45-56.	1.8	1
3569	New Genes Interacted With Recent Whole-Genome Duplicates in the Fast Stem Growth of Bamboos. Molecular Biology and Evolution, 2021, 38, 5752-5768.	3.5	28
3570	Aspergillus fumigatus versus Genus Aspergillus: Conservation, Adaptive Evolution and Specific Virulence Genes. Microorganisms, 2021, 9, 2014.	1.6	4
3571	Exploring the GRAS gene family in common bean (Phaseolus vulgaris L.): characterization, evolutionary relationships, and expression analyses in response to abiotic stresses. Planta, 2021, 254, 84.	1.6	12
3572	Rambutan genome revealed gene networks for spine formation and aril development. Plant Journal, 2021, 108, 1037-1052.	2.8	7
3573	Unraveling Gene Content Variation Across Eukaryotic Giant Viruses Based on Network Analyses and Host Associations. Virus Evolution, 2021, 7, veab081.	2.2	5
3574	TransLnc: a comprehensive resource for translatable lncRNAs extends immunopeptidome. Nucleic Acids Research, 2022, 50, D413-D420.	6.5	16
3575	Identification of the Biosynthetic Gene Cluster for the Organoarsenical Antibiotic Arsinothricin. Microbiology Spectrum, 2021, 9, e0050221.	1.2	14
3576	KinOrtho: a method for mapping human kinase orthologs across the tree of life and illuminating understudied kinases. BMC Bioinformatics, 2021, 22, 446.	1.2	13
3578	The endemic Helicobacter pylori population in Southern Vietnam has both South East Asian and European origins. Gut Pathogens, 2021, 13, 57.	1.6	6
3579	Epigenetic and transcriptional responses underlying mangrove adaptation to UV-B. IScience, 2021, 24, 103148.	1.9	4
3580	Variability of the Pr77 sequence of L1Tc retrotransposon among six T. cruzi strains belonging to different discrete typing units (DTUs). Acta Tropica, 2021, 222, 106053.	0.9	1
3581	Chromosome-scale genomes provide new insights into subspecies divergence and evolutionary characteristics of the giant panda. Science Bulletin, 2021, 66, 2002-2013.	4.3	13
3582	Extreme physiology: Biomass and transcriptional profiling of three abandoned Agave cultivars. Industrial Crops and Products, 2021, 172, 114043.	2.5	16

#	Article	IF	Citations
3583	The draft genome of the Asian corn borer yields insights into ecological adaptation of a devastating maize pest. Insect Biochemistry and Molecular Biology, 2021, 138, 103638.	1.2	8
3584	Evolutionarily conserved transcriptional landscape of the heart defining the chamber specific physiology. Genomics, 2021, 113, 3782-3792.	1.3	1
3585	The chromosome-based genome provides insights into the evolution in water spinach. Scientia Horticulturae, 2021, 289, 110501.	1.7	13
3586	MiDSystem: A comprehensive online system for de novo assembly and analysis of microbial genomes. New Biotechnology, 2021, 65, 42-52.	2.4	2
3587	Phylogenomics, divergence time estimation and trait evolution provide a new look into the Gracilariales (Rhodophyta). Molecular Phylogenetics and Evolution, 2021, 165, 107294.	1.2	22
3588	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. Cell Surface, 2021, 7, 100050.	1.5	16
3589	Transcriptomic and proteomic analyses of venom glands from scorpions Liocheles australasiae, Mesobuthus martensii, and Scorpio maurus palmatus. Peptides, 2021, 146, 170643.	1.2	6
3591	The Draft Genome Sequence of a New Land-Hopper Platorchestia hallaensis. Frontiers in Genetics, 2020, 11, 621301.	1.1	1
3592	Genome-Wide Identification and Comparative Analysis of ARF Family Genes in Three Apiaceae Species. Frontiers in Genetics, 2020, 11, 590535.	1.1	9
3593	Ancestral sequence reconstruction - An underused approach to understand the evolution of gene function in plants?. Computational and Structural Biotechnology Journal, 2021, 19, 1579-1594.	1.9	10
3594	The landscape of lncRNAs in Cydia pomonella provides insights into their signatures and potential roles in transcriptional regulation. BMC Genomics, 2021, 22, 4.	1.2	8
3595	Nutrient availability regulates proline/alanine transporters in Trypanosoma brucei. Journal of Biological Chemistry, 2021, 296, 100566.	1.6	7
3596	Genome and transcriptome of Papaver somniferum Chinese landrace CHM indicates that massive genome expansion contributes to high benzylisoquinoline alkaloid biosynthesis. Horticulture Research, 2021, 8, 5.	2.9	22
3597	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	13.7	85
3598	Expansion within the CYP71D subfamily drives the heterocyclization of tanshinones synthesis in Salvia miltiorrhiza. Nature Communications, 2021, 12, 685.	5.8	94
3599	Analysis of intraspecies diversity reveals a subset of highly variable plant immune receptors and predicts their binding sites. Plant Cell, 2021, 33, 998-1015.	3.1	45
3600	Rapid protein evolution, organellar reductions, and invasive intronic elements in the marine aerobic parasite dinoflagellate Amoebophrya spp. BMC Biology, 2021, 19, 1.	1.7	135
3601	Draft Genome of the Edible Oriental Insect Protaetia brevitarsis seulensis. Frontiers in Genetics, 2020, 11, 593994.	1.1	3

#	ARTICLE	IF	CITATIONS
3603	Comparative analysis of the <i>TCP</i> gene family in celery, coriander and carrot (family) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	6.2	9
3604	The hard clam genome reveals massive expansion and diversification of inhibitors of apoptosis in Bivalvia. BMC Biology, 2021, 19, 15.	1.7	52
3605	Analysis of Long Non-Coding RNA in Cryptosporidium parvum Reveals Significant Stage-Specific Antisense Transcription. Frontiers in Cellular and Infection Microbiology, 2020, 10, 608298.	1.8	21
3606	Comprehensive analysis of full-length transcriptomes of Schizothorax prenanti by single-molecule long-read sequencing. Genomics, 2022, 114, 456-464.	1.3	14
3607	XenoCluster: A Grid Computing Approach to Finding Ancient Evolutionary Genetic Anomalies. Lecture Notes in Computer Science, 2005, , 355-366.	1.0	3
3609	A Parsimony Approach to Genome-Wide Ortholog Assignment. Lecture Notes in Computer Science, 2006, , 578-594.	1.0	11
3611	Reactome â€“ A Knowledgebase of Biological Pathways. Lecture Notes in Computer Science, 2006, , 710-719.	1.0	4
3612	The Potential of Family-Free Genome Comparison. Computational Biology, 2013, , 287-307.	0.1	12
3613	Selecting Targets from Eukaryotic Parasites for Structural Genomics and Drug Discovery. Methods in Molecular Biology, 2014, 1140, 53-59.	0.4	5
3614	The Eukaryotic Pathogen Databases: A Functional Genomic Resource Integrating Data from Human and Veterinary Parasites. Methods in Molecular Biology, 2015, 1201, 1-18.	0.4	16
3615	Defining Orthologs and Pangenome Size Metrics. Methods in Molecular Biology, 2015, 1231, 191-202.	0.4	12
3616	Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. Methods in Molecular Biology, 2015, 1231, 15-29.	0.4	7
3617	Fundamentals of Comparative Genome Analysis in Caenorhabditis Nematodes. Methods in Molecular Biology, 2015, 1327, 11-21.	0.4	3
3618	A Guide to the PLAZA 3.0 Plant Comparative Genomic Database. Methods in Molecular Biology, 2017, 1533, 183-200.	0.4	11
3619	Inferring Orthology and Paralogy. Methods in Molecular Biology, 2019, 1910, 149-175.	0.4	84
3620	Microarray Probe Mapping and Annotation in Cross-Species Comparative Toxicogenomics. Methods in Molecular Biology, 2008, 460, 159-183.	0.4	2
3621	Reactome Knowledgebase of Human Biological Pathways and Processes. Methods in Molecular Biology, 2011, 694, 49-61.	0.4	84
3622	Genomics and Bioinformatics of the PVC Superphylum. , 2013, , 165-193.		2

#	Article	IF	Citations
3623	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 153-166.		1
3624	Foxtail Millet (Setaria italica L.): Potential of Smaller Millet for Future Breeding. , 2019, , 133-163.		6
3625	Computational Strategies for Eukaryotic Pangenome Analyses. , 2020, , 293-307.		8
3626	A Review of Pangenome Tools and Recent Studies. , 2020, , 89-112.		21
3627	The Reyan 7-33-97 Rubber Tree Genome: Insight into Its Structure, Composition and Application. Compendium of Plant Genomes, 2020, , 13-40.	0.3	3
3628	Oh Brother, Where Art Thou? Finding Orthologs in the Twilight and Midnight Zones of Sequence Similarity. , 2016, , 393-419.		4
3629	A Method for Inferring Biological Functions Using Homologous Genes Among Three Genomes. , 2007, , 69-80.		1
3630	Baculovirus Phylogeny Based on Genome Rearrangements. Lecture Notes in Computer Science, 2007, , 69-82.	1.0	3
3631	The Genome Sequence of Meloidogyne incognita Unveils Mechanisms of Adaptation to Plant-Parasitism in Metazoa. , 2009, , 287-302.		3
3632	3 Phylogenomics for the Study of Fungal Biology. , 2014, , 61-79.		3
3633	Orthology Relation and Gene Tree Correction: Complexity Results. Lecture Notes in Computer Science, 2015, , 66-79.	1.0	9
3634	Genome Sequencing. , 2019, , 1-16.		2
3635	An easy and robust method for isolation and validation of single-nucleotide polymorphic markers from a first Erysiphe alphitoides draft genome. Mycological Progress, 2020, 19, 615-628.	0.5	6
3636	Natronorubrum halophilum sp. nov. isolated from two inland salt lakes. Journal of Microbiology, 2020, 58, 105-112.	1.3	20
3637	The Penium margaritaceum Genome: Hallmarks of the Origins of Land Plants. Cell, 2020, 181, 1097-1111.e12.	13.5	153
3638	Survey on the phage resistance mechanisms displayed by a dairy Lactobacillus helveticus strain. Food Microbiology, 2017, 66, 110-116.	2.1	22
3639	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
3640	Phylotranscriptomics in Cucurbitaceae Reveal Multiple Whole-Genome Duplications and Key Morphological and Molecular Innovations. Molecular Plant, 2020, 13, 1117-1133.	3.9	89

#	ARTICLE	IF	CITATIONS
3641	Shifts in a Phenanthrene-Degrading Microbial Community are Driven by Carbohydrate Metabolism Selection in a Ryegrass Rhizosphere. Environmental Science & Technology, 2021, 55, 962-973.	4.6	37
3643	A chromosome-level reference genome of non-heading Chinese cabbage [Brassica campestris (syn.) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	51
3644	A chromosome-scale genome assembly of Isatis indigotica, an important medicinal plant used in traditional Chinese medicine. Horticulture Research, 2020, 7, 18.	2.9	58
3645	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. Nature Biotechnology, 2019, 37, 179-185.	9.4	402
3646	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. Scientific Data, 2018, 5, 180114.	2.4	26
3647	Comparative genomics and transcriptome analysis of Aspergillus niger and metabolic engineering for citrate production. Scientific Reports, 2017, 7, 41040.	1.6	43
3648	DeepNOG: fast and accurate protein orthologous group assignment. Bioinformatics, 2021, 36, 5304-5312.	1.8	16
3649	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
3650	Chromosomal-Level Genome Assembly of Silver Sillago (Sillago sihama). Genome Biology and Evolution, 2021, 13, .	1.1	6
3651	Chromosomal genome of <i>Triplophysa bleekeri</i> provides insights into its evolution and environmental adaptation. GigaScience, 2020, 9, .	3.3	19
3652	Ruthenibacterium lactatiformans gen. nov., sp. nov., an anaerobic, lactate-producing member of the family Ruminococcaceae isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3041-3049.	0.8	36
3653	Characterization of clinical and environmental isolates of Vibrio cidicii sp. nov., a close relative of Vibrio navarrensis. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4148-4155.	0.8	21
3654	Prevotella rara sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3818-3825.	0.8	14
3655	Planctomonas deserti gen. nov., sp. nov., a new member of the family Microbacteriaceae isolated from soil of the Taklamakan desert. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 616-624.	0.8	15
3656	Genome-based taxonomic classification within the family Thermoactinomycetaceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2028-2036.	0.8	33
3657	Genome analysis-based union of the genus Mesoplasma with the genus Entomoplasma. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2735-2738.	0.8	44
3658	Salinigranum halophilum sp. nov., isolated from marine solar salterns. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1648-1655.	0.8	11
3659	Halostella pelagica sp. nov. and Halostella litorea sp. nov., isolated from salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1969-1976.	0.8	26

#	Article	IF	Citations
3660	Pectobacterium parvum sp. nov., having a Salmonella SPI-1-like Type III secretion system and low virulence. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2440-2448.	0.8	51
3661	Salinibaculum litoreum gen. nov., sp. nov., isolated from salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2879-2887.	0.8	13
3662	Roseomonas selenitidurans sp. nov., isolated from urban soil, and emended description of Roseomonas frigidaquae. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5937-5942.	0.8	8
3663	Region-specific diversification of the highly virulent serotype 1 Streptococcus pneumoniae. Microbial Genomics, 2015, 1, e000027.	1.0	27
3664	Plasmodium parasites of birds have the most AT-rich genes of eukaryotes. Microbial Genomics, 2018, 4, .	1.0	25
3665	chewBBACA: A complete suite for gene-by-gene schema creation and strain identification. Microbial Genomics, 2018, 4, .	1.0	201
3666	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. Microbial Genomics, 2018, 4, .	1.0	18
3667	Comparative genomic analysis of three intestinal species reveals reductions in secreted pathogenesis determinants in bovine-specific and non-pathogenic Cryptosporidium species. Microbial Genomics, 2020, 6, .	1.0	13
3668	Genome analysis of a clinical isolate of Shewanella sp. uncovered an active hybrid integrative and conjugative element carrying an integron platform inserted in a novel genomic locus. Microbiology (United Kingdom), 2016, 162, 1335-1345.	0.7	7
3669	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
3798	A chromosomeâ€scale genome assembly of <i>Antheraea pernyi</i> (Saturniidae, Lepidoptera). Molecular Ecology Resources, 2020, 20, 1372-1383.	2.2	20
3799	Taxonomy of the Family <i>Campylobacteraceae</i>. , 0, , 1-25.		66
3800	THE EFFECT OF MASSIVE GENE LOSS FOLLOWING WHOLE GENOME DUPLICATION ON THE ALGORITHMIC RECONSTRUCTION OF THE ANCESTRAL POPULUS DIPLOID. , 2008, , .		3
3801	CLUSTERING OF MAIN ORTHOLOGS FOR MULTIPLE GENOMES. , 2007, , .		3
3804	DeeplyEssential: a deep neural network for predicting essential genes in microbes. BMC Bioinformatics, 2020, 21, 367.	1.2	17
3807	PanFunPro: PAN-genome analysis based on FUNctional PROfiles. F1000Research, 0, 2, 265.	0.8	17
3808	An explanatory evo-devo model for the developmental hourglass. F1000Research, 2014, 3, 156.	0.8	7
3809	An explanatory evo-devo model for the developmental hourglass. F1000Research, 2014, 3, 156.	0.8	16

#	Article	IF	Citations
3810	Complete genome of Pieris rapae, a resilient alien, a cabbage pest, and a source of anti-cancer proteins. F1000Research, 2016, 5, 2631.	0.8	47
3811	An improved Plasmodium cynomolgi genome assembly reveals an unexpected methyltransferase gene expansion. Wellcome Open Research, 2017, 2, 42.	0.9	43
3812	Comparative genomics identifies male accessory gland proteins in five Glossina species. Wellcome Open Research, 2017, 2, 73.	0.9	6
3813	Comparative genomics identifies male accessory gland proteins in five Glossina species. Wellcome Open Research, 2017, 2, 73.	0.9	8
3814	Long read assemblies of geographically dispersed Plasmodium falciparum isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	0.9	114
3815	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	0.9	13
3816	Genomic and transcriptomic comparisons of closely related malaria parasites differing in virulence and sequestration pattern. Wellcome Open Research, 2018, 3, 142.	0.9	11
3817	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. Wellcome Open Research, 2019, 4, 193.	0.9	64
3818	A new Plasmodium vivax reference sequence with improved assembly of the subtelomeres reveals an abundance of pir genes. Wellcome Open Research, 2016, 1, 4.	0.9	118
3819	Genomic evidence of adaptive evolution in emergent Vibrio parahaemolyticus ecotypes. Elementa, 2016, 4, .	1.1	9
3820	Hal: an Automated Pipeline for Phylogenetic Analyses of Genomic Data. PLOS Currents, 2011, 3, RRN1213.	1.4	65
3821	Red Algal Phylogenomics Provides a Robust Framework for Inferring Evolution of Key Metabolic Pathways. PLOS Currents, 2016, 8, .	1.4	14
3822	Building a Phylogenomic Pipeline for the Eukaryotic Tree of Life - Addressing Deep Phylogenies with Genome-Scale Data. PLOS Currents, 2014, 6, .	1.4	30
3823	Characterization of Greenbeard Genes Involved in Long-Distance Kind Discrimination in a Microbial Eukaryote. PLoS Biology, 2016, 14, e1002431.	2.6	49
3824	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. PLoS Biology, 2017, 15, e2002527.	2.6	67
3825	Conservation in Mammals of Genes Associated with Aggression-Related Behavioral Phenotypes in Honey Bees. PLoS Computational Biology, 2016, 12, e1004921.	1.5	14
3826	Widespread position-specific conservation of synonymous rare codons within coding sequences. PLoS Computational Biology, 2017, 13, e1005531.	1.5	98
3827	Analysis of the Basidiomycete Coprinopsis cinerea Reveals Conservation of the Core Meiotic Expression Program over Half a Billion Years of Evolution. PLoS Genetics, 2010, 6, e1001135.	1.5	38

#	ARTICLE	IF	CITATIONS
3828	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
3829	Comparative Genomic Analysis of Drechmeria coniospora Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. PLoS Genetics, 2016, 12, e1006017.	1.5	45
3830	The Landscape of A-to-I RNA Editome Is Shaped by Both Positive and Purifying Selection. PLoS Genetics, 2016, 12, e1006191.	1.5	72
3831	Culture-free genome-wide locus sequence typing (GLST) provides new perspectives on Trypanosoma cruzi dispersal and infection complexity. PLoS Genetics, 2020, 16, e1009170.	1.5	7
3832	Cryptic Diversity within the Major Trypanosomiasis Vector Glossina fuscipes Revealed by Molecular Markers. PLoS Neglected Tropical Diseases, 2011, 5, e1266.	1.3	22
3833	A Multilayer Network Approach for Guiding Drug Repositioning in Neglected Diseases. PLoS Neglected Tropical Diseases, 2016, 10, e0004300.	1.3	38
3834	Identification and Analysis of the Role of Superoxide Dismutases Isoforms in the Pathogenesis of Paracoccidioides spp.. PLoS Neglected Tropical Diseases, 2016, 10, e0004481.	1.3	58
3835	The Princeton Protein Orthology Database (P-POD): A Comparative Genomics Analysis Tool for Biologists. PLoS ONE, 2007, 2, e766.	1.1	86
3836	Functional Equivalency Inferred from â€œAuthoritative Sourcesâ€• in Networks of Homologous Proteins. PLoS ONE, 2009, 4, e5898.	1.1	2
3837	Gene Context Analysis in the Integrated Microbial Genomes (IMG) Data Management System. PLoS ONE, 2009, 4, e7979.	1.1	54
3838	Identification of Novel Pathogenicity Loci in Clostridium perfringens Strains That Cause Avian Necrotic Enteritis. PLoS ONE, 2010, 5, e10795.	1.1	91
3839	progressiveMauve: Multiple Genome Alignment with Gene Gain, Loss and Rearrangement. PLoS ONE, 2010, 5, e11147.	1.1	3,652
3840	Genome Erosion in a Nitrogen-Fixing Vertically Transmitted Endosymbiotic Multicellular Cyanobacterium. PLoS ONE, 2010, 5, e11486.	1.1	178
3841	Phylogenomic Analysis of Marine Roseobacters. PLoS ONE, 2010, 5, e11604.	1.1	29
3842	Inference of Surface Membrane Factors of HIV-1 Infection through Functional Interaction Networks. PLoS ONE, 2010, 5, e13139.	1.1	7
3843	Characterization of the Deleted in Autism 1 Protein Family: Implications for Studying Cognitive Disorders. PLoS ONE, 2011, 6, e14547.	1.1	26
3844	Analysis of Ultra Low Genome Conservation in Clostridium difficile. PLoS ONE, 2010, 5, e15147.	1.1	55
3845	ePlant and the 3D Data Display Initiative: Integrative Systems Biology on the World Wide Web. PLoS ONE, 2011, 6, e15237.	1.1	43

#	ARTICLE	IF	CITATIONS
3846	New Implications on Genomic Adaptation Derived from the Helicobacter pylori Genome Comparison. PLoS ONE, 2011, 6, e17300.	1.1	15
3847	Finding Single Copy Genes Out of Sequenced Genomes for Multilocus Phylogenetics in Non-Model Fungi. PLoS ONE, 2011, 6, e18803.	1.1	50
3848	OrthoList: A Compendium of C. elegans Genes with Human Orthologs. PLoS ONE, 2011, 6, e20085.	1.1	378
3849	HelmCoP: An Online Resource for Helminth Functional Genomics and Drug and Vaccine Targets Prioritization. PLoS ONE, 2011, 6, e21832.	1.1	17
3850	The Genome Sequence of the North-European Cucumber (Cucumis sativus L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	1.1	112
3851	An Essential Farnesylated Kinesin in Trypanosoma brucei. PLoS ONE, 2011, 6, e26508.	1.1	4
3852	Whole-Genome Comparison of Two Campylobacter jejuni Isolates of the Same Sequence Type Reveals Multiple Loci of Different Ancestral Lineage. PLoS ONE, 2011, 6, e27121.	1.1	25
3853	Whole Genome Characterization of the Mechanisms of Daptomycin Resistance in Clinical and Laboratory Derived Isolates of Staphylococcus aureus. PLoS ONE, 2012, 7, e28316.	1.1	202
3854	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
3855	Pyrosequencing-Based Comparative Genome Analysis of Vibrio vulnificus Environmental Isolates. PLoS ONE, 2012, 7, e37553.	1.1	64
3856	Comparative Genomic Analysis of Soybean Flowering Genes. PLoS ONE, 2012, 7, e38250.	1.1	99
3857	The Complete Genome Sequence of Natrinema sp. J7-2, a Haloarchaeon Capable of Growth on Synthetic Media without Amino Acid Supplements. PLoS ONE, 2012, 7, e41621.	1.1	31
3858	GenoSets: Visual Analytic Methods for Comparative Genomics. PLoS ONE, 2012, 7, e46401.	1.1	13
3859	Bioinformatic Inference of Specific and General Transcription Factor Binding Sites in the Plant Pathogen Phytophthora infestans. PLoS ONE, 2012, 7, e51295.	1.1	13
3860	Inferring Hierarchical Orthologous Groups from Orthologous Gene Pairs. PLoS ONE, 2013, 8, e53786.	1.1	152
3861	Complete Plastid Genome Sequence of the Basal Asterid Ardisia polysticta Miq. and Comparative Analyses of Asterid Plastid Genomes. PLoS ONE, 2013, 8, e62548.	1.1	39
3862	Secretome Analysis of the Pine Wood Nematode Bursaphelenchus xylophilus Reveals the Tangled Roots of Parasitism and Its Potential for Molecular Mimicry. PLoS ONE, 2013, 8, e67377.	1.1	98
3863	A Lover and a Fighter: The Genome Sequence of an Entomopathogenic Nematode Heterorhabditis bacteriophora. PLoS ONE, 2013, 8, e69618.	1.1	89

#	ARTICLE	IF	CITATIONS
3864	Functional Divergence and Convergent Evolution in the Plastid-Targeted Glyceraldehyde-3-Phosphate Dehydrogenases of Diverse Eukaryotic Algae. PLoS ONE, 2013, 8, e70396.	1.1	9
3865	A Comparative Genome Analysis of PME and PMEI Families Reveals the Evolution of Pectin Metabolism in Plant Cell Walls. PLoS ONE, 2013, 8, e72082.	1.1	87
3866	Cultivation and Complete Genome Sequencing of Gloeobacter kilaueensis sp. nov., from a Lava Cave in KÄ«lauea Caldera, Hawai'i. PLoS ONE, 2013, 8, e76376.	1.1	85
3867	Differential Stress Transcriptome Landscape of Historic and Recently Emerged Hypervirulent Strains of Clostridium difficile Strains Determined Using RNA-seq. PLoS ONE, 2013, 8, e78489.	1.1	22
3868	Comparative and Phylogenomic Evidence That the Alphaproteobacterium HIMB59 Is Not a Member of the Oceanic SAR11 Clade. PLoS ONE, 2013, 8, e78858.	1.1	38
3869	Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151. PLoS ONE, 2013, 8, e79704.	1.1	42
3870	POGs2: A Web Portal to Facilitate Cross-Species Inferences About Protein Architecture and Function in Plants. PLoS ONE, 2013, 8, e82569.	1.1	19
3871	Sequence Divergence and Conservation in Genomes of Helicobacter cetorum Strains from a Dolphin and a Whale. PLoS ONE, 2013, 8, e83177.	1.1	23
3872	Genomic Evolution of 11 Type Strains within Family Planctomycetaceae. PLoS ONE, 2014, 9, e86752.	1.1	18
3873	A Pepper MSRB2 Gene Confers Drought Tolerance in Rice through the Protection of Chloroplast-Targeted Genes. PLoS ONE, 2014, 9, e90588.	1.1	21
3874	Comparative Genomics and Phylogenomics of Hemotrophic Mycoplasmas. PLoS ONE, 2014, 9, e91445.	1.1	17
3875	The Draft Genome Sequence of European Pear (Pyrus communis L. â€˜Bartlettâ€™). PLoS ONE, 2014, 9, e92644.	1.1	241
3876	Comparative Genome Analysis of Wheat Blue Dwarf Phytoplasma, an Obligate Pathogen That Causes Wheat Blue Dwarf Disease in China. PLoS ONE, 2014, 9, e96436.	1.1	46
3877	A Survey of Innovation through Duplication in the Reduced Genomes of Twelve Parasites. PLoS ONE, 2014, 9, e99213.	1.1	7
3878	Comparative Genomics of the Bacterial Genus Streptococcus Illuminates Evolutionary Implications of Species Groups. PLoS ONE, 2014, 9, e101229.	1.1	76
3879	De Novo Transcriptomes of a Mixotrophic and a Heterotrophic Ciliate from Marine Plankton. PLoS ONE, 2014, 9, e101418.	1.1	29
3880	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
3881	Analysis of the Na+/Ca2+ Exchanger Gene Family within the Phylum Nematoda. PLoS ONE, 2014, 9, e112841.	1.1	14

#	Article	IF	Citations
3882	Complete Chloroplast Genome Sequence of Omani Lime (Citrus aurantiifolia) and Comparative Analysis within the Rosids. PLoS ONE, 2014, 9, e113049.	1.1	60
3883	Synergy: A Web Resource for Exploring Gene Regulation in Synechocystis sp. PCC6803. PLoS ONE, 2014, 9, e113496.	1.1	4
3884	What It Takes to Be a Pseudomonas aeruginosa? The Core Genome of the Opportunistic Pathogen Updated. PLoS ONE, 2015, 10, e0126468.	1.1	91
3885	Complete Genome Sequence of Sporisorium scitamineum and Biotrophic Interaction Transcriptome with Sugarcane. PLoS ONE, 2015, 10, e0129318.	1.1	93
3886	Complete Genome Sequence of a High Lipid-Producing Strain of Mucor circinelloides WJ11 and Comparative Genome Analysis with a Low Lipid-Producing Strain CBS 277.49. PLoS ONE, 2015, 10, e0137543.	1.1	52
3887	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
3888	Genome Survey Sequencing for the Characterization of the Genetic Background of Rosa roxburghii Tratt and Leaf Ascorbate Metabolism Genes. PLoS ONE, 2016, 11, e0147530.	1.1	60
3889	Genomic Comparative Study of Bovine Mastitis Escherichia coli. PLoS ONE, 2016, 11, e0147954.	1.1	63
3890	Comparative Analysis of Lacinutrix Genomes and Their Association with Bacterial Habitat. PLoS ONE, 2016, 11, e0148889.	1.1	9
3891	Genomic and Genetic Diversity within the Pseudomonas fluorescens Complex. PLoS ONE, 2016, 11, e0150183.	1.1	171
3892	Hybridization Capture Using RAD Probes (hyRAD), a New Tool for Performing Genomic Analyses on Collection Specimens. PLoS ONE, 2016, 11, e0151651.	1.1	121
3893	SpinachDB: A Well-Characterized Genomic Database for Gene Family Classification and SNP Information of Spinach. PLoS ONE, 2016, 11, e0152706.	1.1	9
3894	An Integrated Bioinformatics Analysis Reveals Divergent Evolutionary Pattern of Oil Biosynthesis in High- and Low-Oil Plants. PLoS ONE, 2016, 11, e0154882.	1.1	21
3895	Sticky Genomes: Using NGS Evidence to Test Hybrid Speciation Hypotheses. PLoS ONE, 2016, 11, e0154911.	1.1	8
3896	Comparative Genomics of Pathogens Causing Brown Spot Disease of Tobacco: Alternaria longipes and Alternaria alternata. PLoS ONE, 2016, 11, e0155258.	1.1	42
3897	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. PLoS ONE, 2016, 11, e0157844.	1.1	49
3898	Whole Genome Sequencing Allows Better Understanding of the Evolutionary History of Leptospira interrogans Serovar Hardjo. PLoS ONE, 2016, 11, e0159387.	1.1	34
3899	Genome Sequence of the Edible Cultivated Mushroom Lentinula edodes (Shiitake) Reveals Insights into Lignocellulose Degradation. PLoS ONE, 2016, 11, e0160336.	1.1	110

#	ARTICLE	IF	CITATIONS
3900	Genome-Wide Comparison of Magnaporthe Species Reveals a Host-Specific Pattern of Secretory Proteins and Transposable Elements. PLoS ONE, 2016, 11, e0162458.	1.1	43
3901	A De Novo Genome Sequence Assembly of the Arabidopsis thaliana Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. PLoS ONE, 2016, 11, e0164321.	1.1	63
3902	Genetic Characteristics and Multiple-PCR Development for Capsular Identification of Specific Serotypes of Campylobacter jejuni. PLoS ONE, 2016, 11, e0165159.	1.1	7
3903	Whole-Genome Sequence Analysis of Bombella intestini LMG 28161T, a Novel Acetic Acid Bacterium Isolated from the Crop of a Red-Tailed Bumble Bee, Bombus lapidarius. PLoS ONE, 2016, 11, e0165611.	1.1	12
3904	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
3905	Comparative genomics of Clavibacter michiganensis subspecies, pathogens of important agricultural crops. PLoS ONE, 2017, 12, e0172295.	1.1	35
3906	Analysis of the complete genome sequence of Nocardia seriolae UTF1, the causative agent of fish nocardiosis: The first reference genome sequence of the fish pathogenic Nocardia species. PLoS ONE, 2017, 12, e0173198.	1.1	41
3907	The physical characteristics of human proteins in different biological functions. PLoS ONE, 2017, 12, e0176234.	1.1	6
3908	Different adaptation strategies of two citrus scion/rootstock combinations in response to drought stress. PLoS ONE, 2017, 12, e0177993.	1.1	28
3909	Transcriptome analysis of Phytophthora litchii reveals pathogenicity arsenals and confirms taxonomic status. PLoS ONE, 2017, 12, e0178245.	1.1	18
3910	Exploring the molecular basis of adaptive evolution in hydrothermal vent crab Austinograea alayseae by transcriptome analysis. PLoS ONE, 2017, 12, e0178417.	1.1	28
3911	Physiological and genomic features of a novel violacein-producing bacterium isolated from surface seawater. PLoS ONE, 2017, 12, e0179997.	1.1	21
3912	Mitochondrial genome evolution in the Saccharomyces sensu stricto complex. PLoS ONE, 2017, 12, e0183035.	1.1	6
3913	Identifying and sequencing a Mycobacterium sp. strain F4 as a potential bioremediation agent for quinclorac. PLoS ONE, 2017, 12, e0185721.	1.1	6
3914	Vegetative compatibility groups partition variation in the virulence of Verticillium dahliae on strawberry. PLoS ONE, 2018, 13, e0191824.	1.1	27
3915	Diversity of Mycobacterium tuberculosis across Evolutionary Scales. PLoS Pathogens, 2015, 11, e1005257.	2.1	70
3916	The <i>Parachlorella</i> Genome and Transcriptome Endorse Active RWP-RK, Meiosis and Flagellar Genes in Trebouxiophycean Algae. Cytologia, 2019, 84, 323-330.	0.2	6
3918	Expression Level Dominance and Homeolog Expression Bias in Recurrent Origins of the Allopolyploid Fern Polypodium hesperium. American Fern Journal, 2019, 109, 224.	0.2	14

#	ARTICLE	IF	CITATIONS
3920	Evolutionary history of the group formerly known as protists using a phylogenomics approach. Revista De La Academia Colombiana De Ciencias Exactas, Fisicas Y Naturales, 2016, 40, 147.	0.0	1
3921	SIRT1 and SIRT3 Deacetylate Homologous Substrates: AceCS1,2 and HMGCS1,2. Aging, 2011, 3, 635-642.	1.4	85
3922	Nematode Genome Announcement: A Draft Genome for Rice Root-Knot Nematode, Meloidogyne graminicola. Journal of Nematology, 2018, 50, 111-116.	0.4	38
3923	In Silico Chemogenomics Drug Repositioning Strategies for Neglected Tropical Diseases. Current Medicinal Chemistry, 2019, 26, 4355-4379.	1.2	24
3924	Complete Genome of Achalarus lyciades, The First Representative of the Eudaminae Subfamily of Skippers. Current Genomics, 2017, 18, 366-374.	0.7	22
3925	Genomic Insights into the Adaptive Convergent Evolution. Current Genomics, 2019, 20, 81-89.	0.7	16
3926	<i>Plasmodium</i> DEH is ER-localized and crucial for oocyst mitotic division during malaria transmission. Life Science Alliance, 2020, 3, e202000879.	1.3	6
3927	Epidemiological investigation of Pseudomonas aeruginosa isolates from a six-year-long hospital outbreak using high-throughput whole genome sequencing. Eurosurveillance, 2013, 18, .	3.9	57
3928	Investigating the natural resistance of blackfoot p-a%%KERN_ERR%%ua Haliotis iris to abalone viral ganglioneuritis using whole transcriptome analysis. Diseases of Aquatic Organisms, 2019, 135, 107-119.	0.5	7
3929	Pan-Genome-Based Analysis as a Framework for Demarcating Two Closely Related Methanotroph Genera Methylocystis and Methylosinus. Microorganisms, 2020, 8, 768.	1.6	15
3930	Generation of Transcript Assemblies and Identification of Single Nucleotide Polymorphisms from Seven Lowland and Upland Cultivars of Switchgrass. Plant Genome, 2014, 7, plantgenome2013.12.0041.	1.6	6
3931	Effect of Sodium Butyrate on Salmonella Enteritidis Infection in Broiler Chickens. Asian Journal of Poultry Science, 2016, 10, 104-110.	0.1	9
3932	Revealing the biotechnological potential of Delftia sp. JD2 by a genomic approach. AIMS Bioengineering, 2016, 3, 156-175.	0.6	23
3933	Function and Homology of Proteins Similar in Sequence. , 2009, , 143-166.		1
3934	Genome-wide identification and evolutionary analysis of nucleotide-binding site-encoding resistance genes in Lotus japonicus (Fabaceae). Genetics and Molecular Research, 2015, 14, 16024-16040.	0.3	10
3935	Whole Genome Enabled Phylogenetic and Secretome Analyses of Two Venturia nashicola Isolates. Plant Pathology Journal, 2020, 36, 98-105.	0.7	5
3936	SFannotation: A Simple and Fast Protein Function Annotation System. Genomics and Informatics, 2014, 12, 76.	0.4	1
3937	Phylogenetic Method for High-Throughput Ortholog Detection. International Journal of Information Engineering and Electronic Business, 2015, 7, 51-59.	1.0	3

#	Article	IF	Citations
3938	Evolutionary routes to biochemical innovation revealed by integrative analysis of a plant-defense related specialized metabolic pathway. ELife, 2017, 6, .	2.8	84
3939	The genome of an intranuclear parasite, Paramicrosporidium saccamoebae, reveals alternative adaptations to obligate intracellular parasitism. ELife, 2017, 6, .	2.8	63
3940	Natural selection and repeated patterns of molecular evolution following allopatric divergence. ELife, 2019, 8, .	2.8	18
3941	The genetic factors of bilaterian evolution. ELife, 2020, 9, .	2.8	44
3942	Evolution of<i>Wolbachia</i>mutualism and reproductive parasitism: insight from two novel strains that co-infect cat fleas. PeerJ, 2020, 8, e10646.	0.9	43
3943	Comparative genomics of<i>Synechococcus</i>and proposal of the new genus<i>Parasynechococcus</i>. PeerJ, 2016, 4, e1522.	0.9	46
3944	The genome and transcriptome of<i>Phalaenopsis</i>yield insights into floral organ development and flowering regulation. PeerJ, 2016, 4, e2017.	0.9	39
3945	Genome-wide identification and characterization of GRAS transcription factors in sacred lotus (<i>Nelumbo nucifera</i>). PeerJ, 2016, 4, e2388.	0.9	31
3946	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. PeerJ, 2014, 2, e332.	0.9	265
3947	Genome-wide identification and characterization of GRAS transcription factors in tomato (<i>Solanum lycopersicum</i>). PeerJ, 2017, 5, e3955.	0.9	50
3948	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. PeerJ, 2018, 6, e4392.	0.9	24
3949	Genome-wide identification and characterization of Dof transcription factors in eggplant (<i>Solanum melongena</i>L.). PeerJ, 2018, 6, e4481.	0.9	24
3950	Global genomic similarity and core genome sequence diversity of the <i>Streptococcus</i> genus as a toolkit to identify closely related bacterial species in complex environments. PeerJ, 2019, 6, e6233.	0.9	12
3951	Mantle transcriptome sequencing of <i>Mytilus</i> spp. and identification of putative biomineralization genes. PeerJ, 2019, 6, e6245.	0.9	21
3952	GenoDup Pipeline: a tool to detect genome duplication using the dS-based method. PeerJ, 2019, 7, e6303.	0.9	7
3953	Adaptive and degenerative evolution of the<i>S-Phase Kinase-Associated Protein 1-Like</i>family in<i>Arabidopsis thaliana</i>. PeerJ, 2019, 7, e6740.	0.9	7
3954	Conservation of transcriptional elements in the obligate symbiont of the whitefly <i>Bemisia tabaci</i>. PeerJ, 2019, 7, e7477.	0.9	6
3955	Comparative analysis of chloroplast genomes for five<i>Dicliptera</i>species (Acanthaceae): molecular structure, phylogenetic relationships, and adaptive evolution. PeerJ, 2020, 8, e8450.	0.9	29

#	ARTICLE	IF	CITATIONS
3956	Genome-wide identification and expression analysis of the <i>VQ</i> gene family in <i>Cicer arietinum</i> and <i>Medicago truncatula</i>. PeerJ, 2020, 8, e8471.	0.9	13
3957	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	6.5	277
3958	A chromosomeâ€scale genome assembly and annotation of the spring orchid (<i>Cymbidium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	2.2	9
3959	High-quality genome assembly of an important biodiesel plant, <i>Euphorbia lathyris</i> L. DNA Research, 2021, 28, .	1.5	11
3961	Genomic and Transcriptomic Insight of Giant Sclerotium Formation of Wood-Decay Fungi. Frontiers in Microbiology, 2021, 12, 746121.	1.5	7
3962	Taxus yunnanensis genome offers insights into gymnosperm phylogeny and taxol production. Communications Biology, 2021, 4, 1203.	2.0	15
3963	Cross-species meta-analysis of transcriptome changes during the morula-to-blastocyst transition: metabolic and physiological changes take center stage. American Journal of Physiology - Cell Physiology, 2021, 321, C913-C931.	2.1	3
3964	Chromosome-Level Genome Assembly of Cyrtotrachelus buqueti and Mining of Its Specific Genes. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	2
3965	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
3966	Distribution of bacteriocin genes in the lineages of Lactiplantibacillus plantarum. Scientific Reports, 2021, 11, 20063.	1.6	15
3967	Colorful Orthology Clustering in Bounded-Degree Similarity Graphs. Journal of Bioinformatics and Computational Biology, 2021, , 2140010.	0.3	1
3968	The Adaptive Evolution and Gigantism Mechanisms of the Hadal â€œSupergiantâ€•Amphipod Alicella gigantea. Frontiers in Marine Science, 2021, 8, .	1.2	4
3969	Identification of Antimicrobial Peptide Genes in Black Rockfish Sebastes schlegelii and Their Responsive Mechanisms to Edwardsiella tarda Infection. Biology, 2021, 10, 1015.	1.3	14
3970	The chromosomeâ€scale genome assembly, annotation and evolution of <i>Rhododendron henanense</i> subsp. <i>lingbaoense</i>. Molecular Ecology Resources, 2022, 22, 988-1001.	2.2	14
3971	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. Molecular Systems Biology, 2021, 17, e10427.	3.2	17
3972	Chromosome-Level Genome Assembly of the Asian Red-Tail Catfish (Hemibagrus wyckioides). Frontiers in Genetics, 2021, 12, 747684.	1.1	12
3973	Comparative Genomics Reveals Recent Adaptive Evolution in Himalayan Giant Honeybee <i>Apis laboriosa</i>. Genome Biology and Evolution, 2021, 13, .	1.1	7
3974	The red flower wintersweet genome provides insights into the evolution of magnoliids and the molecular mechanism for tepal color development. Plant Journal, 2021, 108, 1662-1678.	2.8	12

#	ARTICLE	IF	CITATIONS
3975	Phylogenetic systematics of Butyrivibrio and Pseudobutyrivibrio genomes illustrate vast taxonomic diversity, open genomes and an abundance of carbohydrate-active enzyme family isoforms. Microbial Genomics, 2021, 7, .	1.0	9
3977	Campylobacter anatolicus sp. nov., a novel member of the genus Campylobacter isolated from feces of Anatolian Ground Squirrel (Spermophilus xanthoprymnus) in Turkey. Systematic and Applied Microbiology, 2021, 44, 126265.	1.2	19
3978	The genome of the black cutworm Agrotis ipsilon. Insect Biochemistry and Molecular Biology, 2021, 139, 103665.	1.2	8
3979	Protein Function Annotation Based on Ortholog Clusters Extracted from Incomplete Genomes Using Combinatorial Optimization. Lecture Notes in Computer Science, 2006, , 99-113.	1.0	0
3980	Cross-Species Comparison Using Expression Data. , 2007, , 147-159.		1
3981	Internal Validation of Ancestral Gene Order Reconstruction in Angiosperm Phylogeny. Lecture Notes in Computer Science, 2008, , 252-264.	1.0	2
3982	Topological Metrics in Blast Data Mining: Plasmid and Nitrogen-Fixing Proteins Case Studies. Communications in Computer and Information Science, 2008, , 207-220.	0.4	0
3983	The Rainbow Prim Algorithm for Selecting Putative Orthologous Protein Sequences. Open Bioinformatics Journal, 2008, 2, 60-63.	1.0	0
3984	Systems Biology and Infectious Diseases. , 2009, , 377-402.		1
3985	A New Approach to Find Orthologous Proteins Using Sequence and Protein-Protein Interaction Similarity. Genomics and Informatics, 2009, 7, 141-147.	0.4	0
3986	Pangenomic Reverse Vaccinology. , 2010, , 203-221.		1
3987	Functional Inference in Microbial Genomics Based on Large-Scale Comparative Analysis. , 2011, , 55-92.		0
3988	Describing the Orthology Signal in a PPI Network at a Functional, Complex Level. Lecture Notes in Computer Science, 2011, , 209-226.	1.0	4
3989	Genomics of Giardia. , 2011, , 95-101.		0
3990	Disease Gene Prioritization. , 0, , .		0
3991	Putting It All Together: The Design of a Pipeline for Genome-Wide Functional Annotation of Fungi in the Modern Era of â€œ-Omicsâ€•Data and Systems Biology. Lecture Notes in Computer Science, 2013, , 113-127.	1.0	1
3992	Domain Architecture Evolution of Metazoan Proteins. , 2013, , 127-144.		0
3993	Cell Cycle Ontology (CCO). , 2013, , 305-309.		0

#	ARTICLE	IF	CITATIONS
3994	OrthoRBH: A streamlined pipeline for mining large gene family sequences in related species. Bioinformation, 2013, 9, 267-269.	0.2	0
3995	Bioinformatic Analysis of Expression Data to Identify Effector Candidates. Methods in Molecular Biology, 2014, 1127, 17-27.	0.4	1
3996	Alternaria Comparative Genomics: The Secret Life of Rots. , 2014, , 45-63.		3
3997	Rough Sets in Ortholog Gene Detection. Lecture Notes in Computer Science, 2014, , 161-168.	1.0	0
4000	Aggregation of Similarity Measures for Ortholog Detection: Validation with Measures Based on Rough Set Theory. Computacion Y Sistemas, 2014, 18, .	0.2	1
4002	Impact of the <i>Toxoplasma gondii</i> Genome Project. , 0, , 309-320.		0
4003	PlasmoDB: The Plasmodium Genome Resource. , 0, , 12-23.		17
4006	Comparative Analysis of Gene Expression: Uncovering Expression Conservation and Divergence Between Salmonella enterica Serovar Typhimurium Strains LT2 and 14028S. Methods in Molecular Biology, 2015, 1231, 125-135.	0.4	0
4018	Effect of Na-butyrate Supplementation on Electromicroscopy, Virulence Gene Expression Analysis and Gut Integrity of Experimentally Induced Salmonella enteritidis in Broiler Chickens. Asian Journal of Poultry Science, 2016, 10, 126-133.	0.1	1
4019	Bioinformatics - Updated Features and Applications. , 2016, , .		4
4023	Influence of sodium butyrate on salmonella infection in broiler chicks. Benha Veterinary Medical Journal, 2016, 31, 21-32.	0.0	2
4024	Bioinformatics Aspects of Foodborne Pathogen Research. , 2017, , 51-64.		0
4025	Finding Genes. , 2017, , 127-141.		0
4026	On Strongly Chordal Graphs That Are Not Leaf Powers. Lecture Notes in Computer Science, 2017, , 386-398.	1.0	2
4063	Genome comparison implies the role of Wsm2 in membrane trafficking and protein degradation. PeerJ, 2018, 6, e4678.	0.9	1
4097	The Genome of Salvia miltiorrhiza. Compendium of Plant Genomes, 2019, , 45-53.	0.3	0
4099	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 1-14.		0
4129	Genomic metrics analyses indicate that Paenibacillus azotofixans is not a later synonym of Paenibacillus durus. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2870-2876.	0.8	6

#	ARTICLE	IF	CITATIONS
4131	Alloscardovia theropitheci sp. nov., isolated from the faeces of gelada baboon, the 'bleeding heart' monkey (Theropithecus gelada). International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3041-3048.	0.8	9
4142	OBSOLETE: NexGen Sequencing Data: Bioinformatic Tools for Visualization and Analysis. , 2020, , .		0
4144	Characterization of the genotype and the phenotype of nontoxigenic strains of Corynebacterium diphtheriae subsp. lausannense isolated in Russian residents. Bulletin of Russian State Medical University, 2020, , .	0.3	0
4154	Genome-based reclassification of Paenibacillus panacisoli DSM 21345T as Paenibacillus massiliensis subsp. panacisoli subsp. nov. and description of Paenibacillus massiliensis subsp. massiliensis subsp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4838-4842.	0.8	10
4156	The Wolfiporia cocos Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotium. Genomics, Proteomics and Bioinformatics, 2020, 18, 455-467.	3.0	11
4164	Chromosome-Level Genome Assembly Reveals Significant Gene Expansion in the Toll and IMD Signaling Pathways of Dendrolimus kikuchii. Frontiers in Genetics, 2021, 12, 728418.	1.1	1
4165	The complete genome sequence of a bile-isolated Stenotrophomonas maltophilia ZT1. Gut Pathogens, 2021, 13, 64.	1.6	0
4166	The Melastoma dodecandrum genome and the evolution of Myrtales. Journal of Genetics and Genomics, 2022, 49, 120-131.	1.7	14
4167	Comparative analysis of transcriptomic data shows the effects of multiple evolutionary selection processes on codon usage in Marsupenaeus japonicus and Marsupenaeus pulchricaudatus. BMC Genomics, 2021, 22, 781.	1.2	6
4169	The Aphelenchus avenae genome highlights evolutionary adaptation to desiccation. Communications Biology, 2021, 4, 1232.	2.0	19
4172	Applications of Network Clustering in Natural Product Research. , 2020, , 239-270.		0
4175	Radiobacillus deserti gen. nov., sp. nov., a UV-resistant bacterium isolated from desert soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6338-6347.	0.8	10
4179	New molecular target for the phylogenetic identification of Leptospira species directly from clinical samples: an alternative gene to 16S rRNA. Revista Da Sociedade Brasileira De Medicina Tropical, 2020, 53, e20190333.	0.4	2
4181	Orthology: Promises and Challenges. , 2020, , 203-228.		10
4183	A Practical Guide to Orthology Resources. , 2020, , 41-77.		2
4184	Structural features of the genome of methicillin-resistant Staphylococcus aureus (MRSA), a ceftaroline-resistant representative of ST239 epidemic clone isolated in Russia. Molekuliarnaia Genetika, Mikrobiologiia I Virusologiia, 2020, 38, 170.	0.1	0
4189	Hydrogeniiclostidium mannosilyticum gen. nov., sp. nov. isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1210-1216.	0.8	14
4190	Nesterenkonia muleiensis sp. nov., a novel actinobacterium isolated from sap of Populus euphratica. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1888-1894.	0.8	5

#	ARTICLE	IF	CITATIONS
4193	Phaffia brasiliana sp. nov., a yeast species isolated from soil in a Cerradoâ€"Atlantic Rain Forest ecotone site in Brazil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	2
4195	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. Bioinformatics, 2022, 38, 612-620.	1.8	4
4196	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. Microbial Genomics, 2021, 7, .	1.0	18
4198	The rumen microbiome inhibits methane formation through dietary choline supplementation. Scientific Reports, 2021, 11, 21761.	1.6	3
4199	Draft genome of the blister beetle, Epicauta chinensis. International Journal of Biological Macromolecules, 2021, 193, 1694-1694.	3.6	4
4205	Data Mining of Malaria Parasite Gene Expression for Possible Translational Research. , 2007, , 1-10.		0
4206	PFP: A Computational Framework for Phylogenetic Footprinting in Prokaryotic Genomes. , 2008, , 110-121.		0
4211	Prometheus, an omics portal for interkingdom comparative genomic analyses. PLoS ONE, 2020, 15, e0240191.	1.1	1
4212	Natronomonas halophila sp. nov. and Natronomonas salina sp. nov., two novel halophilic archaea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5686-5692.	0.8	9
4213	Acidiluteibacter ferrifornacis gen. nov., sp. nov., a new member of the Flavobacteriales from Tielu Harbour, Hainan, PR China. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5812-5817.	0.8	7
4216	Genome-Wide Analyses Provide Insights into the Scavenging Lifestyle of the Striped Hyena (<i>Hyaena) Tj ETQq0 0 0 rgBT /Overlock 10	0.9	3
4218	Structural Features of the Genome of Methicillin-Resistant Staphylococcus aureus (MRSA), a Ceftaroline-Resistant Representative of the Epidemic ST239 Clone Isolated in Russia. Molecular Genetics, Microbiology and Virology, 2020, 35, 210-220.	0.0	1
4220	Whole Genome Analysis of the Red-Crowned Crane Provides Insight into Avian Longevity. Molecules and Cells, 2020, 43, 86-95.	1.0	6
4221	Transcriptome based identification and validation of heat stress transcription factors in wheat progenitor species Aegilops speltoides. Scientific Reports, 2021, 11, 22049.	1.6	9
4222	Centromere-Specific Retrotransposons and Very-Long-Chain Fatty Acid Biosynthesis in the Genome of Yellowhorn (Xanthoceras sorbifolium, Sapindaceae), an Oil-Producing Tree With Significant Drought Resistance. Frontiers in Plant Science, 2021, 12, 766389.	1.7	6
4223	Patho-epigenetics: histone deacetylases as targets of pathogens and therapeutics. MicroLife, 2021, 2, .	1.0	9
4224	Reconstruction of body mass evolution in the Cetartiodactyla and mammals using phylogenomic data. , 0, 1, .		1
4225	The Chloranthus sessilifolius genome provides insight into early diversification of angiosperms. Nature Communications, 2021, 12, 6929.	5.8	29

#	Article	IF	Citations
4226	Longâ€read assembly of the Chinese indigenous Ningxiang pig genome and identification of genetic variations in fat metabolism among different breeds. Molecular Ecology Resources, 2022, 22, 1508-1520.	2.2	9
4227	Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms. Frontiers in Cell and Developmental Biology, 2021, 9, 749963.	1.8	3
4228	Chloranthus genome provides insights into the early diversification of angiosperms. Nature Communications, 2021, 12, 6930.	5.8	44
4229	The Physalis floridana genome provides insights into the biochemical and morphological evolution of Physalis fruits. Horticulture Research, 2021, 8, 244.	2.9	15
4230	Chromosome-Scale Genome Assemblies of Two Korean Cucumber Inbred Lines. Frontiers in Genetics, 2021, 12, 733188.	1.1	4
4231	Chromosome-Scale Reference Genome of Amphicarpaea edgeworthii: A New Resource for Amphicarpic Plants Research and Complex Flowering Pattern. Frontiers in Plant Science, 2021, 12, 770660.	1.7	3
4232	Roseomonas oleicola sp. nov., isolated from an oil production mixture in Yumen Oilfield, and emended description of Roseomonas frigidaquae. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	10
4233	Analysis of pir gene expression across the Plasmodium life cycle. Malaria Journal, 2021, 20, 445.	0.8	9
4234	Accelerating Complete Phytoplasma Genome Assembly by Immunoprecipitation-Based Enrichment and MinION-Based DNA Sequencing for Comparative Analyses. Frontiers in Microbiology, 2021, 12, 766221.	1.5	15
4235	Safety and Health Issues Associated with Fibre Reinforced Polymer Composites in Various Industrial Sectors. Composites Science and Technology, 2022, , 211-228.	0.4	0
4238	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
4239	The first highâ€quality chromosomal genome assembly of a medicinal and edible plant Arctium lappa. Molecular Ecology Resources, 2021, , .	2.2	11
4240	Chromosomeâ€level assembly of the <i>Neolamarckia cadamba</i> genome provides insights into the evolution of cadambine biosynthesis. Plant Journal, 2022, 109, 891-908.	2.8	19
4241	High-Quality Genomes and High-Density Genetic Map Facilitate the Identification of Genes From a Weedy Rice. Frontiers in Plant Science, 2021, 12, 775051.	1.7	7
4242	Telomere-to-telomere genome assembly of asparaginase-producing Trichoderma simmonsii. BMC Genomics, 2021, 22, 830.	1.2	9
4243	Integrative genome, transcriptome, microRNA, and degradome analysis of water dropwort (Oenanthe) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	31
4244	The Cymbidium genome reveals the evolution of unique morphological traits. Horticulture Research, 2021, 8, 255.	2.9	33
4245	A chromosomeâ€level genome of <i>Portunus trituberculatus</i> provides insights into its evolution, salinity adaptation and sex determination. Molecular Ecology Resources, 2022, 22, 1606-1625.	2.2	11

#	ARTICLE	IF	CITATIONS
4247	A multispecies amplicon sequencing approach for genetic diversity assessments in grassland plant species. Molecular Ecology Resources, 2022, 22, 1725-1745.	2.2	6
4248	De novo Transcriptome Assembly of Senna occidentalis Sheds Light on the Anthraquinone Biosynthesis Pathway. Frontiers in Plant Science, 2021, 12, 773553.	1.7	4
4249	Genome sequencing and transcriptomic analysis of the Andean killifish Orestias ascotanensis reveals adaptation to high-altitude aquatic life. Genomics, 2022, 114, 305-315.	1.3	5
4250	Alleleâ€aware chromosomeâ€scale assembly of the allopolyploid genome of hexaploid Ma bamboo (<i>Dendrocalamus latiflorus</i> Munro). Journal of Integrative Plant Biology, 2022, 64, 649-670.	4.1	24
4251	Examining the Relationship Between the Testate Amoeba Hyalosphenia papilio (Arcellinida, Amoebozoa) and its Associated Intracellular Microalgae Using Molecular and Microscopic Methods. Protist, 2022, 173, 125853.	0.6	2
4252	Mining the Genome of Bacillus velezensis VB7 (CP047587) for MAMP Genes and Non-Ribosomal Peptide Synthetase Gene Clusters Conferring Antiviral and Antifungal Activity. Microorganisms, 2021, 9, 2511.	1.6	22
4253	Phylogenetic Analysis of the SQUAMOSA Promoter-Binding Protein-Like Genes in Four Ipomoea Species and Expression Profiling of the IbSPLs During Storage Root Development in Sweet Potato (Ipomoea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	9
4254	Chromosomal-level genome and multi-omics dataset of <i>Pueraria lobata</i> var. <i>thomsonii</i> provide new insights into legume family and the isoflavone and puerarin biosynthesis pathways. Horticulture Research, 2022, 9, .	2.9	10
4255	Genome sequencing and population resequencing provide insights into the genetic basis of domestication and diversity of vegetable soybean. Horticulture Research, 2022, 9, .	2.9	10
4256	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
4257	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
4258	Phylotranscriptomics Resolves the Phylogeny of Pooideae and Uncovers Factors for Their Adaptive Evolution. Molecular Biology and Evolution, 2022, 39, .	3.5	31
4259	Long-read genome sequencing provides molecular insights into scavenging and societal complexity in spotted hyena Crocuta crocuta. Molecular Biology and Evolution, 2022, , .	3.5	1
4261	Chromosome-level genome assembly of the shuttles hoppfish, <i>Periophthalmus modestus</i>. GigaScience, 2022, 11, .	3.3	4
4263	Codon usage in the flatworm Schistosoma mansoni is shaped by the mutational bias towards A+T and translational selection, which increases GC-ending codons in highly expressed genes. Molecular and Biochemical Parasitology, 2022, 247, 111445.	0.5	6
4264	Signatures of selection in recently domesticated macadamia. Nature Communications, 2022, 13, 242.	5.8	14
4267	Chromosome-Level Assembly of the Chinese Hooksnout Carp (Opsariichthys bidens) Genome Using PacBio Sequencing and Hi-C Technology. Frontiers in Genetics, 2021, 12, 788547.	1.1	3
4268	Chromosome-level genome assembly of the fully mycoheterotrophic orchid <i>Gastrodia elata</i>. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	15

#	ARTICLE	IF	CITATIONS
4269	Characterization of a Novel Hot-Spring Cyanobacterium Leptodesmis sichuanensis sp. Nov. and Genomic Insights of Molecular Adaptations Into Its Habitat. Frontiers in Microbiology, 2021, 12, 739625.	1.5	9
4271	Quantitative Insights into the Contribution of Nematocysts to the Adaptive Success of Cnidarians Based on Proteomic Analysis. Biology, 2022, 11, 91.	1.3	2
4272	An RNA Interference Tool to Silence Genes in Sarcoptes scabiei Eggs. International Journal of Molecular Sciences, 2022, 23, 873.	1.8	2
4273	Phenolic degradation by catechol dioxygenases is associated with pathogenic fungi with a necrotrophic lifestyle in the Ceratocystidaceae. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
4274	A chromosomeâ€scale reference genome assembly of yellow mangrove (<i>Bruguiera parviflora</i>) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. Molecular Ecology Resources, 2022, 22, 1939-1953.	2.2	13
4276	Long- read sequencing and de novo assembly of the cynomolgus macaque genome. Journal of Genetics and Genomics, 2022, , .	1.7	1
4277	The responses of harmful dinoflagellate Karenia mikimotoi to simulated ocean acidification at the transcriptional level. Harmful Algae, 2022, 111, 102167.	2.2	3
4278	A well-supported nuclear phylogeny of Poaceae and implications for the evolution of C4 photosynthesis. Molecular Plant, 2022, 15, 755-777.	3.9	47
4280	The Diesel Tree Sindora glabra Genome Provides Insights Into the Evolution of Oleoresin Biosynthesis. Frontiers in Plant Science, 2021, 12, 794830.	1.7	0
4281	Universal gene co-expression network reveals receptor-like protein genes involved in broad-spectrum resistance in pepper (Capsicum annuum L.). Horticulture Research, 2022, , .	2.9	10
4282	Modular evolution of secretion systems and virulence plasmids in a bacterial species complex. BMC Biology, 2022, 20, 16.	1.7	16
4283	Genome survey sequence of black carp provides insights into developmentâ€related gene duplications. Journal of the World Aquaculture Society, 2022, 53, 1197-1214.	1.2	0
4285	Chromosome-Level Genome Assembly of the Rare and Endangered Tropical Plant Speranskia yunnanensis (Euphorbiaceae). Frontiers in Genetics, 2021, 12, 755564.	1.1	1
4286	A core and pan gene map of Leptospira genus and its interactions with human host. Microbial Pathogenesis, 2022, 162, 105347.	1.3	5
4287	The Chinese pine genome and methylome unveil key features of conifer evolution. Cell, 2022, 185, 204-217.e14.	13.5	151
4288	Identification, Molecular Characteristics, and Evolution of GRF Gene Family in Foxtail Millet (Setaria) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	10
4289	Genome Sequences of Two Strains of Prototheca wickerhamii Provide Insight Into the Protothecosis Evolution. Frontiers in Cellular and Infection Microbiology, 2022, 12, 797017.	1.8	2
4290	Titanium dioxide-mediated fatty acids promoted carotenoid synthesis in Phaffia rhodozyma PR106 analyzed whole genome. Bioresource Technology, 2022, 347, 126699.	4.8	5

#	Article	IF	Citations
4291	Triplication is the main evolutionary driving force of NLP transcription factor family in Chinese cabbage and related species. International Journal of Biological Macromolecules, 2022, 201, 492-506.	3.6	4
4292	Host Adaptation in<i>Legionellales</i>Is 1.9 Ga, Coincident with Eukaryogenesis. Molecular Biology and Evolution, 2022, 39, .	3.5	15
4293	Genomic Analysis of Stropharia rugosoannulata Reveals Its Nutritional Strategy and Application Potential in Bioremediation. Journal of Fungi (Basel, Switzerland), 2022, 8, 162.	1.5	5
4294	Traces of transposable elements in genome dark matter co-opted by flowering gene regulation networks. , 0, 2, .		3
4295	Genomic Comparisons and Phenotypic Diversity of Dickeya zeae Strains Causing Bacterial Soft Rot of Banana in China. Frontiers in Plant Science, 2022, 13, 822829.	1.7	2
4297	The genome of the rice variety LTH provides insight into its universal susceptibility mechanism to worldwide rice blast fungal strains. Computational and Structural Biotechnology Journal, 2022, 20, 1012-1026.	1.9	16
4298	Complete Genome Sequencing and Comparative Analysis of the Clinically-Derived Apiotrichum mycotoxinivorans Strain GMU1709. Frontiers in Cellular and Infection Microbiology, 2022, 12, 834015.	1.8	3
4299	The Poly-Glutamate Motif of GmMATE4 Regulates Its Isoflavone Transport Activity. Membranes, 2022, 12, 206.	1.4	4
4300	A New Gene Family Diagnostic for Intracellular Biomineralization of Amorphous Ca Carbonates by Cyanobacteria. Genome Biology and Evolution, 2022, 14, .	1.1	14
4301	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. Nature Communications, 2022, 13, 682.	5.8	59
4303	Genomic insights into the evolution of the critically endangered softâ€shelled turtle <i>Rafetus swinhoei</i>. Molecular Ecology Resources, 2022, 22, 1972-1985.	2.2	9
4304	Extensive sequence divergence between the reference genomes of Taraxacum kok-saghyz and Taraxacum mongolicum. Science China Life Sciences, 2022, 65, 515-528.	2.3	26
4305	HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. Frontiers in Bioinformatics, 2021, 1, .	1.0	5
4306	The long non-coding RNA landscape of Candida yeast pathogens. Nature Communications, 2021, 12, 7317.	5.8	10
4308	Interactomes: Experimental and In Silico Approaches. Advances in Experimental Medicine and Biology, 2021, 1346, 107-117.	0.8	1
4309	Comparative Transcriptome Analysis Reveals Different Mechanisms of Adaptation to Environment among Three Species of Saussurea DC.. Phyton, 2022, 91, 1517-1528.	0.4	1
4310	A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. GigaScience, 2022, 11, .	3.3	6
4311	High-quality chromosome-level genome assembly of Tibetan fox (<i>Vulpes</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.9	4

#	ARTICLE	IF	CITATIONS
4312	Applications of microbial omics in healthcare. , 2022, , 227-248.		0
4313	Amplicon-based and metagenomic approaches provide insights into toxigenic potential in understudied Atlantic Canadian lakes. Facets, 2022, 7, 194-214.	1.1	3
4314	Chromosome-Scale Cerasus Humilis Genome Assembly Reveals Gene Family Evolution and Possible Genomic Basis of Calcium Accumulation in Fruits. SSRN Electronic Journal, 0, , .	0.4	0
4315	Comprehensive Genome Analysis of Halolamina pelagica CDK2: Insights into Abiotic Stress Tolerance Genes. Journal of Pure and Applied Microbiology, 2022, 16, 460-470.	0.3	1
4316	The Antarctic Weddell seal genome reveals evidence of selection on cardiovascular phenotype and lipid handling. Communications Biology, 2022, 5, 140.	2.0	5
4317	A High-Quality, Chromosome-Level Genome Provides Insights Into Determinate Flowering Time and Color of Cotton Rose (Hibiscus mutabilis). Frontiers in Plant Science, 2022, 13, 818206.	1.7	3
4318	A myxozoan genome reveals mosaic evolution in a parasitic cnidarian. BMC Biology, 2022, 20, 51.	1.7	8
4319	Was the Last Bacterial Common Ancestor a Monoderm after All?. Genes, 2022, 13, 376.	1.0	6
4321	Comparative Genomic Analysis Reveals Preserved Features in Organohalide-Respiring <i>Sulfurospirillum</i> Strains. MSphere, 2022, 7, e0093121.	1.3	3
4322	Comparative Genome Analysis of â€˜Candidatus Phytoplasma luffaeâ€™ Reveals the Influential Roles of Potential Mobile Units in Phytoplasma Evolution. Frontiers in Microbiology, 2022, 13, 773608.	1.5	15
4323	The Chromosome-Scale Reference Genome of Macadamia tetraphylla Provides Insights Into Fatty Acid Biosynthesis. Frontiers in Genetics, 2022, 13, 835363.	1.1	4
4324	Genome-Wide Identification and Expression Profiling of CONSTANS-Like Genes in Pepper (Capsicum) Tj ETQq1 1 0.784314 rgBT /Overlo Plant Science, 2022, 13, 828209.	1.7	3
4325	A glimpse at an early stage of microbe domestication revealed in the variable genome of <i>Torulaspora delbrueckii</i>, an emergent industrial yeast. Molecular Ecology, 2023, 32, 2396-2412.	2.0	12
4326	Drivers of intraspecific differentiation of an alpine coldâ€•tolerant herb, <i>Notopterygium oviforme</i> : roles of isolation by distance and ecological factors. Journal of Systematics and Evolution, 0, , .	1.6	1
4327	Demographic history shapes genomic variation in an intracellular parasite with a wide geographical distribution. Molecular Ecology, 2022, 31, 2528-2544.	2.0	13
4328	Population-Genomic Analysis Identifies a Low Rate of Global Adaptive Fixation in the Proteins of the Cyclical Parthenogen<i>Daphnia magna</i>. Molecular Biology and Evolution, 2022, 39, .	3.5	8
4330	Genomic adaptations for arboreal locomotion in Asian flying treefrogs. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116342119.	3.3	6
4331	RNA-Seq reveals miRNA role in thermogenic regulation in brown adipose tissues of goats. BMC Genomics, 2022, 23, 186.	1.2	7

#	Article	IF	Citations
4332	Flavobacterium selenitireducens sp. nov., isolated from rhizosphere soil of ancient mulberry. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	6
4333	Pangenome Analysis of the Soilborne Fungal Phytopathogen Rhizoctonia solani and Development of a Comprehensive Web Resource: RsolaniDB. Frontiers in Microbiology, 2022, 13, 839524.	1.5	14
4334	Chromosome-Level Genome Assembly for Acer pseudosieboldianum and Highlights to Mechanisms for Leaf Color and Shape Change. Frontiers in Plant Science, 2022, 13, 850054.	1.7	7
4335	A chromosomeâ€level genome assembly of <i>Paracymoriza distinctalis</i> (Lepidoptera: Crambidae:) Tj ETQq1 1 0.784314 rgBT /Ove	0.6	0
4336	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. BMC Biology, 2022, 20, 79.	1.7	12
4337	Lysobacter ciconiae sp. nov., and Lysobacter avium sp. nov., isolated from the faeces of an Oriental stork. Journal of Microbiology, 2022, 60, 469-477.	1.3	11
4338	Transcriptome analyses shed light on floral organ morphogenesis and bract color formation in Bougainvillea. BMC Plant Biology, 2022, 22, 97.	1.6	3
4339	Distinguishing Evolutionary Conservation from Derivedness. Life, 2022, 12, 440.	1.1	1
4340	Chromosome-Scale Assembly of the Dendrobium nobile Genome Provides Insights Into the Molecular Mechanism of the Biosynthesis of the Medicinal Active Ingredient of Dendrobium. Frontiers in Genetics, 2022, 13, 844622.	1.1	21
4341	The evolution and competitive strategies of <i>Akkermansia muciniphila</i> in gut. Gut Microbes, 2022, 14, 2025017.	4.3	25
4342	Genetically distant bacteriophages select for unique genomic changes in <i>Enterococcus faecalis</i>. MicrobiologyOpen, 2022, 11, e1273.	1.2	2
4343	Comparative genomic analysis of high-altitude adaptation for Mongolia Mastiff, Tibetan Mastiff, and Canis Lupus. Genomics, 2022, , 110359.	1.3	0
4344	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
4345	A Comparative Analysis of Weizmannia coagulans Genomes Unravels the Genetic Potential for Biotechnological Applications. International Journal of Molecular Sciences, 2022, 23, 3135.	1.8	11
4346	Draft genomes assembly and annotation of Carex parvula and Carex kokanica reveals stress-specific genes. Scientific Reports, 2022, 12, 4970.	1.6	7
4347	The genome of an apodid holothuroid (Chiridota heheva) provides insights into its adaptation to a deep-sea reducing environment. Communications Biology, 2022, 5, 224.	2.0	15
4348	The adaptive evolution of <i>Euryale ferox</i> to the aquatic environment through paleoâ€hexaploidization. Plant Journal, 2022, 110, 627-645.	2.8	12
4350	Comparative Genomics of <i>Fusarium circinatum</i> Isolates Used to Screen Southern Pines for Pitch Canker Resistance. Molecular Plant-Microbe Interactions, 2022, 35, 477-487.	1.4	1

#	ARTICLE	IF	CITATIONS
4351	Chromosome-scale Echinococcus granulosus (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. Communications Biology, 2022, 5, 199.	2.0	7
4352	Genome sequence and population genomics provide insights into chromosomal evolution and phytochemical innovation of <i>Hippophae rhamnoides</i>. Plant Biotechnology Journal, 2022, 20, 1257-1273.	4.1	17
4353	Phylotranscriptomic insights into a Mesoproterozoicâ€"Neoproterozoic origin and early radiation of green seaweeds (Ulvophyceae). Nature Communications, 2022, 13, 1610.	5.8	21
4354	The new Haemaphysalis longicornis genome provides insights into its requisite biological traits. Genomics, 2022, 114, 110317.	1.3	9
4355	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
4356	Inter-paralog amino acid inversion events in large phylogenies of duplicated proteins. PLoS Computational Biology, 2022, 18, e1010016.	1.5	2
4358	Chromosome-level genome assembly of grass carp (Ctenopharyngodon idella) provides insights into its genome evolution. BMC Genomics, 2022, 23, 271.	1.2	21
4359	Transposon insertions regulate genomeâ€wide alleleâ€specific expression and underpin flower colour variations in apple (<i>Malus</i> spp.). Plant Biotechnology Journal, 2022, 20, 1285-1297.	4.1	21
4360	Population genomics of the grapevine pathogen Eutypa lata reveals evidence for population expansion and intraspecific differences in secondary metabolite gene clusters. PLoS Genetics, 2022, 18, e1010153.	1.5	10
4361	Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. Plant Journal, 2022, 110, 1498-1515.	2.8	21
4362	Halorussus halobius sp. nov., Halorussus marinus sp. nov. and Halorussus pelagicus sp. nov., isolated from salted brown alga Laminaria. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	12
4363	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
4364	A Chromosome-Level Reference Genome of Chinese Balloon Flower (Platycodon grandiflorus). Frontiers in Genetics, 2022, 13, 869784.	1.1	7
4365	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
4366	A synthetic â€˜essentialomeâ€™ for axenic culturing of â€˜Candidatus Liberibacter asiaticusâ€™. BMC Research Notes, 2022, 15, 125.	0.6	4
4367	Chromosomeâ€scale genome assembly provides insights into speciation of allotetraploid and massive biomass accumulation of elephant grass (<i>Pennisetum purpureum</i> Schum.). Molecular Ecology Resources, 2022, 22, 2363-2378.	2.2	11
4368	De novo genome assembly of <i>Bradysia cellarum</i> (Diptera: Sciaridae), a notorious pest in traditional special vegetables in China. Insect Molecular Biology, 2022, 31, 508-518.	1.0	3
4369	Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes. Genome Research, 2022, , .	2.4	21

#	Article	IF	Citations
4370	Genome-based taxonomy of genera Halomicrobium and Halosiccatus, and description of Halomicrobium salinisoli sp. nov. Systematic and Applied Microbiology, 2022, 45, 126308.	1.2	24
4371	A new and effective genes-based method for phylogenetic analysis of Klebsiella pneumoniae. Infection, Genetics and Evolution, 2022, 100, 105275.	1.0	2
4372	Chromosome-scale Cerasus humilis genome assembly reveals gene family evolution and possible genomic basis of calcium accumulation in fruits. Scientia Horticulturae, 2022, 299, 111012.	1.7	5
4373	Topology of the redox network during induction of photosynthesis as revealed by time-resolved proteomics in tobacco. Science Advances, 2021, 7, eabi8307.	4.7	27
4374	The Frequency and Topology of Pseudoorthologs. Systematic Biology, 2022, 71, 649-659.	2.7	10
4375	Whole-Genome Sequencing of<i>Acer catalpifolium</i>Reveals Evolutionary History of Endangered Species. Genome Biology and Evolution, 2021, 13, .	1.1	7
4376	Genetic diversity of Leptospira isolates in Lao PDR and genome analysis of an outbreak strain. PLoS Neglected Tropical Diseases, 2021, 15, e0010076.	1.3	5
4377	Haloprofundus salilacus sp. nov., Haloprofundus halobius sp. nov. and Haloprofundus salinisoli sp. nov.: three extremely halophilic archaea isolated from salt lake and saline soil. Extremophiles, 2022, 26, 6.	0.9	23
4378	Alcanivorax limicola sp. nov., isolated from a soda alkali-saline soil. Archives of Microbiology, 2022, 204, 106.	1.0	2
4379	A Chromosome-Level Genome Assembly of Mozambique Tilapia (Oreochromis mossambicus) Reveals the Structure of Sex Determining Regions. Frontiers in Genetics, 2021, 12, 796211.	1.1	5
4380	Chromosome-Level Genome Assembly and HazelOmics Database Construction Provides Insights Into Unsaturated Fatty Acid Synthesis and Cold Resistance in Hazelnut (Corylus heterophylla). Frontiers in Plant Science, 2021, 12, 766548.	1.7	7
4381	Genomic analyses provide insights into spinach domestication and the genetic basis of agronomic traits. Nature Communications, 2021, 12, 7246.	5.8	34
4382	Genomic analysis of ElsinoÃ« arachidis reveals its potential pathogenic mechanism and the biosynthesis pathway of elsinochrome toxin. PLoS ONE, 2021, 16, e0261487.	1.1	3
4383	Genetic structure and evolutionary diversity of mating-type (MAT) loci inÂHypsizygus marmoreus. IMA Fungus, 2021, 12, 35.	1.7	9
4384	Cryptosporidium felis differs from other Cryptosporidium spp. in codon usage. Microbial Genomics, 2021, 7, .	1.0	3
4385	Deciphering Evolutionary Dynamics of WRKY I Genes in Rosaceae Species. Frontiers in Ecology and Evolution, 2021, 9, .	1.1	0
4386	Machine learning prediction of novel pectinolytic enzymes in Aspergillus niger through integrating heterogeneous (post-) genomics data. Microbial Genomics, 2021, 7, .	1.0	2
4387	New data and collaborations at the<i>Saccharomyces</i>Genome Database: updated reference genome, alleles, and the Alliance of Genome Resources. Genetics, 2022, 220, .	1.2	34

#	ARTICLE	IF	CITATIONS
4389	Genome Sequence of Chrysotila roscoffensis, a Coccolithphore Contributed to Global Biogeochemical Cycles. Genes, 2022, 13, 40.	1.0	2
4390	Comparative Genomics Provides Insights into Adaptive Evolution in Tactile-Foraging Birds. Genes, 2022, 13, 678.	1.0	1
4391	High-quality chromosome-scale de novo assembly of the Paspalum notatum â€˜Fluggeâ€™ genome. BMC Genomics, 2022, 23, 293.	1.2	1
4392	Whole-Genome Sequence and Comparative Analysis of Trichoderma asperellum ND-1 Reveal Its Unique Enzymatic System for Efficient Biomass Degradation. Catalysts, 2022, 12, 437.	1.6	9
4393	Genome-Wide Study of Conidiation-Related Genes in the Aphid-Obligate Fungal Pathogen Conidiobolus obscurus (Entomophthoromycotina). Journal of Fungi (Basel, Switzerland), 2022, 8, 389.	1.5	4
4394	Transcriptome analysis provides new insights into cold adaptation of corsac fox (<i>Vulpes) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	0.8	3
4395	Chromosomeâ€level genome assembly for the hornedâ€gall aphid provides insights into interactions between gallâ€making insect and its host plant. Ecology and Evolution, 2022, 12, e8815.	0.8	8
4396	A chromosome-level genome of the kuruma shrimp (Marsupenaeus japonicus) provides insights into its evolution and cold-resistance mechanism. Genomics, 2022, 114, 110373.	1.3	8
4875	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in Aralia elata. Nature Communications, 2022, 13, 2224.	5.8	34
4876	Genomes of leafy and leafless Platanthera orchids illuminate the evolution of mycoheterotrophy. Nature Plants, 2022, 8, 373-388.	4.7	36
4877	Advances in phylogenomics. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2014, 36, 669-78.	0.1	0
4878	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study Streptococcus pyogenes. Methods in Molecular Biology, 2022, 2449, 299-324.	0.4	1
4879	Molecular Characterization of a Flatworm Girardia Isolate from Guanajuato, Mexico. SSRN Electronic Journal, 0, , .	0.4	0
4881	The Unusual Metalloprotease-Rich Venom Proteome of the Australian Elapid Snake Hoplocephalus stephensii. Toxins, 2022, 14, 314.	1.5	2
4882	Speciation with gene flow between two Neotropical sympatric species (<i>Pitcairnia</i> spp.:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 182	0.8	4
4883	Phase separation driven by interchangeable properties in the intrinsically disordered regions of protein paralogs. Communications Biology, 2022, 5, 400.	2.0	13
4884	Survival and Genome Diversity of Vibrio parahaemolyticus Isolated from Edible Aquatic Animals. Diversity, 2022, 14, 350.	0.7	7
4886	The genome sequencing and comparative analysis of a wild kiwifruit Actinidia eriantha. Molecular Horticulture, 2022, 2, .	2.3	13

#	ARTICLE	IF	CITATIONS
4887	Helicobacter turcicus sp. nov., a catalase-negative new member of the Helicobacter genus, isolated from Anatolian Ground Squirrel (Spermophilus xanthoprymnus) in Turkey. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
4888	ProtPathDB: A Web-based Resource of Parasite Proteases. Current Bioinformatics, 2022, 17, 710-722.	0.7	0
4889	The Quest for Orthologs orthology benchmark service in 2022. Nucleic Acids Research, 2022, 50, W623-W632.	6.5	29
4890	MLST analysis of genetic diversity of Bacillus coagulans strains to evaluate effects on constipation model. Food Science and Human Wellness, 2022, 11, 815-827.	2.2	3
4891	Description of the two novel species of the genus Helicobacter: Helicobacter anatolicus sp. nov., and Helicobacter kayseriensis sp. nov., isolated from feces of urban wild birds. Systematic and Applied Microbiology, 2022, 45, 126326.	1.2	9
4892	Giant <i>Starship</i> Elements Mobilize Accessory Genes in Fungal Genomes. Molecular Biology and Evolution, 2022, 39, .	3.5	39
4893	The chromosomeâ€level genome assembly of the Japanese yellowtail jack <i>Seriola aureovittata</i> provides insights into genome evolution and efficient oxygen transport. Molecular Ecology Resources, 2022, 22, 2701-2712.	2.2	5
4894	Modeling the effect of rRNA-mRNA interactions and mRNA folding on mRNA translation in chloroplasts. Computational and Structural Biotechnology Journal, 2022, 20, 2521-2538.	1.9	1
4896	Natrinema halophilum sp. nov., Natrinema salinisoli sp. nov., Natrinema amylolyticum sp. nov. and Haloterrigena alkaliphila sp. nov., four extremely halophilic archaea isolated from salt mine, saline soil and salt lake. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	21
4900	Effects of Bacillus coagulans GBI-30, 6086 as an adjunct starter culture on the production of yogurt. Food Research International, 2022, 160, 111398.	2.9	7
4901	A chromosome-level genome assembly of the pollinating fig wasp <i>Valisia javana</i>. DNA Research, 2022, 29, .	1.5	3
4902	Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. MBio, 2022, 13, .	1.8	4
4903	Pan-Genomes Provide Insights into the Genetic Basis of Auricularia heimuer Domestication. Journal of Fungi (Basel, Switzerland), 2022, 8, 581.	1.5	1
4904	Genetic characterization of potential venom resistance proteins in California ground squirrels (<i>Otospermophilus beecheyi</i>) using transcriptome analyses. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2023, 340, 259-269.	0.6	2
4905	Characterising genome architectures using genome decomposition analysis. BMC Genomics, 2022, 23, .	1.2	2
4906	Clade-specific genes and the evolutionary origin of novelty; new tools in the toolkit. Seminars in Cell and Developmental Biology, 2023, 145, 52-59.	2.3	6
4907	Chromosome-Level Genome Assembly of Acanthogobius ommaturus Provides Insights Into Evolution and Lipid Metabolism. Frontiers in Marine Science, 2022, 9, .	1.2	3
4908	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

#	ARTICLE	IF	CITATIONS
4909	Genomic insights into positive selection during barley domestication. BMC Plant Biology, 2022, 22, .	1.6	3
4910	High-quality chromosome-level genome assembly of Litsea coreana L. provides insights into Magnoliids evolution and flavonoid biosynthesis. Genomics, 2022, 114, 110394.	1.3	2
4911	Using all Gene Families Vastly Expands Data Available for Phylogenomic Inference. Molecular Biology and Evolution, 2022, 39, .	3.5	7
4912	Transcriptome Mining Provides Insights into Cell Wall Metabolism and Fiber Lignification in Agave tequilana Weber. Plants, 2022, 11, 1496.	1.6	2
4913	Genome, genetic evolution, and environmental adaptation mechanisms of Schizophyllum commune in deep subseafloor coal-bearing sediments. IScience, 2022, 25, 104417.	1.9	8
4914	Enhancing the Phytoremediation of Heavy Metals by Combining Hyperaccumulator and Heavy Metal-Resistant Plant Growth-Promoting Bacteria. Frontiers in Plant Science, 2022, 13, .	1.7	8
4915	Modern vaccine development via reverse vaccinology to combat antimicrobial resistance. Life Sciences, 2022, 302, 120660.	2.0	5
4917	Chromosome-level genome assembly of the black widow spider<i>Latrodectus elegans</i>illuminates composition and evolution of venom and silk proteins. GigaScience, 2022, 11, .	3.3	9
4918	Chromosomal-Level Reference Genome of the Moth Heortia Vitessoides (Lepidoptera: Crambidae), A Major Pest of Agarwood-Producing Trees. SSRN Electronic Journal, 0, , .	0.4	0
4919	A chromosome-level genome assembly of <i>Artocarpus nanchuanensis</i> (Moraceae), an extremely endangered fruit tree. GigaScience, 2022, 11, .	3.3	3
4920	The Genetic Adaptations of Toxoptera Aurantia Facilitated its Rapid Multiple Plant Hosts Dispersal and Invasion. SSRN Electronic Journal, 0, , .	0.4	0
4921	The Spruce Budworm Genome: Reconstructing the Evolutionary History of Antifreeze Proteins. Genome Biology and Evolution, 2022, 14, .	1.1	3
4922	Genetic Drift and Host-Adaptive Features Likely Underlie the Cladogenesis of Insect-Associated Lachnospiraceae. Genome Biology and Evolution, 2022, 14, .	1.1	4
4923	The Antarctic Moss Pohlia nutans Genome Provides Insights Into the Evolution of Bryophytes and the Adaptation to Extreme Terrestrial Habitats. Frontiers in Plant Science, 0, 13, .	1.7	9
4924	A chromosome-level genome assembly for the rabbit tapeworm Taenia pisiformis. Gene, 2022, 834, 146650.	1.0	2
4925	Expression Profile of Genes Related to the Th17 Pathway in Macrophages Infected by Leishmania major and Leishmania amazonensis: The Use of Gene Regulatory Networks in Modeling This Pathway. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	2
4926	Chromosome-level and haplotype-resolved genome provides insight into the tetraploid hybrid origin of patchouli. Nature Communications, 2022, 13, .	5.8	20
4927	Transcriptional Basis for Haustorium Formation and Host Establishment in Hemiparasitic Psittacanthus schiedeanus Mistletoes. Frontiers in Genetics, 0, 13, .	1.1	4

#	Article	IF	Citations
4928	Comparative Genomic Analyses Provide Insight Into the Pathogenicity of Metschnikowia bicuspidata LNES0119. Frontiers in Microbiology, 0, 13, .	1.5	7
4929	Gene Conversion Explains Elevated Diversity in the Immunity Modulating APL1 Gene of the Malaria Vector Anopheles funestus. Genes, 2022, 13, 1102.	1.0	2
4930	Genomic Characterization of Lactobacillus delbrueckii Strains with Probiotics Properties. Frontiers in Bioinformatics, 0, 2, .	1.0	6
4931	Complete genome sequence and phylogenetic analysis of medicinal plant <i>Abrus cantoniensis</i> for evolutionary research and germplasm utilization. Plant Genome, 0, , .	1.6	2
4932	Heterotrophic Sulfur Oxidation of Halomonas titanicae SOB56 and Its Habitat Adaptation to the Hydrothermal Environment. Frontiers in Microbiology, 0, 13, .	1.5	3
4933	A chromosome-level genome assembly and annotation of the maize elite breeding line Dan340. GigaByte, 0, 2022, 1-8.	0.0	2
4934	De novo assembly provides new insights into the evolution of Elaeagnus angustifolia L.. Plant Methods, 2022, 18, .	1.9	3
4935	Molecular characterization of a flatworm Girardia isolate from Guanajuato, Mexico. Developmental Biology, 2022, 489, 165-177.	0.9	1
4936	Chromosome-level genome assemblies of four wild peach species provide insights into genome evolution and genetic basis of stress resistance. BMC Biology, 2022, 20, .	1.7	13
4937	Comparative genomics reveals low levels of inter- and intraspecies diversity in the causal agents of dwarf and common bunt of wheat and hint at conspecificity of Tilletia caries and T. laevis. IMA Fungus, 2022, 13, .	1.7	5
4938	Loci underlying leaf agronomic traits identified by re-sequencing celery accessions based on an assembled genome. IScience, 2022, 25, 104565.	1.9	6
4940	The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. GigaScience, 2022, 11, .	3.3	13
4942	Integrative genomics analysis of the ever-shrinking pectin methylesterase (PME) gene family in foxtail		

#	Article	IF	Citations
4949	The genome of <i>Prunus humilis</i> provides new insights to drought adaption and population diversity. DNA Research, 2022, 29, .	1.5	4
4950	Multi-Species Transcriptome Assemblies of Cultivated and Wild Lentils (Lens sp.) Provide a First Glimpse at the Lentil Pangenome. Agronomy, 2022, 12, 1619.	1.3	6
4951	Phylotranscriptomics Illuminates the Placement of Whole Genome Duplications and Gene Retention in Ferns. Frontiers in Plant Science, 0, 13, .	1.7	10
4952	A chromosomeâ€level genome of <i>Syringa oblata</i> provides new insights into chromosome formation in Oleaceae and evolutionary history of lilacs. Plant Journal, 2022, 111, 836-848.	2.8	9
4953	A de novo assembled high-quality chromosome-scale Trifolium pratense genome and fine-scale phylogenetic analysis. BMC Plant Biology, 2022, 22, .	1.6	6
4954	Complete Genome Sequences of Ezakiella coagulans C0061C1 and Fenollaria massiliensis C0061C2. Microbiology Resource Announcements, 0, , .	0.3	1
4955	Identification of Peptoniphilus vaginalis-Like Bacteria, Peptoniphilus septimus sp. nov., From Blood Cultures in a Cervical Cancer Patient Receiving Chemotherapy: Case and Implications. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	3
4956	Genome-Wide Identification, Characterization, and Comparative Analysis of NLR Resistance Genes in Coffea spp.. Frontiers in Plant Science, 0, 13, .	1.7	1
4957	The chromosome-scale genome of Phoebe bournei reveals contrasting fates of terpene synthase (TPS)-a and TPS-b subfamilies. Plant Communications, 2022, 3, 100410.	3.6	24
4958	A chromosome-level genome assembly of the jade perch (Scortum barcoo). Scientific Data, 2022, 9, .	2.4	3
4960	Haplotypeâ€resolved genome assembly of <i>Bletilla striata</i> (Thunb.) Reichb.f. to elucidate medicinal value. Plant Journal, 2022, 111, 1340-1353.	2.8	22
4961	Phenotype-genotype analysis of Latilactobacills curvatus from different niches: Carbohydrate metabolism, antibiotic resistance, bacteriocin, phage fragments and linkages with CRISPR-Cas systems. Food Research International, 2022, 160, 111640.	2.9	7
4962	Complete Genome Sequence of <i>Curtobacterium</i> sp. C1, a Beneficial Endophyte with the Potential for In-Plant Salinity Stress Alleviation. Molecular Plant-Microbe Interactions, 0, , .	1.4	3
4963	Whole-Genome Sequencing and Comparative Genome Analysis of Fusarium solani-melongenae Causing Fusarium Root and Stem Rot in Sweetpotatoes. Microbiology Spectrum, 2022, 10, .	1.2	7
4964	Marine gregarine genomes reveal the breadth of apicomplexan diversity with a partially conserved glideosome machinery. BMC Genomics, 2022, 23, .	1.2	7
4965	The chromosome-scale genome provides insights into pigmentation in Acer rubrum. Plant Physiology and Biochemistry, 2022, 186, 322-333.	2.8	1
4966	Genome sequencing reveals chromosome fusion and extensive expansion of genes related to secondary metabolism in <i>Artemisia argyi</i>. Plant Biotechnology Journal, 2022, 20, 1902-1915.	4.1	25
4967	Pan-genome analysis of three main Chinese chestnut varieties. Frontiers in Plant Science, 0, 13, .	1.7	5

#	Article	IF	Citations
4968	Genome-wide identification and comparative analysis of MATE gene family in Cucurbitaceae species and their regulatory role in melon (Cucumis melo) under salt stress. Horticulture Environment and Biotechnology, 0, , .	0.7	9
4969	The genome of <i>Dioscorea zingiberensis</i> sheds light on the biosynthesis, origin and evolution of the medicinally important diosgenin saponins. Horticulture Research, 2022, 9, .	2.9	14
4970	Genomic divergence of <i>Stellera chamaejasme</i> through local selection across the Qinghaiâ€"Tibet plateau and northern China. Molecular Ecology, 2022, 31, 4782-4796.	2.0	15
4971	Chromosome-Level Genome Assembly of the Butter Clam <i>Saxidomus purpuratus</i>. Genome Biology and Evolution, 2022, 14, .	1.1	1
4972	A chromosome-level genome assembly of Styphnolobium japonicum combined with comparative genomic analyses offers insights on the evolution of flavonoid and lignin biosynthesis. Industrial Crops and Products, 2022, 187, 115336.	2.5	2
4973	Insights into chromosomal evolution and sex determination of <i>Pseudobagrus ussuriensis</i> (Bagridae, Siluriformes) based on a chromosome-level genome. DNA Research, 2022, 29, .	1.5	3
4974	Chromosome-level genome of Tibetan naked carp (<i>Gymnocypris przewalskii</i>) provides insights into Tibetan highland adaptation. DNA Research, 2022, 29, .	1.5	9
4975	Comparative genomic analysis of Echinococcus multilocularis with other tapeworms. , 2022, 77, 2743-2750.		0
4976	Chromosomal-level reference genome of the moth Heortia vitessoides (Lepidoptera: Crambidae), a major pest of agarwood-producing trees. Genomics, 2022, 114, 110440.	1.3	2
4977	Testing candidate genes linked to corolla shape variation of a pollinator shift in Rhytidophyllum (Gesneriaceae). PLoS ONE, 2022, 17, e0267540.	1.1	1
4978	Comparative Analysis of Enzyme Production Patterns of Lignocellulose Degradation of Two White Rot Fungi: Obba rivulosa and Gelatoporia subvermispora. Biomolecules, 2022, 12, 1017.	1.8	5
4979	Comparative genomics reveals the molecular mechanism of salt adaptation for zoysiagrasses. BMC Plant Biology, 2022, 22, .	1.6	5
4980	Effectors from a Bacterial Vector-Borne Pathogen Exhibit Diverse Subcellular Localization, Expression Profiles, and Manipulation of Plant Defense. Molecular Plant-Microbe Interactions, 2022, 35, 1067-1080.	1.4	3
4981	Complete gammaproteobacterial endosymbiont genome assembly from a seep tubeworm Lamellibrachia satsuma. Journal of Microbiology, 2022, 60, 916-927.	1.3	1
4982	Signatures of adaptive evolution in platyrrhine primate genomes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
4983	Nuclear-specific gene expression in heterokaryons of the filamentous ascomycete <i>Neurospora tetrasperma</i>. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, .	1.2	1
4984	Chromosomal-level genome of velvet bean (<i>Mucuna pruriens</i>) provides resources for L-DOPA synthetic research and development. DNA Research, 2022, 29, .	1.5	3
4985	Bioinformatics and its role in the study of the evolution and probiotic potential of lactic acid bacteria. Food Science and Biotechnology, 2023, 32, 389-412.	1.2	4

#	Article	IF	Citations
4986	A High-Quality Genome Assembly of Sorghum dochna. Frontiers in Genetics, 0, 13, .	1.1	2
4987	Dysfunction of Ras-GAP protein AfgapA contributes to hypoxia fitness in Aspergillus fumigatus. Current Genetics, 0, , .	0.8	1
4988	Chromosome-level genome assembly and population genomic analyses provide insights into adaptive evolution of the red turpentine beetle, Dendroctonus valens. BMC Biology, 2022, 20, .	1.7	5
4989	Complete genome sequence of a multiple-stress-tolerant bacterium Halomonas piezotolerans NBT06E8T isolated from a deep-sea sediment sample of the New Britain Trench. 3 Biotech, 2022, 12, .	1.1	1
4990	Comparative Genome and Evolution Analyses of an Endangered Stony Coral Species <i>Dendrophyllia cribrosa</i> Near Dokdo Islands in the East Sea. Genome Biology and Evolution, 2022, 14, .	1.1	1
4991	De Novo Whole-Genome Sequencing and Assembly of the Yellow-Throated Bunting (Emberiza elegans) Provides Insights into Its Evolutionary Adaptation. Animals, 2022, 12, 2004.	1.0	0
4992	Comparative analysis reveals distinctive genomic features of Taiwan hot-spring cyanobacterium Thermosynechococcus sp. TA-1. Frontiers in Microbiology, 0, 13, .	1.5	2
4993	In Silico Analysis of Potential Drug Targets for Protozoan Infections. Medicinal Chemistry, 2023, 19, 91-98.	0.7	1
4994	Behavioral innovation and genomic novelty are associated with the exploitation of a challenging dietary opportunity by an avivorous bat. IScience, 2022, 25, 104973.	1.9	7
4995	Whole-Genome Sequence of Beauveria bassiana JEF-350, a Strain with High Insecticidal Activity against Melon Thrips (Thrips palmi). Microbiology Resource Announcements, 2022, 11, .	0.3	1
4996	De Novo Long-Read Whole-Genome Assemblies and the Comparative Pan-Genome Analysis of Ascochyta Blight Pathogens Affecting Field Pea. Journal of Fungi (Basel, Switzerland), 2022, 8, 884.	1.5	0
4997	Citrus Pan-Genome to Breeding Database (CPBD): A comprehensive genome database for citrus breeding. Molecular Plant, 2022, 15, 1503-1505.	3.9	39
4998	Metabacillus rhizolycopersici sp. nov., Isolated from the Rhizosphere Soil of Tomato Plants. Current Microbiology, 2022, 79, .	1.0	0
5000	Improved genome assembly provides new insights into the environmental adaptation of the American cockroach, <i>Periplaneta americana</i>. Archives of Insect Biochemistry and Physiology, 2022, 111, .	0.6	3
5002	The De Novo Genome Assembly of Olea europaea subsp. cuspidate, a Widely Distributed Olive Close Relative. Frontiers in Genetics, 0, 13, .	1.1	2
5003	A chromosome-level genome assembly provides insights into the environmental adaptability and outbreaks of Chlorops oryzae. Communications Biology, 2022, 5, .	2.0	0
5004	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
5005	Genomic Analysis Reveals Adaptation of <i>Vibrio campbellii</i> to the Hadal Ocean. Applied and Environmental Microbiology, 2022, 88, .	1.4	5

#	Article	IF	Citations
5006	Exploring the medicinally important secondary metabolites landscape through the lens of transcriptome data in fenugreek (Trigonella foenum graecum L.). Scientific Reports, 2022, 12, .	1.6	9
5007	Comprehensive genome sequence analysis of the devastating tobacco bacterial phytopathogen Ralstonia solanacearum strain FJ1003. Frontiers in Genetics, 0, 13, .	1.1	1
5008	Chromosome-level assembly of Gymnocypris eckloni genome. Scientific Data, 2022, 9, .	2.4	5
5009	A chromosome-level genome of the helmet catfish (Cranoglanis bouderius). Frontiers in Genetics, 0, 13, .	1.1	2
5010	Genomic investigation of the Chinese alligator reveals wildâ€extinct genetic diversity and genomic consequences of their continuous decline. Molecular Ecology Resources, 2023, 23, 294-311.	2.2	4
5011	Shewanella oncorhynchi sp. nov., a novel member of the genus Shewanella, isolated from Rainbow Trout (Oncorhynchus mykiss). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	11
5012	Genomic and transcriptomic analyses provide insights into valuable fatty acid biosynthesis and environmental adaptation of yellowhorn. Frontiers in Plant Science, 0, 13, .	1.7	2
5013	Testing Phylogenetic Stability with Variable Taxon Sampling. Methods in Molecular Biology, 2022, , 167-188.	0.4	1
5014	Reconstructing Gene Gains and Losses with BadiRate. Methods in Molecular Biology, 2022, , 213-232.	0.4	1
5015	Chromosomal-level genome of macadamia (<i>Macadamia integrifolia</i>). , 2022, 1, 1-9.		4
5017	Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar â€˜Changxianggeng 1813â€™ Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice. International Journal of Molecular Sciences, 2022, 23, 9705.	1.8	5
5020	Multiâ€omics provides new insights into the domestication and improvement of dark jute () Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.8	1
5022	Comparative Genome Analysis Reveals the Genomic Basis of Semi-Aquatic Adaptation in American Mink (Neovison vison). Animals, 2022, 12, 2385.	1.0	2
5023	Transcriptome analysis provides insight into adaptive mechanisms of scallops under environmental stress. Frontiers in Marine Science, 0, 9, .	1.2	7
5024	The complete mitochondrial genome of Isochrysis galbana harbors a unique repeat structure and a specific trans-spliced cox1 gene. Frontiers in Microbiology, 0, 13, .	1.5	1
5025	First Report and Comparative Genomic Analysis of a Mycoplasma mycoides Subspecies capri HN-A in Hainan Island. Microorganisms, 2022, 10, 1908.	1.6	0
5028	Development and Optimization of a Selective Whole-Genome Amplification To Study Plasmodium ovale Spp.. Microbiology Spectrum, 2022, 10, .	1.2	3
5030	The genetic architecture of phenotypic diversity in the Betta fish (<i>Betta splendens</i>). Science Advances, 2022, 8, .	4.7	10

#	Article	IF	Citations
5031	Elevation of Clavibacter michiganensis subsp. californiensis to species level as Clavibacter californiensis sp. nov., merging and re-classification of Clavibacter michiganensis subsp. chilensis and Clavibacter michiganensis subsp. phaseoli as Clavibacter phaseoli sp. nov. based on complete genome in silico analyses. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	4
5032	Transcriptome profiling of barley and tomato shoot and root meristems unravels physiological variations underlying photoperiodic sensitivity. PLoS ONE, 2022, 17, e0265981.	1.1	0
5033	IPGA: A handy integrated prokaryotes genome and panâ€genome analysis web service. , 2022, 1, .		19
5035	The coral <i>Acropora loripes</i> genome reveals an alternative pathway for cysteine biosynthesis in animals. Science Advances, 2022, 8, .	4.7	10
5036	De novo assembly and annotation of the CHOZNÂ® GS ^{âˆ’/âˆ’} genome supports highâ€throughput genomeâ€scale screening. Biotechnology and Bioengineering, 0, , .	1.7	4
5037	Chromosomeâ€level genome assembly and functional characterization of terpene synthases provide insights into the volatile terpenoid biosynthesis of <i>Wurfbainia villosa</i>. Plant Journal, 2022, 112, 630-645.	2.8	13
5039	A genome for <i>Cissus</i> illustrates features underlying its evolutionary success in dry savannas. Horticulture Research, 2022, 9, .	2.9	3
5040	Chromosome-level genome assembly and resequencing of camphor tree (<i>Cinnamomum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf biosynthesis of <i>Cinnamomum</i>. Horticulture Research, 2022, 9, .	2.9	5
5041	Pan-Genome Analysis of Campylobacter: Insights on the Genomic Diversity and Virulence Profile. Microbiology Spectrum, 2022, 10, .	1.2	8
5042	Identification of Candidate Ice Nucleation Activity (INA) Genes in Fusarium avenaceum by Combining Phenotypic Characterization with Comparative Genomics and Transcriptomics. Journal of Fungi (Basel, Switzerland), 2022, 8, 958.	1.5	3
5044	A chromosome-level genome assembly of the potato grouper (Epinephelus tukula). Genomics, 2022, 114, 110473.	1.3	2
5045	Evolution of isoformâ€level gene expression patterns across tissues during lotus species divergence. Plant Journal, 2022, 112, 830-846.	2.8	1
5046	Pan-genome evolution and its association with divergence of metabolic functions in Bifidobacterium genus. World Journal of Microbiology and Biotechnology, 2022, 38, .	1.7	1
5047	Novel genome sequence of Chinese cavefish (<i>Triplophysa rosa</i>) reveals pervasive relaxation of natural selection in cavefish genomes. Molecular Ecology, 2022, 31, 5831-5845.	2.0	12
5048	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
5049	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and withinâ€host species divergence. Transboundary and Emerging Diseases, 2022, 69, 3468-3484.	1.3	4
5050	A chromosome-level genome assembly for Dracaena cochinchinensis reveals the molecular basis of its longevity and formation of dragonâ€™s blood. Plant Communications, 2022, 3, 100456.	3.6	6
5051	Comparative transcriptomics analysis pipeline for the meta-analysis of phylogenetically divergent datasets (CoRMAP). BMC Bioinformatics, 2022, 23, .	1.2	2

#	ARTICLE	IF	CITATIONS
5052	The complex genome and adaptive evolution of polyploid Chinese pepper (<i>Zanthoxylum armatum</i>) Tj ETQq0 0 0 rgBT /Overlock 1	4.1	10
5053	HSDatabaseâ€"a database of highly similar duplicate genes from plants, animals, and algae. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	2
5054	Phylogenomics provides insights into the evolution of cactophily and host plant shifts in Drosophila. Molecular Phylogenetics and Evolution, 2023, 178, 107653.	1.2	4
5055	Chromosome-Level Assembly of Male Opsariichthys bidens Genome Provides Insights into the Regulation of the GnRH Signaling Pathway and Genome Evolution. Biology, 2022, 11, 1500.	1.3	3
5056	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. BMC Biology, 2022, 20, .	1.7	5
5057	EchinoDB: an update to the web-based application for genomic and transcriptomic data on echinoderms. BMC Genomic Data, 2022, 23, .	0.7	1
5058	Whole-genome sequencing and comparative genomic analysis of a pathogenic Enterocytozoon hepatopenaei strain isolated from Litopenaeus vannamei. Aquaculture International, 2023, 31, 523-546.	1.1	4
5059	The chromosomeâ€level genome of <i>Akebia trifoliata</i> as an important resource to study plant evolution and environmental adaptation in the Cretaceous. Plant Journal, 2022, 112, 1316-1330.	2.8	14
5060	Identification of shared bacterial strains in the vaginal microbiota of related and unrelated reproductive-age mothers and daughters using genome-resolved metagenomics. PLoS ONE, 2022, 17, e0275908.	1.1	5
5062	Karyotype variation, spontaneous genome rearrangements affecting chemical insensitivity, and expression level polymorphisms in the plant pathogen Phytophthora infestans revealed using its first chromosome-scale assembly. PLoS Pathogens, 2022, 18, e1010869.	2.1	4
5063	OrthoSNAP: A tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. PLoS Biology, 2022, 20, e3001827.	2.6	10
5064	Genomic insights into the physiology of Quinella, an iconic uncultured rumen bacterium. Nature Communications, 2022, 13, .	5.8	10
5065	The Chromosome-level genome of Aesculus wilsonii provides new insights into terpenoid biosynthesis and Aesculus evolution. Frontiers in Plant Science, 0, 13, .	1.7	1
5066	Integrated Omic Approaches Reveal Molecular Mechanisms of Tolerance during Soybean and Meloidogyne incognita Interactions. Plants, 2022, 11, 2744.	1.6	4
5067	Haladaptatus halobius sp. nov. and Haladaptatus salinisoli sp. nov., two extremely halophilic archaea isolated from Gobi saline soil. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
5068	De novo genome assembly and annotation of Holothuria scabra (Jaeger, 1833) from nanopore sequencing reads. Genes and Genomics, 2022, 44, 1487-1498.	0.5	3
5069	De-novo genome assembly and annotation of sobaity seabream Sparidentex hasta. Frontiers in Genetics, 0, 13, .	1.1	1
5070	An overview of online resources for intra-species detection of gene duplications. Frontiers in Genetics, 0, 13, .	1.1	1

#	ARTICLE	IF	CITATIONS
5072	A Chromosome-Scale Genome Assembly of Mitragyna speciosa (Kratom) and the Assessment of Its Genetic Diversity in Thailand. Biology, 2022, 11, 1492.	1.3	2
5073	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in <i>Ganoderma</i>. Molecular Ecology Resources, 0, , .	2.2	4
5074	Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. Plant Communications, 2022, 3, 100464.	3.6	6
5075	A chromosome-level genome of Semiothisa cinerearia provides insights into its genome evolution and control. BMC Genomics, 2022, 23, .	1.2	1
5076	Comparative transcriptome and proteome analyses of the longissimus dorsi muscle for explaining the difference between donkey meat and other meats. Animal Biotechnology, 2023, 34, 3085-3098.	0.7	1
5077	Genome Evolution of a Symbiont Population for Pathogen Defense in Honeybees. Genome Biology and Evolution, 2022, 14, .	1.1	6
5079	CRISPR-based oligo recombineering prioritizes apicomplexan cysteines for drug discovery. Nature Microbiology, 2022, 7, 1891-1905.	5.9	13
5081	Comparative Genomic Analysis of 31 <i>Phytophthora</i> Genomes Reveals Genome Plasticity and Horizontal Gene Transfer. Molecular Plant-Microbe Interactions, 2023, 36, 26-46.	1.4	6
5082	Worms and gills, plates and spines: the evolutionary origins and incredible disparity of deuterostomes revealed by fossils, genes, and development. Biological Reviews, 2023, 98, 316-351.	4.7	12
5083	In-silico approach of identifying novel therapeutic targets against Yersinia pestis using pan and subtractive genomic analysis. Computational Biology and Chemistry, 2022, 101, 107784.	1.1	2
5084	Chromosome-level genome assembly of the bar-headed goose (Anser indicus). Scientific Data, 2022, 9, .	2.4	2
5085	Phylogenomics as an effective approach to untangle cross-species hybridization event: A case study in the family Nymphaeaceae. Frontiers in Genetics, 0, 13, .	1.1	3
5087	Olfactory and gustatory receptor genes in fig wasps: Evolutionary insights from comparative studies. Gene, 2023, 850, 146953.	1.0	6
5088	The whole-genome assembly of an endangered Salicaceae species: <i>Chosenia arbutifolia</i> (Pall.) A. Skv. GigaScience, 2022, 11, .	3.3	1
5089	The Soursop Genome (Annona muricata L., Annonaceae). Compendium of Plant Genomes, 2022, , 149-174.	0.3	0
5090	Identification of sex-linked marker and candidate sex determination gene in ornamental fish, African scat (Scatophagus tetracanthus). Aquaculture, 2023, 563, 739023.	1.7	1
5091	Wholeâ€genome assembly and annotation for the little yellow croaker (<i>Larimichthys polyactis</i>) provide insights into the evolution of hermaphroditism and gonochorism. Molecular Ecology Resources, 2023, 23, 632-658.	2.2	4
5092	<scp>NGSEP</scp> 4: Efficient and accurate identification of orthogroups and wholeâ€genome alignment. Molecular Ecology Resources, 2023, 23, 712-724.	2.2	7

#	Article	IF	Citations
5093	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
5094	CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses, 2022, 14, 2534.	1.5	6
5095	Chromosome-level genome assembly of Dongxiang wild rice (Oryza rufipogon) provides insights into resistance to disease and freezing. Frontiers in Genetics, 0, 13, .	1.1	2
5097	Wholeâ€genome resequencing reveals complex effects of geographicalâ€"palaeoclimatic interactions on diversification of moustache toads in East Asia. Molecular Ecology, 2023, 32, 644-659.	2.0	2
5099	HGTree v2.0: a comprehensive database update for horizontal gene transfer (HGT) events detected by the tree-reconciliation method. Nucleic Acids Research, 2023, 51, D1010-D1018.	6.5	5
5102	Metagenome-assembled genome extraction and analysis from microbiomes using KBase. Nature Protocols, 2023, 18, 208-238.	5.5	7
5103	OrthoDB v11: annotation of orthologs in the widest sampling of organismal diversity. Nucleic Acids Research, 2023, 51, D445-D451.	6.5	76
5104	Dissection of Besnoitia besnoiti intermediate host life cycle stages: From morphology to gene expression. PLoS Pathogens, 2022, 18, e1010955.	2.1	3
5107	A Chromosome-level assembly of the Japanese eel genome, insights into gene duplication and chromosomal reorganization. GigaScience, 2022, 11, .	3.3	4
5108	Transcriptomics-based Analysis of the Response of Sugar Content in Litchi Pulp to Foliar Calcium Fertilizer Treatment. Journal of the American Society for Horticultural Science, 2023, 148, 9-20.	0.5	0
5109	Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in Acer palmatum. International Journal of Biological Macromolecules, 2023, 227, 93-104.	3.6	4
5110	New Papiliotrema laurentii UFV-1 strains with improved acetic acid tolerance selected by adaptive laboratory evolution. Fungal Genetics and Biology, 2023, 164, 103765.	0.9	2
5111	Phylogeny Trees asÂaÂTool toÂCompare Inference Algorithms ofÂOrthologs. Lecture Notes in Computer Science, 2022, , 128-139.	1.0	0
5112	First Report and Comparative Genomic Analysis of Mycoplasma capricolum subsp. capricolum HN-B in Hainan Island, China. Microorganisms, 2022, 10, 2298.	1.6	0
5113	Chromosome-Level Genome Assembly and Multi-Omics Dataset Provide Insights into Isoflavone and Puerarin Biosynthesis in Pueraria lobata (Wild.) Ohwi. Biomolecules, 2022, 12, 1731.	1.8	0
5114	Evolutionary Diversity of Dus2 Enzymes Reveals Novel Structural and Functional Features among Members of the RNA Dihydrouridine Synthases Family. Biomolecules, 2022, 12, 1760.	1.8	0
5115	Genomic basis of the giga-chromosomes and giga-genome of tree peony Paeonia ostii. Nature Communications, 2022, 13, .	5.8	16
5116	Comparative Genomics Reveal the Utilization Ability of Variable Carbohydrates as Key Genetic Features of Listeria Pathogens in Their Pathogenic Lifestyles. Pathogens, 2022, 11, 1430.	1.2	1

#	ARTICLE	IF	CITATIONS
5117	Vaginal microbiome-host interactions modeled in a human vagina-on-a-chip. Microbiome, 2022, 10, .	4.9	35
5119	The first genome sequence of Phomopsis vexans: a fungal pathogen causing Phomopsis blight in eggplant. , 0, , .		1
5120	A new order, Entrophosporales, and three new Entrophospora species in Glomeromycota. Frontiers in Microbiology, 0, 13, .	1.5	16
5121	Phylogenomics and the flowering plant tree of life. Journal of Integrative Plant Biology, 2023, 65, 299-323.	4.1	25
5122	Identification of Novel Bile Salt-Tolerant Genes in Lactobacillus Using Comparative Genomics and Its Application in the Rapid Screening of Tolerant Strains. Microorganisms, 2022, 10, 2371.	1.6	4
5126	A draft genome of the medicinal plant Cremastra appendiculata (D. Don) provides insights into the colchicine biosynthetic pathway. Communications Biology, 2022, 5, .	2.0	4
5128	Different Effects of Different Lactobacillus acidophilus Strains on DSS-Induced Colitis. International Journal of Molecular Sciences, 2022, 23, 14841.	1.8	4
5129	Comparative genomics of five <i>Valsa</i> species gives insights on their pathogenicity evolution. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	0
5130	Comparative Genomics for Evolutionary Cell Biology Using AMOEBAE: Understanding the Golgi and Beyond. Methods in Molecular Biology, 2023, , 431-452.	0.4	7
5131	Linolenic Acid-Derived Oxylipins Inhibit Aflatoxin Biosynthesis in <i>Aspergillus flavus</i> through Activation of Imizoquin Biosynthesis. Journal of Agricultural and Food Chemistry, 2022, 70, 15928-15944.	2.4	1
5132	The draft genome of Andean Rhodopseudomonas sp. strain AZUL predicts genome plasticity and adaptation to chemical homeostasis. BMC Microbiology, 2022, 22, .	1.3	0
5133	Molecular evolution and signatures of selective pressures on Bos, focusing on the Nelore breed (Bos) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	0
5134	Actin cytoskeleton and complex cell architecture in an Asgard archaeon. Nature, 2023, 613, 332-339.	13.7	55
5135	Whole-genome analysis revealed the growth-promoting mechanism of endophytic bacterial strain Q2H1 in potato plants. Frontiers in Microbiology, 0, 13, .	1.5	4
5136	Karyotype evolution of the Asterids insights from the first genome sequences of the family Cornaceae. DNA Research, 2023, 30, .	1.5	2
5137	A highly quality genome sequence of <i>Penicillium oxalicum</i> species isolated from the root of <i>Ixora chinensis</i> in Vietnam. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	1
5138	Transcriptome Analysis on the Underlying Physiological Mechanism of Calcium and Magnesium Resolving â€œSugar Recedingâ€•in â€˜Feizixiaoâ€™ Litchi Pulp. Horticulturae, 2022, 8, 1197.	1.2	0
5139	Jack of all trades: Genome assembly of Wild Jack and comparative genomics of Artocarpus. Frontiers in Plant Science, 0, 13, .	1.7	1

#	ARTICLE	IF	CITATIONS
5140	Syringa oblata genome provides new insights into molecular mechanism of flower color differences among individuals and biosynthesis of its flower volatiles. Frontiers in Plant Science, 0, 13, .	1.7	0
5141	The Sugar Metabolic Model of Aspergillus niger Can Only Be Reliably Transferred to Fungi of Its Phylum. Journal of Fungi (Basel, Switzerland), 2022, 8, 1315.	1.5	6
5142	Differences in genetic flux in invasive Streptococcus pneumoniae associated with bacteraemia and meningitis. Heliyon, 2022, 8, e12229.	1.4	0
5144	High-quality genome of Diaphanosoma dubium provides insights into molecular basis of its broad ecological adaptation. IScience, 2023, 26, 106006.	1.9	0
5145	A chromosome-level genome assembly of the<i>Henosepilachna vigintioctomaculata</i>provides insights into the evolution of ladybird beetles. DNA Research, 2023, 30, .	1.5	2
5146	Biased mutations and gene losses underlying diploidization of the tetraploid broomcorn millet genome. Plant Journal, 2023, 113, 787-801.	2.8	4
5147	Sipunculus nudus genome provides insights into evolution of spiralian phyla and development. Frontiers in Marine Science, 0, 9, .	1.2	1
5148	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
5150	Comprehensive analysis of 84 Faecalibacterium prausnitzii strains uncovers their genetic diversity, functional characteristics, and potential risks. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	6
5151	Single-cell transcriptomics unveils xylem cell development and evolution. Genome Biology, 2023, 24, .	3.8	24
5152	A chromosomeâ€level genome assembly of radish (<i>Raphanus sativus</i> L.) reveals insights into genome adaptation and differential bolting regulation. Plant Biotechnology Journal, 2023, 21, 990-1004.	4.1	14
5153	Legionella maioricensis sp. nov., a new species isolated from the hot water distribution systems of a hospital and a shopping center during routine sampling. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	3
5154	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort (Oenanthe sinensis). Industrial Crops and Products, 2023, 193, 116203.	2.5	7
5155	Phylogenomic resolution of order- and family-level monocot relationships using 602 single-copy nuclear genes and 1375 BUSCO genes. Frontiers in Plant Science, 0, 13, .	1.7	10
5156	Phylotranscriptomic Analyses of Mycoheterotrophic Monocots Show a Continuum of Convergent Evolutionary Changes in Expressed Nuclear Genes From Three Independent Nonphotosynthetic Lineages. Genome Biology and Evolution, 2023, 15, .	1.1	5
5157	Genomic insight into Myroides oncorhynchi sp. nov., a new member of the Myroides genus, isolated from the internal organ of rainbow trout (Oncorhynchus mykiss). Antonie Van Leeuwenhoek, 2023, 116, 291-302.	0.7	1
5158	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
5159	The Chromosome-Scale Genomes of Exserohilum rostratum and Bipolaris zeicola Pathogenic Fungi Causing Rice Spikelet Rot Disease. Journal of Fungi (Basel, Switzerland), 2023, 9, 177.	1.5	1

#	Article	IF	Citations
5161	PlantTribes2: Tools for comparative gene family analysis in plant genomics. Frontiers in Plant Science, 0, 13, .	1.7	5
5162	Population genetic analysis of the microsporidium <i>Ordospora colligata</i> reveals the role of natural selection and phylogeography on its extremely compact and reduced genome. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	3
5163	A Robust Methodology for Assessing Homoeolog-Specific Expression. Methods in Molecular Biology, 2023, , 251-258.	0.4	0
5164	Isolation of vB_AsaM_LPM4 reveals the dynamics of Prophage 3 in Aeromonas salmonicida subsp. salmonicida. Archives of Virology, 2023, 168, .	0.9	1
5166	Characterization and genome-wide sequence analysis of an ectomycorrhizal fungus Pisolithus albus, a potential source for reclamation of degraded lands. 3 Biotech, 2023, 13, .	1.1	1
5170	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. Journal of Advanced Research, 2024, 56, 15-29.	4.4	3
5171	Analyses of a chromosome-scale genome assembly reveal the origin and evolution of cultivated chrysanthemum. Nature Communications, 2023, 14, .	5.8	25
5173	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
5174	Chromosome-level genome of the bean bug Megacopta cribraria in native range, provides insights into adaptation and pest management. International Journal of Biological Macromolecules, 2023, 237, 123989.	3.6	0
5175	Phylogenomic analyses of Camellia support reticulate evolution among major clades. Molecular Phylogenetics and Evolution, 2023, 182, 107744.	1.2	3
5176	Seeing is believing: Understanding functions of NPR1 and its paralogs in plant immunity through cellular and structural analyses. Current Opinion in Plant Biology, 2023, 73, 102352.	3.5	7
5177	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of Poncirus polyandra. Genomics, 2023, 115, 110617.	1.3	1
5178	The Populus koreana genome provides insights into the biosynthesis of plant aroma. Industrial Crops and Products, 2023, 197, 116453.	2.5	1
5179	Sugars and sucrose transporters in pollinia of <i>Phalaenopsis aphrodite</i> (<i>Orchidaceae</i>). Journal of Experimental Botany, 2023, 74, 2556-2571.	2.4	1
5180	Apical Secretory Glycoprotein Complex Contributes to Cell Attachment and Entry by Cryptosporidium parvum. MBio, 2023, 14, .	1.8	1
5181	The chromosome-level genome and key genes associated with mud-dwelling behavior and adaptations of hypoxia and noxious environments in loach (Misgurnus anguillicaudatus). BMC Biology, 2023, 21, .	1.7	2
5182	Inference of Ancient Polyploidy from Genomic Data. Methods in Molecular Biology, 2023, , 3-18.	0.4	2
5183	Genome-based reclassification of Anoxybacillus salavatliensis Cihan et al. 2011 as a later heterotypic synonym of Anoxybacillus gonensis Belduz et al. 2003. Antonie Van Leeuwenhoek, 2023, 116, 415-423.	0.7	1

#	Article	IF	Citations
5184	Chromosome-Level Assembly of Flowering Cherry (Prunus campanulata) Provides Insight into Anthocyanin Accumulation. Genes, 2023, 14, 389.	1.0	1
5185	PANAS: Pipeline and a Case Study to Obtain Synonymous and Nonsynonymous Substitution Rates in Genes of Platyhelminthes. Comparative Parasitology, 2023, 90, .	0.0	1
5186	Interplay between transcriptional regulators and <scp>VapBC toxinâ€"antitoxin</scp> loci during thermal stress response in extremely thermoacidophilic archaea. Environmental Microbiology, 2023, 25, 1200-1215.	1.8	4
5187	Genome and haplotype provide insights into the population differentiation and breeding improvement of Gossypium barbadense. Journal of Advanced Research, 2023, 54, 15-27.	4.4	2
5188	The genome of Magnolia hypoleuca provides a new insight into cold tolerance and the evolutionary position of magnoliids. Frontiers in Plant Science, 0, 14, .	1.7	3
5189	Genome assembly, resequencing and genomeâ€wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry. Plant Journal, 2023, 114, 519-533.	2.8	4
5190	A gap-free and haplotype-resolved lemon genome provides insights into flavor synthesis and huanglongbing (HLB) tolerance. Horticulture Research, 2023, 10, .	2.9	6
5191	An improved reference genome for Trifolium subterraneum L. provides insight into molecular diversity and intra-specific phylogeny. Frontiers in Plant Science, 0, 14, .	1.7	5
5192	Physiological and genomic insights into abiotic stress of halophilic archaeon Natrinema altunense 4.1R isolated from a saline ecosystem of Tunisian desert. Genetica, 2023, 151, 133-152.	0.5	2
5193	Genomic diversity in Fructobacillus spp. isolated from fructose-rich niches. PLoS ONE, 2023, 18, e0281839.	1.1	3
5194	Identification and Phylogenetic Analysis of the R2R3-MYB Subfamily in Brassica napus. Plants, 2023, 12, 886.	1.6	4
5195	OrthoPhy: A Program to Construct Ortholog Data Sets Using Taxonomic Information. Genome Biology and Evolution, 2023, 15, .	1.1	0
5196	Genomic characterization of coexisting anatoxin-producing and non-toxigenic Microcoleus subspecies in benthic mats from the Wolastoq, New Brunswick, Canada. Harmful Algae, 2023, 124, 102405.	2.2	6
5197	Challenges and opportunities of strain diversity in gut microbiome research. Frontiers in Microbiology, 0, 14, .	1.5	4
5198	Comparative Genomic Analysis and Physiological Properties of Limosilactobacillus fermentum SMFM2017-NK2 with Ability to Inflammatory Bowel Disease. Microorganisms, 2023, 11, 547.	1.6	1
5199	A chromosome-level genome assembly for Erianthus fulvus provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. Plant Communications, 2023, 4, 100562.	3.6	4
5200	Subspecies-level genome comparison of Lactobacillus delbrueckii. Scientific Reports, 2023, 13, .	1.6	7
5201	Transcript annotation of Chinese sturgeon (Acipenser sinensis) using Iso-seq and RNA-seq data. Scientific Data, 2023, 10, .	2.4	2

#	ARTICLE	IF	CITATIONS
5202	Synteny Identifies Reliable Orthologs for Phylogenomics and Comparative Genomics of the Brassicaceae. Genome Biology and Evolution, 2023, 15, .	1.1	3
5203	Genomic characterization and molecular dating of the novel bacterium Permianibacter aggregans HW001T, which originated from Permian ground water. Marine Life Science and Technology, 2023, 5, 12-27.	1.8	0
5204	ProteInfer, deep neural networks for protein functional inference. ELife, 0, 12, .	2.8	31
5205	Draft Genome and Biological Characteristics of Fusarium solani and Fusarium oxysporum Causing Black Rot in Gastrodia elata. International Journal of Molecular Sciences, 2023, 24, 4545.	1.8	0
5207	Chromosomeâ€level reference genome of <i>Tetrastigma hemsleyanum</i> (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. Plant Journal, 2023, 114, 805-823.	2.8	5
5208	De novo assembly of a chromosome-level reference genome of the ornamental butterfly Sericinus montelus based on nanopore sequencing and Hi-C analysis. Frontiers in Genetics, 0, 14, .	1.1	0
5209	The giant diploid faba genome unlocks variation in a global protein crop. Nature, 2023, 615, 652-659.	13.7	40
5210	Chromosome-level genome assembly of <i>Phrynocephalus forsythii</i> using third-generation DNA sequencing and Hi-C analysis. DNA Research, 2023, 30, .	1.5	0
5211	A phylogenomic analysis of Limosilactobacillus reuteri reveals ancient and stable evolutionary relationships with rodents and birds and zoonotic transmission to humans. BMC Biology, 2023, 21, .	1.7	8
5213	Revealing evolution of tropane alkaloid biosynthesis by analyzing two genomes in the Solanaceae family. Nature Communications, 2023, 14, .	5.8	12
5214	Large-Scale Identification of Known and Novel RRNPP Quorum-Sensing Systems by RRNPP_Detector Captures Novel Features of Bacterial, Plasmidic, and Viral Coevolution. Molecular Biology and Evolution, 2023, 40, .	3.5	1
5216	Genomic Analysis of the Deep-Sea Bacterium Shewanella sp. MTB7 Reveals Backgrounds Related to Its Deep-Sea Environment Adaptation. Microorganisms, 2023, 11, 798.	1.6	1
5217	Toward novel treatment against filariasis: Insight into genome-wide co-evolutionary analysis of filarial nematodes and Wolbachia. Frontiers in Microbiology, 0, 14, .	1.5	0
5219	Rapid adaptations of Legionella pneumophila to the human host. Microbial Genomics, 2023, 9, .	1.0	0
5220	Comparative Genomics Analysis of Ganoderma Orthologs Involved in Plant-Pathogenesis. Forests, 2023, 14, 653.	0.9	3
5221	Genomeâ€wide comparative analysis between <i>Cranoglanis bouderius</i> and <i>Pangasianodon hypophthalmus</i>: Reveal the genes related to resistance to lowâ€temperature stress. Journal of the World Aquaculture Society, 2023, 54, 1367-1385.	1.2	1
5224	Nuclear phylogeny and insights into whole-genome duplications and reproductive development of Solanaceae plants. Plant Communications, 2023, 4, 100595.	3.6	8
5226	Characterization and Genome Analysis of Cladobotryum mycophilum, the Causal Agent of Cobweb Disease of Morchella sextelata in China. Journal of Fungi (Basel, Switzerland), 2023, 9, 411.	1.5	1

#	Article	IF	Citations
5228	Highly contiguous genomes of human clinical isolates of Giardia duodenalis reveal assemblage- and sub-assemblage-specific presenceâ€“absence variation in protein-coding genes. Microbial Genomics, 2023, 9, .	1.0	1
5230	LncRNA-encoded peptides: the case of the lncRNA gene located downstream of EIN2. Functional and Integrative Genomics, 2023, 23, .	1.4	0
5232	Microsporeâ€expressed <scp>SCULP1</scp> is required for <i>p</i>â€coumaroylation of sporopollenin, exine integrity, and pollen development in wheat. New Phytologist, 2023, 239, 102-115.	3.5	0
5233	Gene loss during a transition to multicellularity. Scientific Reports, 2023, 13, .	1.6	3
5235	Chromosome-scale genome assembly of <i>Prunus pusilliflora</i> provides novel insights into genome evolution, disease resistance, and dormancy release in <i>Cerasus</i> L<i>.</i>. Horticulture Research, 0, , .	2.9	1
5236	The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics. GigaScience, 2022, 12, .	3.3	3
5237	Monkeypox virus: phylogenomics, hostâ€“pathogen interactome and mutational cascade. Microbial Genomics, 2023, 9, .	1.0	2
5239	Chromosome-level genome assembly of <i>Salvia miltiorrhiza</i> with orange roots uncovers the role of Sm2OGD3 in catalyzing 15,16-dehydrogenation of tanshinones. Horticulture Research, 2023, 10, .	2.9	4
5240	Flagellar Genes Are Associated with the Colonization Persistence Phenotype of the Drosophila melanogaster Microbiota. Microbiology Spectrum, 2023, 11, .	1.2	3
5241	Genome Organization of Four Brazilian Xanthomonas albilineans Strains Does Not Correlate with Aggressiveness. Microbiology Spectrum, 0, , .	1.2	1
5242	Systematical Characterization of the AT-Hook Gene Family in Juglans regia L. and the Functional Analysis of the JrAHL2 in Flower Induction and Hypocotyl Elongation. International Journal of Molecular Sciences, 2023, 24, 7244.	1.8	0
5245	Origin and diversification of a Himalayan orchid genus Pleione. Molecular Phylogenetics and Evolution, 2023, 184, 107797.	1.2	0
5309	Inferring Clusters ofÂOrthologous andÂParalogous Transcripts. Lecture Notes in Computer Science, 2023, , 19-34.	1.0	0
5349	Bioinformatics study to unravel the role of rhizobiome to biologically control the pathogens in vegetables. , 2023, , 267-284.		0
5356	A Transferable Machine Learning Framework for Predicting Transcriptional Responses of Genes Across Species. Methods in Molecular Biology, 2023, , 361-379.	0.4	0
5376	Approaches to increase the validity of gene family identification using manual homology search tools. Genetica, 0, , .	0.5	0