

HMMER web server: interactive sequence similarity search

Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
3	Finding Protein and Nucleotide Similarities with FASTA. Current Protocols in Bioinformatics, 2003, 4, Unit3.9.	25.8	55
4	Computational approaches to selecting and optimising targets for structural biology. Methods, 2011, 55, 3-11.	3.8	7
5	Complete Genome Sequence of the Soybean Symbiont Bradyrhizobium japonicum Strain USDA6T. Genes, 2011, 2, 763-787.	2.4	108
6	Evolution and Quantitative Comparison of Genome-Wide Protein Domain Distributions. Genes, 2011, 2, 912-924.	2.4	9
7	Context-dependent conservation of DNA methyltransferases in bacteria. Nucleic Acids Research, 2012, 40, 7066-7073.	14.5	60
8	Side-chain rotamer changes upon ligand binding: common, crucial, correlate with entropy and rearrange hydrogen bonding. Bioinformatics, 2012, 28, i423-i430.	4.1	61
9	Characterization and Prediction of Protein Phosphorylation Hotspots in Arabidopsis thaliana. Frontiers in Plant Science, 2012, 3, 207.	3.6	22
10	Whole Genome Analysis of Leptospira icterohaemolyticum Provides Insight into Leptospiral Evolution and Pathogenicity. PLoS Neglected Tropical Diseases, 2012, 6, e1853.	3.0	60
11	A common ancestry for BAP1 and Uch37 regulators. Bioinformatics, 2012, 28, 1953-1956.	4.1	48
12	TIGRFAMs and Genome Properties in 2013. Nucleic Acids Research, 2012, 41, D387-D395.	14.5	484
13	ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria. Nucleic Acids Research, 2012, 40, D621-D626.	14.5	206
14	Reannotation of the Corynebacterium diphtheriae NCTC13129 genome as a new approach to studying gene targets connected to virulence and pathogenicity in diphtheria. Open Access Bioinformatics, 2012, , 1.	0.9	6
15	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. Nucleic Acids Research, 2012, 41, D483-D489.	14.5	238
16	Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. Briefings in Bioinformatics, 2012, 13, 696-710.	6.5	70
17	Visualizing the protein sequence universe. , 2012, , .		3
18	Enriching miRNA binding site specificity with sequence profile based filtering of 3'-UTR region of mRNA. , 2012, , .		0
19	The RCSB Protein Data Bank: new resources for research and education. Nucleic Acids Research, 2012, 41, D475-D482.	14.5	418
20	Targeting the ERAD pathway via inhibition of signal peptide peptidase for antiparasitic therapeutic design. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21486-21491.	7.1	89

#	ARTICLE	IF	CITATIONS
21	A machine learning framework for trait based genomics. , 2012, , .		3
22	BIPS: BIANA Interolog Prediction Server. A tool for proteinâ€“protein interaction inference. Nucleic Acids Research, 2012, 40, W147-W151.	14.5	57
23	Evolutionary History and Genome Organization of DUF1220 Protein Domains. G3: Genes, Genomes, Genetics, 2012, 2, 977-986.	1.8	69
24	BioJava: an open-source framework for bioinformatics in 2012. Bioinformatics, 2012, 28, 2693-2695.	4.1	160
25	Sequence, Structure, and Evolution of Cellulases in Glycoside Hydrolase Family 48. Journal of Biological Chemistry, 2012, 287, 41068-41077.	3.4	32
26	BioShell Threader: protein homology detection based on sequence profiles and secondary structure profiles. Nucleic Acids Research, 2012, 40, W257-W262.	14.5	10
27	Draft Genome Sequence of Staphylococcus aureus ST672, an Emerging Disease Clone from India. Journal of Bacteriology, 2012, 194, 6946-6947.	2.2	8
29	Evolutionary adaptation of plant annexins has diversified their molecular structures, interactions and functional roles. New Phytologist, 2012, 196, 695-712.	7.3	145
30	Homology Modeling: Generating Structural Models to Understand Protein Function and Mechanism. Biological and Medical Physics Series, 2012, , 97-116.	0.4	9
31	Localisation of a family of complexâ€“forming Î²â€“barrels in the <i>T. vaginalis</i> hydrogenosomal membrane. FEBS Letters, 2012, 586, 4038-4045.	2.8	4
33	Distant plant homologues: donâ€™t throw out the baby. Trends in Plant Science, 2012, 17, 126-128.	8.8	3
34	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.	3.4	132
35	Reference databases for taxonomic assignment in metagenomics. Briefings in Bioinformatics, 2012, 13, 682-695.	6.5	82
36	Diversity, classification and function of the plant protein kinase superfamily. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2619-2639.	4.0	277
37	Taxonomic binning of metagenome samples generated by next-generation sequencing technologies. Briefings in Bioinformatics, 2012, 13, 646-655.	6.5	98
38	Fungal Smn and Spf30 homologues are mainly present in filamentous fungi and genomes with many introns: Implications for spinal muscular atrophy. Gene, 2012, 491, 135-141.	2.2	11
39	Evolution of prokaryotic homologues of the eukaryotic SEFIR protein domain. Gene, 2012, 492, 160-166.	2.2	12
40	Profile-based short linear protein motif discovery. BMC Bioinformatics, 2012, 13, 104.	2.6	14

#	ARTICLE	IF	CITATIONS
41	Identifying structural domains of proteins using clustering. BMC Bioinformatics, 2012, 13, 286.	2.6	11
42	The mammalian PYHIN gene family: Phylogeny, evolution and expression. BMC Evolutionary Biology, 2012, 12, 140.	3.2	168
43	Re-annotation of the CAZy genes of <i>Trichoderma reesei</i> and transcription in the presence of lignocellulosic substrates. Microbial Cell Factories, 2012, 11, 134.	4.0	173
44	Molecular characterization of the hexose transporter gene in benzimidazole resistant and susceptible populations of <i>Trypanosoma cruzi</i> . Parasites and Vectors, 2012, 5, 161.	2.5	11
45	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. Advances in Botanical Research, 2012, 64, 383-427.	1.1	11
46	DADP: the database of anuran defense peptides. Bioinformatics, 2012, 28, 1406-1407.	4.1	163
47	A Galaxy Workflow for the Functional Annotation of Metagenomic Samples. Lecture Notes in Computer Science, 2012, , 247-253.	1.3	3
48	Phylogenetic Approaches to Natural Product Structure Prediction. Methods in Enzymology, 2012, 517, 161-182.	1.0	35
49	Using protein-domain information for multiple sequence alignment. , 2012, , .		2
50	New trends in peptide-based anti-biofilm strategies: a review of recent achievements and bioinformatic approaches. Biofouling, 2012, 28, 1033-1061.	2.2	128
51	MicroRNAs and essential components of the microRNA processing machinery are not encoded in the genome of the ctenophore <i>Mnemiopsis leidyi</i> . BMC Genomics, 2012, 13, 714.	2.8	43
52	PIPS: Pathogenicity Island Prediction Software. PLoS ONE, 2012, 7, e30848.	2.5	70
53	Genome-Wide Identification and Mapping of NBS-Encoding Resistance Genes in <i>Solanum tuberosum</i> Group Phureja. PLoS ONE, 2012, 7, e34775.	2.5	107
54	Classification of HIV-1 Sequences Using Profile Hidden Markov Models. PLoS ONE, 2012, 7, e36566.	2.5	7
55	Oligonucleotide Primers for Targeted Amplification of Single-Copy Nuclear Genes in Apocritan Hymenoptera. PLoS ONE, 2012, 7, e39826.	2.5	10
56	Large-Scale Transcriptome Analysis of Retroelements in the Migratory Locust, <i>Locusta migratoria</i> . PLoS ONE, 2012, 7, e40532.	2.5	30
57	Functional and Structural Comparison of Pyrrolnitrin- and Iprodione-Induced Modifications in the Class III Histidine-Kinase Bos1 of <i>Botrytis cinerea</i> . PLoS ONE, 2012, 7, e42520.	2.5	62
58	Unique Features of Odorant-Binding Proteins of the Parasitoid Wasp <i>Nasonia vitripennis</i> Revealed by Genome Annotation and Comparative Analyses. PLoS ONE, 2012, 7, e43034.	2.5	62

#	ARTICLE	IF	CITATIONS
59	Genome-Wide Identification and Analysis of MAPK and MAPKK Gene Families in <i>Brachypodium distachyon</i> . PLoS ONE, 2012, 7, e46744.	2.5	99
60	Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 2012, 13, 711-727.	6.5	150
61	Accurate de novo structure prediction of large transmembrane protein domains using fragment-assembly and correlated mutation analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1540-7.	7.1	176
62	Identification of antimicrobial peptides from teleosts and anurans in expressed sequence tag databases using conserved signal sequences. FEBS Journal, 2012, 279, 724-736.	4.7	23
63	The use of evolutionary patterns in protein annotation. Current Opinion in Structural Biology, 2012, 22, 316-325.	5.7	28
64	PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for examining phage diversity. BMC Bioinformatics, 2012, 13, 37.	2.6	21
65	Predict impact of single amino acid change upon protein structure. BMC Genomics, 2012, 13, S4.	2.8	48
66	De novo prediction of the genomic components and capabilities for microbial plant biomass degradation from (meta-)genomes. Biotechnology for Biofuels, 2013, 6, 24.	6.2	18
67	Identification of novel arthropod vector G protein-coupled receptors. Parasites and Vectors, 2013, 6, 150.	2.5	9
68	Genome-Wide Analysis of the AP2/ERF Gene Family in <i>Prunus mume</i> . Plant Molecular Biology Reporter, 2013, 31, 741-750.	1.8	77
69	FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. Mitochondrion, 2013, 13, 357-359.	3.4	3
70	Accurate and universal delineation of prokaryotic species. Nature Methods, 2013, 10, 881-884.	19.0	311
71	A novel <i>hAT</i> element in <i>Bombyx mori</i> and <i>hodnius prolixus</i> : its relationship with miniature inverted repeat transposable elements ( <i>MITEs</i> ) and horizontal transfer. Insect Molecular Biology, 2013, 22, 584-596.	2.0	15
72	Tam41 Is a CDP-Diacylglycerol Synthase Required for Cardiolipin Biosynthesis in Mitochondria. Cell Metabolism, 2013, 17, 709-718.	16.2	135
73	Gene Loss and Adaptation to Hominids Underlie the Ancient Origin of HIV-1. Cell Host and Microbe, 2013, 14, 85-92.	11.0	93
74	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. Nature, 2013, 500, 350-353.	27.8	466
75	An automated graphics tool for comparative genomics: the Coulson plot generator. BMC Bioinformatics, 2013, 14, 141.	2.6	30
76	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. BMC Evolutionary Biology, 2013, 13, 33.	3.2	123

#	ARTICLE	IF	CITATIONS
77	Evolutionary origins, molecular cloning and expression of carotenoid hydroxylases in eukaryotic photosynthetic algae. BMC Genomics, 2013, 14, 457.	2.8	31
78	Variant surface antigens of malaria parasites: functional and evolutionary insights from comparative gene family classification and analysis. BMC Genomics, 2013, 14, 427.	2.8	65
79	Identification and analysis of MKK and MPK gene families in canola ( <i>Brassica napus</i> L.). BMC Genomics, 2013, 14, 392.	2.8	75
80	Genome-wide analysis of histone modifiers in tomato: gaining an insight into their developmental roles. BMC Genomics, 2013, 14, 57.	2.8	125
81	phiBIOTICS: catalogue of therapeutic enzybiotics, relevant research studies and practical applications. BMC Microbiology, 2013, 13, 53.	3.3	20
82	The pattern of Phosphate transporter 1 genes evolutionary divergence in <i>Glycine max</i> L.. BMC Plant Biology, 2013, 13, 48.	3.6	72
83	Designing and benchmarking the MULTICOM protein structure prediction system. BMC Structural Biology, 2013, 13, 2.	2.3	25
84	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. Human Genetics, 2013, 132, 899-911.	3.8	13
85	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. Biotechnology Advances, 2013, 31, 1109-1119.	11.7	23
86	Comparative analysis of <i>Leishmania</i> exoproteomes: Implication for hostâ€“pathogen interactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2653-2662.	2.3	8
87	Identification of hidden relationships from the coupling of Hydrophobic Cluster Analysis and Domain Architecture information. Bioinformatics, 2013, 29, 1726-1733.	4.1	29
89	A phenylalanine rotameric switch for signal-state control in bacterial chemoreceptors. Nature Communications, 2013, 4, 2881.	12.8	37
90	Viral pathogen discovery. Current Opinion in Microbiology, 2013, 16, 468-478.	5.1	190
91	Making automated multiple alignments of very large numbers of protein sequences. Bioinformatics, 2013, 29, 989-995.	4.1	49
92	Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and Oomycetes. BMC Genomics, 2013, 14, S7.	2.8	72
93	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . BMC Genomics, 2013, 14, 664.	2.8	99
94	KEGG orthology-based annotation of the predicted proteome of <i>Acropora digitifera</i> : ZoophyteBase - an open access and searchable database of a coral genome. BMC Genomics, 2013, 14, 509.	2.8	51
95	Molecular epidemiology of <i>Plasmodium vivax</i> in Latin America: polymorphism and evolutionary relationships of the circumsporozoite gene. Malaria Journal, 2013, 12, 243.	2.3	27

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96	Spatial expression of transcription factors in Drosophila embryonic organ development. <i>Genome Biology</i> , 2013, 14, R140.	9.6	135
97	Probabilistic grammatical model for helix-helix contact site classification. <i>Algorithms for Molecular Biology</i> , 2013, 8, 31.	1.2	6
98	A new computational strategy for predicting essential genes. <i>BMC Genomics</i> , 2013, 14, 910.	2.8	34
99	Exploring the "dark matter" of a mammalian proteome by protein structure and function modeling. <i>Proteome Science</i> , 2013, 11, 47.	1.7	9
100	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in <i>Phytophthora sojae</i> . <i>BMC Genomics</i> , 2013, 14, 839.	2.8	30
101	Evolution and dynamics of megaplasmiids with genome sizes larger than 100 kb in the <i>Bacillus cereus</i> group. <i>BMC Evolutionary Biology</i> , 2013, 13, 262.	3.2	36
102	Identification of the type II cytochrome c maturation pathway in anammox bacteria by comparative genomics. <i>BMC Microbiology</i> , 2013, 13, 265.	3.3	23
103	The vertebrate ancestral repertoire of visual opsins, transducin alpha subunits and oxytocin/vasopressin receptors was established by duplication of their shared genomic region in the two rounds of early vertebrate genome duplications. <i>BMC Evolutionary Biology</i> , 2013, 13, 238.	3.2	111
104	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	1.0	28
105	Prediction of enzymatic activity of proteins based on structural and functional domains. , 2013, , .		1
106	Protein Substrates of a Novel Secretion System Are Numerous in the Bacteroidetes Phylum and Have in Common a Cleavable C-Terminal Secretion Signal, Extensive Post-Translational Modification, and Cell-Surface Attachment. <i>Journal of Proteome Research</i> , 2013, 12, 4449-4461.	3.7	120
107	<i>Bacillus thuringiensis</i> Metalloproteinase Bmp1 Functions as a Nematicidal Virulence Factor. <i>Applied and Environmental Microbiology</i> , 2013, 79, 460-468.	3.1	46
108	Ferredoxin:thioredoxin reductase (FTR) links the regulation of oxygenic photosynthesis to deeply rooted bacteria. <i>Planta</i> , 2013, 237, 619-635.	3.2	31
109	Genes expressed by the biological control bacterium <i>Pseudomonas protegens</i> on seed surfaces under the control of the global regulators <i>GacA</i> and <i>RpoS</i> . <i>Environmental Microbiology</i> , 2013, 15, 716-735.	3.8	41
110	Using comparative genomics to uncover new kinds of protein-based metabolic organelles in bacteria. <i>Protein Science</i> , 2013, 22, 179-195.	7.6	108
111	Identification of Immunity-related Genes in Arabidopsis and Cassava Using Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 345-353.	6.9	8
112	Development of an ELISA for the quantification of the C-terminal decapeptide prothymosin $\pm$ (100-109) in sera of mice infected with bacteria. <i>Journal of Immunological Methods</i> , 2013, 395, 54-62.	1.4	10
113	Two-component signal transduction in <i>Agaricus bisporus</i> : A comparative genomic analysis with other basidiomycetes through the web-based tool BASID2CS. <i>Fungal Genetics and Biology</i> , 2013, 55, 77-84.	2.1	6

#	ARTICLE	IF	CITATIONS
114	Hieranoid: Hierarchical Orthology Inference. Journal of Molecular Biology, 2013, 425, 2072-2081.	4.2	38
115	Selecting age-related functional characteristics in the human gut microbiome. Microbiome, 2013, 1, 2.	11.1	45
116	Using <scp>I</scp>llumina next generation sequencing technologies to sequence multigene families in <i>de novo</i> species. Molecular Ecology Resources, 2013, 13, 510-521.	4.8	16
117	Untangling the transcriptome from fungus-infected plant tissues. Gene, 2013, 519, 238-244.	2.2	6
118	Using Analyses of Amino Acid Coevolution to Understand Protein Structure and Function. Methods in Enzymology, 2013, 523, 191-212.	1.0	13
119	Genome-wide identification, molecular evolution and expression analyses of the phospholipase D gene family in three Rosaceae species. Scientia Horticulturae, 2013, 153, 13-21.	3.6	20
120	The discovery of Foxl2 paralogs in chondrichthyan, coelacanth and tetrapod genomes reveals an ancient duplication in vertebrates. Heredity, 2013, 111, 57-65.	2.6	22
121	A systematic quantitative proteomic examination of multidrug resistance in Acinetobacter baumannii. Journal of Proteomics, 2013, 84, 17-39.	2.4	44
122	Genome mining for methanobactins. BMC Biology, 2013, 11, 17.	3.8	64
123	Evidence for the widespread distribution of CRISPR-Cas system in the Phylum<i>Cyanobacteria</i>. RNA Biology, 2013, 10, 687-693.	3.1	86
124	Identification of Cyclic Nucleotide Gated Channels Using Regular Expressions. Methods in Molecular Biology, 2013, 1016, 207-224.	0.9	23
125	Deep sequencing of non-ribosomal peptide synthetases and polyketide synthases from the microbiomes of Australian marine sponges. ISME Journal, 2013, 7, 1842-1851.	9.8	53
126	Comparative Genomics of a Plant-Pathogenic Fungus,<i>Pyrenophora tritici-repentis</i>, Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	1.8	167
127	Pathway Databases: Making Chemical and Biological Sense of the Genomic Data Flood. Chemistry and Biology, 2013, 20, 629-635.	6.0	20
128	<i>In silico</i> study of human aquaporin AQP11 and AQP12 channels. Protein Science, 2013, 22, 455-466.	7.6	32
130	Protein Engineering and Stabilization from Sequence Statistics. Methods in Enzymology, 2013, 523, 237-256.	1.0	25
131	Genome-wide survey and expression analysis of the MADS-box gene family in soybean. Molecular Biology Reports, 2013, 40, 3901-3911.	2.3	60
132	Analysis of a deep transcriptome from the mantle tissue of Patella vulgata Linnaeus (Mollusca:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 230-243.	2.4	53



#	ARTICLE	IF	CITATIONS
134	BioSmalltalk: a pure object system and library for bioinformatics. Bioinformatics, 2013, 29, 2355-2356.	4.1	2
135	Mutagenesis of Individual Pentatricopeptide Repeat Motifs Affects RNA Binding Activity and Reveals Functional Partitioning of <i>Arabidopsis</i> PROTON GRADIENT REGULATION3 Å. Plant Cell, 2013, 25, 3079-3088.	6.6	38
136	Proteolytic activation of Chlamydia trachomatis HTRA is mediated by PDZ1 domain interactions with protease domain loops L3 and LC and beta strand Î²5. Cellular and Molecular Biology Letters, 2013, 18, 522-37.	7.0	10
137	Calciomics: integrative studies of Ca <sup>2+</sup> -binding proteins and their interactomes in biological systems. Metallomics, 2013, 5, 29-42.	2.4	77
138	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. ISME Journal, 2013, 7, 2287-2300.	9.8	113
139	Short tandem repeats in the inhibitory domain of the mineralocorticoid receptor: prediction of a Î²-solenoid structure. BMC Structural Biology, 2013, 13, 17.	2.3	10
140	Type I pyridoxal 5â€²-phosphate dependent enzymatic domains embedded within multimodular nonribosomal peptide synthetase and polyketide synthase assembly lines. BMC Structural Biology, 2013, 13, 26.	2.3	22
141	Small, Smaller, Smallest: The Origins and Evolution of Ancient Dual Symbioses in a Phloem-Feeding Insect. Genome Biology and Evolution, 2013, 5, 1675-1688.	2.5	276
142	BiDaS: a web-based Monte Carlo BioData Simulator based on sequence/feature characteristics. Nucleic Acids Research, 2013, 41, W582-W586.	14.5	7
143	Overexpression of a BAHD Acyltransferase, <i>OsAt10</i> , Alters Rice Cell Wall Hydroxycinnamic Acid Content and Saccharification Å Å. Plant Physiology, 2013, 161, 1615-1633.	4.8	164
144	Comparative genomics in <i>Chlamydomonas</i> and <i>Plasmodium</i> identifies an ancient nuclear envelope protein family essential for sexual reproduction in protists, fungi, plants, and vertebrates. Genes and Development, 2013, 27, 1198-1215.	5.9	87
145	A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. Genome Research, 2013, 23, 1839-1851.	5.5	30
146	Protein signature-based estimation of metagenomic abundances including all domains of life and viruses. Bioinformatics, 2013, 29, 973-980.	4.1	36
147	Analysis of the Sam50 translocase of Excavate organisms supports evolution of divergent organelles from a common endosymbiotic event. Bioscience Reports, 2013, 33, .	2.4	2
148	Assembly of the Type II Secretion System such as Found in Vibrio cholerae Depends on the Novel Pilotin AspS. PLoS Pathogens, 2013, 9, e1003117.	4.7	59
149	The Conserved ADAMTS-like Protein Lonely heart Mediates Matrix Formation and Cardiac Tissue Integrity. PLoS Genetics, 2013, 9, e1003616.	3.5	48
150	A Conserved Helicase Processivity Factor Is Needed for Conjugation and Replication of an Integrative and Conjugative Element. PLoS Genetics, 2013, 9, e1003198.	3.5	44
151	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across Cochliobolus Pathogens. PLoS Genetics, 2013, 9, e1003233.	3.5	232

#	ARTICLE	IF	CITATIONS
152	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. International Journal of Molecular Sciences, 2013, 14, 11444-11483.	4.1	8
153	When parasitic wasps hijacked viruses: genomic and functional evolution of polydnaviruses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130051.	4.0	150
154	Construction and validation of a homology model of the human voltage-gated proton channel hHV1. Journal of General Physiology, 2013, 141, 445-465.	1.9	75
155	Overview of organohalide-respiring bacteria and a proposal for a classification system for reductive dehalogenases. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120322.	4.0	266
156	Genetic Control and Comparative Genomic Analysis of Flowering Time in Setaria (Poaceae). G3: Genes, Genomes, Genetics, 2013, 3, 283-295.	1.8	97
157	Identification and Analysis of a Novel Dimerization Domain Shared by Various Members of c-Jun N-terminal Kinase (JNK) Scaffold Proteins. Journal of Biological Chemistry, 2013, 288, 7294-7304.	3.4	15
158	<i>RAPID omics</i> : a web server for large-scale prediction of protein-RNA interactions. Bioinformatics, 2013, 29, 2928-2930.	4.1	247
159	The Genetic Architecture of Degenerin/Epithelial Sodium Channels in <i>Drosophila</i> . G3: Genes, Genomes, Genetics, 2013, 3, 441-450.	1.8	85
160	Sfr13 is a member of a large family of asymmetrically 1 localized Sfi1-repeat proteins and is important for basal body separation and stability in <i>Tetrahymena thermophila</i> . Journal of Cell Science, 2013, 126, 1659-71.	2.0	14
161	An Experimentally Tested Scenario for the Structural Evolution of Eukaryotic Cys2His2 Zinc Fingers from Eubacterial Ros Homologs. Molecular Biology and Evolution, 2013, 30, 1504-1513.	8.9	23
162	Global analysis of <i>Drosophila</i> Cys2-His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. Genome Research, 2013, 23, 928-940.	5.5	70
163	Phylogenetic Analyses Uncover a Novel Clade of Transferrin in Nonmammalian Vertebrates. Molecular Biology and Evolution, 2013, 30, 894-905.	8.9	13
164	Strategies and molecular tools to fight antimicrobial resistance: resistome, transcriptome, and antimicrobial peptides. Frontiers in Microbiology, 2013, 4, 412.	3.5	51
165	SecReT4: a web-based bacterial type IV secretion system resource. Nucleic Acids Research, 2013, 41, D660-D665.	14.5	100
166	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. Nucleic Acids Research, 2013, 41, 4549-4564.	14.5	108
167	BmTEdb: a collective database of transposable elements in the silkworm genome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat055.	3.0	34
168	Contact potentials via wavelet transform for prediction of subcellular localizations in gram negative bacterial proteins. , 2013, 2013, 643-6.		0
169	Structure and Evolution of Chlorate Reduction Composite Transposons. MBio, 2013, 4, .	4.1	64

#	ARTICLE	IF	CITATIONS
170	DIALIGN at GOBICSâ€”multiple sequence alignment using various sources of external information. Nucleic Acids Research, 2013, 41, W3-W7.	14.5	45
171	PIECE: a database for plant gene structure comparison and evolution. Nucleic Acids Research, 2013, 41, D1159-D1166.	14.5	50
172	Differentiation of <i>Bacillus anthracis</i> , <i>B. cereus</i> , and <i>B. thuringiensis</i> on the Basis of the <i>csaB</i> Gene Reflects Host Source. Applied and Environmental Microbiology, 2013, 79, 3860-3863.	3.1	10
173	The Draft Genome and Transcriptome of <i>Panagrellus redivivus</i> Are Shaped by the Harsh Demands of a Free-Living Lifestyle. Genetics, 2013, 193, 1279-1295.	2.9	57
174	Structural characterization of T7 tail machinery reveals a conserved tubular structure among other <i>Podoviridae</i> family members and suggests a common mechanism for DNA delivery. Bacteriophage, 2013, 3, e27011.	1.9	4
175	Evolutionary cell biology of chromosome segregation: insights from trypanosomes. Open Biology, 2013, 3, 130023.	3.6	70
176	A pipeline of programs for collecting and analyzing group II intron retroelement sequences from GenBank. Mobile DNA, 2013, 4, 28.	3.6	12
177	A comparative hidden Markov model analysis pipeline identifies proteins characteristic of cereal-infecting fungi. BMC Genomics, 2013, 14, 807.	2.8	26
178	Genome sequence of the <i>Litoreibacter arenae</i> type strain (DSM 19593T), a member of the <i>Roseobacter</i> clade isolated from sea sand. Standards in Genomic Sciences, 2013, 9, 117-127.	1.5	8
179	Genome sequence of the reddish-pigmented <i>Rubellimicrobium thermophilum</i> type strain (DSM 16684T), a member of the <i>Roseobacter</i> clade. Standards in Genomic Sciences, 2013, 8, 480-490.	1.5	6
180	A potential source for cellulolytic enzyme discovery and environmental aspects revealed through metagenomics of Brazilian mangroves. AMB Express, 2013, 3, 65.	3.0	40
181	The Complete Genome Sequence of <i>Proteus mirabilis</i> Strain BB2000 Reveals Differences from the <i>P. mirabilis</i> Reference Strain. Genome Announcements, 2013, 1, .	0.8	25
182	MisPred: a resource for identification of erroneous protein sequences in public databases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat053.	3.0	17
183	Complete Genome Sequence of the Thermophilic and Facultatively Chemolithoautotrophic Sulfate Reducer <i>Archaeoglobus sulfaticallidus</i> Strain PM70-1 <sup>T</sup> . Genome Announcements, 2013, 1, .	0.8	8
184	Conserved-residue mutations in Wzy affect O-antigen polymerization and Wzz-mediated chain-length regulation in <i>Pseudomonas aeruginosa</i> PAO1. Scientific Reports, 2013, 3, 3441.	3.3	40
185	Re-annotation of the genome sequence of <i>Helicobacter pylori</i> 26695. Journal of Integrative Bioinformatics, 2013, 10, 66-78.	1.5	17
186	Genome-wide Membrane Protein Structure Prediction. Current Genomics, 2013, 14, 324-329.	1.6	24
187	Sequencing and De Novo Assembly of the Western Tarnished Plant Bug ( <i>Lygus hesperus</i> ) Transcriptome. PLoS ONE, 2013, 8, e55105.	2.5	49

#	ARTICLE	IF	CITATIONS
188	Horizontal Transfer of a Subtilisin Gene from Plants into an Ancestor of the Plant Pathogenic Fungal Genus <i>Colletotrichum</i> . PLoS ONE, 2013, 8, e59078.	2.5	28
189	Genome-Wide Expression Analysis of Soybean MADS Genes Showing Potential Function in the Seed Development. PLoS ONE, 2013, 8, e62288.	2.5	40
190	A Novel Predicted Calcium-Regulated Kinase Family Implicated in Neurological Disorders. PLoS ONE, 2013, 8, e66427.	2.5	40
191	An Improved Method for TAL Effectors DNA-Binding Sites Prediction Reveals Functional Convergence in TAL Repertoires of <i>Xanthomonas oryzae</i> Strains. PLoS ONE, 2013, 8, e68464.	2.5	102
192	Revising the Taxonomic Distribution, Origin and Evolution of Ribosome Inactivating Protein Genes. PLoS ONE, 2013, 8, e72825.	2.5	37
193	Evolutionary History of Chordate PAX Genes: Dynamics of Change in a Complex Gene Family. PLoS ONE, 2013, 8, e73560.	2.5	20
194	Transcriptome Sequencing and Differential Gene Expression Analysis of Delayed Gland Morphogenesis in <i>Gossypium australe</i> during Seed Germination. PLoS ONE, 2013, 8, e75323.	2.5	26
195	Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences. PLoS ONE, 2013, 8, e75458.	2.5	7
196	Comparative Genomic Analysis of Multi-Subunit Tethering Complexes Demonstrates an Ancient Pan-Eukaryotic Complement and Sculpting in Apicomplexa. PLoS ONE, 2013, 8, e76278.	2.5	61
197	Diversity and Evolution of Bacterial Twin Arginine Translocase Protein, TatC, Reveals a Protein Secretion System That Is Evolving to Fit Its Environmental Niche. PLoS ONE, 2013, 8, e78742.	2.5	23
198	De novo Assembly and Characterization of the Global Transcriptome for <i>Rhyacionia leptotubula</i> Using Illumina Paired-End Sequencing. PLoS ONE, 2013, 8, e81096.	2.5	13
199	Functional Environmental Screening of a Metagenomic Library Identifies <i>stlA</i> ; A Unique Salt Tolerance Locus from the Human Gut Microbiome. PLoS ONE, 2013, 8, e82985.	2.5	39
200	Inferring the Brassica rapa Interactome Using Protein-Protein Interaction Data from Arabidopsis thaliana. Frontiers in Plant Science, 2012, 3, 297.	3.6	25
201	Diversity of reductive dehalogenase genes from environmental samples and enrichment cultures identified with degenerate primer PCR screens. Frontiers in Microbiology, 2013, 4, 341.	3.5	44
202	Transcriptome Analysis of the Oil-Rich Tea Plant, <i>Camellia oleifera</i> , Reveals Candidate Genes Related to Lipid Metabolism. PLoS ONE, 2014, 9, e104150.	2.5	73
203	Comprehensive Analysis of Alternative Splicing in <i>Digitalis purpurea</i> by Strand-Specific RNA-Seq. PLoS ONE, 2014, 9, e106001.	2.5	12
204	Sequencing, De Novo Assembly and Annotation of the Colorado Potato Beetle, <i>Leptinotarsa decemlineata</i> , Transcriptome. PLoS ONE, 2014, 9, e86012.	2.5	60
205	Training Set Selection for the Prediction of Essential Genes. PLoS ONE, 2014, 9, e86805.	2.5	38

#	ARTICLE	IF	CITATIONS
206	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. PLoS ONE, 2014, 9, e87723.	2.5	47
207	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. PLoS ONE, 2014, 9, e93907.	2.5	112
208	Metagenomic Identification of a Novel Salt Tolerance Gene from the Human Gut Microbiome Which Encodes a Membrane Protein with Homology to a brp/blh-Family $\beta^2$ -Carotene 15,15- $\alpha$ -Monooxygenase. PLoS ONE, 2014, 9, e103318.	2.5	36
209	De Novo Assembly of the Perennial Ryegrass Transcriptome Using an RNA-Seq Strategy. PLoS ONE, 2014, 9, e103567.	2.5	44
210	Transcriptome of American Oysters, Crassostrea virginica, in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. PLoS ONE, 2014, 9, e105097.	2.5	74
211	Combining Structural Modeling with Ensemble Machine Learning to Accurately Predict Protein Fold Stability and Binding Affinity Effects upon Mutation. PLoS ONE, 2014, 9, e107353.	2.5	71
212	Hybrid and Rogue Kinases Encoded in the Genomes of Model Eukaryotes. PLoS ONE, 2014, 9, e107956.	2.5	3
213	Protein Domain Analysis of Genomic Sequence Data Reveals Regulation of LRR Related Domains in Plant Transpiration in Ficus. PLoS ONE, 2014, 9, e108719.	2.5	4
214	A Hybrid Non-Ribosomal Peptide/Polyketide Synthetase Containing Fatty-Acyl Ligase (FAAL) Synthesizes the $\beta^2$ -Amino Fatty Acid Lipopeptides Puwainaphycins in the Cyanobacterium Cylandrospermum alatosporum. PLoS ONE, 2014, 9, e111904.	2.5	54
215	The Genome of the Generalist Plant Pathogen Fusarium avenaceum Is Enriched with Genes Involved in Redox, Signaling and Secondary Metabolism. PLoS ONE, 2014, 9, e112703.	2.5	78
216	Genome-Wide Identification and Comprehensive Analyses of the Kinomes in Four Pathogenic Microsporidia Species. PLoS ONE, 2014, 9, e115890.	2.5	8
217	Effects of different compost amendments on the abundance and composition of alkB harboring bacterial communities in a soil under industrial use contaminated with hydrocarbons. Frontiers in Microbiology, 2014, 5, 96.	3.5	33
218	Ancient association between cation leak channels and Mid1 proteins is conserved in fungi and animals. Frontiers in Molecular Neuroscience, 2014, 7, 15.	2.9	29
219	Is Five Percent Too Small? Analysis of the Overlaps between Disorder, Coiled Coil and Collagen Predictions in Complete Proteomes. Proteomes, 2014, 2, 72-83.	3.5	5
220	Use of Bioinformatics Tools in Different Spheres of Life Sciences. Journal of Data Mining in Genomics & Proteomics, 2014, 05, .	0.5	16
221	In Silico Sequence Analysis Reveals New Characteristics of Fungal NADPH Oxidase Genes. Mycobiology, 2014, 42, 241-248.	1.7	1
222	Mining the Dark Matter of the Cancer Proteome for Novel Biomarkers. Current Cancer Therapy Reviews, 2014, 9, 265-277.	0.3	9
223	Proteogenomics in microbiology: Taking the right turn at the junction of genomics and proteomics. Proteomics, 2014, 14, 2360-2675.	2.2	28

#	ARTICLE	IF	CITATIONS
224	Assessment of optimized Markov models in protein fold classification. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450016.	0.8	5
225	REPERTOIRE OF PROTEIN KINASES ENCODED IN THE GENOME OF ZEBRAFISH SHOWS REMARKABLY LARGE POPULATION OF PIM KINASES. Journal of Bioinformatics and Computational Biology, 2014, 12, 1350014.	0.8	3
226	Nemertean Toxin Genes Revealed through Transcriptome Sequencing. Genome Biology and Evolution, 2014, 6, 3314-3325.	2.5	22
227	Integrating protein structural dynamics and evolutionary analysis with Bio3D. BMC Bioinformatics, 2014, 15, 399.	2.6	292
228	Metatranscriptomic analysis of lignocellulolytic microbial communities involved in high-solids decomposition of rice straw. Biotechnology for Biofuels, 2014, 7, 495.	6.2	40
229	New gene models and alternative splicing in the maize pathogen Colletotrichum graminicola revealed by RNA-Seq analysis. BMC Genomics, 2014, 15, 842.	2.8	59
230	An Expanded Genomic Representation of the Phylum Cyanobacteria. Genome Biology and Evolution, 2014, 6, 1031-1045.	2.5	326
231	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. BMC Plant Biology, 2014, 14, 329.	3.6	42
232	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (Citrus) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	2.3	52
233	Comparative genomics of planktonic Flavobacteriaceae from the Gulf of Maine using metagenomic data. Microbiome, 2014, 2, 34.	11.1	28
234	The Case for an Early Biological Origin of DNA. Journal of Molecular Evolution, 2014, 79, 204-212.	1.8	25
235	Motif depletion in bacteriophages infecting hosts with CRISPR systems. BMC Genomics, 2014, 15, 663.	2.8	9
236	Maize protein phosphatase gene family: identification and molecular characterization. BMC Genomics, 2014, 15, 773.	2.8	55
237	Pogo-like Transposases Have Been Repeatedly Domesticated into CENP-B-Related Proteins. Genome Biology and Evolution, 2014, 6, 2008-2016.	2.5	38
238	Deorphanizing the human transmembrane genome: A landscape of uncharacterized membrane proteins. Acta Pharmacologica Sinica, 2014, 35, 11-23.	6.1	34
239	Genomic versatility and functional variation between two dominant heterotrophic symbionts of deep-sea <i>Osedax</i> worms. ISME Journal, 2014, 8, 908-924.	9.8	32
240	Compositional Biases among Synonymous Substitutions Cause Conflict between Gene and Protein Trees for Plastid Origins. Molecular Biology and Evolution, 2014, 31, 1697-1709.	8.9	49
241	Correcting for Differential Transcript Coverage Reveals a Strong Relationship between Alternative Splicing and Organism Complexity. Molecular Biology and Evolution, 2014, 31, 1402-1413.	8.9	124



#	ARTICLE	IF	CITATIONS
242	Improving Contact Prediction along Three Dimensions. PLoS Computational Biology, 2014, 10, e1003847.	3.2	71
243	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. BioMed Research International, 2014, 2014, 1-9.	1.9	3
244	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. Frontiers in Plant Science, 2014, 5, 372.	3.6	45
245	TM6SF2 and MAC30, new enzyme homologs in sterol metabolism and common metabolic disease. Frontiers in Genetics, 2014, 5, 439.	2.3	50
246	Genome Sequencing and Comparative Genomics of the Broad Host-Range Pathogen Rhizoctonia solani AG8. PLoS Genetics, 2014, 10, e1004281.	3.5	145
247	Fur Is the Master Regulator of the Extraintestinal Pathogenic Escherichia coli Response to Serum. MBio, 2014, 5, .	4.1	31
248	Genomic Sequence of the Yeast Kluyveromyces marxianus CCT 7735 (UFV-3), a Highly Lactose-Fermenting Yeast Isolated from the Brazilian Dairy Industry. Genome Announcements, 2014, 2, .	0.8	23
249	Microbial Succession in the Gut: Directional Trends of Taxonomic and Functional Change in a Birth Cohort of Spanish Infants. PLoS Genetics, 2014, 10, e1004406.	3.5	164
250	Gene Expansion Shapes Genome Architecture in the Human Pathogen Lichtheimia corymbifera: An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). PLoS Genetics, 2014, 10, e1004496.	3.5	80
251	Identification of Diversity-Generating Retroelements in Human Microbiomes. International Journal of Molecular Sciences, 2014, 15, 14234-14246.	4.1	37
252	Insilico analysis of hypothetical proteins unveils putative metabolic pathways and essential genes in Leishmania donovani. Frontiers in Genetics, 2014, 5, 291.	2.3	31
253	Genome-wide comparative analysis of NBS-encoding genes between Brassica species and Arabidopsis thaliana. BMC Genomics, 2014, 15, 3.	2.8	147
254	Identification of Giardia lamblia DHHC Proteins and the Role of Protein S-palmitoylation in the Encystation Process. PLoS Neglected Tropical Diseases, 2014, 8, e2997.	3.0	23
255	ARBitrator: a software pipeline for on-demand retrieval of auto-curated <i>nifH</i> sequences from GenBank. Bioinformatics, 2014, 30, 2883-2890.	4.1	55
256	Managing, Analysing, and Integrating Big Data in Medical Bioinformatics: Open Problems and Future Perspectives. BioMed Research International, 2014, 2014, 1-13.	1.9	118
257	Potential Conservation of Circadian Clock Proteins in the phylum Nematoda as Revealed by Bioinformatic Searches. PLoS ONE, 2014, 9, e112871.	2.5	13
258	Inducible Defenses Stay Up Late: Temporal Patterns of Immune Gene Expression in <i>Tenebrio molitor</i>. G3: Genes, Genomes, Genetics, 2014, 4, 947-955.	1.8	78
259	High-Resolution Profiling of Novel Transcribed Regions During Rat Spermatogenesis1. Biology of Reproduction, 2014, 91, 5.	2.7	50

#	ARTICLE	IF	CITATIONS
260	Wormhole: Wisely Predicting Multidimensional Branches. , 2014, , .		12
261	Identification of Ancient Greek Papyrus Fragments Using Genetic Sequence Alignment Algorithms. , 2014, , .		5
262	Metagenome-Wide Association of Microbial Determinants of Host Phenotype in <i>Drosophila melanogaster</i> . MBio, 2014, 5, e01631-14.	4.1	112
263	Paternally Transmitted Mitochondria Express a New Gene of Potential Viral Origin. Genome Biology and Evolution, 2014, 6, 391-405.	2.5	50
264	Evidence of Extensive DNA Transfer between <i>Bacteroidales</i> Species within the Human Gut. MBio, 2014, 5, e01305-14.	4.1	126
265	Powerful Sequence Similarity Search Methods and In-Depth Manual Analyses Can Identify Remote Homologs in Many Apparently “Orphan” Viral Proteins. Journal of Virology, 2014, 88, 10-20.	3.4	116
266	Secreted Proteomes of Different Developmental Stages of the Gastrointestinal Nematode <i>Nippostrongylus brasiliensis</i> . Molecular and Cellular Proteomics, 2014, 13, 2736-2751.	3.8	88
267	Molecular analyses of gut contents: elucidating the feeding of co-occurring salps in the Lazarev Sea from a different perspective. Antarctic Science, 2014, 26, 545-553.	0.9	16
268	Crystal structure of a feruloyl esterase belonging to the tannase family: A disulfide bond near a catalytic triad. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2857-2867.	2.6	68
269	Functional elucidation of antibacterial phage ORFans targeting <i>Pseudomonas aeruginosa</i> . Cellular Microbiology, 2014, 16, 1822-1835.	2.1	47
270	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. Nucleic Acids Research, 2014, 42, D364-D373.	14.5	156
271	Differential Genome Evolution Between Companion Symbionts in an Insect-Bacterial Symbiosis. MBio, 2014, 5, e01697-14.	4.1	70
272	Dynamic Analysis of Embedded Software Using Execution Replay. , 2014, , .		1
273	The Structure-Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	14.5	210
274	An Ancient Autoproteolytic Domain Found in GAIN, ZU5 and Nucleoporin98. Journal of Molecular Biology, 2014, 426, 3935-3945.	4.2	11
275	Clustal Omega. Current Protocols in Bioinformatics, 2014, 48, 3.13.1-16.	25.8	461
276	Using the MEROPS Database for Proteolytic Enzymes and Their Inhibitors and Substrates. Current Protocols in Bioinformatics, 2014, 48, 1.25.1-33.	25.8	39
277	Dissection of Hexosyl- and Sialyltransferase Domains in the Bifunctional Capsule Polymerases from <i>Neisseria meningitidis</i> W and Y Defines a New Sialyltransferase Family. Journal of Biological Chemistry, 2014, 289, 33945-33957.	3.4	21



#	ARTICLE	IF	CITATIONS
278	Phylogenetic analysis of CDK and cyclin proteins in premetazoan lineages. BMC Evolutionary Biology, 2014, 14, 10.	3.2	114
279	Interspecific and intraspecific gene variability in a 1-Mb region containing the highest density of NBS-LRR genes found in the melon genome. BMC Genomics, 2014, 15, 1131.	2.8	16
280	Genomic characterisation of the effector complement of the potato cyst nematode <i>Globodera pallida</i> . BMC Genomics, 2014, 15, 923.	2.8	81
281	RNA sequencing and de novo assembly of the digestive gland transcriptome in <i>Mytilus galloprovincialis</i> fed with toxinogenic and non-toxic strains of <i>Alexandrium minutum</i> . BMC Research Notes, 2014, 7, 722.	1.4	47
282	Dynamic evolution of the GnRH receptor gene family in vertebrates. BMC Evolutionary Biology, 2014, 14, 215.	3.2	30
283	Non-specific lipid transfer proteins in maize. BMC Plant Biology, 2014, 14, 281.	3.6	82
284	Arabidopsis ANGULATA10 is required for thylakoid biogenesis and mesophyll development. Journal of Experimental Botany, 2014, 65, 2391-2404.	4.8	13
285	A Subfamily of Putative Cytokinin Receptors Is Revealed by an Analysis of the Evolution of the Two-Component Signaling System of Plants. Plant Physiology, 2014, 165, 227-237.	4.8	37
286	3did: a catalog of domain-based interactions of known three-dimensional structure. Nucleic Acids Research, 2014, 42, D374-D379.	14.5	249
288	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. Nucleic Acids Research, 2014, 42, e172-e172.	14.5	33
289	PASTA: Ultra-Large Multiple Sequence Alignment. Lecture Notes in Computer Science, 2014, , 177-191.	1.3	48
290	An improved predictive recognition model for Cys2-His2 zinc finger proteins. Nucleic Acids Research, 2014, 42, 4800-4812.	14.5	66
291	In vivo function and comparative genomic analyses of the <i>Drosophila</i> gut microbiota identify candidate symbiosis factors. Frontiers in Microbiology, 2014, 5, 576.	3.5	72
292	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	2.5	153
293	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. Genome Biology, 2014, 15, R39.	9.6	245
294	IDEAL in 2014 illustrates interaction networks composed of intrinsically disordered proteins and their binding partners. Nucleic Acids Research, 2014, 42, D320-D325.	14.5	88
295	The interplay of restriction-modification systems with mobile genetic elements and their prokaryotic hosts. Nucleic Acids Research, 2014, 42, 10618-10631.	14.5	246
296	Structural analysis of arabinose-5-phosphate isomerase from <i>Bacteroides fragilis</i> and functional implications. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2640-2651.	2.5	0

#	ARTICLE	IF	CITATIONS
297	Longin and <scp>GAF</scp> Domains: Structural Evolution and Adaptation to the Subcellular Trafficking Machinery. <i>Traffic</i> , 2014, 15, 104-121.	2.7	40
298	Discovery of Unconventional Kinetochores in Kinetoplastids. <i>Cell</i> , 2014, 156, 1247-1258.	28.9	217
299	Proteins Feel More Than They See: Fine-Tuning of Binding Affinity by Properties of the Non-Interacting Surface. <i>Journal of Molecular Biology</i> , 2014, 426, 2632-2652.	4.2	103
300	Enrichment and characterization of an anaerobic cellulolytic microbial consortium SQD-1.1 from mangrove soil. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 465-474.	3.6	28
301	Identification and characterization of CBL and CIPK gene families in canola ( <i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2014, 14, 8.	3.6	133
302	Skylign: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models. <i>BMC Bioinformatics</i> , 2014, 15, 7.	2.6	298
303	Quantitative prediction of the effect of genetic variation using hidden Markov models. <i>BMC Bioinformatics</i> , 2014, 15, 5.	2.6	22
304	Conserved CO-FT regulons contribute to the photoperiod flowering control in soybean. <i>BMC Plant Biology</i> , 2014, 14, 9.	3.6	73
305	Development of novel EST-derived resistance gene markers in hop ( <i>Humulus lupulus</i> L.). <i>Molecular Breeding</i> , 2014, 33, 61-74.	2.1	6
306	Identification and expression profile analysis of the protein kinase gene superfamily in maize development. <i>Molecular Breeding</i> , 2014, 33, 155-172.	2.1	43
307	Influence of N- and/or C-terminal regions on activity, expression, characteristics and structure of lipase from <i>Geobacillus</i> sp. 95. <i>Extremophiles</i> , 2014, 18, 131-145.	2.3	18
308	Genome-wide identification and expression analysis of the mitogen-activated protein kinase gene family from banana suggest involvement of specific members in different stages of fruit ripening. <i>Functional and Integrative Genomics</i> , 2014, 14, 161-175.	3.5	47
309	Use of Whole Genome Shotgun Metagenomics: A Practical Guide for the Microbiome-Minded Physician Scientist. <i>Seminars in Reproductive Medicine</i> , 2014, 32, 005-013.	1.1	19
310	Structural Fold and Binding Sites of the Human Na <sup>+</sup> -Phosphate Cotransporter NaPi-II. <i>Biophysical Journal</i> , 2014, 106, 1268-1279.	0.5	42
311	FGF Signaling Emerged Concomitantly with the Origin of Eumetazoans. <i>Molecular Biology and Evolution</i> , 2014, 31, 310-318.	8.9	23
312	Live Genomics for Pathogen Monitoring in Public Health. <i>Pathogens</i> , 2014, 3, 93-108.	2.8	4
313	On the Origin and Evolution of Plant Brassinosteroid Receptor Kinases. <i>Journal of Molecular Evolution</i> , 2014, 78, 118-129.	1.8	28
314	Genomic comparison of sporeforming bacilli isolated from milk. <i>BMC Genomics</i> , 2014, 15, 26.	2.8	27

#	ARTICLE	IF	CITATIONS
315	SECRETOOL: integrated secretome analysis tool for fungi. Amino Acids, 2014, 46, 471-473.	2.7	46
316	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1819-1828.	2.6	36
317	The Characterization of Sponge NLRs Provides Insight into the Origin and Evolution of This Innate Immune Gene Family in Animals. Molecular Biology and Evolution, 2014, 31, 106-120.	8.9	86
318	Reconstructing a Thauera genome from a hydrogenotrophic-denitrifying consortium using metagenomic sequence data. Applied Microbiology and Biotechnology, 2014, 98, 6885-6895.	3.6	38
319	Bacterial phylogeny structures soil resistomes across habitats. Nature, 2014, 509, 612-616.	27.8	973
320	Systematic analysis of a wasp parasitism arsenal. Molecular Ecology, 2014, 23, 890-901.	3.9	108
321	footprintDB: a database of transcription factors with annotated cis elements and binding interfaces. Bioinformatics, 2014, 30, 258-265.	4.1	72
322	A View to a Kill: The Bacterial Type VI Secretion System. Cell Host and Microbe, 2014, 15, 9-21.	11.0	523
323	Marine Tubeworm Metamorphosis Induced by Arrays of Bacterial Phage Tail-Like Structures. Science, 2014, 343, 529-533.	12.6	223
324	Selecting Protein Families for Environmental Features Based on Manifold Regularization. IEEE Transactions on Nanobioscience, 2014, 13, 104-108.	3.3	1
325	Green genes: bioinformatics and systems-biology innovations drive algal biotechnology. Trends in Biotechnology, 2014, 32, 617-626.	9.3	53
326	Alkaline phosphatases in microbialites and bacterioplankton from Alchichica soda lake, Mexico. FEMS Microbiology Ecology, 2014, 90, n/a-n/a.	2.7	33
327	Normal Mode Dynamics Comparison of Proteins. Israel Journal of Chemistry, 2014, 54, 1118-1125.	2.3	4
328	The <i>urora</i> kinase in <i>Trypanosoma brucei</i> undergoes post-translational modifications and is targeted to various subcellular locations through binding to <i>TbCPC</i> 1. Molecular Microbiology, 2014, 91, 256-274.	2.5	12
329	Multiple enzymatic activities of ParB/Srx superfamily mediate sexual conflict among conjugative plasmids. Nature Communications, 2014, 5, 5322.	12.8	28
330	Phenylethanol promotes adhesion and biofilm formation of the antagonistic yeast <i>Kloeckera apiculata</i> for the control of blue mold on citrus. FEMS Yeast Research, 2014, 14, 536-546.	2.3	63
331	One origin for metallo- $\beta$ -lactamase activity, or two? An investigation assessing a diverse set of reconstructed ancestral sequences based on a sample of phylogenetic trees. Journal of Molecular Evolution, 2014, 79, 117-129.	1.8	23
332	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.	2.6	30

#	ARTICLE	IF	CITATIONS
333	NMR Solution Structure of the Terminal Immunoglobulin-like Domain from the Leptospira Host-Interacting Outer Membrane Protein, LigB. <i>Biochemistry</i> , 2014, 53, 5249-5260.	2.5	20
334	Efficient Data Race Detection for C/C++ Programs Using Dynamic Granularity. , 2014, , .		17
335	Novel divergent nidovirus in a python with pneumonia. <i>Journal of General Virology</i> , 2014, 95, 2480-2485.	2.9	41
336	HNH proteins are a widespread component of phage DNA packaging machines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6022-6027.	7.1	110
337	Mitreicin A , an endolysin-like bacteriolytic enzyme from a newly isolated soil streptomycete. <i>Letters in Applied Microbiology</i> , 2014, 58, 493-502.	2.2	6
338	<sc>GIL</sc>, a new c-di-GMP-binding protein domain involved in regulation of cellulose synthesis in enterobacteria. <i>Molecular Microbiology</i> , 2014, 93, 439-452.	2.5	118
339	Genome Reconstruction and Gene Expression of <i>Candidatus Accumulibacter phosphatis</i> Clade IB Performing Biological Phosphorus Removal. <i>Environmental Science &amp; Technology</i> , 2014, 48, 10363-10371.	10.0	64
340	T cell transcripts and T cell activities in the gills of the teleost fish sea bass ( <i>Dicentrarchus labrax</i> ). <i>Developmental and Comparative Immunology</i> , 2014, 47, 309-318.	2.3	58
341	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. <i>Rna</i> , 2014, 20, 1337-1348.	3.5	34
342	Three-dimensional protein structure prediction: Methods and computational strategies. <i>Computational Biology and Chemistry</i> , 2014, 53, 251-276.	2.3	160
343	The quest for a unified view of bacterial land colonization. <i>ISME Journal</i> , 2014, 8, 1358-1369.	9.8	21
344	Understanding the antagonism of retinoblastoma protein dephosphorylation by PNUTS provides insights into the PP1 regulatory code. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4097-4102.	7.1	112
345	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
346	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. <i>Genomics</i> , 2014, 104, 1-7.	2.9	19
347	A Type VI Secretion-Related Pathway in <i>Bacteroidetes</i> Mediates Interbacterial Antagonism. <i>Cell Host and Microbe</i> , 2014, 16, 227-236.	11.0	311
348	Characterization of Thermolide Biosynthetic Genes and a New Thermolide from Sister Thermophilic Fungi. <i>Organic Letters</i> , 2014, 16, 3744-3747.	4.6	23
349	Dynamic recruitment of amino acid transporters to the insect/symbiont interface. <i>Molecular Ecology</i> , 2014, 23, 1608-1623.	3.9	57
350	New phylogenomic and comparative analyses provide corroborating evidence that Myxozoa is Cnidaria. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 10-18.	2.7	34

#	ARTICLE	IF	CITATIONS
351	A family of starch-active polysaccharide monooxygenases. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13822-13827.	7.1	222
352	Identification and phylogenetic analyses of VAS <sub>t</sub> , an uncharacterized protein domain associated with lipid-binding domains in Eukaryotes. BMC Bioinformatics, 2014, 15, 222.	2.6	38
353	Osiris: accessible and reproducible phylogenetic and phylogenomic analyses within the Galaxy workflow management system. BMC Bioinformatics, 2014, 15, 230.	2.6	36
354	Enhancing HMM-based protein profile-profile alignment with structural features and evolutionary coupling information. BMC Bioinformatics, 2014, 15, 252.	2.6	8
355	Paleo-evolutionary plasticity of plant disease resistance genes. BMC Genomics, 2014, 15, 187.	2.8	51
356	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	2.8	91
357	Characterization of the MLO gene family in Rosaceae and gene expression analysis in <i>Malus domestica</i> . BMC Genomics, 2014, 15, 618.	2.8	97
358	Modular organization and reticulate evolution of the ORF1 of Jockey superfamily transposable elements. Mobile DNA, 2014, 5, 19.	3.6	11
359	Prediction and functional analysis of the sweet orange protein-protein interaction network. BMC Plant Biology, 2014, 14, 213.	3.6	30
360	The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. Cell, 2014, 158, 1187-1198.	28.9	152
361	Evidence supporting the existence of a NUPR1-like family of helix-loop-helix chromatin proteins related to, yet distinct from, AT hook-containing HMG proteins. Journal of Molecular Modeling, 2014, 20, 2357.	1.8	15
362	Analysis of novel <i>kitasatosporae</i> reveals significant evolutionary changes in conserved developmental genes between <i>Kitasatospora</i> and <i>Streptomyces</i> . Antonie Van Leeuwenhoek, 2014, 106, 365-380.	1.7	34
363	Molecular characterization and phylogenetic analysis of the genome of porcine torovirus. Archives of Virology, 2014, 159, 773-778.	2.1	21
364	Diversity of the metal-transporting P1B-type ATPases. Journal of Biological Inorganic Chemistry, 2014, 19, 947-960.	2.6	98
365	Protein kinase structure, expression and regulation in maize drought signaling. Molecular Breeding, 2014, 34, 583-602.	2.1	16
366	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
367	<i>In vitro</i> evaluation of the mucin-adhesion ability and probiotic potential of <i>Lactobacillus mucosae</i> LM1. Journal of Applied Microbiology, 2014, 117, 485-497.	3.1	109
368	Rapid Evolution of Cellulosome Modules by Comparative Analyses of Five Clostridiales Genomes. Bioenergy Research, 2014, 7, 1369-1381.	3.9	0

#	ARTICLE	IF	CITATIONS
369	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. BMC Bioinformatics, 2014, 15, 75.	2.6	1
370	Characterization of the pigmented shell-forming proteome of the common grove snail <i>Cepaea nemoralis</i> . BMC Genomics, 2014, 15, 249.	2.8	76
371	A customized Web portal for the genome of the ctenophore <i>Mnemiopsis leidyi</i> . BMC Genomics, 2014, 15, 316.	2.8	28
372	A network-based approach to identify substrate classes of bacterial glycosyltransferases. BMC Genomics, 2014, 15, 349.	2.8	337
373	Dramatic expansion of the black widow toxin arsenal uncovered by multi-tissue transcriptomics and venom proteomics. BMC Genomics, 2014, 15, 366.	2.8	93
374	Comparative genomic analysis of the R2R3 MYB secondary cell wall regulators of Arabidopsis, poplar, rice, maize, and switchgrass. BMC Plant Biology, 2014, 14, 135.	3.6	74
375	Proteomic Profile of <i>Cryptococcus neoformans</i> Biofilm Reveals Changes in Metabolic Processes. Journal of Proteome Research, 2014, 13, 1545-1559.	3.7	58
376	SearchDOGS Bacteria, Software That Provides Automated Identification of Potentially Missed Genes in Annotated Bacterial Genomes. Journal of Bacteriology, 2014, 196, 2030-2042.	2.2	12
377	Draft Genome Sequence of <i>Trueperella pyogenes</i> , Isolated from the Infected Uterus of a Postpartum Cow with Metritis. Genome Announcements, 2014, 2, .	0.8	11
378	Repurposing TRASH: Emergence of the enzyme organomercurial lyase from a non-catalytic zinc finger scaffold. Journal of Structural Biology, 2014, 188, 16-21.	2.8	11
379	CDK phosphorylation of SLD-2 is required for replication initiation and germline development in <i>C. elegans</i> . Journal of Cell Biology, 2014, 204, 507-522.	5.2	21
380	Genetic diversity of the unicellular nitrogen-fixing cyanobacteria <i>UCYN-A</i> and its prymnesiophyte host. Environmental Microbiology, 2014, 16, 3238-3249.	3.8	118
381	Genome-wide identification, characterisation and expression analysis of the MADS-box gene family in <i>Prunus mume</i> . Molecular Genetics and Genomics, 2014, 289, 903-920.	2.1	102
382	The myosin motor domain-containing chitin synthase PdChsVII is required for development, cell wall integrity and virulence in the citrus postharvest pathogen <i>Penicillium digitatum</i> . Fungal Genetics and Biology, 2014, 67, 58-70.	2.1	38
383	Genomic analysis and expression investigation of caleosin gene family in Arabidopsis. Biochemical and Biophysical Research Communications, 2014, 448, 365-371.	2.1	37
384	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. Molecular Biology of the Cell, 2014, 25, 1421-1436.	2.1	26
385	<i>MEROPS</i> : the database of proteolytic enzymes, their substrates and inhibitors. Nucleic Acids Research, 2014, 42, D503-D509.	14.5	782
386	Identifying Pathogenicity Islands in Bacterial Pathogenomics Using Computational Approaches. Pathogens, 2014, 3, 36-56.	2.8	78

#	ARTICLE	IF	CITATIONS
387	Leptospiral Pathogenomics. <i>Pathogens</i> , 2014, 3, 280-308.	2.8	94
388	Integrative workflows for metagenomic analysis. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 70.	3.7	32
389	Complete genome sequence of DSM 30083T, the type strain (U5/41T) of <i>Escherichia coli</i> , and a proposal for delineating subspecies in microbial taxonomy. <i>Standards in Genomic Sciences</i> , 2014, 9, 2.	1.5	454
390	Quality scores for 32,000 genomes. <i>Standards in Genomic Sciences</i> , 2014, 9, 20.	1.5	36
391	Mapping genomic features to functional traits through microbial whole genome sequences. <i>International Journal of Bioinformatics Research and Applications</i> , 2014, 10, 461.	0.2	6
392	The Genome Sequence of a Type ST239 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate from a Malaysian Hospital. <i>Standards in Genomic Sciences</i> , 2014, 9, 933-939.	1.5	2
393	Non-contiguous finished genome sequence and description of <i>Sulfurimonas hongkongensis</i> sp. nov., a strictly anaerobic denitrifying, hydrogen- and sulfur-oxidizing chemolithoautotroph isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 1302-1310.	1.5	30
394	Complete genome sequence of the bacteriochlorophyll a-containing <i>Roseobacterium elongatum</i> type strain (DSM 19469T), a representative of the <i>Roseobacter</i> group isolated from Australian coast sand. <i>Standards in Genomic Sciences</i> , 2014, 9, 840-854.	1.5	4
395	Genome sequence of the <i>Wenxinia marina</i> type strain (DSM 24838T), a representative of the <i>Roseobacter</i> group isolated from oilfield sediments. <i>Standards in Genomic Sciences</i> , 2014, 9, 855-865.	1.5	3
396	Genome sequence of the pink to light reddish-pigmented <i>Rubellimicrobium mesophilum</i> type strain (DSM 19309T), a representative of the <i>Roseobacter</i> group isolated from soil, and emended description of the species. <i>Standards in Genomic Sciences</i> , 2014, 9, 902-913.	1.5	12
397	A meta-approach for improving the prediction and the functional annotation of ortholog groups. <i>BMC Genomics</i> , 2014, 15, S16.	2.8	20
398	Optimisation of miRNA-mRNA relationship prediction using biological features. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 45.	0.3	2
399	Identification of the meiotic toolkit in diatoms and exploration of meiosis-specific SPO11 and RAD51 homologs in the sexual species <i>Pseudo-nitzschia multistriata</i> and <i>Seminavis robusta</i> . <i>BMC Genomics</i> , 2015, 16, 930.	2.8	53
400	Genomic and expression analysis of transition proteins in <i>Drosophila</i> . <i>Spermatogenesis</i> , 2015, 5, e1178518.	0.8	5
401	Gene expression profiling during adventitious root formation in carnation stem cuttings. <i>BMC Genomics</i> , 2015, 16, 789.	2.8	67
402	SmedGD 2.0: The <i>Schmidtea mediterranea</i> genome database. <i>Genesis</i> , 2015, 53, 535-546.	1.6	114
403	Activity-Dependent Neuroprotective Protein (ADNP): A Case Study for Highly Conserved Chordata-Specific Genes Shaping the Brain and Mutated in Cancer. <i>Journal of Alzheimer's Disease</i> , 2015, 45, 57-73.	2.6	44
404	Transcriptomic variation of hepatopancreas reveals the energy metabolism and biological processes associated with molting in Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Scientific Reports</i> , 2015, 5, 14015.	3.3	91



#	ARTICLE	IF	CITATIONS
405	Lactococcus garvieae: a small bacteria and a big data world. Health Information Science and Systems, 2015, 3, S5.	5.2	8
406	An integrated database of wood-formation related genes in plants. Scientific Reports, 2015, 5, 11422.	3.3	3
407	Tracing the structural evolution of eukaryotic ATP binding cassette transporter superfamily. Scientific Reports, 2015, 5, 16724.	3.3	55
408	TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. Evolutionary Bioinformatics, 2015, 11, EBO.S23873.	1.2	37
409	Genome-wide Identification of WRKY Genes in the Desert Poplar Populus euphratica and Adaptive Evolution of the Genes in Response to Salt Stress. Evolutionary Bioinformatics, 2015, 11s1, EBO.S22067.	1.2	20
410	Identification of an Ideal-like Fingerprint for a Protein Fold using Overlapped Conserved Residues based Approach. Scientific Reports, 2015, 4, 5643.	3.3	6
411	A Novel Mitosomal $\beta$ -Barrel Outer Membrane Protein in Entamoeba. Scientific Reports, 2015, 5, 8545.	3.3	16
412	WaspAtlas: a <i>Nasonia vitripennis</i> gene database and analysis platform. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav103.	3.0	18
413	Dimeric interactions and complex formation using direct coevolutionary couplings. Scientific Reports, 2015, 5, 13652.	3.3	75
414	Draft genome sequences for the obligate bacterial predators Bacteriovorax spp. of four phylogenetic clusters. Standards in Genomic Sciences, 2015, 10, 11.	1.5	12
415	A large-scale conformation sampling and evaluation server for protein tertiary structure prediction and its assessment in CASP11. BMC Bioinformatics, 2015, 16, 337.	2.6	19
416	Longitudinal analysis of the peripheral B cell repertoire reveals unique effects of immunization with a new influenza virus strain. Genome Medicine, 2015, 7, 124.	8.2	35
417	The genomic landscape of ribosomal peptides containing thiazole and oxazole heterocycles. BMC Genomics, 2015, 16, 778.	2.8	68
418	Genetics and physiology of cell wall polysaccharides in the model C4 grass, Setaria viridis spp. BMC Plant Biology, 2015, 15, 236.	3.6	16
419	Fecal virome analysis of three carnivores reveals a novel nodavirus and multiple gemycircularviruses. Virology Journal, 2015, 12, 79.	3.4	29
420	Genome sequence of the Roseovarius mucosus type strain (DSM 17069T), a bacteriochlorophyll a-containing representative of the marine Roseobacter group isolated from the dinoflagellate Alexandrium ostenfeldii. Standards in Genomic Sciences, 2015, 10, 17.	1.5	12
421	Ultra-large alignments using phylogeny-aware profiles. Genome Biology, 2015, 16, 124.	8.8	113
422	A novel RING finger in the C-terminal domain of the coatomer protein $\beta$ -COP. Biology Direct, 2015, 10, 70.	4.6	7



#	ARTICLE	IF	CITATIONS
423	MnTEdb, a collective resource for mulberry transposable elements. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	25
424	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav052-bav052.	3.0	13
425	The human oral metaproteome reveals potential biomarkers for caries disease. Proteomics, 2015, 15, 3497-3507.	2.2	66
426	Parameterizing sequence alignment with an explicit evolutionary model. BMC Bioinformatics, 2015, 16, 406.	2.6	26
427	Comparative genomics between human and animal associated subspecies of the Mycobacterium avium complex: a basis for pathogenicity. BMC Genomics, 2015, 16, 695.	2.8	22
428	Origin and evolution of the enhancer of split complex. BMC Genomics, 2015, 16, 712.	2.8	8
429	The genome of Dasychira pudibunda nucleopolyhedrovirus (DapuNPV) reveals novel genetic connection between baculoviruses infecting moths of the Lymantriidae family. BMC Genomics, 2015, 16, 759.	2.8	11
430	Transcriptomic profiling of host-parasite interactions in the microsporidian Trachipleistophora hominis. BMC Genomics, 2015, 16, 983.	2.8	30
431	A bioinformatic survey of RNA-binding proteins in Plasmodium. BMC Genomics, 2015, 16, 890.	2.8	79
432	Three-dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. BMC Structural Biology, 2015, 15, 20.	2.3	4
433	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200.	8.8	77
434	The UBR-box and its relationship to binuclear RING-like treble clef zinc fingers. Biology Direct, 2015, 10, 36.	4.6	7
435	Bacterial calpains and the evolution of the calpain (C2) family of peptidases. Biology Direct, 2015, 10, 66.	4.6	15
436	Evolutionary loss of peroxisomes “not limited to parasites. Biology Direct, 2015, 10, 74.	4.6	29
437	Genome sequence of the pink-pigmented marine bacterium Loktanella hongkongensis type strain (UST950701-009PT), a representative of the Roseobacter group. Standards in Genomic Sciences, 2015, 10, 51.	1.5	1
438	Expanding the Imine Reductase Toolbox by Exploring the Bacterial Protein Sequence Space. ChemBioChem, 2015, 16, 1749-1756.	2.6	93
439	CNL Disease Resistance Genes in Soybean and Their Evolutionary Divergence. Evolutionary Bioinformatics, 2015, 11, EBO.S21782.	1.2	30
440	The <sc>P</sc>sp system of <sc>Mycobacterium tuberculosis</sc> integrates envelope stress-sensing and envelope-preserving functions. Molecular Microbiology, 2015, 97, 408-422.	2.5	42

#	ARTICLE	IF	CITATIONS
441	Draft Genome Sequence of Yellow Pigmented <i>Jeotgalibacillus alimentarius</i> JY-13 T , the First Halophile Strain of the Genus <i>Jeotgalibacillus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	2
442	A peptide resource for the analysis of <i>Staphylococcus aureus</i> in host-pathogen interaction studies. <i>Proteomics</i> , 2015, 15, 3648-3661.	2.2	24
443	Quantitative functional characterization of conserved molecular interactions in the active site of mannitol 2â€dehydrogenase. <i>Protein Science</i> , 2015, 24, 936-945.	7.6	5
444	The Quantification of Representative Sequences pipeline for amplicon sequencing: case study on withinâ€population <scp>ITS</scp>1 sequence variation in a microparasite infecting <i><scp>D</scp>aphnia</i>. <i>Molecular Ecology Resources</i> , 2015, 15, 1385-1395.	4.8	7
445	New Insights on the Terpenome of the Red Seaweed <i>Laurencia dendroidea</i> (Florideophyceae,) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 582	4.6	39
446	Managing and Documenting Legacy Scientific Workflows. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 65-87.	1.5	3
447	Genome, Proteome and Structure of a T7-Like Bacteriophage of the Kiwifruit Canker Phytopathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>Viruses</i> , 2015, 7, 3361-3379.	3.3	26
448	Structural Conservation and Functional Diversity of the Poxvirus Immune Evasion (PIE) Domain Superfamily. <i>Viruses</i> , 2015, 7, 4873-4893.	3.3	37
449	Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. <i>Viruses</i> , 2015, 7, 5388-5409.	3.3	16
450	Genome-Wide Identification and Expression Analyses of Aquaporin Gene Family during Development and Abiotic Stress in Banana. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19728-19751.	4.1	69
451	Genome comparison of two <i>Exiguobacterium</i> strains from high altitude andean lakes with different arsenic resistance: identification and 3D modeling of the Acr3 efflux pump. <i>Frontiers in Environmental Science</i> , 2015, 3, .	3.3	54
452	Recovering full-length viral genomes from metagenomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1069.	3.5	29
453	Metagenomic evidence for reciprocal particle exchange between the mainstem estuary and lateral bay sediments of the lower Columbia River. <i>Frontiers in Microbiology</i> , 2015, 6, 1074.	3.5	11
454	Antibacterial phage ORFans of <i>Pseudomonas aeruginosa</i> phage LUZ24 reveal a novel MvaT inhibiting protein. <i>Frontiers in Microbiology</i> , 2015, 6, 1242.	3.5	31
455	Comparative Genomic Insights into Ecophysiology of Neutrophilic, Microaerophilic Iron Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 1265.	3.5	78
456	Comparative Analysis of Secretomes from Ectomycorrhizal Fungi with an Emphasis on Small-Secreted Proteins. <i>Frontiers in Microbiology</i> , 2015, 6, 1278.	3.5	127
457	Anatomy of protein disorder, flexibility and disease-related mutations. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 47.	3.5	16
458	Genome-wide identification and characterization of the Dof gene family in <i>Medicago truncatula</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 10645-10657.	0.2	24

#	ARTICLE	IF	CITATIONS
459	Genome-Wide Comparative Analysis Reveals Similar Types of NBS Genes in Hybrid Citrus sinensis Genome and Original Citrus clementine Genome and Provides New Insights into Non-TIR NBS Genes. PLoS ONE, 2015, 10, e0121893.	2.5	9
460	In silico Neuropeptidome of Female Macrobrachium rosenbergii Based on Transcriptome and Peptide Mining of Eyestalk, Central Nervous System and Ovary. PLoS ONE, 2015, 10, e0123848.	2.5	113
461	Genome-Wide SNP Identification and Characterization in Two Soybean Cultivars with Contrasting Mungbean Yellow Mosaic India Virus Disease Resistance Traits. PLoS ONE, 2015, 10, e0123897.	2.5	34
462	The Homeobox Genes of Caenorhabditis elegans and Insights into Their Spatio-Temporal Expression Dynamics during Embryogenesis. PLoS ONE, 2015, 10, e0126947.	2.5	31
463	Structure Analysis Uncovers a Highly Diverse but Structurally Conserved Effector Family in Phytopathogenic Fungi. PLoS Pathogens, 2015, 11, e1005228.	4.7	188
464	Identification of Ohnolog Genes Originating from Whole Genome Duplication in Early Vertebrates, Based on Synteny Comparison across Multiple Genomes. PLoS Computational Biology, 2015, 11, e1004394.	3.2	113
465	Regulation of Clostridium difficile Spore Formation by the SpoIIQ and SpoIIIA Proteins. PLoS Genetics, 2015, 11, e1005562.	3.5	55
466	Modulation of Ambient Temperature-Dependent Flowering in Arabidopsis thaliana by Natural Variation of FLOWERING LOCUS M. PLoS Genetics, 2015, 11, e1005588.	3.5	103
467	De Novo Regulatory Motif Discovery Identifies Significant Motifs in Promoters of Five Classes of Plant Dehydrin Genes. PLoS ONE, 2015, 10, e0129016.	2.5	27
468	A de novo Assembly of the Common Frog (Rana temporaria) Transcriptome and Comparison of Transcription Following Exposure to Ranavirus and Batrachochytrium dendrobatidis. PLoS ONE, 2015, 10, e0130500.	2.5	32
469	In Silico/In Vivo Insights into the Functional and Evolutionary Pathway of Pseudomonas aeruginosa Oleate-Diol Synthase. Discovery of a New Bacterial Di-Heme Cytochrome C Peroxidase Subfamily. PLoS ONE, 2015, 10, e0131462.	2.5	11
470	The Origin and Evolution of Baeyer-Villiger Monooxygenases (BVMOs): An Ancestral Family of Flavin Monooxygenases. PLoS ONE, 2015, 10, e0132689.	2.5	42
471	Assembly and Analysis of Differential Transcriptome Responses of Hevea brasiliensis on Interaction with Microcyclus ulei. PLoS ONE, 2015, 10, e0134837.	2.5	18
472	Bioinformatics Analysis Reveals Abundant Short Alpha-Helices as a Common Structural Feature of Oomycete RxLR Effector Proteins. PLoS ONE, 2015, 10, e0135240.	2.5	16
473	Genome-Wide Identification and Expression Analysis of the NAC Transcription Factor Family in Cassava. PLoS ONE, 2015, 10, e0136993.	2.5	73
474	Evolution of a Novel Antiviral Immune-Signaling Interaction by Partial-Gene Duplication. PLoS ONE, 2015, 10, e0137276.	2.5	9
475	Biochemical Characterization of Putative Adenylate Dimethylallyltransferase and Cytokinin Dehydrogenase from Nostoc sp. PCC 7120. PLoS ONE, 2015, 10, e0138468.	2.5	19
476	De Novo Assembly and Genome Analyses of the Marine-Derived Scopulariopsis brevicaulis Strain LF580 Unravels Life-Style Traits and Anticancerous Scopularide Biosynthetic Gene Cluster. PLoS ONE, 2015, 10, e0140398.	2.5	34

#	ARTICLE	IF	CITATIONS
477	Coevolved Mutations Reveal Distinct Architectures for Two Core Proteins in the Bacterial Flagellar Motor. PLoS ONE, 2015, 10, e0142407.	2.5	8
478	Complete Genomic and Lysis-Cassette Characterization of the Novel Phage, KBNP1315, which Infects Avian Pathogenic Escherichia coli (APEC). PLoS ONE, 2015, 10, e0142504.	2.5	16
479	Comparative Genomic and Phylogenomic Analyses Reveal a Conserved Core Genome Shared by Estuarine and Oceanic Cyanopodoviruses. PLoS ONE, 2015, 10, e0142962.	2.5	48
480	Cysteine-Rich Atrial Secretory Protein from the Snail Achatina achatina: Purification and Structural Characterization. PLoS ONE, 2015, 10, e0138787.	2.5	5
481	The auxin response factor gene family in banana: genome-wide identification and expression analyses during development, ripening, and abiotic stress. Frontiers in Plant Science, 2015, 6, 742.	3.6	131
482	Genome-wide identification and transcriptional expression analysis of mitogen-activated protein kinase and mitogen-activated protein kinase kinase genes in Capsicum annum. Frontiers in Plant Science, 2015, 6, 780.	3.6	53
483	Global analysis of WRKY transcription factor superfamily in Setaria identifies potential candidates involved in abiotic stress signaling. Frontiers in Plant Science, 2015, 6, 910.	3.6	96
484	Genome-wide gene phylogeny of CIPK family in cassava and expression analysis of partial drought-induced genes. Frontiers in Plant Science, 2015, 6, 914.	3.6	67
485	De novo Transcriptome Assembly of a Chinese Locoweed (Oxytropis ochrocephala) Species Provides Insights into Genes Associated with Drought, Salinity, and Cold Tolerance. Frontiers in Plant Science, 2015, 6, 1086.	3.6	23
486	<i>Pseudomonas aeruginosa</i> Exopolyphosphatase Is Also a Polyphosphate: ADP Phosphotransferase. Enzyme Research, 2015, 2015, 1-13.	1.8	9
487	Computational Analysis of the Binding Specificities of PH Domains. BioMed Research International, 2015, 2015, 1-11.	1.9	22
488	Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. ELife, 2015, 4, e06974.	6.0	198
489	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. ELife, 2015, 4, e07966.	6.0	50
490	Inside the Pan-genome - Methods and Software Overview. Current Genomics, 2015, 16, 245-252.	1.6	79
491	Metagenomic Analysis of Chicken Gut Microbiota for Improving Metabolism and Health of Chickens – A Review. Asian-Australasian Journal of Animal Sciences, 2015, 28, 1217-1225.	2.4	90
492	Big Data Applications in Health Sciences and Epidemiology. Handbook of Statistics, 2015, , 171-202.	0.6	9
493	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	12.6	617
494	Histone chaperones in Arabidopsis and rice: genome-wide identification, phylogeny, architecture and transcriptional regulation. BMC Plant Biology, 2015, 15, 42.	3.6	44

#	ARTICLE	IF	CITATIONS
495	Genome-Wide Analysis in Three <i>Fusarium</i> Pathogens Identifies Rapidly Evolving Chromosomes and Genes Associated with Pathogenicity. <i>Genome Biology and Evolution</i> , 2015, 7, 1613-1627.	2.5	77
496	A male-determining factor in the mosquito <i>Aedes aegypti</i> . <i>Science</i> , 2015, 348, 1268-1270.	12.6	266
497	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	4.1	17
498	The maize ( <i>Zea mays</i> ssp. <i>mays</i> var. B73) genome encodes 33 members of the purple acid phosphatase family. <i>Frontiers in Plant Science</i> , 2015, 6, 341.	3.6	51
499	Genome-wide survey and expression analysis of the PUB family in Chinese cabbage ( <i>Brassica rapa</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.1	37
500	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2367-2382.	8.9	66
501	The central nervous system transcriptome of the weakly electric brown ghost knifefish ( <i>Apteronotus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	19
502	A genetic map of cassava ( <i>Manihot esculenta</i> Crantz) with integrated physical mapping of immunity-related genes. <i>BMC Genomics</i> , 2015, 16, 190.	2.8	65
503	Pan-genome dynamics of <i>Pseudomonas</i> gene complements enriched across hexachlorocyclohexane dumpsite. <i>BMC Genomics</i> , 2015, 16, 313.	2.8	19
504	A novel essential domain perspective for exploring gene essentiality. <i>Bioinformatics</i> , 2015, 31, 2921-2929.	4.1	7
505	Identification and distribution of the NBS-LRR gene family in the Cassava genome. <i>BMC Genomics</i> , 2015, 16, 360.	2.8	130
506	Predicting Sub-cellular Location of Proteins Based on Hierarchical Clustering and Hidden Markov Models. <i>Lecture Notes in Computer Science</i> , 2015, , 256-263.	1.3	1
507	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, W30-W38.	14.5	849
508	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	2.5	22
509	Comparative genomic analysis of seven <i>Mycoplasma hyosynoviae</i> strains. <i>MicrobiologyOpen</i> , 2015, 4, 343-359.	3.0	13
510	Combined computational and experimental analysis of a complex of ribonuclease III and the regulatory macrodomain protein, YmdB. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 459-472.	2.6	12
511	Multiple conformations are a conserved and regulatory feature of the <i>RB1</i> 5' UTR. <i>Rna</i> , 2015, 21, 1274-1285.	3.5	60
512	Dead enzymes in the aldehyde dehydrogenase gene family: role in drug metabolism and toxicology. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2015, 11, 1839-1847.	3.3	12

#	ARTICLE	IF	CITATIONS
513	The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. <i>Genome Biology and Evolution</i> , 2015, 7, 1713-1727.	2.5	36
514	Evolutionary divergence of the plant elicitor peptides (Peps) and their receptors: interfamily incompatibility of perception but compatibility of downstream signalling. <i>Journal of Experimental Botany</i> , 2015, 66, 5315-5325.	4.8	77
515	Regulation of DNA replication at the end of the mitochondrial D-loop involves the helicase TWINKLE and a conserved sequence element. <i>Nucleic Acids Research</i> , 2015, 43, 9262-9275.	14.5	81
516	Discovery of an essential nucleotidylating activity associated with a newly delineated conserved domain in the RNA polymerase-containing protein of all nidoviruses. <i>Nucleic Acids Research</i> , 2015, 43, 8416-8434.	14.5	197
517	Recognition of Farsi handwriting strokes using profile HMM. , 2015, , .		0
518	Draft Genome Sequence of <i>Jeotgalibacillus soli</i> DSM 23228, a Bacterium Isolated from Alkaline Sandy Soil. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
519	Two Proteins Form a Heteromeric Bacterial Self-Recognition Complex in Which Variable Subdomains Determine Allele-Restricted Binding. <i>MBio</i> , 2015, 6, e00251.	4.1	33
520	Evolution of Hox-like genes in Cnidaria: Study of Hydra Hox repertoire reveals tailor-made Hox-code for Cnidarians. <i>Mechanisms of Development</i> , 2015, 138, 87-96.	1.7	15
521	Genome-wide identification and evolutionary analyses of bZIP transcription factors in wheat and its relatives and expression profiles of anther development related TabZIP genes. <i>BMC Genomics</i> , 2015, 16, 976.	2.8	56
522	Uridylation and adenylation of RNAs. <i>Science China Life Sciences</i> , 2015, 58, 1057-1066.	4.9	25
523	JPred4: a protein secondary structure prediction server. <i>Nucleic Acids Research</i> , 2015, 43, W389-W394.	14.5	1,546
524	Phylogeny, Morphology, and Metabolic and Invasive Capabilities of Epicellular Fish Coccidium <i>Goussia janae</i> . <i>Protist</i> , 2015, 166, 659-676.	1.5	16
525	Genomes to natural products PRediction Informatics for Secondary Metabolomes (PRISM). <i>Nucleic Acids Research</i> , 2015, 43, gkv1012.	14.5	210
526	Complete genome sequence of and proposal of <i>Thermophilum uzonense</i> sp. nov. a novel hyperthermophilic crenarchaeon and emended description of the genus <i>Thermophilum</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 122.	1.5	23
527	The eyestalk transcriptome of red swamp crayfish <i>Procambarus clarkii</i> . <i>Gene</i> , 2015, 557, 28-34.	2.2	60
528	PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. <i>Journal of Computational Biology</i> , 2015, 22, 377-386.	1.6	360
529	The complete mitochondrial DNA of <i>Tegillarca granosa</i> and comparative mitogenomic analyses of three Arcidae species. <i>Gene</i> , 2015, 557, 61-70.	2.2	20
530	In silico identification and expression analysis of MscS like gene family in rice. <i>Plant Gene</i> , 2015, 1, 8-17.	2.3	12

#	ARTICLE	IF	CITATIONS
531	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	4.2	23
532	Starvation-response may not involve Atg1-dependent autophagy induction in non-unikont parasites. <i>Scientific Reports</i> , 2014, 4, 5829.	3.3	18
533	Genome-wide analysis of the GRAS gene family in <i>Prunus mume</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 303-317.	2.1	74
534	Genome-wide identification, sequence characterization, and protein-protein interaction properties of DDB1 (damaged DNA binding protein-1)-binding WD40-repeat family members in <i>Solanum lycopersicum</i> . <i>Planta</i> , 2015, 241, 1337-1350.	3.2	10
535	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. <i>Plant Molecular Biology</i> , 2015, 87, 473-487.	3.9	115
536	Genome-wide analysis of the calcium-dependent protein kinase gene family in <i>Gossypium raimondii</i> . <i>Journal of Integrative Agriculture</i> , 2015, 14, 29-41.	3.5	20
537	Botulinum neurotoxin homologs in non- <i>Clostridium</i> species. <i>FEBS Letters</i> , 2015, 589, 342-348.	2.8	85
538	Molecular evolution and expression of the CRAL_TRIO protein family in insects. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 62, 168-173.	2.7	13
539	<i>Plasmodium vivax</i> trophozoite-stage proteomes. <i>Journal of Proteomics</i> , 2015, 115, 157-176.	2.4	29
540	Phosphorylation of innate immune adaptor proteins MAVS, STING, and TRIF induces IRF3 activation. <i>Science</i> , 2015, 347, aaa2630.	12.6	1,280
541	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015, 5, 8069.	3.3	144
542	<scp>SecReT6</scp>: a web-based resource for type <scp>VI</scp> secretion systems found in bacteria. <i>Environmental Microbiology</i> , 2015, 17, 2196-2202.	3.8	170
543	Vaccinia Virus Protein A49 Is an Unexpected Member of the B-cell Lymphoma (Bcl)-2 Protein Family. <i>Journal of Biological Chemistry</i> , 2015, 290, 5991-6002.	3.4	49
544	Structural basis for assembly and function of the Nup82 complex in the nuclear pore scaffold. <i>Journal of Cell Biology</i> , 2015, 208, 283-297.	5.2	64
545	Evolution of plant virus movement proteins from the 30K superfamily and of their homologs integrated in plant genomes. <i>Virology</i> , 2015, 476, 304-315.	2.4	65
546	The Role of Palmitoylation for Protein Recruitment to the Inner Membrane Complex of the Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2015, 290, 1712-1728.	3.4	66
547	<i>Xylella fastidiosa</i> Esterase Rather than Hydroxynitrile Lyase. <i>ChemBioChem</i> , 2015, 16, 625-630.	2.6	6
548	Proteasomal Control of Cytokinin Synthesis Protects <i>Mycobacterium tuberculosis</i> against Nitric Oxide. <i>Molecular Cell</i> , 2015, 57, 984-994.	9.7	101



#	ARTICLE	IF	CITATIONS
549	Research Resource: The Dynamic Transcriptional Profile of Sertoli Cells During the Progression of Spermatogenesis. <i>Molecular Endocrinology</i> , 2015, 29, 627-642.	3.7	74
550	Annotation of proteins of unknown function: initial enzyme results. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 43-54.	1.2	16
551	Transfection of <i>Sclerotinia sclerotiorum</i> with <i>In Vitro</i> Transcripts of a Naturally Occurring Interspecific Recombinant of <i>Sclerotinia sclerotiorum</i> Hypovirus 2 Significantly Reduces Virulence of the Fungus. <i>Journal of Virology</i> , 2015, 89, 5060-5071.	3.4	84
552	Prediction of Indel flanking regions in protein sequences using a variable-order Markov model. <i>Bioinformatics</i> , 2015, 31, 40-47.	4.1	5
553	Ancient dynamin segments capture early stages of host-mitochondrial integration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2800-2805.	7.1	41
554	RNA interference against gut osmoregulatory genes in phloem-feeding insects. <i>Journal of Insect Physiology</i> , 2015, 79, 105-112.	2.0	63
555	The aspartate aminotransferase-like domain of Firmicutes MocR transcriptional regulators. <i>Computational Biology and Chemistry</i> , 2015, 58, 55-61.	2.3	16
556	Characterization of the secretome of <i>Plasmopara viticola</i> by de novo transcriptome analysis. <i>Physiological and Molecular Plant Pathology</i> , 2015, 91, 1-10.	2.5	64
557	The insertion domain 1 of class IIA dimeric glycyl-tRNA synthetase is a rubredoxin-like zinc ribbon. <i>Journal of Structural Biology</i> , 2015, 190, 38-46.	2.8	5
558	Comparative analysis of essential genes in prokaryotic genomic islands. <i>Scientific Reports</i> , 2015, 5, 12561.	3.3	11
559	Eco-Evolutionary Dynamics of Episomes among Ecologically Cohesive Bacterial Populations. <i>MBio</i> , 2015, 6, e00552-15.	4.1	25
560	Unmasking alternative splicing inside protein-coding exons defines exons and their role in proteome plasticity. <i>Genome Research</i> , 2015, 25, 995-1007.	5.5	150
561	Cytosuclear Interactions in the Evolution of Animal Mitochondrial tRNA Metabolism. <i>Genome Biology and Evolution</i> , 2015, 7, 2089-2101.	2.5	44
562	Genome-Wide Identification and Evolution of HECT Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2015, 16, 8517-8535.	4.1	15
563	Combining metagenomics, metatranscriptomics and viromics to explore novel microbial interactions: towards a systems-level understanding of human microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 390-401.	4.1	182
564	A feature analysis of lower solubility proteins in three eukaryotic systems. <i>Journal of Proteomics</i> , 2015, 118, 21-38.	2.4	15
565	Turning <i>Escherichia coli</i> into a Frataxin-Dependent Organism. <i>PLoS Genetics</i> , 2015, 11, e1005134.	3.5	19
566	The interactome of soybean GmWRKY53 using yeast 2-hybrid library screening to saturation. <i>Plant Signaling and Behavior</i> , 2015, 10, e1028705.	2.4	11



#	ARTICLE	IF	CITATIONS
567	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011.	3.5	29
568	Genome and Phylogenetic Analyses of <i>Trypanosoma evansi</i> Reveal Extensive Similarity to <i>T. brucei</i> and Multiple Independent Origins for Dyskinetoplasty. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3404.	3.0	124
569	A Suggested New Bacteriophage Genus, “Kp34likevirus”, within the Autographivirinae Subfamily of Podoviridae. <i>Viruses</i> , 2015, 7, 1804-1822.	3.3	38
570	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. <i>EBioMedicine</i> , 2015, 2, 968-984.	6.1	306
571	Comparative Genomics of <i>Streptococcus pyogenes</i> M1 isolates differing in virulence and propensity to cause systemic infection in mice. <i>International Journal of Medical Microbiology</i> , 2015, 305, 532-543.	3.6	37
572	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015, 43, W134-W140.	14.5	73
573	Genome-wide identification of the auxin response factor (ARF) gene family and expression analysis of its role associated with pistil development in Japanese apricot ( <i>Prunus mume</i> Sieb. et Zucc). <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	2.1	22
575	Origin and evolution of lysyl oxidases. <i>Scientific Reports</i> , 2015, 5, 10568.	3.3	86
576	The radish genome and comprehensive gene expression profile of tuberous root formation and development. <i>Scientific Reports</i> , 2015, 5, 10835.	3.3	154
577	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 445-450.	2.1	4
578	Evolutionary Dynamics of the Cellulose Synthase Gene Superfamily in Grasses. <i>Plant Physiology</i> , 2015, 168, 968-983.	4.8	55
579	Soybean kinome: functional classification and gene expression patterns. <i>Journal of Experimental Botany</i> , 2015, 66, 1919-1934.	4.8	43
580	A wheat ABC transporter contributes to both grain formation and mycotoxin tolerance. <i>Journal of Experimental Botany</i> , 2015, 66, 2583-2593.	4.8	104
581	Predicting Peptide-Mediated Interactions on a Genome-Wide Scale. <i>PLoS Computational Biology</i> , 2015, 11, e1004248.	3.2	16
582	Maximum-Likelihood Tree Estimation Using Codon Substitution Models with Multiple Partitions. <i>Molecular Biology and Evolution</i> , 2015, 32, 2208-2216.	8.9	14
583	All-atom 3D structure prediction of transmembrane $\beta^2$ -barrel proteins from sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5413-5418.	7.1	53
584	Complete genome of <i>Jeotgalibacillus malaysiensis</i> D5 T consisting of a chromosome and a circular megaplasmid. <i>Journal of Biotechnology</i> , 2015, 204, 13-14.	3.8	8
585	BRENDA in 2015: exciting developments in its 25th year of existence. <i>Nucleic Acids Research</i> , 2015, 43, D439-D446.	14.5	183

#	ARTICLE	IF	CITATIONS
586	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	8.8	330
587	NIEluter: Predicting peptides eluted from HLA class I molecules. <i>Journal of Immunological Methods</i> , 2015, 422, 22-27.	1.4	18
588	Islander: a database of precisely mapped genomic islands in tRNA and tmRNA genes. <i>Nucleic Acids Research</i> , 2015, 43, D48-D53.	14.5	94
589	Sequencing of allotetraploid cotton ( <i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
590	Biochemical functional predictions for protein structures of unknown or uncertain function. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 182-191.	4.1	77
591	A Previously Uncharacterized, Nonphotosynthetic Member of the Chromatiaceae Is the Primary CO <sub>2</sub> -Fixing Constituent in a Self-Regenerating Biocathode. <i>Applied and Environmental Microbiology</i> , 2015, 81, 699-712.	3.1	89
592	Genome sequence of cultivated Upland cotton ( <i>Gossypium hirsutum</i> TM-1) provides insights into genome evolution. <i>Nature Biotechnology</i> , 2015, 33, 524-530.	17.5	1,064
593	Thermostable chitinase II from <i>Thermomyces lanuginosus</i> SSBP: Cloning, structure prediction and molecular dynamics simulations. <i>Journal of Theoretical Biology</i> , 2015, 374, 107-114.	1.7	53
594	Widespread Macromolecular Interaction Perturbations in Human Genetic Disorders. <i>Cell</i> , 2015, 161, 647-660.	28.9	482
595	Genomic and transcriptomic analysis of the endophytic fungus <i>Pestalotiopsis fici</i> reveals its lifestyle and high potential for synthesis of natural products. <i>BMC Genomics</i> , 2015, 16, 28.	2.8	102
596	Comprehensive analysis of CCCH-type zinc finger family genes facilitates functional gene discovery and reflects recent allopolyploidization event in tetraploid switchgrass. <i>BMC Genomics</i> , 2015, 16, 129.	2.8	38
597	Retained duplicate genes in green alga <i>Chlamydomonas reinhardtii</i> tend to be stress responsive and experience frequent response gains. <i>BMC Genomics</i> , 2015, 16, 149.	2.8	12
598	A RNA-seq approach to identify putative toxins from acrorhagi in aggressive and non-aggressive <i>Anthopleura elegantissima</i> polyps. <i>BMC Genomics</i> , 2015, 16, 221.	2.8	60
599	Comparative transcriptome analysis within the <i>Lolium/Festuca</i> species complex reveals high sequence conservation. <i>BMC Genomics</i> , 2015, 16, 249.	2.8	24
600	A genome-wide analysis of MADS-box genes in peach [ <i>Prunus persica</i> (L.) Batsch]. <i>BMC Plant Biology</i> , 2015, 15, 41.	3.6	93
601	The evolution of WRKY transcription factors. <i>BMC Plant Biology</i> , 2015, 15, 66.	3.6	204
602	Domain atrophy creates rare cases of functional partial protein domains. <i>Genome Biology</i> , 2015, 16, 88.	8.8	23
603	Sex-specific and developmental expression of Dmrt genes in the starlet sea anemone, <i>Nematostella vectensis</i> . <i>EvoDevo</i> , 2015, 6, 13.	3.2	8

#	ARTICLE	IF	CITATIONS
604	Genome-wide identification and analysis of the MADS-box gene family in sesame. <i>Gene</i> , 2015, 569, 66-76.	2.2	37
605	Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota. <i>Current Biology</i> , 2015, 25, 1682-1693.	3.9	342
606	Mosaic genome of endobacteria in arbuscular mycorrhizal fungi: Transkingdom gene transfer in an ancient mycoplasma-fungus association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7785-7790.	7.1	103
607	Long non-coding RNA discovery across the genus <i>Anopheles</i> reveals conserved secondary structures within and beyond the <i>Gambiae</i> complex. <i>BMC Genomics</i> , 2015, 16, 337.	2.8	85
608	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	12.6	357
609	Genome Sequence, Comparative Analysis, and Evolutionary Insights into Chitinases of Entomopathogenic Fungus <i>Hirsutella thompsonii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 916-930.	2.5	39
610	Homozygous MED25 mutation implicated in eye intellectual disability syndrome. <i>Human Genetics</i> , 2015, 134, 577-587.	3.8	18
611	Discovering short linear protein motif based on selective training of profile hidden Markov models. <i>Journal of Theoretical Biology</i> , 2015, 377, 75-84.	1.7	5
612	Feature extraction by statistical contact potentials and wavelet transform for predicting subcellular localizations in gram negative bacterial proteins. <i>Journal of Theoretical Biology</i> , 2015, 364, 121-130.	1.7	5
613	KAPPA, a simple algorithm for discovery and clustering of proteins defined by a key amino acid pattern: a case study of the cysteine-rich proteins. <i>Bioinformatics</i> , 2015, 31, 1716-1723.	4.1	6
614	Identification and expression analysis of the SQUAMOSA promoter-binding protein (SBP)-box gene family in <i>Prunus mume</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 1701-1715.	2.1	58
615	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, D76-D81.	14.5	287
616	Functional diversification of the dehydrin gene family in apple and its contribution to cold acclimation during dormancy. <i>Physiologia Plantarum</i> , 2015, 155, 315-329.	5.2	18
617	In silico approaches for the identification of virulence candidates amongst hypothetical proteins of <i>Mycoplasma pneumoniae</i> 309. <i>Computational Biology and Chemistry</i> , 2015, 59, 67-80.	2.3	26
618	LYRA, a webserver for lymphocyte receptor structural modeling. <i>Nucleic Acids Research</i> , 2015, 43, W349-W355.	14.5	75
619	The mysterious nature of bacterial surface (gliding) motility: A focal adhesion-based mechanism in <i>Myxococcus xanthus</i> . <i>Seminars in Cell and Developmental Biology</i> , 2015, 46, 143-154.	5.0	60
620	Transcriptome profiling provides new insights into the formation of floral scent in <i>Hedychium coronarium</i> . <i>BMC Genomics</i> , 2015, 16, 470.	2.8	70
621	TMFoldRec: a statistical potential-based transmembrane protein fold recognition tool. <i>BMC Bioinformatics</i> , 2015, 16, 201.	2.6	11

#	ARTICLE	IF	CITATIONS
622	Capturing coevolutionary signals in repeat proteins. BMC Bioinformatics, 2015, 16, 207.	2.6	24
623	Evolutionary insights from de novo transcriptome assembly and SNP discovery in California white oaks. BMC Genomics, 2015, 16, 552.	2.8	31
624	Aspergillus niger membrane-associated proteome analysis for the identification of glucose transporters. Biotechnology for Biofuels, 2015, 8, 150.	6.2	43
625	REC-1 and HIM-5 distribute meiotic crossovers and function redundantly in meiotic double-strand break formation in <i>Caenorhabditis elegans</i> . Genes and Development, 2015, 29, 1969-1979.	5.9	19
626	De novo assembly of the Carcinus maenas transcriptome and characterization of innate immune system pathways. BMC Genomics, 2015, 16, 458.	2.8	48
627	Application of a systematic exoproteogenomic profiling workflow on lactobacillus mucosae LM1. , 2015, , .		0
628	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. Genome Biology and Evolution, 2015, 7, 1815-1826.	2.5	27
629	STAC: A New Domain Associated with Transmembrane Solute Transport and Two-Component Signal Transduction Systems. Journal of Molecular Biology, 2015, 427, 3327-3339.	4.2	17
630	Localization and Evolution of Putative Triose Phosphate Translocators in the Diatom <i>Phaeodactylum tricornutum</i> . Genome Biology and Evolution, 2015, 7, 2955-2969.	2.5	53
631	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.	2.8	66
632	An automated Genomes-to-Natural Products platform (GNP) for the discovery of modular natural products. Nature Communications, 2015, 6, 8421.	12.8	123
633	Genomic Analysis of Pure Cultures and Communities. Springer Protocols, 2015, , 5-27.	0.3	16
634	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. Environmental Science & Technology, 2015, 49, 12628-12640.	10.0	72
635	SANSparallel: interactive homology search against Uniprot. Nucleic Acids Research, 2015, 43, W24-W29.	14.5	38
636	Whole transcriptome profiling of the vernalization process in Lilium longiflorum (cultivar White) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 1	2.8	45
637	LncRNA-ID: Long non-coding RNA IDentification using balanced random forests. Bioinformatics, 2015, 31, 3897-3905.	4.1	85
638	Complete mitochondrial genome of Anadara vellicata (Bivalvia: Arcidae): A unique gene order and large atypical non-coding region. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 16, 73-82.	1.0	7
639	Origins and evolvability of the PAX family. Seminars in Cell and Developmental Biology, 2015, 44, 64-74.	5.0	40

#	ARTICLE	IF	CITATIONS
640	Widespread Recurrent Patterns of Rapid Repeat Evolution in the Kinetochore Scaffold KNL1. <i>Genome Biology and Evolution</i> , 2015, 7, 2383-2393.	2.5	40
641	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian) Tj ETQq1 1 0.784314 rgBT /Overl esterases and an arabinopyranosidase. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10031-10046.	3.6	36
642	PECAS: prokaryotic and eukaryotic classical analysis of secretome. <i>Amino Acids</i> , 2015, 47, 2659-2663.	2.7	7
643	<i>Ebola</i>virus</i> comparative genomics. <i>FEMS Microbiology Reviews</i> , 2015, 39, 764-778.	8.6	54
644	Distribution of Ribonucleoprotein and Protein-Only RNase P in Eukarya. <i>Molecular Biology and Evolution</i> , 2015, 32, msv187.	8.9	56
645	Genome-wide identification and expression analysis of WNK kinase gene family in rice. <i>Computational Biology and Chemistry</i> , 2015, 59, 56-66.	2.3	16
646	Hammock: a hidden Markov model-based peptide clustering algorithm to identify protein-interaction consensus motifs in large datasets. <i>Bioinformatics</i> , 2016, 32, 9-16.	4.1	35
647	Resistance gene analogs involved in tolerant cassavaâ€“geminivirus interaction that shows a recovery phenotype. <i>Virus Genes</i> , 2015, 51, 393-407.	1.6	17
648	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . <i>Genome Biology</i> , 2015, 16, 143.	9.6	122
649	The <i>Enterobacterium Trabulsiella odontotermitis</i> Presents Novel Adaptations Related to Its Association with Fungus-Growing Termites. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6577-6588.	3.1	18
650	<i>QQS</i> orphan gene regulates carbon and nitrogen partitioning across species via NF-YC interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14734-14739.	7.1	109
651	The Kuâ€“Mar zinc finger: A segment-swapped zinc ribbon in MarR-like transcription regulators related to the Ku bridge. <i>Journal of Structural Biology</i> , 2015, 191, 281-289.	2.8	7
652	An Architecture Proposal Based in Intelligent Algorithms for Motifs Discovery in Genetic Expressions. <i>Lecture Notes in Computer Science</i> , 2015, , 261-269.	1.3	0
653	Integrative genomic mining for enzyme function to enable engineering of a non-natural biosynthetic pathway. <i>Nature Communications</i> , 2015, 6, 10005.	12.8	77
654	Family resemblances: A common fold for some dimeric ion-coupled secondary transporters. <i>Journal of General Physiology</i> , 2015, 146, 423-434.	1.9	30
655	Polyketide synthesis genes associated with toxin production in two species of <i>Gambierdiscus</i> (Dinophyceae). <i>BMC Genomics</i> , 2015, 16, 410.	2.8	56
656	Automated Identification of Dipeptide Natural Products by an Informatic Search Algorithm. <i>ChemBioChem</i> , 2015, 16, 223-227.	2.6	9
657	The cell envelope proteome of <i>Aggregatibacter actinomycetemcomitans</i>. <i>Molecular Oral Microbiology</i> , 2015, 30, 97-110.	2.7	9

#	ARTICLE	IF	CITATIONS
659	Structural, evolutionary and functional analysis of the <scp>NAC</scp> domain protein family in <i>Eucalyptus</i>. <i>New Phytologist</i> , 2015, 206, 1337-1350.	7.3	69
660	Integrative data analysis indicates an intrinsic disordered domain character of Argonaute-binding motifs. <i>Bioinformatics</i> , 2015, 31, 332-339.	4.1	9
661	Genome-wide analysis of the MADS-box gene family in <i>Brassica rapa</i> (Chinese cabbage). <i>Molecular Genetics and Genomics</i> , 2015, 290, 239-255.	2.1	80
662	Genome-wide investigation and transcriptome analysis of the WRKY gene family in <i>Gossypium</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 151-171.	2.1	69
663	Characterization of hypothetical protein VNG0128C from <i>Halobacterium</i> NRC-1 reveals GALE like activity and its involvement in Leloir pathway of galactose metabolism. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1743-1755.	3.5	2
664	The genome of the Pacific oyster <i>Crassostrea gigas</i> brings new insights on the massive expansion of the C1q gene family in <i>Bivalvia</i> . <i>Developmental and Comparative Immunology</i> , 2015, 49, 59-71.	2.3	95
665	BurrH: a new modular DNA binding protein for genome engineering. <i>Scientific Reports</i> , 2014, 4, 3831.	3.3	45
666	Phylostratigraphic Bias Creates Spurious Patterns of Genome Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 258-267.	8.9	107
667	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. <i>ISME Journal</i> , 2015, 9, 207-216.	9.8	540
668	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae <i>Nannochloropsis</i> . <i>Scientific Reports</i> , 2014, 4, 5454.	3.3	75
669	Identification, Characterization and Expression Profiling of Dicer-Like, Argonaute and RNA-Dependent RNA Polymerase Gene Families in Foxtail Millet. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 43-55.	1.8	54
670	T12BioP “ Topological Indices to BioPolymers. A Graphical “ Numerical Approach for Bioinformatics. , 2016, , .		0
671	Functional annotation of putative conserved proteins from <i>Borrelia burgdorferi</i> to find potential drug targets. <i>International Journal of Computational Biology and Drug Design</i> , 2016, 9, 295.	0.3	4
672	In silico analyses of mitochondrial ORFans in freshwater mussels ( <i>Bivalvia</i> : Unionoida) provide a framework for future studies of their origin and function. <i>BMC Genomics</i> , 2016, 17, 597.	2.8	38
673	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. <i>BMC Genomics</i> , 2016, 17, 892.	2.8	14
674	Accurate Identification of Cancerlectins through Hybrid Machine Learning Technology. <i>International Journal of Genomics</i> , 2016, 2016, 1-11.	1.6	23
675	Multi-OMICs and Genome Editing Perspectives on Liver Cancer Signaling Networks. <i>BioMed Research International</i> , 2016, 2016, 1-14.	1.9	7
676	Genome-Wide Identification of Long Noncoding RNAs in Human Intervertebral Disc Degeneration by RNA Sequencing. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	41



#	ARTICLE	IF	CITATIONS
677	Unravelling the functional genetics of dinoflagellates: a review of approaches and opportunities. <i>Perspectives in Phycology</i> , 2016, 3, 37-52.	1.9	42
678	Application of the MAFFT sequence alignment program to large dataâ€”reexamination of the usefulness of chained guide trees. <i>Bioinformatics</i> , 2016, 32, 3246-3251.	4.1	276
679	Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. <i>Frontiers in Genetics</i> , 2015, 6, 361.	2.3	57
680	Microevolution Analysis of <i>Bacillus coahuilensis</i> Unveils Differences in Phosphorus Acquisition Strategies and Their Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 58.	3.5	17
681	Phylogenetic and Functional Substrate Specificity for Endolithic Microbial Communities in Hyper-Arid Environments. <i>Frontiers in Microbiology</i> , 2016, 7, 301.	3.5	60
682	A Bacteriophage-Acquired O-Antigen Polymerase (Wzy <sup>Î²</sup> ) from <i>P. aeruginosa</i> Serotype O16 Performs a Varied Mechanism Compared to Its Cognate Wzy <sup>Î±</sup> . <i>Frontiers in Microbiology</i> , 2016, 7, 393.	3.5	7
683	Genome-Centric Analysis of Microbial Populations Enriched by Hydraulic Fracture Fluid Additives in a Coal Bed Methane Production Well. <i>Frontiers in Microbiology</i> , 2016, 7, 731.	3.5	67
684	Genomic and Metagenomic Analysis of Diversity-Generating Retroelements Associated with <i>Treponema denticola</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 852.	3.5	13
685	Not All Particles Are Equal: The Selective Enrichment of Particle-Associated Bacteria from the Mediterranean Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 996.	3.5	36
686	Microbial Community Responses to Increased Water and Organic Matter in the Arid Soils of the McMurdo Dry Valleys, Antarctica. <i>Frontiers in Microbiology</i> , 2016, 7, 1040.	3.5	59
687	Expanding the Knowledge on Lignocellulolytic and Redox Enzymes of Worker and Soldier Castes from the Lower Termite <i>Coptotermes gestroi</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1518.	3.5	26
688	Genome Sequencing of <i>Sulfolobus</i> sp. A20 from Costa Rica and Comparative Analyses of the Putative Pathways of Carbon, Nitrogen, and Sulfur Metabolism in Various <i>Sulfolobus</i> Strains. <i>Frontiers in Microbiology</i> , 2016, 7, 1902.	3.5	26
689	Widespread Inter- and Intra-Domain Horizontal Gene Transfer of d-Amino Acid Metabolism Enzymes in Eukaryotes. <i>Frontiers in Microbiology</i> , 2016, 7, 2001.	3.5	28
690	De Novo Assembly and Characterization of Bud, Leaf and Flowers Transcriptome from <i>Juglans Regia</i> L. for the Identification and Characterization of New EST-SSRs. <i>Forests</i> , 2016, 7, 247.	2.1	52
691	Genome-Wide Survey Reveals Transcriptional Differences Underlying the Contrasting Trichome Phenotypes of Two Sister Desert Poplars. <i>Genes</i> , 2016, 7, 111.	2.4	25
692	Prediction of Toxin Genes from Chinese Yellow Catfish Based on Transcriptomic and Proteomic Sequencing. <i>International Journal of Molecular Sciences</i> , 2016, 17, 556.	4.1	14
693	Evolution and expression of the phosphodiesterase 6 genes unveils vertebrate novelty to control photosensitivity. <i>BMC Evolutionary Biology</i> , 2016, 16, 124.	3.2	46
694	Identification and functional characterization of novel xylose transporters from the cell factories <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 148.	6.2	71

#	ARTICLE	IF	CITATIONS
695	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus <i>Leptospira</i> . PLoS Neglected Tropical Diseases, 2016, 10, e0004403.	3.0	253
696	Discovery and Characterization of a Thermostable and Highly Halotolerant GH5 Cellulase from an Icelandic Hot Spring Isolate. PLoS ONE, 2016, 11, e0146454.	2.5	61
697	Dimerization and Transactivation Domains as Candidates for Functional Modulation and Diversity of Sox9. PLoS ONE, 2016, 11, e0156199.	2.5	8
698	Maximum-Entropy Models of Sequenced Immune Repertoires Predict Antigen-Antibody Affinity. PLoS Computational Biology, 2016, 12, e1004870.	3.2	26
699	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. PLoS Computational Biology, 2016, 12, e1004991.	3.2	21
700	De Novo Assembled Wheat Transcriptomes Delineate Differentially Expressed Host Genes in Response to Leaf Rust Infection. PLoS ONE, 2016, 11, e0148453.	2.5	36
701	Identification of Highly Variable Supernumerary Chromosome Segments in an Asexual Pathogen. PLoS ONE, 2016, 11, e0158183.	2.5	12
702	The De Novo Transcriptome and Its Functional Annotation in the Seed Beetle <i>Callosobruchus maculatus</i> . PLoS ONE, 2016, 11, e0158565.	2.5	52
703	aPPRove: An HMM-Based Method for Accurate Prediction of RNA-Pentatricopeptide Repeat Protein Binding Events. PLoS ONE, 2016, 11, e0160645.	2.5	14
704	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus <i>Aspergillus cristatus</i> . BMC Genomics, 2016, 17, 428.	2.8	55
705	Global Analysis of WRKY Genes and Their Response to Dehydration and Salt Stress in Soybean. Frontiers in Plant Science, 2016, 7, 9.	3.6	126
706	Genome-Wide Identification and Expression Analysis of the WRKY Gene Family in Cassava. Frontiers in Plant Science, 2016, 7, 25.	3.6	96
707	The Pokeweed Leaf mRNA Transcriptome and Its Regulation by Jasmonic Acid. Frontiers in Plant Science, 2016, 7, 283.	3.6	30
708	Genome-Wide Identification and Characterization of WRKY Gene Family in Peanut. Frontiers in Plant Science, 2016, 7, 534.	3.6	102
709	Transcriptome Profile Analysis from Different Sex Types of <i>Ginkgo biloba</i> L.. Frontiers in Plant Science, 2016, 7, 871.	3.6	21
710	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.	3.6	75
711	Genome-Wide Identification and Expression Analysis of the Mitogen-Activated Protein Kinase Gene Family in Cassava. Frontiers in Plant Science, 2016, 7, 1294.	3.6	31
712	Genome-Wide Identification, Characterization and Expression Analysis of the TCP Gene Family in <i>Prunus mume</i> . Frontiers in Plant Science, 2016, 7, 1301.	3.6	41



#	ARTICLE	IF	CITATIONS
713	Genome-Wide Characterization of the MADS-Box Gene Family in Radish ( <i>Raphanus sativus</i> L.) and Assessment of Its Roles in Flowering and Floral Organogenesis. <i>Frontiers in Plant Science</i> , 2016, 07, 1390.	3.6	41
714	Genome-Wide Identification, Phylogeny, and Expression Analyses of the 14-3-3 Family Reveal Their Involvement in the Development, Ripening, and Abiotic Stress Response in Banana. <i>Frontiers in Plant Science</i> , 2016, 7, 1442.	3.6	21
715	A Developmental Transcriptome Map for Allotetraploid <i>Arachis hypogaea</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1446.	3.6	178
716	Genome-Wide Survey of Flavonoid Biosynthesis Genes and Gene Expression Analysis between Black- and Yellow-Seeded <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1755.	3.6	44
717	Long Noncoding RNA Identification: Comparing Machine Learning Based Tools for Long Noncoding Transcripts Discrimination. <i>BioMed Research International</i> , 2016, 2016, 1-14.	1.9	1,176
718	Genome-centric resolution of microbial diversity, metabolism and interactions in anaerobic digestion. <i>Environmental Microbiology</i> , 2016, 18, 3144-3158.	3.8	123
719	Genomic analysis of snub-nosed monkeys ( <i>Rhinopithecus</i> ) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	21.4	109
720	Long Non-Coding RNAs (lncRNAs) of Sea Cucumber: Large-Scale Prediction, Expression Profiling, Non-Coding Network Construction, and lncRNA-microRNA-Gene Interaction Analysis of lncRNAs in <i>Apostichopus japonicus</i> and <i>Holothuria glaberrima</i> During LPS Challenge and Radial Organ Complex Regeneration. <i>Marine Biotechnology</i> , 2016, 18, 485-499.	2.4	30
721	Catechol dioxygenases catalyzing the first step in Norway spruce phenolic degradation are key virulence factors in the bark beetle-vectored fungus <i>Endoconidiophora polonica</i> . <i>Plant Physiology</i> , 2016, 171, pp.01916.2015.	4.8	75
722	Evolution and protein interactions of AP2 proteins in Brassicaceae: Evidence linking development and environmental responses. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 549-563.	8.5	16
723	Potential Mechanisms for Microbial Energy Acquisition in Oxidic Deep-Sea Sediments. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4232-4243.	3.1	51
724	Mutations in Encephalomyocarditis Virus 3A Protein Uncouple the Dependency of Genome Replication on Host Factors Phosphatidylinositol 4-Kinase III $\alpha$ and Oxysterol-Binding Protein. <i>MSphere</i> , 2016, 1, .	2.9	18
725	Methanogenic paraffin degradation proceeds via alkane addition to fumarate by <i>Smithella</i> spp. mediated by a syntrophic coupling with hydrogenotrophic methanogens. <i>Environmental Microbiology</i> , 2016, 18, 2604-2619.	3.8	71
726	Functional and topological diversity of LOV domain photoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1442-51.	7.1	125
727	Microalgal bioengineering for sustainable energy development: Recent transgenesis and metabolic engineering strategies. <i>Biotechnology Journal</i> , 2016, 11, 303-314.	3.5	44
728	Microbial Fe(III) oxide reduction potential in C-hocolate P-ots hot spring, Yellowstone National Park. <i>Geobiology</i> , 2016, 14, 255-275.	2.4	59
729	Proteomic analysis of the venom and venom sac of the woodwasp, <i>Sirex noctilio</i> - Towards understanding its biological impact. <i>Journal of Proteomics</i> , 2016, 146, 195-206.	2.4	23
730	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 12.13.1-12.13.25.	25.8	21

#	ARTICLE	IF	CITATIONS
731	Diatom Vacuolar 1,6- $\alpha$ -D-GlcNAc 6-Phosphate Transglycosylases can Functionally Complement the Respective Yeast Mutants. Journal of Eukaryotic Microbiology, 2016, 63, 536-546.	1.7	29
732	ECDYSTEROID AND CHITINASE FLUCTUATIONS IN THE WESTERN TARNISHED PLANT BUG (<i>Lygus Tj ETQq1 1 0.784314 rgBT /Overlo Physiology, 2016, 92, 108-126.	1.5	3
733	Identification and characterization of toxins in the venom gland of the Chinese bird spider,<i>Haplopelma hainanum</i>, by transcriptomic analysis. Insect Science, 2016, 23, 487-499.	3.0	14
734	Transcriptomic profile of tobacco in response to Alternaria longipes and Alternaria alternata infections. Scientific Reports, 2016, 6, 25635.	3.3	16
735	Genome-wide analysis of the AP2/ERF family in Musa species reveals divergence and neofunctionalisation during evolution. Scientific Reports, 2016, 6, 18878.	3.3	75
736	Superoxide dismutase 2 knockdown leads to defects in locomotor activity, sensitivity to paraquat, and increased cuticle pigmentation in Tribolium castaneum. Scientific Reports, 2016, 6, 29583.	3.3	21
737	Ligand-biased regulation of PtdIns(3,4,5)P3-dependent signal transduction in GPCR control of pituitary hormone release. Endocrinology, 2016, 158, en.2016-1552.	2.8	3
738	Direct coevolutionary couplings reflect biophysical residue interactions in proteins. Journal of Chemical Physics, 2016, 145, 174102.	3.0	22
739	Phylogenomics-guided discovery of a novel conserved cassette of short linear motifs in BubR1 essential for the spindle checkpoint. Open Biology, 2016, 6, 160315.	3.6	33
740	HIPPI: highly accurate protein family classification with ensembles of HMMs. BMC Genomics, 2016, 17, 765.	2.8	17
741	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
742	Prediction and characterization of protein-protein interaction network in Bacillus licheniformis WX-02. Scientific Reports, 2016, 6, 19486.	3.3	12
743	Automated detection of ncRNAs in the draft genome sequence of a colonial tunicate: the carpet sea squirt Didemnum vexillum. BMC Genomics, 2016, 17, 691.	2.8	10
744	Classification of the treble clef zinc finger: noteworthy lessons for structure and function evolution. Scientific Reports, 2016, 6, 32070.	3.3	17
745	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. BMC Biotechnology, 2016, 16, 47.	3.3	91
746	Comparative phylogenomic analysis provides insights into TCP gene functions in Sorghum. Scientific Reports, 2016, 6, 38488.	3.3	48
747	Selective pressure against horizontally acquired prokaryotic genes as a driving force of plastid evolution. Scientific Reports, 2016, 6, 19036.	3.3	12
748	Genome-wide identification, phylogeny, and expression analysis of pectin methylesterases reveal their major role in cotton fiber development. BMC Genomics, 2016, 17, 1000.	2.8	42

#	ARTICLE	IF	CITATIONS
749	Metagenomic mining for thermostable esterolytic enzymes uncovers a new family of bacterial esterases. <i>Scientific Reports</i> , 2016, 6, 38886.	3.3	53
750	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	3.4	38
751	A Stochastic Point Cloud Sampling Method for Multi-Template Protein Comparative Modeling. <i>Scientific Reports</i> , 2016, 6, 25687.	3.3	8
752	Pentatricopeptide repeat proteins in maize. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	21
753	(Meta)genomic insights into the pathogenome of <i>Cellulosimicrobium cellulans</i> . <i>Scientific Reports</i> , 2016, 6, 25527.	3.3	20
754	Identification of lipoxygenase (LOX) genes from legumes and their responses in wild type and cultivated peanut upon <i>Aspergillus flavus</i> infection. <i>Scientific Reports</i> , 2016, 6, 35245.	3.3	52
755	The phylogeny of C/S1 bZIP transcription factors reveals a shared algal ancestry and the pre-angiosperm translational regulation of S1 transcripts. <i>Scientific Reports</i> , 2016, 6, 30444.	3.3	27
756	Production of hemolysin BL by <i>Bacillus cereus</i> group isolates of dairy origin is associated with whole-genome phylogenetic clade. <i>BMC Genomics</i> , 2016, 17, 581.	2.8	77
757	Modulation of gut microbiota and delayed immunosenescence as a result of syringaresinol consumption in middle-aged mice. <i>Scientific Reports</i> , 2016, 6, 39026.	3.3	46
758	Genome-wide characterization of the $\beta$ -1,3-glucanase gene family in <i>Gossypium</i> by comparative analysis. <i>Scientific Reports</i> , 2016, 6, 29044.	3.3	16
759	Broken TALEs: Transcription Activator-like Effectors Populate Partly Folded States. <i>Biophysical Journal</i> , 2016, 111, 2395-2403.	0.5	10
760	Genome-wide characterization and analysis of bZIP transcription factor gene family related to abiotic stress in cassava. <i>Scientific Reports</i> , 2016, 6, 22783.	3.3	97
761	CMsearch: simultaneous exploration of protein sequence space and structure space improves not only protein homology detection but also protein structure prediction. <i>Bioinformatics</i> , 2016, 32, i332-i340.	4.1	52
762	The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. <i>Scientific Reports</i> , 2016, 6, 28594.	3.3	118
763	From Genomes to Phenotypes: Traitair, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	3.8	102
764	Expansion and diversification of the MSDIN family of cyclic peptide genes in the poisonous agarics <i>Amanita phalloides</i> and <i>A. bisporigera</i> . <i>BMC Genomics</i> , 2016, 17, 1038.	2.8	37
765	dbEM: A database of epigenetic modifiers curated from cancerous and normal genomes. <i>Scientific Reports</i> , 2016, 6, 19340.	3.3	58
766	Multi-tissue transcriptomics for construction of a comprehensive gene resource for the terrestrial snail <i>Theba pisana</i> . <i>Scientific Reports</i> , 2016, 6, 20685.	3.3	10

#	ARTICLE	IF	CITATIONS
767	Structure-Function Relationships in L-Amino Acid Deaminase, a Flavoprotein Belonging to a Novel Class of Biotechnologically Relevant Enzymes. <i>Journal of Biological Chemistry</i> , 2016, 291, 10457-10475.	3.4	46
768	Computational prospecting the great viral unknown. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw077.	1.8	56
769	Connectivity to the surface determines diversity patterns in subsurface aquifers of the Fennoscandian shield. <i>ISME Journal</i> , 2016, 10, 2447-2458.	9.8	93
770	A computational model for predicting fusion peptide of retroviruses. <i>Computational Biology and Chemistry</i> , 2016, 61, 245-250.	2.3	5
771	Metagenomic analysis between free-living and cultured <i>Epinephelus fuscoguttatus</i> under different environmental conditions in Indonesian waters. <i>Marine Pollution Bulletin</i> , 2016, 110, 726-734.	5.0	19
772	“Every Gene Is Everywhere but the Environment Selects” Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. <i>Genome Biology and Evolution</i> , 2016, 8, 1388-1400.	2.5	82
773	Characterization of the Cadherin-Catenin Complex of the Sea Anemone <i>Nematostella vectensis</i> and Implications for the Evolution of Metazoan Cell-Cell Adhesion. <i>Molecular Biology and Evolution</i> , 2016, 33, 2016-2029.	8.9	22
774	Protein architecture and core residues in unwound $\alpha$ -helices provide insights to the transport function of plant AtCHX17. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1983-1998.	2.6	16
775	Regulation of genetic flux between bacteria by restriction-modification systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5658-5663.	7.1	161
776	Evolutionary Changes on the Way to Clathrin-Mediated Endocytosis in Animals. <i>Genome Biology and Evolution</i> , 2016, 8, 588-606.	2.5	23
777	Dynamic Evolution of Nitric Oxide Detoxifying Flavohemoglobins, a Family of Single-Protein Metabolic Modules in Bacteria and Eukaryotes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1979-1987.	8.9	46
778	Refined <i>Pichia pastoris</i> reference genome sequence. <i>Journal of Biotechnology</i> , 2016, 235, 121-131.	3.8	84
779	Delineation of Steroid-Degrading Microorganisms through Comparative Genomic Analysis. <i>MBio</i> , 2016, 7, e00166.	4.1	107
780	Mitochondrial Genomes of <i>Anopheles</i> ( <i>Kerteszia</i> ) (Diptera: Culicidae) From the Atlantic Forest, Brazil. <i>Journal of Medical Entomology</i> , 2016, 53, 790-797.	1.8	17
781	De novo transcriptome analysis reveals tissue-specific differences in gene expression in <i>Salix arbutifolia</i> . <i>Trees - Structure and Function</i> , 2016, 30, 1647-1655.	1.9	4
782	SPAR: a random forest-based predictor for self-interacting proteins with fine-grained domain information. <i>Amino Acids</i> , 2016, 48, 1655-1665.	2.7	25
783	Comprehensive analysis of NAC transcription factors in diploid <i>Gossypium</i> : sequence conservation and expression analysis uncover their roles during fiber development. <i>Science China Life Sciences</i> , 2016, 59, 142-153.	4.9	24
784	Genome-wide identification and characterization of the Dof gene family in moso bamboo ( <i>Phyllostachys heterocycla</i> var. <i>pubescens</i> ). <i>Genes and Genomics</i> , 2016, 38, 733-745.	1.4	14

#	ARTICLE	IF	CITATIONS
785	A Eukaryote without a Mitochondrial Organelle. <i>Current Biology</i> , 2016, 26, 1274-1284.	3.9	302
786	Characterizing gene sets using discriminative random walks with restart on heterogeneous biological networks. <i>Bioinformatics</i> , 2016, 32, 2167-2175.	4.1	38
787	The homologous identification of the stem rust resistance genes Rpg5, Adf3 and RGA1 in the relatives of barley. <i>Cytology and Genetics</i> , 2016, 50, 96-105.	0.5	1
788	Presence of a carboxy-terminal pseudorepeat and disease-like pseudohyperphosphorylation critically influence tau's interaction with microtubules in axon-like processes. <i>Molecular Biology of the Cell</i> , 2016, 27, 3537-3549.	2.1	53
789	Benchmarking the next generation of homology inference tools. <i>Bioinformatics</i> , 2016, 32, 2636-2641.	4.1	14
790	Voltage-Gated Sodium Channels. <i>Current Topics in Membranes</i> , 2016, 78, 261-286.	0.9	21
791	High rates of microbial dinitrogen fixation and sulfate reduction associated with the Mediterranean seagrass <i>Posidonia oceanica</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 476-483.	2.8	56
792	Concomitant emergence of the antisense protein gene of HIV-1 and of the pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11537-11542.	7.1	64
793	F-box genes: Genome-wide expansion, evolution and their contribution to pollen growth in pear ( <i>Pyrus bretschneideri</i> ). <i>Plant Science</i> , 2016, 253, 164-175.	3.6	42
794	Draft Genome Sequence of Marine Sponge Symbiont <i>Pseudoalteromonas luteoviolacea</i> IPB1, Isolated from Hilo, Hawaii. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
795	Genomic charting of ribosomally synthesized natural product chemical space facilitates targeted mining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6343-E6351.	7.1	127
796	Using <sc>HHsearch</sc> to tackle proteins of unknown function: A pilot study with <sc>PH</sc> domains. <i>Traffic</i> , 2016, 17, 1214-1226.	2.7	51
797	LINEs between Species: Evolutionary Dynamics of LINE-1 Retrotransposons across the Eukaryotic Tree of Life. <i>Genome Biology and Evolution</i> , 2016, 8, 3301-3322.	2.5	66
798	An atypical segment swap in the DN and DC domains of the Acr_tran family resistance-nodulation-cell division pump. <i>Journal of Structural Biology</i> , 2016, 196, 358-363.	2.8	1
799	Terpene synthase genes in eukaryotes beyond plants and fungi: Occurrence in social amoebae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12132-12137.	7.1	92
800	Genome-wide survey and phylogeny of S-Ribosylhomocysteine (LuxS) enzyme in bacterial genomes. <i>BMC Genomics</i> , 2016, 17, 742.	2.8	12
801	A Eukaryotic-like Serine/Threonine Kinase Protects Staphylococci against Phages. <i>Cell Host and Microbe</i> , 2016, 20, 471-481.	11.0	72
802	Detection of N2O-producing fungi in environment using nitrite reductase gene (nirK)-targeting primers. <i>Fungal Biology</i> , 2016, 120, 1479-1492.	2.5	25

#	ARTICLE	IF	CITATIONS
803	Advances in the characterization of RNA-binding proteins. Wiley Interdisciplinary Reviews RNA, 2016, 7, 793-810.	6.4	89
804	An alphabaculovirus isolated from dead <i>Lymantria dispar</i> larvae shows high genetic similarity to baculovirus previously isolated from <i>Lymantria monacha</i> – An example of adaptation to a new host. Journal of Invertebrate Pathology, 2016, 139, 56-66.	3.2	11
805	Identification and Correction of Erroneous Protein Sequences in Public Databases. Methods in Molecular Biology, 2016, 1415, 179-192.	0.9	1
806	When predator becomes prey: investigating the salivary transcriptome of the shark-feeding leech <i>Pontobdella macrothela</i> (Hirudinea: Piscicolidae). Zoological Journal of the Linnean Society, 2016, , .	2.3	10
807	Putative binding mode of <i>Escherichia coli</i> exopolyphosphatase and polyphosphates based on a hybrid in silico/biochemical approach. Archives of Biochemistry and Biophysics, 2016, 606, 64-72.	3.0	1
808	Diverse gene functions in a soil mobilome. Soil Biology and Biochemistry, 2016, 101, 175-183.	8.8	24
809	Transcription Factors Involved in Plant Drought Tolerance Regulation. , 2016, , 315-358.		1
810	Conservation of the C-type lectin fold for accommodating massive sequence variation in archaeal diversity-generating retroelements. BMC Structural Biology, 2016, 16, 13.	2.3	15
811	Comparative analyses of ubiquitin-like <i>ATG8</i> and cysteine protease <i>ATG4</i> autophagy genes in the plant lineage and cross-kingdom processing of ATG8 by ATG4. Autophagy, 2016, 12, 2054-2068.	9.1	50
812	Baseplate assembly of phage Mu: Defining the conserved core components of contractile-tailed phages and related bacterial systems. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10174-10179.	7.1	46
813	Eye development and photoreceptor differentiation in the cephalopod <i>Doryteuthis pealeii</i> . Development (Cambridge), 2016, 143, 3168-81.	2.5	24
814	Improved glycerol to ethanol conversion by <i>E. coli</i> using a metagenomic fragment isolated from an anaerobic reactor. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 1405-1416.	3.0	18
815	Uncovering Earth's virome. Nature, 2016, 536, 425-430.	27.8	880
816	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5163-71.	7.1	211
817	Genome sequence and comparative analysis of clavicipitaceous insect-pathogenic fungus <i>Aschersonia badia</i> with <i>Metarhizium</i> spp.. BMC Genomics, 2016, 17, 367.	2.8	12
818	Identification of Multiple Phytotoxins Produced by <i>Fusarium virguliforme</i> Including a Phytotoxic Effector (FvNIS1) Associated With Sudden Death Syndrome Foliar Symptoms. Molecular Plant-Microbe Interactions, 2016, 29, 96-108.	2.6	53
819	The role of ADP-ribosylation in regulating DNA interstrand crosslink repair. Journal of Cell Science, 2016, 129, 3845-3858.	2.0	15
820	Identification and characterization of the GhHsp20 gene family in <i>Gossypium hirsutum</i> . Scientific Reports, 2016, 6, 32517.	3.3	29



#	ARTICLE	IF	CITATIONS
821	The ERF transcription factor family in cassava: genome-wide characterization and expression analyses against drought stress. <i>Scientific Reports</i> , 2016, 6, 37379.	3.3	33
822	A Fungal Effector With Host Nuclear Localization and DNA-Binding Properties Is Required for Maize Anthracnose Development. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 83-95.	2.6	58
823	The genome sequence of the outbreeding globe artichoke constructed de novo incorporating a phase-aware low-pass sequencing strategy of F1 progeny. <i>Scientific Reports</i> , 2016, 6, 19427.	3.3	106
824	Near complete genome sequence of the animal feed probiotic, <i>Bacillus amyloliquefaciens</i> H57. <i>Standards in Genomic Sciences</i> , 2016, 11, 60.	1.5	16
825	Identification of transcription hubs that control lipid metabolism and carbon concentrating mechanism in model microalgae <i>chlamydomonas reinhardtii</i> using regulatory networks: Regulatory networks hubs in <i>C. reinhardtii</i> that control lipid and carbon concentrating metabolic pathways. , 2016, , ,		1
826	Characterization of a venom gland-associated rhabdovirus in the parasitoid wasp <i>Diachasmimorpha longicauda</i> . <i>Journal of Insect Physiology</i> , 2016, 91-92, 48-55.	2.0	15
827	Peptidase specificity from the substrate cleavage collection in the MEROPS database and a tool to measure cleavage site conservation. <i>Biochimie</i> , 2016, 122, 5-30.	2.6	54
828	Origins and Evolution of tetherin , an Orphan Antiviral Gene. <i>Cell Host and Microbe</i> , 2016, 20, 189-201.	11.0	35
829	A Catalytically Competent Terpene Synthase Inferred Using Ancestral Sequence Reconstruction Strategy. <i>ACS Catalysis</i> , 2016, 6, 5345-5349.	11.2	2
830	ATP6AP1 deficiency causes an immunodeficiency with hepatopathy, cognitive impairment and abnormal protein glycosylation. <i>Nature Communications</i> , 2016, 7, 11600.	12.8	110
831	Novel Genomic and Evolutionary Insight of WRKY Transcription Factors in Plant Lineage. <i>Scientific Reports</i> , 2016, 6, 37309.	3.3	55
832	Improved metagenome assemblies and taxonomic binning using long-read circular consensus sequence data. <i>Scientific Reports</i> , 2016, 6, 25373.	3.3	139
833	Monolignol ferulate conjugates are naturally incorporated into plant lignins. <i>Science Advances</i> , 2016, 2, e1600393.	10.3	147
834	dRHP-PseRA: detecting remote homology proteins using profile-based pseudo protein sequence and rank aggregation. <i>Scientific Reports</i> , 2016, 6, 32333.	3.3	84
835	Metagenomic analysis and functional characterization of the biogas microbiome using high throughput shotgun sequencing and a novel binning strategy. <i>Biotechnology for Biofuels</i> , 2016, 9, 26.	6.2	248
836	Expansion of Lysine-rich Repeats in Plasmodium Proteins Generates Novel Localization Sequences That Target the Periphery of the Host Erythrocyte. <i>Journal of Biological Chemistry</i> , 2016, 291, 26188-26207.	3.4	32
837	Antibody-Based Therapy for Enterococcal Catheter-Associated Urinary Tract Infections. <i>MBio</i> , 2016, 7, .	4.1	48
838	Absence of N-terminal acetyltransferase diversification during evolution of eukaryotic organisms. <i>Scientific Reports</i> , 2016, 6, 21304.	3.3	41





#	ARTICLE	IF	CITATIONS
857	Evolution of the Tim17 protein family. <i>Biology Direct</i> , 2016, 11, 54.	4.6	56
858	A comprehensive view of the web-resources related to sericulture. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw086.	3.0	3
859	Heterotrophic <i>Proteobacteria</i> in the vicinity of diffuse hydrothermal venting. <i>Environmental Microbiology</i> , 2016, 18, 4348-4368.	3.8	63
860	A phospholipase A <sub>1</sub> antibacterial Type VI secretion effector interacts directly with the C-terminal domain of the VgrG spike protein for delivery. <i>Molecular Microbiology</i> , 2016, 99, 1099-1118.	2.5	179
861	Transcription factors in microalgae: genome-wide prediction and comparative analysis. <i>BMC Genomics</i> , 2016, 17, 282.	2.8	52
862	Marine Fungi. , 2016, , 99-153.		8
863	Long noncoding RNAs expressed in human hepatic stellate cells form networks with extracellular matrix proteins. <i>Genome Medicine</i> , 2016, 8, 31.	8.2	59
864	Permanent draft genome sequence of <i>Desulfurococcus mobilis</i> type strain DSM 2161, a thermoacidophilic sulfur-reducing crenarchaeon isolated from acidic hot springs of Hveravellir, Iceland. <i>Standards in Genomic Sciences</i> , 2016, 11, 3.	1.5	2
865	Applications of Bio-molecular Databases in Bioinformatics. <i>Studies in Computational Intelligence</i> , 2016, , 329-351.	0.9	4
866	The evolution of genome mining in microbes – a review. <i>Natural Product Reports</i> , 2016, 33, 988-1005.	10.3	538
867	Mitochondrial selfish elements and the evolution of biological novelties. <i>Environmental Epigenetics</i> , 2016, 62, 687-697.	1.8	34
868	Ancient Eukaryotic Origin and Evolutionary Plasticity of Nuclear Lamina. <i>Genome Biology and Evolution</i> , 2016, 8, 2663-2671.	2.5	57
869	A Leucine-Rich Repeat Receptor-like Kinase from the Antarctic Moss <i>Pohlia nutans</i> Confers Salinity and ABA Stress Tolerance. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1136-1145.	1.8	8
870	Consensus protein design. <i>Protein Engineering, Design and Selection</i> , 2016, 29, 245-251.	2.1	160
871	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 34-44.	1.0	22
872	Medical Imaging in Clinical Applications. <i>Studies in Computational Intelligence</i> , 2016, , .	0.9	13
873	Functional Characterization of Maize C2H2 Zinc-Finger Gene Family. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 761-776.	1.8	27
874	Environmental Breviatea harbour mutualistic <i>Arcobacter</i> epibionts. <i>Nature</i> , 2016, 534, 254-258.	27.8	68

#	ARTICLE	IF	CITATIONS
875	Holding it together: rapid evolution and positive selection in the synaptonemal complex of <i>Drosophila</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 91.	3.2	24
876	Comparative genomics and prediction of conditionally dispensable sequences in legume "infecting" <i>Fusarium oxysporum</i> formae speciales facilitates identification of candidate effectors. <i>BMC Genomics</i> , 2016, 17, 191.	2.8	109
877	Comparative transcriptomics and proteomics of three different aphid species identifies core and diverse effector sets. <i>BMC Genomics</i> , 2016, 17, 172.	2.8	92
878	CrAgDb "a database of annotated <i>Cryptosporidium parvum</i> haplotype repertoire in archaeal genomes. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw030.	1.8	9
879	Comparative Genomics of Interreplicore Translocations in Bacteria: A Measure of Chromosome Topology?. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1597-1606.	1.8	11
880	Finding Protein and Nucleotide Similarities with FASTA. <i>Current Protocols in Bioinformatics</i> , 2016, 53, 3.9.1-3.9.25.	25.8	92
881	E <sub>scp</sub> effector <sub>P</sub> : predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016, 210, 743-761.	7.3	438
882	Genome Structural Diversity among 31 <i>Bordetella pertussis</i> Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. <i>MSphere</i> , 2016, 1, .	2.9	51
883	The evolution of ERMIONE in mitochondrial biogenesis and lipid homeostasis: An evolutionary view from comparative cell biology. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2016, 1861, 900-912.	2.4	49
884	CAMP <sub>R3</sub> : a database on sequences, structures and signatures of antimicrobial peptides: Table 1.. <i>Nucleic Acids Research</i> , 2016, 44, D1094-D1097.	14.5	521
885	Functional divergence of GhCFE5 homoeologs revealed in cotton fiber and <i>Arabidopsis</i> root cell development. <i>Plant Cell Reports</i> , 2016, 35, 867-881.	5.6	17
886	Mycobacterial Pan-Genome Analysis Suggests Important Role of Plasmids in the Radiation of Type VII Secretion Systems. <i>Genome Biology and Evolution</i> , 2016, 8, 387-402.	2.5	81
887	Screening and discovery of lineage-specific mitochondrial membrane proteins in <i>Entamoeba histolytica</i> . <i>Molecular and Biochemical Parasitology</i> , 2016, 209, 10-17.	1.1	13
888	Metagenomic assessment of the functional potential of the rumen microbiome in Holstein dairy cows. <i>Anaerobe</i> , 2016, 38, 50-60.	2.1	93
889	Lineage-Specific Patterns of Genome Deterioration in Obligate Symbionts of Sharpshooter Leafhoppers. <i>Genome Biology and Evolution</i> , 2016, 8, 296-301.	2.5	28
890	<i>i</i> RAPID <i>i</i> signature: identification of ribonucleoproteins and RNA-binding regions. <i>Bioinformatics</i> , 2016, 32, 773-775.	4.1	129
891	Long noncoding RNAs in T lymphocytes. <i>Journal of Leukocyte Biology</i> , 2016, 99, 31-44.	3.3	31
892	In silico identification of BESS-DC genes and expression analysis in the silkworm, <i>Bombyx mori</i> . <i>Gene</i> , 2016, 575, 478-487.	2.2	2

#	ARTICLE	IF	CITATIONS
893	De novo analysis of transcriptome reveals genes associated with leaf abscission in sugarcane ( <i>Saccharum officinarum</i> L.). <i>BMC Genomics</i> , 2016, 17, 195.	2.8	51
894	Proteome distribution between nucleoplasm and nucleolus and its relation to ribosome biogenesis in <i>Arabidopsis thaliana</i> . <i>RNA Biology</i> , 2016, 13, 441-454.	3.1	48
895	Evolutionary distinctiveness of fatty acid and polyketide synthesis in eukaryotes. <i>ISME Journal</i> , 2016, 10, 1877-1890.	9.8	72
896	New features of desiccation tolerance in the lichen photobiont <i>Trebouxia gelatinosa</i> are revealed by a transcriptomic approach. <i>Plant Molecular Biology</i> , 2016, 91, 319-339.	3.9	69
897	In-silico identification of candidate genes for fertility restoration in cytoplasmic male sterile perennial ryegrass ( <i>Lolium perenne</i> L.). <i>Genome Biology and Evolution</i> , 2016, 9, evw047.	2.5	22
898	The CopC Family: Structural and Bioinformatic Insights into a Diverse Group of Periplasmic Copper Binding Proteins. <i>Biochemistry</i> , 2016, 55, 2278-2290.	2.5	78
899	Accurate contact predictions using covariation techniques and machine learning. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 145-151.	2.6	48
900	Genome Sequence and Analysis of <i>Escherichia coli</i> MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. <i>Genome Biology and Evolution</i> , 2016, 8, 742-752.	2.5	35
901	The mid-developmental transition and the evolution of animal body plans. <i>Nature</i> , 2016, 531, 637-641.	27.8	231
902	Ecological Genomics of the Uncultivated Marine Roseobacter Lineage CHAB-I-5. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2100-2111.	3.1	50
903	Identification and Functional Prediction of Large Intergenic Noncoding RNAs (lincRNAs) in Rainbow Trout ( <i>Oncorhynchus mykiss</i> ). <i>Marine Biotechnology</i> , 2016, 18, 271-282.	2.4	53
904	Tracing the Archaeal Origins of Eukaryotic Membrane-Trafficking System Building Blocks. <i>Molecular Biology and Evolution</i> , 2016, 33, 1528-1541.	8.9	77
905	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
906	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing. <i>Cell</i> , 2016, 164, 805-817.	28.9	479
907	Assembly and clustering of natural antibiotics guides target identification. <i>Nature Chemical Biology</i> , 2016, 12, 233-239.	8.0	86
908	Genome-wide analysis of CrRLK1L gene family in <i>Gossypium</i> and identification of candidate CrRLK1L genes related to fiber development. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1137-1154.	2.1	27
909	Chitosan enhances parasitism of <i>Meloidogyne javanica</i> eggs by the nematophagous fungus <i>Pochonia chlamydosporia</i> . <i>Fungal Biology</i> , 2016, 120, 572-585.	2.5	51
910	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	12.8	189

#	ARTICLE	IF	CITATIONS
911	Early Folding Events, Local Interactions, and Conservation of Protein Backbone Rigidity. Biophysical Journal, 2016, 110, 572-583.	0.5	23
912	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. Applied and Environmental Microbiology, 2016, 82, 2872-2883.	3.1	102
913	<i>In silico</i> identification, phylogeny and expression analysis of expansin superfamily in <i>Medicago truncatula</i> . Biotechnology and Biotechnological Equipment, 2016, 30, 197-203.	1.3	7
914	Gene Family Expansions in Aphids Maintained by Endosymbiotic and Nonsymbiotic Traits. Genome Biology and Evolution, 2016, 8, 753-764.	2.5	27
915	Protein Structure Is Related to RNA Structural Reactivity In Vivo. Journal of Molecular Biology, 2016, 428, 758-766.	4.2	14
916	Coiled-coil domain containing 42 ( Ccdc 42) is necessary for proper sperm development and male fertility in the mouse. Developmental Biology, 2016, 412, 208-218.	2.0	54
917	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. Molecular and Cellular Proteomics, 2016, 15, 236-245.	3.8	68
918	Current updates on computer aided protein modeling and designing. International Journal of Biological Macromolecules, 2016, 85, 48-62.	7.5	123
919	Reverse transcriptase genes are highly abundant and transcriptionally active in marine plankton assemblages. ISME Journal, 2016, 10, 1134-1146.	9.8	35
920	Prediction of Type II Toxin-Antitoxin Loci in Klebsiella pneumoniae Genome Sequences. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 143-149.	3.6	22
921	Neurospora crassa transcriptomics reveals oxidative stress and plasma membrane homeostasis biology genes as key targets in response to chitosan. Molecular BioSystems, 2016, 12, 391-403.	2.9	30
922	Genome-wide analysis and expression patterns of ZF-HD transcription factors under different developmental tissues and abiotic stresses in Chinese cabbage. Molecular Genetics and Genomics, 2016, 291, 1451-1464.	2.1	53
923	Genome-wide identification and phylogenetic analysis of plant RNA binding proteins comprising both RNA recognition motifs and contiguous glycine residues. Molecular Genetics and Genomics, 2016, 291, 763-773.	2.1	10
924	Transcriptome profiling of the cysticercus stage of the laboratory model Taenia crassiceps, strain ORF. Acta Tropica, 2016, 154, 50-62.	2.0	13
925	deepBase v2.0: identification, expression, evolution and function of small RNAs, lncRNAs and circular RNAs from deep-sequencing data. Nucleic Acids Research, 2016, 44, D196-D202.	14.5	203
926	Hidden Markov models for gene sequence classification. Pattern Analysis and Applications, 2016, 19, 793-805.	4.6	9
927	Complete genome analysis of Clostridium bornimense strain M2/40T: A new acidogenic Clostridium species isolated from a mesophilic two-phase laboratory-scale biogas reactor. Journal of Biotechnology, 2016, 232, 38-49.	3.8	19
928	Multiple Origins of Eukaryotic <i>cox15</i> Suggest Horizontal Gene Transfer from Bacteria to Jakobid Mitochondrial DNA. Molecular Biology and Evolution, 2016, 33, 122-133.	8.9	21

#	ARTICLE	IF	CITATIONS
929	The complement of family M1 aminopeptidases of <i>Haemonchus contortus</i> – Biotechnological implications. <i>Biotechnology Advances</i> , 2016, 34, 65-76.	11.7	8
930	Plant Bioinformatics. <i>Methods in Molecular Biology</i> , 2016, .	0.9	11
931	Evolutionary history of PEPC genes in green plants: Implications for the evolution of CAM in orchids. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 559-564.	2.7	39
932	Proteomic Tools for the Analysis of Cytoskeleton Proteins. <i>Methods in Molecular Biology</i> , 2016, 1365, 385-413.	0.9	1
933	Identification of Genes Conferring Tolerance to Lignocellulose-Derived Inhibitors by Functional Selections in Soil Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 528-537.	3.1	20
934	Cytoskeleton Methods and Protocols. <i>Methods in Molecular Biology</i> , 2016, 1365, v-vi.	0.9	5
936	Dormancy-associated MADS-box genes and microRNAs jointly control dormancy transition in pear ( <i>Pyrus pyrifolia</i> white pear group) flower bud. <i>Journal of Experimental Botany</i> , 2016, 67, 239-257.	4.8	170
937	Cloning, expression, and molecular dynamics simulations of a xylosidase obtained from <i>Thermomyces lanuginosus</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1681-1692.	3.5	45
938	Rapid and enhanced remote homology detection by cascading hidden Markov model searches in sequence space. <i>Bioinformatics</i> , 2016, 32, 338-344.	4.1	5
939	Quantitative proteomic analysis of <i>Araucaria angustifolia</i> (Bertol.) Kuntze cell lines with contrasting embryogenic potential. <i>Journal of Proteomics</i> , 2016, 130, 180-189.	2.4	40
940	GDSL esterase/lipase genes in <i>Brassica rapa</i> L.: genome-wide identification and expression analysis. <i>Molecular Genetics and Genomics</i> , 2016, 291, 531-542.	2.1	62
941	Hepatic Long Intergenic Noncoding RNAs: High Promoter Conservation and Dynamic, Sex-Dependent Transcriptional Regulation by Growth Hormone. <i>Molecular and Cellular Biology</i> , 2016, 36, 50-69.	2.3	39
942	Genome-wide survey and expression analysis of the calcium-dependent protein kinase gene family in cassava. <i>Molecular Genetics and Genomics</i> , 2016, 291, 241-253.	2.1	36
943	Computational recognition for long non-coding RNA (lncRNA): Software and databases. <i>Briefings in Bioinformatics</i> , 2017, 18, 9-27.	6.5	42
944	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. <i>ISME Journal</i> , 2017, 11, 237-247.	9.8	298
945	The repetitive DNA element BncDNA, enriched in the B chromosome of the cichlid fish <i>Astatotilapia latifasciata</i> , transcribes a potentially noncoding RNA. <i>Chromosoma</i> , 2017, 126, 313-323.	2.2	31
946	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	3.8	212
947	An integrated and comprehensive transcriptome reveals immune-related genes and signal pathways in topmouth culter ( <i>Culter alburnus</i> ). <i>Aquaculture Research</i> , 2017, 48, 2231-2242.	1.8	5

#	ARTICLE	IF	CITATIONS
948	Broad taxonomic characterization of <i>Verticillium</i> wilt resistance genes reveals an ancient origin of the tomato Ve1 immune receptor. <i>Molecular Plant Pathology</i> , 2017, 18, 195-209.	4.2	58
949	Structure prediction and functional analyses of a thermostable lipase obtained from <i>Shewanella putrefaciens</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2123-2135.	3.5	34
950	Hidden Markov Models for Protein Domain Homology Identification and Analysis. <i>Methods in Molecular Biology</i> , 2017, 1555, 47-58.	0.9	3
951	Identification of functional enolase genes of the silkworm <i>Bombyx mori</i> from public databases with a combination of dry and wet bench processes. <i>BMC Genomics</i> , 2017, 18, 83.	2.8	12
952	Discovery and metagenomic analysis of an anammox bacterial enrichment related to <i>Candidatus Brocadia caroliniensis</i> in a full-scale glycerol-fed nitrification-denitrification separate centrate treatment process. <i>Water Research</i> , 2017, 111, 265-273.	11.3	122
953	Traditional versus 3â€² RNA-seq in a non-model species. <i>Genomics Data</i> , 2017, 11, 9-16.	1.3	35
954	Mechanism of Deletion Removing All Dystrophin Exons in a Canine Model for DMD Implicates Concerted Evolution of X Chromosome Pseudogenes. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 4, 62-71.	4.1	6
955	Diversity of Microbial Carbohydrate-Active enZymes (CAZymes) Associated with Freshwater and Soil Samples from Caatinga Biome. <i>Microbial Ecology</i> , 2017, 74, 89-105.	2.8	19
956	Identification and evolutionary analysis of long non-coding RNAs in zebra finch. <i>BMC Genomics</i> , 2017, 18, 117.	2.8	13
957	Genome-wide identification and analysis of biotic and abiotic stress regulation of small heat shock protein ( HSP20 ) family genes in bread wheat. <i>Journal of Plant Physiology</i> , 2017, 211, 100-113.	3.5	112
958	Multiple resistance to pirimiphos-methyl and bifenthrin in <i>Tribolium castaneum</i> involves the activity of lipases, esterases, and laccase2. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 195, 27-43.	2.6	14
959	De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. <i>Scientific Reports</i> , 2017, 7, 40472.	3.3	18
960	No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, msw284.	8.9	74
961	Genome Sequencing of the Behavior Manipulating Virus LbFV Reveals a Possible New Virus Family. <i>Genome Biology and Evolution</i> , 2016, 8, 3718-3739.	2.5	21
962	Exploring the genomic diversity of black yeasts and relatives ( <i>Chaetothyriales</i> , <i>Ascomycota</i> ). <i>Studies in Mycology</i> , 2017, 86, 1-28.	7.2	144
963	Introduction to Hidden Markov Models and Its Applications in Biology. <i>Methods in Molecular Biology</i> , 2017, 1552, 1-12.	0.9	8
964	Complete genome sequence of <i>Lysinibacillus sphaericus</i> LMG 22257, a strain with ureolytic activity inducing calcium carbonate precipitation. <i>Journal of Biotechnology</i> , 2017, 246, 33-35.	3.8	5
965	Genomic Microdiversity of <i>Bifidobacterium pseudocatenulatum</i> Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention. <i>MBio</i> , 2017, 8, .	4.1	43



#	ARTICLE	IF	CITATIONS
966	Expansion and stress responses of the AP2/EREBP superfamily in cotton. BMC Genomics, 2017, 18, 118.	2.8	80
967	Effect of light and prey availability on gene expression of the mixotrophic chrysophyte, <i>Ochromonas</i> sp.. BMC Genomics, 2017, 18, 163.	2.8	28
968	Not all predicted CRISPR-Cas systems are equal: isolated cas genes and classes of CRISPR like elements. BMC Bioinformatics, 2017, 18, 92.	2.6	160
969	Loggerhead sea turtle embryos ( <i>Caretta caretta</i> ) regulate expression of stress response and developmental genes when exposed to a biologically realistic heat stress. Molecular Ecology, 2017, 26, 2978-2992.	3.9	39
970	Statoviruses, A novel taxon of RNA viruses present in the gastrointestinal tracts of diverse mammals. Virology, 2017, 504, 36-44.	2.4	16
971	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. Scientific Reports, 2017, 7, 44103.	3.3	67
972	Role of Modular Polyketide Synthases in the Production of Polyether Ladder Compounds in <i>Ciguatoin</i> -Producing <i>Gambierdiscus polynesiensis</i> and <i>G. excentricus</i> (Dinophyceae). Journal of Eukaryotic Microbiology, 2017, 64, 691-706.	1.7	31
973	Lateral Gene Transfer in the Adaptation of the Anaerobic Parasite <i>Blastocystis</i> to the Gut. Current Biology, 2017, 27, 807-820.	3.9	94
974	De novo transcriptome assemblies of four accessions of the metal hyperaccumulator plant <i>Noccaea caerulescens</i> . Scientific Data, 2017, 4, 160131.	5.3	38
975	Functional characterization of AGAMOUS-subfamily members from cotton during reproductive development and in response to plant hormones. Plant Reproduction, 2017, 30, 19-39.	2.2	12
976	Comparative transcriptome analysis of two contrasting watermelon genotypes during fruit development and ripening. BMC Genomics, 2017, 18, 3.	2.8	72
977	Leaf transcriptome analysis of a subtropical evergreen broadleaf plant, wild oil-tea camellia ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	2.8	46
978	Complete genome sequence of <i>Jiangella gansuensis</i> strain YIM 002T (DSM 44835T), the type species of the genus <i>Jiangella</i> and source of new antibiotic compounds. Standards in Genomic Sciences, 2017, 12, 21.	1.5	9
979	Genome-wide identification of the TIFY gene family in three cultivated <i>Gossypium</i> species and the expression of JAZ genes. Scientific Reports, 2017, 7, 42418.	3.3	46
980	Computational tools for exploring sequence databases as a resource for antimicrobial peptides. Biotechnology Advances, 2017, 35, 337-349.	11.7	111
981	LoaP is a broadly conserved antiterminator protein that regulates antibiotic gene clusters in <i>Bacillus amyloliquefaciens</i> . Nature Microbiology, 2017, 2, 17003.	13.3	45
982	Origins and challenges of viral dark matter. Virus Research, 2017, 239, 136-142.	2.2	167
983	Arabidopsis E3 ubiquitin ligase PLANT U-box13 (<sc>PUB</sc>13) regulates chitin receptor LYSIN MOTIF RECEPTOR KINASE5 (<sc>LYK</sc>5) protein abundance. New Phytologist, 2017, 214, 1646-1656.	7.3	114

#	ARTICLE	IF	CITATIONS
984	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	21.4	316
985	De novo RNA sequence assembly during in vivo inflammatory stress reveals hundreds of unannotated lincRNAs in human blood CD14+ monocytes and in adipose tissue. <i>Physiological Genomics</i> , 2017, 49, 287-305.	2.3	9
986	Melody Retrieval and Classification Using Biologically-Inspired Techniques. <i>Lecture Notes in Computer Science</i> , 2017, , 49-64.	1.3	0
987	Genomics and evolution of protein phosphatases. <i>Science Signaling</i> , 2017, 10, .	3.6	206
988	Genome-wide identification and characterization of NB-ARC resistant genes in wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 58	5.6	30
989	MARS: A protein family involved in the formation of vertical skeletal elements. <i>Journal of Structural Biology</i> , 2017, 198, 92-102.	2.8	13
990	Functional and evolutionary characterization of Ohr proteins in eukaryotes reveals many active homologs among pathogenic fungi. <i>Redox Biology</i> , 2017, 12, 600-609.	9.0	15
991	<i>Staphylococcus sciuri</i> bacteriophages double-convert for staphylokinase and phospholipase, mediate interspecies plasmid transduction, and package mecA gene. <i>Scientific Reports</i> , 2017, 7, 46319.	3.3	48
992	Genome-wide identification, characterization of the MADS-box gene family in Chinese jujube and their involvement in flower development. <i>Scientific Reports</i> , 2017, 7, 1025.	3.3	42
993	The plastid outer membrane localized LPTD1 is important for glycerolipid remodelling under phosphate starvation. <i>Plant, Cell and Environment</i> , 2017, 40, 1643-1657.	5.7	13
994	Transcriptomic changes in an animal-bacterial symbiosis under modeled microgravity conditions. <i>Scientific Reports</i> , 2017, 7, 46318.	3.3	19
995	Protein-Carbohydrate Interactions. <i>Methods in Molecular Biology</i> , 2017, , .	0.9	4
996	A Concurrent Subtractive Assembly Approach for Identification of Disease Associated Sub-metagenomes. <i>Lecture Notes in Computer Science</i> , 2017, 2017, 18-33.	1.3	8
997	Metagenomics and CAZyme Discovery. <i>Methods in Molecular Biology</i> , 2017, 1588, 255-277.	0.9	19
998	Structures of closed and open conformations of dimeric human ATM. <i>Science Advances</i> , 2017, 3, e1700933.	10.3	91
999	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	2.8	11
1000	Tracking microbial colonization in fecal microbiota transplantation experiments via genome-resolved metagenomics. <i>Microbiome</i> , 2017, 5, 50.	11.1	78
1001	Identification and allelic dissection uncover roles of lncRNAs in secondary growth of <i>Populus tomentosa</i> . <i>DNA Research</i> , 2017, 24, 473-486.	3.4	37

#	ARTICLE	IF	CITATIONS
1002	Genetic hurdles limit the arms race between <i>Prochlorococcus</i> and the T7-like podoviruses infecting them. ISME Journal, 2017, 11, 1836-1851.	9.8	36
1003	Comparative genomic analysis of SET domain family reveals the origin, expansion, and putative function of the arthropod-specific SmydA genes as histone modifiers in insects. GigaScience, 2017, 6, 1-16.	6.4	19
1004	Lateral gene transfer of <i>p</i> -cresol- and indole-producing enzymes from environmental bacteria to <i>Mastigamoeba balamuthi</i> . Environmental Microbiology, 2017, 19, 1091-1102.	3.8	10
1006	Tomato root microbiota and <i>Phytophthora parasitica</i> -associated disease. Microbiome, 2017, 5, 56.	11.1	65
1007	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. Journal of Biological Chemistry, 2017, 292, 13271-13283.	3.4	26
1008	Phylogenomic Synteny Network Analysis of MADS-Box Transcription Factor Genes Reveals Lineage-Specific Transpositions, Ancient Tandem Duplications, and Deep Positional Conservation. Plant Cell, 2017, 29, 1278-1292.	6.6	106
1009	Functional annotation and analysis of the <i>Ornithodoros moubata</i> midgut genes differentially expressed after blood feeding. Ticks and Tick-borne Diseases, 2017, 8, 693-708.	2.7	34
1010	Comparative genomic analysis of innate immunity reveals novel and conserved components in crustacean food crop species. BMC Genomics, 2017, 18, 389.	2.8	37
1011	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. Emerging Microbes and Infections, 2017, 6, 1-7.	6.5	44
1012	Phylogenomics. , 2017, , .		47
1013	De novo assembly, functional annotation, and analysis of the giant reed ( <i>Arundo donax</i> L.) leaf transcriptome provide tools for the development of a biofuel feedstock. Biotechnology for Biofuels, 2017, 10, 138.	6.2	37
1014	Plant Argonaute Proteins. Methods in Molecular Biology, 2017, , .	0.9	1
1015	Permanent Draft Genome Sequence of <i>Desulfurococcus amylolyticus</i> Strain Z-533 <sup>T</sup> , a Peptide and Starch Degradar Isolated from Thermal Springs in the Kamchatka Peninsula and Kunashir Island, Russia. Genome Announcements, 2017, 5, .	0.8	2
1016	Phylogenetic and Evolutionary Analysis of Plant ARGONAUTES. Methods in Molecular Biology, 2017, 1640, 267-294.	0.9	9
1017	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. Nature Microbiology, 2017, 2, 17045.	13.3	62
1018	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. Scientific Reports, 2017, 7, 44598.	3.3	340
1019	Epipodial Tentacle Gene Expression and Predetermined Resilience to Summer Mortality in the Commercially Important Greenlip Abalone, <i>Haliotis laevigata</i> . Marine Biotechnology, 2017, 19, 191-205.	2.4	22
1020	A footprint of desiccation tolerance in the genome of <i>Xerophyta viscosa</i> . Nature Plants, 2017, 3, 17038.	9.3	123

#	ARTICLE	IF	CITATIONS
1021	Engineering bacterial thiosulfate and tetrathionate sensors for detecting gut inflammation. <i>Molecular Systems Biology</i> , 2017, 13, 923.	7.2	194
1022	An integrated approach to identify cytochrome P450 superfamilies in plant species within the malvids. , 2017, , .		0
1023	Eros is a novel transmembrane protein that controls the phagocyte respiratory burst and is essential for innate immunity. <i>Journal of Experimental Medicine</i> , 2017, 214, 1111-1128.	8.5	50
1024	Highly potent host external immunity acts as a strong selective force enhancing rapid parasite virulence evolution. <i>Environmental Microbiology</i> , 2017, 19, 2090-2100.	3.8	11
1025	On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria. <i>Science</i> , 2017, 355, 1436-1440.	12.6	344
1026	Malaria parasites possess a telomere repeat-binding protein that shares ancestry with transcription factor IIIA. <i>Nature Microbiology</i> , 2017, 2, 17033.	13.3	17
1027	Phylogeny-Based Systematization of Arabidopsis Proteins with Histone H1 Globular Domain. <i>Plant Physiology</i> , 2017, 174, 27-34.	4.8	28
1028	De novo transcriptome assembly reveals high transcriptional complexity in <i>Pisum sativum</i> axillary buds and shows rapid changes in expression of diurnally regulated genes. <i>BMC Genomics</i> , 2017, 18, 221.	2.8	24
1029	Transcriptional sequencing and analysis of major genes involved in the adventitious root formation of mango cotyledon segments. <i>Planta</i> , 2017, 245, 1193-1213.	3.2	13
1030	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	27.8	471
1031	Xyloglucan breakdown by endo-xyloglucanase family 74 from <i>Aspergillus fumigatus</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2893-2903.	3.6	33
1032	De novo sequencing and comparative analysis of peduncle transcriptomes in <i>Hovenia acerba</i> . <i>Agri Gene</i> , 2017, 3, 32-36.	1.9	2
1033	Genome-wide identification, cloning and characterization of SNARE genes in bread wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.9	1
1034	Genome analysis of <i>Chlamydia trachomatis</i> for functional characterization of hypothetical proteins to discover novel drug targets. <i>International Journal of Biological Macromolecules</i> , 2017, 96, 234-240.	7.5	28
1035	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.9	14
1036	BindML/BindML+: Detecting Protein-Protein Interaction Interface Propensity from Amino Acid Substitution Patterns. <i>Methods in Molecular Biology</i> , 2017, 1529, 279-289.	0.9	4
1037	The evolution of function within the Nudix homology clan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 775-811.	2.6	53
1038	Potential of semiarid soil from Caatinga biome as a novel source for mining lignocellulose-degrading enzymes. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw248.	2.7	15

#	ARTICLE	IF	CITATIONS
1039	Comparative analysis of tree peony petal development by transcriptome sequencing. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	10
1040	Spontaneous circadian rhythms in a cold-adapted natural isolate of <i>Aureobasidium pullulans</i> . <i>Scientific Reports</i> , 2017, 7, 13837.	3.3	15
1041	Algorithms for matching partially labelled sequence graphs. <i>Algorithms for Molecular Biology</i> , 2017, 12, 24.	1.2	1
1042	Potential and pitfalls in the genetic diagnosis of kidney diseases. <i>CKJ: Clinical Kidney Journal</i> , 2017, 10, 581-585.	2.9	7
1043	<i>Chlamydomonas reinhardtii</i> LFO1 Is an IsdG Family Heme Oxygenase. <i>MSphere</i> , 2017, 2, .	2.9	15
1044	Genome scanning for identification and mapping of receptor-like kinase (RLK) gene superfamily in <i>Solanum tuberosum</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 755-765.	3.1	10
1045	Olfactory Ionotropic Receptors in Mosquito <i>Aedes albopictus</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2017, 54, 1229-1235.	1.8	16
1046	Paralogs of the C-Terminal Domain of the Cyanobacterial Orange Carotenoid Protein Are Carotenoid Donors to Helical Carotenoid Proteins. <i>Plant Physiology</i> , 2017, 175, 1283-1303.	4.8	52
1047	Ctenophore relationships and their placement as the sister group to all other animals. <i>Nature Ecology and Evolution</i> , 2017, 1, 1737-1746.	7.8	202
1048	Genomic adaptation to polyphagy and insecticides in a major East Asian noctuid pest. <i>Nature Ecology and Evolution</i> , 2017, 1, 1747-1756.	7.8	269
1049	A Lytic <i>Providencia rettgeri</i> Virus of Potential Therapeutic Value Is a Deep-Branching Member of the <i>T5virus</i> Genus. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	13
1050	Both modular and single-domain Type I polyketide synthases are expressed in the brevetoxin-producing dinoflagellate, <i>Karenia brevis</i> (Dinophyceae). <i>Journal of Phycology</i> , 2017, 53, 1325-1339.	2.3	28
1051	Functional Annotation of Hypothetical proteins of <i>Lactobacillus rhamnosus</i> . , 2017, , .		1
1052	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	3.3	24
1053	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12003-12008.	7.1	90
1054	Elucidating Substrate Promiscuity within the FabI Enzyme Family. <i>ACS Chemical Biology</i> , 2017, 12, 2465-2473.	3.4	17
1055	Structural and evolutionary analysis of <i>Leishmania Alba</i> proteins. <i>Molecular and Biochemical Parasitology</i> , 2017, 217, 23-31.	1.1	12
1056	Large-Scale Phylogenomics of the <i>Lactobacillus casei</i> Group Highlights Taxonomic Inconsistencies and Reveals Novel Clade-Associated Features. <i>MSystems</i> , 2017, 2, .	3.8	79

#	ARTICLE	IF	CITATIONS
1057	The periplasmic transaminase PtaA of <i>Pseudomonas fluorescens</i> converts the glutamic acid residue at the pyoverdine fluorophore to $\alpha$ -ketoglutaric acid. <i>Journal of Biological Chemistry</i> , 2017, 292, 18660-18671.	3.4	8
1058	De novo transcriptome assembly for the spiny mouse ( <i>Acomys cahirinus</i> ). <i>Scientific Reports</i> , 2017, 7, 8996.	3.3	37
1059	De novo transcriptome sequencing of <i>Camellia sasanqua</i> and the analysis of major candidate genes related to floral traits. <i>Plant Physiology and Biochemistry</i> , 2017, 120, 103-111.	5.8	16
1060	Comparative secretome analysis of <i>Rhizoctonia solani</i> isolates with different host ranges reveals unique secretomes and cell death inducing effectors. <i>Scientific Reports</i> , 2017, 7, 10410.	3.3	62
1061	Identification of biosynthetic gene clusters from metagenomic libraries using PPTase complementation in a <i>Streptomyces</i> host. <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	34
1062	Nontargeted virus sequence discovery pipeline and virus clustering for metagenomic data. <i>Nature Protocols</i> , 2017, 12, 1673-1682.	12.0	115
1063	Evolution of sex-dependent mtDNA transmission in freshwater mussels ( <i>Bivalvia</i> : Unionida). <i>Scientific Reports</i> , 2017, 7, 1551.	3.3	40
1064	Metazoan Ribosome Inactivating Protein encoding genes acquired by Horizontal Gene Transfer. <i>Scientific Reports</i> , 2017, 7, 1863.	3.3	16
1065	Transcriptomes and expression profiling of deep-sea corals from the Red Sea provide insight into the biology of azooxanthellate corals. <i>Scientific Reports</i> , 2017, 7, 6442.	3.3	21
1066	<i>Heterodera schachtii</i> Tyrosinase-like protein - a novel nematode effector modulating plant hormone homeostasis. <i>Scientific Reports</i> , 2017, 7, 6874.	3.3	33
1067	Taxonomic and functional patterns across soil microbial communities of global biomes. <i>Science of the Total Environment</i> , 2017, 609, 1064-1074.	8.0	32
1068	Identification and functionality prediction of pathogenesis-related protein 1 from legume family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2066-2080.	2.6	10
1069	Nidovirus-Associated Proliferative Pneumonia in the Green Tree Python ( <i>Morelia viridis</i> ). <i>Journal of Virology</i> , 2017, 91, .	3.4	41
1070	Evolutionary Dynamics of Male Reproductive Genes in the <i>Drosophila virilis</i> Subgroup. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3145-3155.	1.8	33
1071	Protein structure prediction: making AWSEM AWSEM-CER by adding evolutionary restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2127-2142.	2.6	23
1072	Annotated Draft Genome Assemblies for the Northern Bobwhite ( <i>Colinus virginianus</i> ) and the Scaled Quail ( <i>Callipepla squamata</i> ) Reveal Disparate Estimates of Modern Genome Diversity and Historic Effective Population Size. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3047-3058.	1.8	20
1073	Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus <i>Pneumocystis jirovecii</i> . <i>MBio</i> , 2017, 8, .	4.1	24
1074	Mountain hare transcriptome and diagnostic markers as resources to monitor hybridization with European hares. <i>Scientific Data</i> , 2017, 4, 170178.	5.3	11

#	ARTICLE	IF	CITATIONS
1075	Molecular Mechanisms for Microbe Recognition and Defense by the Red Seaweed <i>Laurencia dendroidea</i> . <i>MSphere</i> , 2017, 2, .	2.9	19
1076	The HMMER Web Server for Protein Sequence Similarity Search. <i>Current Protocols in Bioinformatics</i> , 2017, 60, 3.15.1-3.15.23.	25.8	119
1077	Comparative functional genomics of the TPR gene family in <i>Arabidopsis</i> , rice and maize. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	10
1078	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	36
1079	The Structure of a Conserved Domain of TamB Reveals a Hydrophobic $\hat{1}^2$ Taco Fold. <i>Structure</i> , 2017, 25, 1898-1906.e5.	3.3	33
1080	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. <i>MBio</i> , 2017, 8, .	4.1	49
1081	Genomic, Transcriptomic, and Phenotypic Analyses of <i>Neisseria meningitidis</i> Isolates from Disease Patients and Their Household Contacts. <i>MSystems</i> , 2017, 2, .	3.8	3
1082	A New Lineage of Eukaryotes Illuminates Early Mitochondrial Genome Reduction. <i>Current Biology</i> , 2017, 27, 3717-3724.e5.	3.9	109
1083	Early emergence of negative regulation of the tyrosine kinase Src by the C-terminal Src kinase. <i>Journal of Biological Chemistry</i> , 2017, 292, 18518-18529.	3.4	7
1084	Genomic data reveal high conservation but divergent evolutionary pattern of Polycomb/Trithorax group genes in arthropods. <i>Insect Science</i> , 2019, 26, 20-34.	3.0	11
1085	The MAPKKK gene family in cassava: Genome-wide identification and expression analysis against drought stress. <i>Scientific Reports</i> , 2017, 7, 14939.	3.3	31
1086	Modular endolysin of Burkholderia AP3 phage has the largest lysozyme-like catalytic subunit discovered to date and no catalytic aspartate residue. <i>Scientific Reports</i> , 2017, 7, 14501.	3.3	28
1087	Role of the nucleotidyl cyclase helical domain in catalytically active dimer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9821-E9828.	7.1	35
1088	KIXBASE: A comprehensive web resource for identification and exploration of KIX domains. <i>Scientific Reports</i> , 2017, 7, 14924.	3.3	5
1089	Idiosyncratic Genome Degradation in a Bacterial Endosymbiont of Periodical Cicadas. <i>Current Biology</i> , 2017, 27, 3568-3575.e3.	3.9	37
1090	Histone methyltransferase 1 regulates the encystation process in the parasite <i>Giardia lamblia</i> . <i>FEBS Journal</i> , 2017, 284, 2396-2409.	4.7	10
1091	Characterization of the antimicrobial peptide family defensins in the Tasmanian devil ( <i>Sarcophilus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2017, 69, 133-143.	2.4	10
1092	A Parallel FastTrack Data Race Detector on Multi-core Systems. , 2017, , .		3



#	ARTICLE	IF	CITATIONS
1093	The calmodulin fused kinase novel gene family is the major system in plants converting Ca <sup>2+</sup> signals to protein phosphorylation responses. <i>Scientific Reports</i> , 2017, 7, 4127.	3.3	12
1094	Metagenomic binning of a marine sponge microbiome reveals unity in defense but metabolic specialization. <i>ISME Journal</i> , 2017, 11, 2465-2478.	9.8	150
1095	Genome-wide identification, evolution, and expression analysis of GATA transcription factors in apple ( <i>Malus domestica</i> Borkh.). <i>Gene</i> , 2017, 627, 460-472.	2.2	26
1096	Genome-wide identification and expression analysis of the lipoxygenase gene family during peach fruit ripening under different postharvest treatments. <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	2.1	22
1097	Plant manipulation through gall formation constrains amino acid transporter evolution in sap-feeding insects. <i>BMC Evolutionary Biology</i> , 2017, 17, 153.	3.2	5
1098	Molecular evolution of globin genes in Gymnotiform electric fishes: relation to hypoxia tolerance. <i>BMC Evolutionary Biology</i> , 2017, 17, 51.	3.2	12
1099	Variability among Cucurbitaceae species (melon, cucumber and watermelon) in a genomic region containing a cluster of NBS-LRR genes. <i>BMC Genomics</i> , 2017, 18, 138.	2.8	16
1100	Sex-specific differences in transcriptome profiles of brain and muscle tissue of the tropical gar. <i>BMC Genomics</i> , 2017, 18, 283.	2.8	13
1101	Three novel <i>Pseudomonas</i> phages isolated from composting provide insights into the evolution and diversity of tailed phages. <i>BMC Genomics</i> , 2017, 18, 346.	2.8	32
1102	OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. <i>BMC Genomics</i> , 2017, 18, 390.	2.8	23
1103	Genome-wide analysis of UDP-glycosyltransferase super family in <i>Brassica rapa</i> and <i>Brassica oleracea</i> reveals its evolutionary history and functional characterization. <i>BMC Genomics</i> , 2017, 18, 474.	2.8	54
1104	Identification and characterization of long intergenic noncoding RNAs in bovine mammary glands. <i>BMC Genomics</i> , 2017, 18, 468.	2.8	103
1105	A candidate RxLR effector from <i>Plasmopara viticola</i> can elicit immune responses in <i>Nicotiana benthamiana</i> . <i>BMC Plant Biology</i> , 2017, 17, 75.	3.6	43
1106	Changes in the neuropeptide content of <i>Biomphalaria</i> ganglia nervous system following <i>Schistosoma</i> infection. <i>Parasites and Vectors</i> , 2017, 10, 275.	2.5	25
1107	Genome-wide characterization of the Rab gene family in <i>Gossypium</i> by comparative analysis. , 2017, 58, 26.		11
1108	Lipidomics. <i>Methods in Molecular Biology</i> , 2017, , .	0.9	10
1109	Single-Cell Alternative Splicing Analysis with Expedition Reveals Splicing Dynamics during Neuron Differentiation. <i>Molecular Cell</i> , 2017, 67, 148-161.e5.	9.7	155
1110	Case-Control Comparison of Enteric Viromes in Captive Rhesus Macaques with Acute or Idiopathic Chronic Diarrhea. <i>Journal of Virology</i> , 2017, 91, .	3.4	46

#	ARTICLE	IF	CITATIONS
1111	Computational Functional Analysis of Lipid Metabolic Enzymes. <i>Methods in Molecular Biology</i> , 2017, 1609, 195-216.	0.9	2
1112	A differentially regulated <scp>AP</scp>2/<scp>ERF</scp> transcription factor gene cluster acts downstream of a <scp>MAP</scp> kinase cascade to modulate terpenoid indole alkaloid biosynthesis in <i>Catharanthus roseus</i>. <i>New Phytologist</i> , 2017, 213, 1107-1123.	7.3	157
1113	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	2.7	21
1114	Phylotype Dynamics of Bacterial P Utilization Genes in Microbialites and Bacterioplankton of a Monomictic Endorheic Lake. <i>Microbial Ecology</i> , 2017, 73, 296-309.	2.8	14
1115	The temperate Burkholderia phage AP3 of the Peduovirinae shows efficient antimicrobial activity against <i>B. cenocepacia</i> of the IIIA lineage. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1203-1216.	3.6	15
1116	Genome-wide identification, characterisation and expression profiles of calcium-dependent protein kinase genes in barley ( <i>Hordeum vulgare</i> L.). <i>Journal of Applied Genetics</i> , 2017, 58, 11-22.	1.9	17
1117	Diversity, expansion, and evolutionary novelty of plant DNA-binding transcription factor families. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 3-20.	1.9	75
1118	COME: a robust coding potential calculation tool for lncRNA identification and characterization based on multiple features. <i>Nucleic Acids Research</i> , 2017, 45, e2-e2.	14.5	102
1119	Molecular dynamics simulation of chitinase I from <i>Thermomyces lanuginosus</i> SSBP</i> to ensure optimal activity. <i>Molecular Simulation</i> , 2017, 43, 480-490.	2.0	8
1120	Natural products as mediators of disease. <i>Natural Product Reports</i> , 2017, 34, 194-219.	10.3	59
1121	Experimental metagenomics and ribosomal profiling of the human skin microbiome. <i>Experimental Dermatology</i> , 2017, 26, 211-219.	2.9	34
1122	Horizontal Gene Transfer of Phytochelatin Synthases from Bacteria to Extremophilic Green Algae. <i>Microbial Ecology</i> , 2017, 73, 50-60.	2.8	27
1123	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. <i>Virus Evolution</i> , 2017, 3, vex024.	4.9	30
1124	A metagenome-derived thermostable Î <sup>2</sup> -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. <i>Scientific Reports</i> , 2017, 7, 17306.	3.3	15
1125	Loss of <i>AvrSr50</i> by somatic exchange in stem rust leads to virulence for <i>Sr50</i> resistance in wheat. <i>Science</i> , 2017, 358, 1607-1610.	12.6	206
1126	MEBS, a software platform to evaluate large (meta)genomic collections according to their metabolic machinery: unraveling the sulfur cycle. <i>GigaScience</i> , 2017, 6, 1-17.	6.4	35
1127	Enhanced Desiccation Tolerance in Mature Cultures of the Streptophytic Green Alga <i>Zygnema circumcarinatum</i> Revealed by Transcriptomics. <i>Plant and Cell Physiology</i> , 2017, 58, 2067-2084.	3.1	95
1128	Searching for Antibiotic Resistance Genes in a Pristine Arctic Wetland. <i>Journal of Contemporary Water Research and Education</i> , 2017, 160, 42-59.	0.7	18

#	ARTICLE	IF	CITATIONS
1129	Virome comparisons in wild-diseased and healthy captive giant pandas. <i>Microbiome</i> , 2017, 5, 90.	11.1	113
1130	Pattern-directed aligned pattern clustering. , 2017, , .		2
1131	The core regulatory network of the abscisic acid pathway in banana: genome-wide identification and expression analyses during development, ripening, and abiotic stress. <i>BMC Plant Biology</i> , 2017, 17, 145.	3.6	51
1132	The complete genome sequence of <i>Ensifer meliloti</i> strain CCMM B554 (FSM-MA), a highly effective nitrogen-fixing microsymbiont of <i>Medicago truncatula</i> Gaertn. <i>Standards in Genomic Sciences</i> , 2017, 12, 75.	1.5	3
1133	CSPred: A machine-learning-based compound model to identify the functional activities of biologically-stable toxins. , 2017, , .		2
1134	GPU-accelerated protein sequence alignment for Jamu prediction. , 2017, , .		0
1135	Managing workflows on top of a cloud computing orchestrator for using heterogeneous environments on e-Science. <i>International Journal of Web and Grid Services</i> , 2017, 13, 375.	0.5	2
1136	Direct AUC optimization of regulatory motifs. <i>Bioinformatics</i> , 2017, 33, i243-i251.	4.1	30
1137	Identification, Classification, and Expression Analysis of GRAS Gene Family in <i>Malus domestica</i> . <i>Frontiers in Physiology</i> , 2017, 8, 253.	2.8	45
1138	Evolutionary Analysis of MIKCC-Type MADS-Box Genes in Gymnosperms and Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 8, 895.	3.6	68
1139	Transcriptome Profiling to Identify Genes Involved in Mesosulfuron-Methyl Resistance in <i>Alopecurus aequalis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1391.	3.6	66
1140	Genome-wide characterization of the aldehyde dehydrogenase gene superfamily in soybean and its potential role in drought stress response. <i>BMC Genomics</i> , 2017, 18, 518.	2.8	59
1141	De novo metatranscriptome assembly and coral gene expression profile of <i>Montipora capitata</i> with growth anomaly. <i>BMC Genomics</i> , 2017, 18, 710.	2.8	22
1142	The purplish bifurcate mussel <i>Mytilisepta virgata</i> gene expression atlas reveals a remarkable tissue functional specialization. <i>BMC Genomics</i> , 2017, 18, 590.	2.8	32
1143	Genome-wide characterization, evolution, and expression analysis of the leucine-rich repeat receptor-like protein kinase (LRR-RLK) gene family in Rosaceae genomes. <i>BMC Genomics</i> , 2017, 18, 763.	2.8	62
1144	Elucidating the Role of Host Long Non-Coding RNA during Viral Infection: Challenges and Paths Forward. <i>Vaccines</i> , 2017, 5, 37.	4.4	12
1145	Cyclic di-GMP differentially tunes a bacterial flagellar motor through a novel class of CheY-like regulators. <i>ELife</i> , 2017, 6, .	6.0	62
1146	Transcriptomic analysis of the response of <i>Acropora millepora</i> to hypo-osmotic stress provides insights into DMSP biosynthesis by corals. <i>BMC Genomics</i> , 2017, 18, 612.	2.8	22

#	ARTICLE	IF	CITATIONS
1147	HiMMe: using genetic patterns as a proxy for genome assembly reliability assessment. BMC Genomics, 2017, 18, 694.	2.8	3
1148	The Enigmatic Origin of Papillomavirus Protein Domains. Viruses, 2017, 9, 240.	3.3	6
1149	Transcriptome Analysis Reveals Long Intergenic Noncoding RNAs Contributed to Growth and Meat Quality Differences between Yorkshire and Wannanhua Pig. Genes, 2017, 8, 203.	2.4	48
1150	De Novo Assembly and Analysis of Tartary Buckwheat ( <i>Fagopyrum tataricum</i> Garetn.) Transcriptome Discloses Key Regulators Involved in Salt-Stress Response. Genes, 2017, 8, 255.	2.4	42
1151	Sequencing and De Novo Assembly of the Toxicodendron radicans (Poison Ivy) Transcriptome. Genes, 2017, 8, 317.	2.4	19
1152	Metagenomic Binning Recovers a Transcriptionally Active Gammaproteobacterium Linking Methanotrophy to Partial Denitrification in an Anoxic Oxygen Minimum Zone. Frontiers in Marine Science, 2017, 4, .	2.5	44
1153	The Holo-Transcriptome of a Calcified Early Branching Metazoan. Frontiers in Marine Science, 2017, 4, .	2.5	19
1154	Insights of Phage-Host Interaction in Hypersaline Ecosystem through Metagenomics Analyses. Frontiers in Microbiology, 2017, 8, 352.	3.5	28
1155	Comparative Genomics of Four Isosphaeraceae Planctomycetes: A Common Pool of Plasmids and Glycoside Hydrolase Genes Shared by Paludisphaera borealis PX4T, Isosphaera pallida IS1BT, Singulisphaera acidiphila DSM 18658T, and Strain SH-PL62. Frontiers in Microbiology, 2017, 8, 412.	3.5	47
1156	Intriguing Interaction of Bacteriophage-Host Association: An Understanding in the Era of Omics. Frontiers in Microbiology, 2017, 8, 559.	3.5	37
1157	The Hybrid Strategy of Thermoactinospira rubra YIM 77501T for Utilizing Cellulose as a Carbon Source at Different Temperatures. Frontiers in Microbiology, 2017, 8, 942.	3.5	17
1158	Comparative Genomics of Facultative Bacterial Symbionts Isolated from European Orius Species Reveals an Ancestral Symbiotic Association. Frontiers in Microbiology, 2017, 8, 1969.	3.5	11
1159	Variation of Carbohydrate-Active Enzyme Patterns in the Gut Microbiota of Italian Healthy Subjects and Type 2 Diabetes Patients. Frontiers in Microbiology, 2017, 8, 2079.	3.5	20
1160	New Techniques for Ancient Proteins: Direct Coupling Analysis Applied on Proteins Involved in Iron Sulfur Cluster Biogenesis. Frontiers in Molecular Biosciences, 2017, 4, 40.	3.5	7
1161	Describing Genomic and Epigenomic Traits Underpinning Emerging Fungal Pathogens. Advances in Genetics, 2017, 100, 73-140.	1.8	17
1162	Evolution of an intricate J-protein network driving protein disaggregation in eukaryotes. ELife, 2017, 6, .	6.0	60
1163	Comparative Genomics of Non-TNL Disease Resistance Genes from Six Plant Species. Genes, 2017, 8, 249.	2.4	34
1164	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between Arabidopsis thaliana and Brassica species uncover effects of whole genome and tandem duplications. BMC Genomics, 2017, 18, 733.	2.8	37

#	ARTICLE	IF	CITATIONS
1165	Transcriptome Analysis of <i>Taxillusi chinensis</i> (DC.) Danser Seeds in Response to Water Loss. PLoS ONE, 2017, 12, e0169177.	2.5	31
1166	PnLRR-RLK27, a novel leucine-rich repeats receptor-like protein kinase from the Antarctic moss <i>Pohlia nutans</i> , positively regulates salinity and oxidation-stress tolerance. PLoS ONE, 2017, 12, e0172869.	2.5	33
1167	Genome-wide analysis of brain and gonad transcripts reveals changes of key sex reversal-related genes expression and signaling pathways in three stages of <i>Monopterus albus</i> . PLoS ONE, 2017, 12, e0173974.	2.5	40
1168	<i>Bacillus</i> sp. JR3 esterase LipJ: A new mesophilic enzyme showing traces of a thermophilic past. PLoS ONE, 2017, 12, e0181029.	2.5	6
1169	Genome-wide identification and analysis of the MADS-box gene family in bread wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	2.5	69
1170	RNA-Seq de novo assembly and differential transcriptome analysis of the nematode <i>Ascaridia galli</i> in relation to in vivo exposure to flubendazole. PLoS ONE, 2017, 12, e0185182.	2.5	11
1171	Activated entomopathogenic nematode infective juveniles release lethal venom proteins. PLoS Pathogens, 2017, 13, e1006302.	4.7	95
1172	Generality of toxins in defensive symbiosis: Ribosome-inactivating proteins and defense against parasitic wasps in <i>Drosophila</i> . PLoS Pathogens, 2017, 13, e1006431.	4.7	82
1173	Pf16 and phiPMW: Expanding the realm of <i>Pseudomonas putida</i> bacteriophages. PLoS ONE, 2017, 12, e0184307.	2.5	7
1174	Genome-wide comparative analysis of putative Pth11-related G protein-coupled receptors in fungi belonging to Pezizomycotina. BMC Microbiology, 2017, 17, 166.	3.3	11
1175	COGcollator: a web server for analysis of distant relationships between homologous protein families. Biology Direct, 2017, 12, 29.	4.6	12
1176	Targeted metatranscriptomics of compost-derived consortia reveals a GH11 exerting an unusual exo-1,4- $\beta$ -xylosidase activity. Biotechnology for Biofuels, 2017, 10, 254.	6.2	30
1177	Viral communities of the human gut: metagenomic analysis of composition and dynamics. Mobile DNA, 2017, 8, 12.	3.6	119
1178	Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple ( <i>Acer saccharum</i> Marsh.). BMC Research Notes, 2017, 10, 369.	1.4	9
1179	Microbial phylogeny determines transcriptional response of resistome to dynamic composting processes. Microbiome, 2017, 5, 103.	11.1	60
1180	Metagenomic Characterization of <i>Candidatus</i> <i>Smithella cisternae</i> Strain M82_1, a Syntrophic Alkane-Degrading Bacteria, Enriched from the Shengli Oil Field. Microbes and Environments, 2017, 32, 234-243.	1.6	26
1181	Evolution of the Metabolic Network Leading to Ascorbate Synthesis and Degradation Using <i>Marchantia polymorpha</i> as a Model System. , 2017, , 417-430.		0
1182	COGNAT: a web server for comparative analysis of genomic neighborhoods. Biology Direct, 2017, 12, 26.	4.6	7

#	ARTICLE	IF	CITATIONS
1183	Protein remote homology detection based on bidirectional long short-term memory. BMC Bioinformatics, 2017, 18, 443.	2.6	57
1184	dBBQs: dataBase of Bacterial Quality scores. BMC Bioinformatics, 2017, 18, 483.	2.6	27
1185	Performance of Hidden Markov Models in Recovering the Standard Classification of Glycoside Hydrolases. Evolutionary Bioinformatics, 2017, 13, 117693431770340.	1.2	7
1186	Infectious polymorphic toxins delivered by outer membrane exchange discriminate kin in myxobacteria. ELife, 2017, 6, .	6.0	70
1187	Myticalins: A Novel Multigenic Family of Linear, Cationic Antimicrobial Peptides from Marine Mussels ( <i>Mytilus</i> spp.). Marine Drugs, 2017, 15, 261.	4.6	54
1188	Genome analysis of the foxtail millet pathogen <i>Sclerospora graminicola</i> reveals the complex effector repertoire of graminicolous downy mildews. BMC Genomics, 2017, 18, 897.	2.8	27
1189	A dual transcript-discovery approach to improve the delimitation of gene features from RNA-seq data in the chicken model. Biology Open, 2018, 7, .	1.2	7
1190	GHOST: global hepatitis outbreak and surveillance technology. BMC Genomics, 2017, 18, 916.	2.8	38
1191	Identification of putative CONSTANS-like genes from the de novo assembled transcriptome of leek. Biologia Plantarum, 2018, 62, 269-276.	1.9	4
1192	A Model for Manganese interaction with <i>Deinococcus radiodurans</i> proteome network involved in ROS response and defense. Journal of Trace Elements in Medicine and Biology, 2018, 50, 465-473.	3.0	23
1193	Genome-wide Identification and Expression Pattern Analysis of Zinc-finger Homeodomain Transcription Factors in Tomato under Abiotic Stress. Journal of the American Society for Horticultural Science, 2018, 143, 14-22.	1.0	11
1194	Identification and functional analysis of germin-like protein Gene family in tea plant ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.6	10
1195	Involvement in surface antigen expression by a moonlighting FG-repeat nucleoporin in trypanosomes. Molecular Biology of the Cell, 2018, 29, 1100-1110.	2.1	5
1196	Biochemical characterization in Norway spruce ( <i>Picea abies</i> ) of SABATH methyltransferases that methylate phytohormones. Phytochemistry, 2018, 149, 146-154.	2.9	17
1197	Identification of a novel aminopolycarboxylic acid siderophore gene cluster encoding the biosynthesis of ethylenediaminesuccinic acid hydroxyarginine (EDHA). Metallomics, 2018, 10, 722-734.	2.4	8
1198	Evolutionary convergence and divergence in archaeal chromosomal proteins and Chromo-like domains from bacteria and eukaryotes. Scientific Reports, 2018, 8, 6196.	3.3	22
1199	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	3.8	376
1200	Metagenomic binning reveals versatile nutrient cycling and distinct adaptive features in alphaproteobacterial symbionts of marine sponges. FEMS Microbiology Ecology, 2018, 94, .	2.7	61

#	ARTICLE	IF	CITATIONS
1201	Transcriptome characterization and screening of molecular markers in ecologically important Himalayan species ( <i>Rhododendron arboreum</i> ). <i>Genome</i> , 2018, 61, 417-428.	2.0	18
1202	Dual Role of Humic Substances As Electron Donor and Shuttle for Dissimilatory Iron Reduction. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5691-5699.	10.0	116
1203	Genome-wide analyses of the bHLH superfamily in crustaceans: reappraisal of higher-order groupings and evidence for lineage-specific duplications. <i>Royal Society Open Science</i> , 2018, 5, 172433.	2.4	5
1204	Termite soldiers contribute to social immunity by synthesizing potent oral secretions. <i>Insect Molecular Biology</i> , 2018, 27, 564-576.	2.0	38
1205	Genome-wide comparative and evolutionary analysis of Calmodulin-binding Transcription Activator (CAMTA) family in <i>Gossypium</i> species. <i>Scientific Reports</i> , 2018, 8, 5573.	3.3	44
1206	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. <i>Molecular Plant Pathology</i> , 2018, 19, 2094-2110.	4.2	350
1207	PpHB22, a member of HD-Zip proteins, activates PpDAM1 to regulate bud dormancy transition in ‘Suli’™ pear ( <i>Pyrus pyrifolia</i> White Pear Group). <i>Plant Physiology and Biochemistry</i> , 2018, 127, 355-365.	5.8	30
1208	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. <i>ACS Chemical Biology</i> , 2018, 13, 1142-1147.	3.4	30
1209	A type VI secretion system effector delivery mechanism dependent on PAAR and a chaperone-co-chaperone complex. <i>Nature Microbiology</i> , 2018, 3, 632-640.	13.3	116
1210	Evolutionary conservation of a core fungal phosphate homeostasis pathway coupled to development in <i>Blastocladiella emersonii</i> . <i>Fungal Genetics and Biology</i> , 2018, 115, 20-32.	2.1	13
1211	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, <i>Scomber colias</i> . <i>Data in Brief</i> , 2018, 18, 276-284.	1.0	7
1212	Identification, evolution and expression analyses of Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit gene family in wheat ( <i>Triticum aestivum</i> L.). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	2.1	3
1213	Phylogeny and evolution of the cholesterol transporter NPC1 in insects. <i>Journal of Insect Physiology</i> , 2018, 107, 157-166.	2.0	13
1214	Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen <i>Candida auris</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	169
1215	Phosphatase activity tunes two-component system sensor detection threshold. <i>Nature Communications</i> , 2018, 9, 1433.	12.8	66
1216	Structural Characterization and Directed Evolution of a Novel Acetyl Xylan Esterase Reveals Thermostability Determinants of the Carbohydrate Esterase 7 Family. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	18
1217	Are Fireworms Venomous? Evidence for the Convergent Evolution of Toxin Homologs in Three Species of Fireworms (Annelida, Amphinomidae). <i>Genome Biology and Evolution</i> , 2018, 10, 249-268.	2.5	30
1218	Novel global effector mining from the transcriptome of early life stages of the soybean cyst nematode <i>Heterodera glycines</i> . <i>Scientific Reports</i> , 2018, 8, 2505.	3.3	31



#	ARTICLE	IF	CITATIONS
1219	Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. <i>DNA Research</i> , 2018, 25, 217-227.	3.4	33
1220	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. <i>Nature Communications</i> , 2018, 9, 448.	12.8	146
1221	Cross-kingdom auxiliary subunit modulation of a voltage-gated sodium channel. <i>Journal of Biological Chemistry</i> , 2018, 293, 4981-4992.	3.4	11
1222	Unraveling Allosteric Mechanisms of Enzymatic Catalysis with an Evolutionary Analysis of Residueâ€“Residue Contact Dynamical Changes. <i>ACS Catalysis</i> , 2018, 8, 2375-2384.	11.2	18
1223	Papain-like cysteine proteases in <i>Carica papaya</i> : lineage-specific gene duplication and expansion. <i>BMC Genomics</i> , 2018, 19, 26.	2.8	28
1224	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. <i>Scientific Data</i> , 2018, 5, 170203.	5.3	449
1225	A peculiar lclR family transcription factor regulates para-hydroxybenzoate catabolism in <i>Streptomyces coelicolor</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1501-1512.	14.5	9
1226	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. <i>MSystems</i> , 2018, 3, .	3.8	68
1227	Transcriptional Response to Lactic Acid Stress in the Hybrid Yeast <i>Zygosaccharomyces parabailii</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	18
1228	Genome-wide identification and analysis of the evolution and expression patterns of the cellulose synthase gene superfamily in <i>Gossypium</i> species. <i>Gene</i> , 2018, 646, 28-38.	2.2	22
1229	Stressâ€“responsive regulation of long nonâ€“coding <sc>RNA</sc> polyadenylation in <i>Oryza sativa</i>. <i>Plant Journal</i> , 2018, 93, 814-827.	5.7	86
1230	Aureo Wiki Ì The repository of the <i>Staphylococcus aureus</i> research and annotation community. <i>International Journal of Medical Microbiology</i> , 2018, 308, 558-568.	3.6	99
1231	Biochemical and biophysical characterization of novel GH10 xylanase prospected from a sugar cane bagasse compost-derived microbial consortia. <i>International Journal of Biological Macromolecules</i> , 2018, 109, 560-568.	7.5	15
1232	<i>ZmCOL3</i>, a CCT gene represses flowering in maize by interfering with the circadian clock and activating expression of <i>ZmCCT</i>. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 465-480.	8.5	43
1233	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018, 20, 1041-1063.	3.8	228
1234	Genome-based classification of micromonosporae with a focus on their biotechnological and ecological potential. <i>Scientific Reports</i> , 2018, 8, 525.	3.3	102
1235	Evolution of the growth hormone, prolactin, prolactin 2 and somatolactin family. <i>General and Comparative Endocrinology</i> , 2018, 264, 94-112.	1.8	45
1236	Genome-wide identification and characterization of SPL transcription factor family and their evolution and expression profiling analysis in cotton. <i>Scientific Reports</i> , 2018, 8, 762.	3.3	56

#	ARTICLE	IF	CITATIONS
1237	Characterization of the late embryogenesis abundant (LEA) proteins family and their role in drought stress tolerance in upland cotton. <i>BMC Genetics</i> , 2018, 19, 6.	2.7	216
1238	Identification of a novel fused gene family implicates convergent evolution in eukaryotic calcium signaling. <i>BMC Genomics</i> , 2018, 19, 306.	2.8	4
1239	â€œCandidatus Paraporphyromonas polyenzymogenesâ€•encodes multi-modular cellulases linked to the type IX secretion system. <i>Microbiome</i> , 2018, 6, 44.	11.1	32
1240	The <i>Phytophthora cactorum</i> genome provides insights into the adaptation to host defense compounds and fungicides. <i>Scientific Reports</i> , 2018, 8, 6534.	3.3	52
1241	Introducing difference recurrence relations for faster semi-global alignment of long sequences. <i>BMC Bioinformatics</i> , 2018, 19, 45.	2.6	75
1242	Comparative genomic analysis of <i>Geosporobacter ferrireducens</i> and its versatility of anaerobic energy metabolism. <i>Journal of Microbiology</i> , 2018, 56, 365-371.	2.8	8
1243	H<sub>v</sub>1 Proton Channels in Dinoflagellates: Not Just for Bioluminescence?. <i>Journal of Eukaryotic Microbiology</i> , 2018, 65, 928-933.	1.7	9
1244	Two-dimensional analysis provides molecular insight into flower scent of <i>Lilium</i> â€˜Siberiaâ€™™. <i>Scientific Reports</i> , 2018, 8, 5352.	3.3	24
1245	Stable Isotope Probing for Microbial Iron Reduction in Chocolate Pots Hot Spring, Yellowstone National Park. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	46
1246	Mannose 6â€phosphateâ€dependent lysosomal enzyme targeting in hydra: a biochemical, immunological and structural elucidation. <i>FEBS Letters</i> , 2018, 592, 1366-1377.	2.8	5
1247	A High-Throughput Mutational Scan of an Intrinsically Disordered Acidic Transcriptional Activation Domain. <i>Cell Systems</i> , 2018, 6, 444-455.e6.	6.2	135
1248	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	5.5	99
1249	Out of Water: The Origin and Early Diversification of Plant <i>R</i>-Genes. <i>Plant Physiology</i> , 2018, 177, 82-89.	4.8	117
1250	Structural and functional analysis of the DOT1Lâ€AF10 complex reveals mechanistic insights into MLL-AF10-associated leukemogenesis. <i>Genes and Development</i> , 2018, 32, 341-346.	5.9	17
1251	How genomes could transform surveillance and facial recognition. <i>Biometric Technology Today</i> , 2018, 2018, 5-7.	0.1	0
1252	Genome-wide analysis of the MADS-box gene family in polyploid cotton ( <i>Gossypium hirsutum</i> ) and in its diploid parental species ( <i>Gossypium arboreum</i> and <i>Gossypium raimondii</i> ). <i>Plant Physiology and Biochemistry</i> , 2018, 127, 169-184.	5.8	30
1253	The BRD3 ET domain recognizes a short peptide motif through a mechanism that is conserved across chromatin remodelers and transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2018, 293, 7160-7175.	3.4	39
1254	Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. <i>Biochemistry</i> , 2018, 57, 3237-3243.	2.5	19

#	ARTICLE	IF	CITATIONS
1255	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018, 7, .	6.4	12
1256	Variations on a theme: evolution of the phage-shock-protein system in Actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 753-760.	1.7	7
1257	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018, 33, 450-462.e10.	16.8	213
1258	De novo synthesis of the sedative valerenic acid in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 94-101.	7.0	21
1259	Draft genome analysis provides insights into the fiber yield, crude protein biosynthesis, and vegetative growth of domesticated ramie ( <i>Boehmeria nivea</i> L. Gaud). <i>DNA Research</i> , 2018, 25, 173-181.	3.4	32
1260	A comprehensive review and comparison of different computational methods for protein remote homology detection. <i>Briefings in Bioinformatics</i> , 2018, 19, 231-244.	6.5	106
1261	Bioinformatics tools for the identification of gene clusters that biosynthesize specialized metabolites. <i>Briefings in Bioinformatics</i> , 2018, 19, 1022-1034.	6.5	88
1262	Evolution of the receptors for growth hormone, prolactin, erythropoietin and thrombopoietin in relation to the vertebrate tetraploidizations. <i>General and Comparative Endocrinology</i> , 2018, 257, 143-160.	1.8	26
1263	LMMO: A Large Margin Approach for Refining Regulatory Motifs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 913-925.	3.0	12
1264	ITSoneDB: a comprehensive collection of eukaryotic ribosomal RNA Internal Transcribed Spacer 1 (ITS1) sequences. <i>Nucleic Acids Research</i> , 2018, 46, D127-D132.	14.5	31
1265	RNA sequencing and analysis of three <i>Lupinus nodulosus</i> provide new insights into specific host-symbiont relationships with compatible and incompatible <i>Bradyrhizobium</i> strains. <i>Plant Science</i> , 2018, 266, 102-116.	3.6	8
1266	Proteome and Structural Organization of the Knob Complex on the Surface of the <i>Plasmodium</i> Infected Red Blood Cell. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1600177.	1.6	13
1267	Characterization of Putative Effectors from the Cereal Cyst Nematode <i>Heterodera avenae</i> . <i>Phytopathology</i> , 2018, 108, 264-274.	2.2	8
1268	Clustal Omega for making accurate alignments of many protein sequences. <i>Protein Science</i> , 2018, 27, 135-145.	7.6	1,286
1269	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. <i>ISME Journal</i> , 2018, 12, 1-16.	9.8	148
1270	Sex determination and differentiation genes in a functional hermaphrodite scallop, <i>Nodipecten subnodosus</i> . <i>Marine Genomics</i> , 2018, 37, 161-175.	1.1	16
1271	Reconstructing High-Quality Large-Scale Metabolic Models with merlin. <i>Methods in Molecular Biology</i> , 2018, 1716, 1-36.	0.9	13
1272	<scp>ApoplastP</scp>: prediction of effectors and plant proteins in the apoplast using machine learning. <i>New Phytologist</i> , 2018, 217, 1764-1778.	7.3	180

#	ARTICLE	IF	CITATIONS
1273	Genome-wide analysis of carotenoid cleavage oxygenase genes and their responses to various phytohormones and abiotic stresses in apple ( <i>Malus domestica</i> ). <i>Plant Physiology and Biochemistry</i> , 2018, 123, 81-93.	5.8	40
1274	Retrieved 16S rRNA and nifH sequences reveal co-dominance of Bradyrhizobium and Ensifer (Sinorhizobium) strains in field-collected root nodules of the promiscuous host <i>Vigna radiata</i> (L.) R. Wilczek. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 485-497.	3.6	23
1275	A Comprehensive Computational Analysis of Mycobacterium Genomes Pinpoints the Genes Co-occurring with YczE, a Membrane Protein Coding Gene Under the Putative Control of a MocR, and Predicts its Function. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 111-125.	3.6	3
1276	Pectin methylesterase inhibitor (PMEI) family can be related to male sterility in Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>pekinensis</i> ). <i>Molecular Genetics and Genomics</i> , 2018, 293, 343-357.	2.1	21
1277	FuzzyID2: A software package for large data set species identification via barcoding and metabarcoding using hidden Markov models and fuzzy set methods. <i>Molecular Ecology Resources</i> , 2018, 18, 666-675.	4.8	11
1278	Genome-wide identification and expression analysis of beta-galactosidase family members during fruit softening of peach [ <i>Prunus persica</i> (L.) Batsch]. <i>Postharvest Biology and Technology</i> , 2018, 136, 111-123.	6.0	39
1279	Combination of type II fatty acid biosynthesis enzymes and thiolases supports a functional $\beta^2$ -oxidation reversal. <i>Metabolic Engineering</i> , 2018, 45, 11-19.	7.0	19
1280	HITS-PR-HHblits: protein remote homology detection by combining PageRank and Hyperlink-Induced Topic Search. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	53
1281	Global transcriptome analysis of the aphelid <i>Paraphelidium tribonemae</i> supports the phagotrophic origin of fungi. <i>Communications Biology</i> , 2018, 1, 231.	4.4	63
1282	Expansion and Functional Divergence of the <i>SHORT VEGETATIVE PHASE</i> ( <i>SVP</i> ) Genes in Eudicots. <i>Genome Biology and Evolution</i> , 2018, 10, 3026-3037.	2.5	32
1283	Shared gene-network signatures between the human heavy metal proteome and neurological disorders and cancer types. <i>Metallomics</i> , 2018, 10, 1678-1686.	2.4	11
1284	New insights into the evolution and functional divergence of the SWEET family in <i>Saccharum</i> based on comparative genomics. <i>BMC Plant Biology</i> , 2018, 18, 270.	3.6	42
1285	Genome-wide detection of terpene synthase genes in holy basil ( <i>Ocimum sanctum</i> L.). <i>PLoS ONE</i> , 2018, 13, e0207097.	2.5	31
1286	Controlling aflatoxin contamination and propagation of <i>Aspergillus flavus</i> by a soy-fermenting <i>Aspergillus oryzae</i> strain. <i>Scientific Reports</i> , 2018, 8, 16871.	3.3	66
1287	Impact of Amoxicillin-Clavulanate followed by Autologous Fecal Microbiota Transplantation on Fecal Microbiome Structure and Metabolic Potential. <i>MSphere</i> , 2018, 3, .	2.9	17
1288	Pivotal role of bZIPs in amylose biosynthesis by genome survey and transcriptome analysis in wheat ( <i>Triticum aestivum</i> L.) mutants. <i>Scientific Reports</i> , 2018, 8, 17240.	3.3	30
1289	Comparative genomics of nuclear envelope proteins. <i>BMC Genomics</i> , 2018, 19, 823.	2.8	9
1290	Genome-wide identification of LRR-containing sequences and the response of these sequences to nematode infection in <i>Arachis duranensis</i> . <i>BMC Plant Biology</i> , 2018, 18, 279.	3.6	22

#	ARTICLE	IF	CITATIONS
1291	Genome-Wide Identification of Flowering-Time Genes in Brassica Species and Reveals a Correlation between Selective Pressure and Expression Patterns of Vernalization-Pathway Genes in Brassica napus. International Journal of Molecular Sciences, 2018, 19, 3632.	4.1	20
1292	LncRNAs in polyploid cotton interspecific hybrids are derived from transposon neofunctionalization. Genome Biology, 2018, 19, 195.	8.8	59
1293	Complete genome sequence of Planococcus sp. PAMC21323 isolated from Antarctica and its metabolic potential to detoxify pollutants. Standards in Genomic Sciences, 2018, 13, 31.	1.5	10
1294	FishTEDB: a collective database of transposable elements identified in the complete genomes of fish. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	40
1295	Methanogenesis on Early Stages of Life: Ancient but Not Primordial. Origins of Life and Evolution of Biospheres, 2018, 48, 407-420.	1.9	16
1296	Coevolving residues inform protein dynamics profiles and disease susceptibility of nSNVs. PLoS Computational Biology, 2018, 14, e1006626.	3.2	12
1297	Comparative De Novo transcriptome analysis of the Australian black-lip and Sydney rock oysters reveals expansion of repetitive elements in Saccostrea genomes. PLoS ONE, 2018, 13, e0206417.	2.5	3
1298	Photoperiod response-related gene SiCOL1 contributes to flowering in sesame. BMC Plant Biology, 2018, 18, 343.	3.6	17
1299	Comparative genomics of downy mildews reveals potential adaptations to biotrophy. BMC Genomics, 2018, 19, 851.	2.8	59
1300	Genome-wide analysis of the pentatricopeptide repeat gene family in different maize genomes and its important role in kernel development. BMC Plant Biology, 2018, 18, 366.	3.6	26
1301	Gut colonization by a novel Clostridium species is associated with the onset of epizootic rabbit enteropathy. Veterinary Research, 2018, 49, 123.	3.0	17
1302	A Phylogenomic Framework and Divergence History of Cephalochordata Amphioxus. Frontiers in Physiology, 2018, 9, 1833.	2.8	11
1303	Expression and Characteristics of Two Glucose-Tolerant GH1 Î2-glucosidases From Actinomadura amylolytica YIM 77502T for Promoting Cellulose Degradation. Frontiers in Microbiology, 2018, 9, 3149.	3.5	17
1304	Reconstructing the evolutionary history of F420-dependent dehydrogenases. Scientific Reports, 2018, 8, 17571.	3.3	18
1305	Bacterial and Archaeal Viruses of Himalayan Hot Springs at Manikaran Modulate Host Genomes. Frontiers in Microbiology, 2018, 9, 3095.	3.5	27
1306	Comparative Analysis of the Nodule Transcriptomes of Ceanothus thyrsiflorus (Rhamnaceae, Rosales) and Datisca glomerata (Datiscaceae, Cucurbitales). Frontiers in Plant Science, 2018, 9, 1629.	3.6	12
1308	The structure of SDS22 provides insights into the mechanism of heterodimer formation with PP1. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 817-824.	0.8	5
1309	Full-length title: NRPPUR database search and in vitro analysis identify an NRPS-PKS biosynthetic gene cluster with a potential antibiotic effect. BMC Bioinformatics, 2018, 19, 463.	2.6	12

#	ARTICLE	IF	CITATIONS
1310	Evolutionary diversity and novelty of DNA repair genes in asexual Bdelloid rotifers. BMC Evolutionary Biology, 2018, 18, 177.	3.2	25
1311	Genome-Wide Analysis of LRR-RLK Gene Family in Four Gossypium Species and Expression Analysis during Cotton Development and Stress Responses. Genes, 2018, 9, 592.	2.4	17
1312	FLIM-MAP: Gene Context Based Identification of Functional Modules in Bacterial Metabolic Pathways. Frontiers in Microbiology, 2018, 9, 2183.	3.5	20
1313	Does mitochondrial DNA evolution in metazoa drive the origin of new mitochondrial proteins?. IUBMB Life, 2018, 70, 1240-1250.	3.4	13
1314	Structural and functional characterisation of the entry point to pyocyanin biosynthesis in <i>Pseudomonas aeruginosa</i> defines a new 3-deoxy-4-arabino-heptulosonate 7-phosphate synthase subclass. Bioscience Reports, 2018, 38, .	2.4	14
1315	Novel Campylobacter concisus lipooligosaccharide is a determinant of inflammatory potential and virulence. Journal of Lipid Research, 2018, 59, 1893-1905.	4.2	4
1316	Biosynthesis of the neurotoxin domoic acid in a bloom-forming diatom. Science, 2018, 361, 1356-1358.	12.6	124
1317	A Subset of Exoribonucleases Serve as Degradative Enzymes for pGpG in c-di-GMP Signaling. Journal of Bacteriology, 2018, 200, .	2.2	24
1318	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. MSphere, 2018, 3, .	2.9	12
1319	Building (Viral) Phylogenetic Trees Using a Maximum Likelihood Approach. Current Protocols in Microbiology, 2018, 51, e63.	6.5	5
1320	Evolutionary Genomics of Metchnikovella incurvata (Metchnikovellidae): An Early Branching Microsporidium. Genome Biology and Evolution, 2018, 10, 2736-2748.	2.5	34
1321	Genome-Wide Characterization of DNA Demethylase Genes and Their Association with Salt Response in Pyrus. Genes, 2018, 9, 398.	2.4	14
1322	Transcriptional recording by CRISPR spacer acquisition from RNA. Nature, 2018, 562, 380-385.	27.8	117
1323	Gold biotechnology: Development and advancements. AIP Conference Proceedings, 2018, , .	0.4	1
1324	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. Genetics, 2018, 210, 883-894.	2.9	21
1325	Characterization of C-ring component assembly in flagellar motors from amino acid coevolution. Royal Society Open Science, 2018, 5, 171854.	2.4	11
1326	Molecular recognition of the beta-glucans laminarin and pustulan by a SusD-like glycan-binding protein of a marine Bacteroidetes. FEBS Journal, 2018, 285, 4465-4481.	4.7	13
1327	Structural Insights into Substrate Selectivity and Activity of Bacterial Polyphosphate Kinases. ACS Catalysis, 2018, 8, 10746-10760.	11.2	48



#	ARTICLE	IF	CITATIONS
1328	De Novo Hepatic Transcriptome Assembly and Systems Level Analysis of Three Species of Dietary Fish, <i>Sardinops sagax</i> , <i>Scomber japonicus</i> , and <i>Pleuronichthys verticalis</i> . <i>Genes</i> , 2018, 9, 521.	2.4	1
1329	Genomic discovery of the hypsin gene and biosynthetic pathways for terpenoids in <i>Hypsizygus marmoreus</i> . <i>BMC Genomics</i> , 2018, 19, 789.	2.8	21
1330	A diversity-generating retroelement encoded by a globally ubiquitous <i>Bacteroides</i> phage. <i>Microbiome</i> , 2018, 6, 191.	11.1	48
1331	Transcriptome Analysis of Bael ( <i>Aegle marmelos</i> (L.) Corr.) a Member of Family Rutaceae. <i>Forests</i> , 2018, 9, 450.	2.1	8
1332	Non-target site-based resistance to tribenuron-methyl and essential involved genes in <i>Myosoton aquaticum</i> (L.). <i>BMC Plant Biology</i> , 2018, 18, 225.	3.6	37
1333	Organic Particles: Heterogeneous Hubs for Microbial Interactions in Aquatic Ecosystems. <i>Frontiers in Microbiology</i> , 2018, 9, 2569.	3.5	51
1334	Microbially Produced Imidazole Propionate Impairs Insulin Signaling through mTORC1. <i>Cell</i> , 2018, 175, 947-961.e17.	28.9	517
1336	Genome-wide identification of tomato ( <i>Solanum lycopersicum</i> L.) lipoxygenases coupled with expression profiles during plant development and in response to methyl-jasmonate and wounding. <i>Journal of Plant Physiology</i> , 2018, 231, 318-328.	3.5	47
1337	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 4276.	12.8	46
1338	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	12.6	757
1339	Genome-Wide Identification and Transcriptional Regulation of Aquaporin Genes in Bread Wheat ( <i>Triticum aestivum</i> L.) under Water Stress. <i>Genes</i> , 2018, 9, 497.	2.4	19
1340	Transcriptome Profiles Reveal the Crucial Roles of Auxin and Cytokinin in the "Shoot Branching" of <i>Cremastra appendiculata</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3354.	4.1	14
1341	MGH: a genome hub for the medicinal plant maca ( <i>Lepidium meyenii</i> ). <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	5
1342	WRKY transcription factors in legumes. <i>BMC Plant Biology</i> , 2018, 18, 243.	3.6	66
1343	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on <i>Streptomyces coelicolor</i> . <i>PLoS Computational Biology</i> , 2018, 14, e1006541.	3.2	228
1344	Species groups distributed across elevational gradients reveal convergent and continuous genetic adaptation to high elevations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10634-E10641.	7.1	57
1345	Comprehensive transcriptome analysis reveals genes in response to water deficit in the leaves of <i>Saccharum narenga</i> (Nees ex Steud.) hack. <i>BMC Plant Biology</i> , 2018, 18, 250.	3.6	35
1346	Genomic Description of "Candidatus Abyssobacterium," a Novel Subsurface Lineage Within the Candidate Phylum Hydrogenedentes. <i>Frontiers in Microbiology</i> , 2018, 9, 1993.	3.5	36



#	ARTICLE	IF	CITATIONS
1347	Dynamical comparison between myoglobin and hemoglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 1176-1183.	2.6	7
1348	De novo transcriptome assembly of the coral <i>Agaricia lamarcki</i> (Lamarck's sheet coral) from mesophotic depth in southwest Puerto Rico. <i>Marine Genomics</i> , 2018, 41, 6-11.	1.1	22
1349	Nature of Long-Range Evolutionary Constraint in Enzymes: Insights from Comparison to Pseudoenzymes with Similar Structures. <i>Molecular Biology and Evolution</i> , 2018, 35, 2597-2606.	8.9	15
1350	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia ( <i>Oreochromis shiranus</i> ) and North African catfish ( <i>Clarias gariepinus</i> ). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	3.0	23
1351	PCR assays for detection of human astroviruses: In silico evaluation and design, and in vitro application to samples collected from patients in the Netherlands. <i>Journal of Clinical Virology</i> , 2018, 108, 83-89.	3.1	7
1352	Shotgun Proteomics Analysis of Saliva and Salivary Gland Tissue from the Common Octopus <i>Octopus vulgaris</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3866-3876.	3.7	15
1353	Host Cell Proteome of <i>Physcomitrella patens</i> Harbors Proteases and Protease Inhibitors under Bioproduction Conditions. <i>Journal of Proteome Research</i> , 2018, 17, 3749-3760.	3.7	19
1354	Factors Influencing Gene Family Size Variation Among Related Species in a Plant Family, Solanaceae. <i>Genome Biology and Evolution</i> , 2018, 10, 2596-2613.	2.5	54
1355	Signaling specificity in the c-di-GMP-dependent network regulating antibiotic synthesis in <i>Lysobacter</i> . <i>Nucleic Acids Research</i> , 2018, 46, 9276-9288.	14.5	55
1356	The Zinc Linchpin Motif in the DNA Repair Glycosylase MUTYH: Identifying the Zn <sup>2+</sup> Ligands and Roles in Damage Recognition and Repair. <i>Journal of the American Chemical Society</i> , 2018, 140, 13260-13271.	13.7	8
1357	Emergence of soil bacterial ecotypes along a climate gradient. <i>Environmental Microbiology</i> , 2018, 20, 4112-4126.	3.8	32
1358	Whole Genome Analysis of Cyclin Dependent Kinase (CDK) Gene Family in Cotton and Functional Evaluation of the Role of CDKF4 Gene in Drought and Salt Stress Tolerance in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2625.	4.1	51
1359	Genome-wide identification and characterization of LRR-RLKs reveal functional conservation of the SIF subfamily in cotton ( <i>Gossypium hirsutum</i> ). <i>BMC Plant Biology</i> , 2018, 18, 185.	3.6	28
1360	Investigating the Composition and Metabolic Potential of Microbial Communities in Chocolate Pots Hot Springs. <i>Frontiers in Microbiology</i> , 2018, 9, 2075.	3.5	19
1362	Toward Reducing Phylostratigraphic Errors and Biases. <i>Genome Biology and Evolution</i> , 2018, 10, 2037-2048.	2.5	20
1363	Origins and structural properties of novel and <i>de novo</i> protein domains during insect evolution. <i>FEBS Journal</i> , 2018, 285, 2605-2625.	4.7	30
1364	Defining the architecture of KPC-2 Carbapenemase: Identifying allosteric networks to fight antibiotics resistance. <i>Scientific Reports</i> , 2018, 8, 12916.	3.3	27
1365	Maize GO Annotation—Methods, Evaluation, and Review (maizeGAMER). <i>Plant Direct</i> , 2018, 2, e00052.	1.9	97

#	ARTICLE	IF	CITATIONS
1366	Proteiniphilum saccharofermentans str. M3/6T isolated from a laboratory biogas reactor is versatile in polysaccharide and oligopeptide utilization as deduced from genome-based metabolic reconstructions. Biotechnology Reports (Amsterdam, Netherlands), 2018, 18, e00254.	4.4	30
1367	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in Aspergillus fumigatus. MBio, 2018, 9, .	4.1	44
1368	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	3.8	604
1369	Revised Phylogeny of the <i>Cellulose Synthase</i> Gene Superfamily: Insights into Cell Wall Evolution. Plant Physiology, 2018, 177, 1124-1141.	4.8	118
1370	Molecular Mechanisms Preventing Senescence in Response to Prolonged Darkness in a Desiccation-Tolerant Plant. Plant Physiology, 2018, 177, 1319-1338.	4.8	26
1371	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	4.1	13
1372	dbCAN2: a meta server for automated carbohydrate-active enzyme annotation. Nucleic Acids Research, 2018, 46, W95-W101.	14.5	1,641
1373	Ecological Engineering Helps Maximize Function in Algal Oil Production. Applied and Environmental Microbiology, 2018, 84, .	3.1	6
1374	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in Ettlia oleoabundans. Algal Research, 2018, 33, 142-155.	4.6	21
1375	Identification on mitogen-activated protein kinase signaling cascades by integrating protein interaction with transcriptional profiling analysis in cotton. Scientific Reports, 2018, 8, 8178.	3.3	17
1376	Discovery of a novel iflavivirus sequence in the eastern paralysis tick Ixodes holocyclus. Archives of Virology, 2018, 163, 2451-2457.	2.1	24
1377	Gene flow prevents mitonuclear co-adaptation: A comparative portrait of sympatric wild types and cybrids in the fish Chrosomus eos. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 77-84.	1.0	1
1378	Comparative genomics of <i>Campylobacter concisus</i> : Analysis of clinical strains reveals genome diversity and pathogenic potential. Emerging Microbes and Infections, 2018, 7, 1-17.	6.5	25
1379	SPTEdb: a database for transposable elements in salicaceous plants. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	12
1380	The transcriptome of flower development provides insight into floral scent formation in Freesia hybrida. Plant Growth Regulation, 2018, 86, 93-104.	3.4	21
1381	Transcriptomic Profiling of Fruit Development in Black Raspberry Rubus coreanus. International Journal of Genomics, 2018, 2018, 1-13.	1.6	7
1382	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion ( <i>MATE</i> ) Family in <i>Gossypium raimondii</i> and <i>Gossypium arboreum</i> and Its Expression Analysis Under Salt, Cadmium, and Drought Stress. G3: Genes, Genomes, Genetics, 2018, 8, 2483-2500.	1.8	56
1383	Cotton Late Embryogenesis Abundant ( <i>LEA2</i> ) Genes Promote Root Growth and Confer Drought Stress Tolerance in Transgenic <i>Arabidopsis thaliana</i> . G3: Genes, Genomes, Genetics, 2018, 8, 2781-2803.	1.8	51

#	ARTICLE	IF	CITATIONS
1384	Genome-wide identification and comprehensive analysis of the NAC transcription factor family in <i>Sesamum indicum</i> . PLoS ONE, 2018, 13, e0199262.	2.5	29
1385	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.	1.9	9
1386	A CAZyme-Rich Genome of a Taxonomically Novel Rhodophyte-Associated Carrageenolytic Marine Bacterium. Marine Biotechnology, 2018, 20, 685-705.	2.4	8
1387	Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evolution, 2018, 4, vey008.	4.9	90
1388	Community dynamics and functional characteristics of naphthalene-degrading populations in contaminated surface sediments and hypoxic/anoxic groundwater. Environmental Microbiology, 2018, 20, 3543-3559.	3.8	22
1389	Use of designed sequences in protein structure recognition. Biology Direct, 2018, 13, 8.	4.6	5
1390	Insights into Avian Incomplete Dosage Compensation: Sex-Biased Gene Expression Coevolves with Sex Chromosome Degeneration in the Common Whitethroat. Genes, 2018, 9, 373.	2.4	13
1391	EqualTDL: illustrating equivalent tandem duplication random loss rearrangements. BMC Bioinformatics, 2018, 19, 192.	2.6	7
1392	Mixed evolutionary origins of endogenous biomass-depolymerizing enzymes in animals. BMC Genomics, 2018, 19, 483.	2.8	8
1393	Guarding the gateway to histidine biosynthesis in plants: <i>Medicago truncatula</i> ATP-phosphoribosyltransferase in relaxed and tense states. Biochemical Journal, 2018, 475, 2681-2697.	3.7	6
1394	Genome-Wide Identification and Expression Analysis of the KUP Family under Abiotic Stress in Cassava ( <i>Manihot esculenta</i> Crantz). Frontiers in Physiology, 2018, 9, 17.	2.8	65
1395	Asymmetric Evolution and Expansion of the NAC Transcription Factor in Polyploidized Cotton. Frontiers in Plant Science, 2018, 9, 47.	3.6	24
1396	Identification of Putative Precursor Genes for the Biosynthesis of Cannabinoid-Like Compound in <i>Radula marginata</i> . Frontiers in Plant Science, 2018, 9, 537.	3.6	28
1397	Murine colitis reveals a disease-associated bacteriophage community. Nature Microbiology, 2018, 3, 1023-1031.	13.3	132
1398	Computational Methodologies in the Exploration of Marine Natural Product Leads. Marine Drugs, 2018, 16, 236.	4.6	70
1399	<i>SECONDARY WALL ASSOCIATED MYB1</i> is a positive regulator of secondary cell wall thickening in <i>Brachypodium distachyon</i> and is not found in the Brassicaceae. Plant Journal, 2018, 96, 532-545.	5.7	20
1400	Cotton rat lung transcriptome reveals host immune response to Respiratory Syncytial Virus infection. Scientific Reports, 2018, 8, 11318.	3.3	10
1401	Genome-Wide Identification and Characterization of WD40 Protein Genes in the Silkworm, <i>Bombyx mori</i> . International Journal of Molecular Sciences, 2018, 19, 527.	4.1	17

#	ARTICLE	IF	CITATIONS
1402	Integrative visual omics of the white-rot fungus <i>Polyporus brumalis</i> exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. <i>Biotechnology for Biofuels</i> , 2018, 11, 201.	6.2	45
1403	SNP hot-spots in the clam parasite QPX. <i>BMC Genomics</i> , 2018, 19, 486.	2.8	2
1404	Genome-Wide Identification, Expression, and Functional Analysis of the Sugar Transporter Gene Family in Cassava ( <i>Manihot esculenta</i> ). <i>International Journal of Molecular Sciences</i> , 2018, 19, 987.	4.1	30
1405	Arachidonic Acid Stress Impacts Pneumococcal Fatty Acid Homeostasis. <i>Frontiers in Microbiology</i> , 2018, 9, 813.	3.5	42
1406	An Engineered Distant Homolog of <i>Pseudomonas syringae</i> TTSS Effector From <i>Physcomitrella patens</i> Can Act as a Bacterial Virulence Factor. <i>Frontiers in Microbiology</i> , 2018, 9, 1060.	3.5	4
1407	Horizontal transfer of BovB and L1 retrotransposons in eukaryotes. <i>Genome Biology</i> , 2018, 19, 85.	8.8	78
1408	Whole genome and transcriptome analysis reveal adaptive strategies and pathogenesis of <i>Calonectria pseudoreteauidii</i> to <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2018, 19, 358.	2.8	15
1409	Genome-Wide Analysis of the GRF Family Reveals Their Involvement in Abiotic Stress Response in Cassava. <i>Genes</i> , 2018, 9, 110.	2.4	23
1410	A Novel G-Protein-Coupled Receptors Gene from Upland Cotton Enhances Salt Stress Tolerance in Transgenic <i>Arabidopsis</i> . <i>Genes</i> , 2018, 9, 209.	2.4	50
1411	Genome-Wide Analyses of Calcium Sensors Reveal Their Involvement in Drought Stress Response and Storage Roots Deterioration after Harvest in Cassava. <i>Genes</i> , 2018, 9, 221.	2.4	9
1412	Horizontal gene transfer of <i>Chlamydia</i> : Novel insights from tree reconciliation. <i>PLoS ONE</i> , 2018, 13, e0195139.	2.5	6
1413	Genome-Wide Identification and Characterization of Tyrosine Kinases in the Silkworm, <i>Bombyx mori</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 934.	4.1	4
1414	Genome-Wide Identification and Expression Analysis of the UGlcAE Gene Family in Tomato. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1583.	4.1	27
1415	The Late Embryogenesis Abundant Protein Family in Cassava ( <i>Manihot esculenta</i> Crantz): Genome-Wide Characterization and Expression during Abiotic Stress. <i>Molecules</i> , 2018, 23, 1196.	3.8	22
1416	<i>Burkholderia cenocepacia</i> Prophages—Prevalence, Chromosome Location and Major Genes Involved. <i>Viruses</i> , 2018, 10, 297.	3.3	16
1417	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	27.8	337
1418	Stable isotope informed genome-resolved metagenomics reveals that <i>Saccharibacteria</i> utilize microbially-processed plant-derived carbon. <i>Microbiome</i> , 2018, 6, 122.	11.1	156
1419	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018, 11, 1024-1037.	8.3	130

#	ARTICLE	IF	CITATIONS
1420	A High-Quality Reference Genome for the Invasive Mosquitofish <i>Gambusia affinis</i> Using a Chicago Library. G3: Genes, Genomes, Genetics, 2018, 8, 1855-1861.	1.8	16
1421	The genome assembly of the fungal pathogen <i>Pyrenochaeta lycopersici</i> from Single-Molecule Real-Time sequencing sheds new light on its biological complexity. PLoS ONE, 2018, 13, e0200217.	2.5	19
1422	Plant annexins and their involvement in stress responses. Environmental and Experimental Botany, 2018, 155, 293-306.	4.2	38
1423	Transcriptome-Guided Identification of Carbohydrate Active Enzymes (CAZy) from the Christmas Island Red Crab, <i>Gecarcoidea natalis</i> and a Vote for the Inclusion of Transcriptome-Derived Crustacean CAZys in Comparative Studies. Marine Biotechnology, 2018, 20, 654-665.	2.4	21
1424	De novo transcriptome assembly of <i>Pueraria montana</i> var. <i>lobata</i> and <i>Neustanthus phaseoloides</i> for the development of eSSR and SNP markers: narrowing the US origin(s) of the invasive kudzu. BMC Genomics, 2018, 19, 439.	2.8	11
1425	<i>Ceratocystis cacaofunesta</i> genome analysis reveals a large expansion of extracellular phosphatidylinositol-specific phospholipase-C genes (PI-PLC). BMC Genomics, 2018, 19, 58.	2.8	19
1426	Plasma virome of cattle from forest region revealed diverse small circular ssDNA viral genomes. Virology Journal, 2018, 15, 11.	3.4	27
1427	Terzyme: a tool for identification and analysis of the plant terpenome. Plant Methods, 2018, 14, 4.	4.3	25
1428	Elucidation of the anti-hyperammonemic mechanism of <i>Lactobacillus amylovorus</i> JBD401 by comparative genomic analysis. BMC Genomics, 2018, 19, 292.	2.8	12
1429	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. G3: Genes, Genomes, Genetics, 2018, 8, 2205-2214.	1.8	22
1430	BioPS: System for screening and assessment of biofuel-production potential of cyanobacteria. PLoS ONE, 2018, 13, e0202002.	2.5	4
1431	Broad Phylogenetic Diversity Associated with Nitrogen Loss through Sulfur Oxidation in a Large Public Marine Aquarium. Applied and Environmental Microbiology, 2018, 84, .	3.1	7
1432	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. Frontiers in Genetics, 2018, 9, 281.	2.3	30
1433	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. Scientific Reports, 2018, 8, 12699.	3.3	37
1434	High-Resolution Temporal and Spatial Patterns of Virome in Wastewater Treatment Systems. Environmental Science & Technology, 2018, 52, 10337-10346.	10.0	25
1435	A coevolution-guided model for the rotor of the bacterial flagellar motor. Scientific Reports, 2018, 8, 11754.	3.3	5
1436	Characterization of the $\beta$ -defensin genes in giant panda. Scientific Reports, 2018, 8, 12308.	3.3	7
1437	Identification and characterization of histone modification gene family reveal their critical responses to flower induction in apple. BMC Plant Biology, 2018, 18, 173.	3.6	21

#	ARTICLE	IF	CITATIONS
1438	Genome-Wide Identification, Characterization and Expression Analyses of Heat Shock Protein-Related Genes in a Highly Invasive Ascidian <i>Ciona savignyi</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1043.	2.8	25
1439	Genome-wide characterization, identification, and expression analysis of the WD40 protein family in cotton. <i>Genome</i> , 2018, 61, 539-547.	2.0	23
1440	Transcriptome response of the foundation plant <i>Spartina alterniflora</i> to the Deepwater Horizon oil spill. <i>Molecular Ecology</i> , 2018, 27, 2986-3000.	3.9	17
1441	Ubiquitin Proteasome pathway proteins as potential drug targets in parasite <i>Trypanosoma cruzi</i> . <i>Scientific Reports</i> , 2018, 8, 8399.	3.3	28
1442	Current strategies to induce secondary metabolites from microbial biosynthetic cryptic gene clusters. <i>Annals of Microbiology</i> , 2018, 68, 419-432.	2.6	19
1443	Luciferase of the Japanese syllid polychaete <i>Odontosyllis umdecimdonga</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 502, 318-323.	2.1	24
1444	Transcriptomic and functional analyses unveil the role of long non-coding RNAs in anthocyanin biosynthesis during sea buckthorn fruit ripening. <i>DNA Research</i> , 2018, 25, 465-476.	3.4	114
1445	Comprehensive analysis of <i>Verticillium nonalfalfae</i> in silico secretome uncovers putative effector proteins expressed during hop invasion. <i>PLoS ONE</i> , 2018, 13, e0198971.	2.5	51
1446	The Evolutionary Consequences of Transposon-Related Pericentromer Expansion in Melon. <i>Genome Biology and Evolution</i> , 2018, 10, 1584-1595.	2.5	20
1447	Superior ab initio identification, annotation and characterisation of TEs and segmental duplications from genome assemblies. <i>PLoS ONE</i> , 2018, 13, e0193588.	2.5	27
1448	Discovering Patterns From Sequences Using Pattern-Directed Aligned Pattern Clustering. <i>IEEE Transactions on Nanobioscience</i> , 2018, 17, 209-218.	3.3	4
1449	Analysis of a vinculin homolog in a sponge (phylum Porifera) reveals that vertebrate-like cell adhesions emerged early in animal evolution. <i>Journal of Biological Chemistry</i> , 2018, 293, 11674-11686.	3.4	25
1450	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of <i>linc-ADAL</i> in adipocyte metabolism. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	42
1451	Transcriptional up-regulation of BAG3, a Chaperone Assisted Selective Autophagy factor, in animal models of KY-deficient hereditary myopathy. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	2.4	3
1452	Dispersal-competition tradeoff in microbiomes in the quest for land colonization. <i>Scientific Reports</i> , 2018, 8, 9451.	3.3	15
1453	Genomics of Actinobacteria With a Focus on Natural Product Biosynthetic Genes. , 2018, , 325-335.		0
1454	FlyXCDBâ€”A Resource for <i>Drosophila</i> Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 3353-3411.	4.2	13
1455	Multi 'omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone. <i>Science of the Total Environment</i> , 2018, 642, 742-753.	8.0	60

#	ARTICLE	IF	CITATIONS
1456	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W200-W204.	14.5	1,432
1457	Assigning biological function using hidden signatures in cystine-stabilized peptide sequences. <i>Scientific Reports</i> , 2018, 8, 9049.	3.3	5
1458	The calcium sensor TaCBL4 and its interacting protein TaCIPK5 are required for wheat resistance to stripe rust fungus. <i>Journal of Experimental Botany</i> , 2018, 69, 4443-4457.	4.8	49
1459	LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. <i>Briefings in Bioinformatics</i> , 2019, 20, 2009-2027.	6.5	98
1460	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. <i>Plant Biotechnology Journal</i> , 2019, 17, 451-460.	8.3	89
1461	The developmental dynamics of the <i>Populus</i> stem transcriptome. <i>Plant Biotechnology Journal</i> , 2019, 17, 206-219.	8.3	112
1462	Infrastructure for High-Performance Computing: Grids and Grid Computing. , 2019, , 230-235.		2
1463	Identification of Homologs. , 2019, , 980-984.		1
1464	Biological Database Searching. , 2019, , 29-38.		0
1465	Protein Three-Dimensional Structure Prediction. , 2019, , 497-511.		4
1466	Cross-species systems analysis of evolutionary toolkits of neurogenomic response to social challenge. <i>Genes, Brain and Behavior</i> , 2019, 18, e12502.	2.2	30
1467	Protein Import into Hydrogenosomes and Mitosomes. <i>Microbiology Monographs</i> , 2019, , 31-84.	0.6	2
1468	Multiple Independent Origins of Apicomplexan-Like Parasites. <i>Current Biology</i> , 2019, 29, 2936-2941.e5.	3.9	84
1469	Elucidating Syntrophic Butyrate-Degrading Populations in Anaerobic Digesters Using Stable-Isotope-Informed Genome-Resolved Metagenomics. <i>MSystems</i> , 2019, 4, .	3.8	19
1470	Characterization of Microalgal Acetyl-CoA Synthetases with High Catalytic Efficiency Reveals Their Regulatory Mechanism and Lipid Engineering Potential. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9569-9578.	5.2	6
1471	Characterization of <i>Pectobacterium carotovorum</i> subsp. <i>carotovorum</i> Bacteriophage PP16 Prospective for Biocontrol of Potato Soft Rot. <i>Microbiology</i> , 2019, 88, 451-460.	1.2	27
1472	The SWEET family genes in strawberry: Identification and expression profiling during fruit development. <i>South African Journal of Botany</i> , 2019, 125, 176-187.	2.5	13
1473	Transcriptome Analysis of Young Ovaries Reveals Candidate Genes Involved in Gamete Formation in <i>Lantana camara</i> . <i>Plants</i> , 2019, 8, 263.	3.5	5



#	ARTICLE	IF	CITATIONS
1474	Cassava AGPase genes and their encoded proteins are different from those of other plants. <i>Planta</i> , 2019, 250, 1621-1635.	3.2	8
1475	The predominance of nucleotidyl activation in bacterial phosphonate biosynthesis. <i>Nature Communications</i> , 2019, 10, 3698.	12.8	16
1476	Transcriptomic analysis of Pacific white shrimp ( <i>Litopenaeus vannamei</i> , Boone 1931) in response to acute hepatopancreatic necrosis disease caused by <i>Vibrio parahaemolyticus</i> . <i>PLoS ONE</i> , 2019, 14, e0220993.	2.5	43
1477	CasPDB: an integrated and annotated database for Cas proteins from bacteria and archaea. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	8
1478	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. <i>PeerJ</i> , 2019, 7, e6741.	2.0	18
1479	Transcriptomic investigation into polyketide toxin synthesis in <i>Ostreopsis</i> (Dinophyceae) species. <i>Environmental Microbiology</i> , 2019, 21, 4196-4211.	3.8	12
1480	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	8.8	21
1481	Genomic analysis of the core components of ABA signaling reveals their possible role in abiotic stress response in cassava. <i>Environmental and Experimental Botany</i> , 2019, 167, 103855.	4.2	11
1482	<i>Labeledella phragmitis</i> sp. nov. and <i>Labeledella populi</i> sp. nov., two endophytic actinobacteria isolated from plants in the Taklamakan Desert and emended description of the genus <i>Labeledella</i> . <i>Systematic and Applied Microbiology</i> , 2019, 42, 126004.	2.8	20
1483	Complete chloroplast genome of <i>Prunus canescens</i> : an endemic shrub in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2381-2382.	0.4	1
1484	The complete chloroplast genome of <i>Vaccinium duclouxii</i> , an endemic species in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2215-2216.	0.4	5
1485	The complete chloroplast genome of <i>Vaccinium fragile</i> (Vacciniaceae), a shrub endemic to China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2310-2311.	0.4	4
1486	Genome-wide identification and expression analysis of the dof (DNA binding with one finger) protein family in monocot and dicot species. <i>Physiological and Molecular Plant Pathology</i> , 2019, 108, 101431.	2.5	3
1487	Transcriptome profile of <i>Corynebacterium pseudotuberculosis</i> in response to iron limitation. <i>BMC Genomics</i> , 2019, 20, 663.	2.8	19
1488	Transcriptome Landscape Variation in the Genus <i>Thymus</i> . <i>Genes</i> , 2019, 10, 620.	2.4	11
1489	Secretomic analyses of <i>Ruminiclostridium papyrosolvens</i> reveal its enzymatic basis for lignocellulose degradation. <i>Biotechnology for Biofuels</i> , 2019, 12, 183.	6.2	24
1490	Genome-Wide Identification and Expression Analysis of the Metacaspase Gene Family in <i>Gossypium</i> Species. <i>Genes</i> , 2019, 10, 527.	2.4	9
1491	Prediction of interresidue contacts with DeepMetaPSICOV in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1092-1099.	2.6	102

#	ARTICLE	IF	CITATIONS
1492	Peat substrate amended with chitin modulates the N-cycle, siderophore and chitinase responses in the lettuce rhizobiome. <i>Scientific Reports</i> , 2019, 9, 9890.	3.3	50
1493	Identification and Functional Investigation of Genome-Encoded, Small, Secreted Peptides in Plants. <i>Current Protocols in Plant Biology</i> , 2019, 4, e20098.	2.8	15
1495	Automated structure prediction of trans-acyltransferase polyketide synthase products. <i>Nature Chemical Biology</i> , 2019, 15, 813-821.	8.0	94
1496	Transcriptome analysis and codominant markers development in caper, a drought tolerant orphan crop with medicinal value. <i>Scientific Reports</i> , 2019, 9, 10411.	3.3	23
1497	Diversification of the type IV filament superfamily into machines for adhesion, protein secretion, DNA uptake, and motility. <i>PLoS Biology</i> , 2019, 17, e3000390.	5.6	121
1498	Phylogenetic Methods to Study Light Signaling. <i>Methods in Molecular Biology</i> , 2019, 2026, 265-276.	0.9	0
1499	Genome wide characterization, evolution and expression analysis of FBA gene family under salt stress in <i>Gossypium</i> species. <i>Biologia (Poland)</i> , 2019, 74, 1539-1552.	1.5	3
1500	iDS372, a Phenotypically Reconciled Model for the Metabolism of <i>Streptococcus pneumoniae</i> Strain R6. <i>Frontiers in Microbiology</i> , 2019, 10, 1283.	3.5	20
1501	Global characterization and expression analysis of interferon regulatory factors in response to <i>Aeromonas hydrophila</i> challenge in Chinese soft-shelled turtle ( <i>Pelodiscus sinensis</i> ). <i>Fish and Shellfish Immunology</i> , 2019, 92, 821-832.	3.6	10
1502	De novo European eel transcriptome provides insights into the evolutionary history of duplicated genes in teleost lineages. <i>PLoS ONE</i> , 2019, 14, e0218085.	2.5	41
1503	Identification of TPX2 Gene Family in Upland Cotton and Its Functional Analysis in Cotton Fiber Development. <i>Genes</i> , 2019, 10, 508.	2.4	8
1504	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019, 15, 803-812.	8.0	97
1505	RNA profiling of human testicular cells identifies syntenic lncRNAs associated with spermatogenesis. <i>Human Reproduction</i> , 2019, 34, 1278-1290.	0.9	35
1506	Genome-Wide Identification and Characterization of JAZ Protein Family in Two <i>Petunia</i> Progenitors. <i>Plants</i> , 2019, 8, 203.	3.5	8
1507	Data-driven computational analysis of allosteric proteins by exploring protein dynamics, residue coevolution and residue interaction networks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, , .	2.4	17
1508	Microbial life cycles link global modularity in regulation to mosaic evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 1184-1196.	7.8	18
1509	Switching of INCENP paralogs controls transitions in mitotic chromosomal passenger complex functions. <i>Cell Cycle</i> , 2019, 18, 2006-2025.	2.6	6
1510	Functional characterization of Gh_A08G1120 (GH3.5) gene reveal their significant role in enhancing drought and salt stress tolerance in cotton. <i>BMC Genetics</i> , 2019, 20, 62.	2.7	39

#	ARTICLE	IF	CITATIONS
1511	Molecular evolution and lineage-specific expansion of the PP2C family in <i>Zea mays</i> . <i>Planta</i> , 2019, 250, 1521-1538.	3.2	51
1512	MerMAIDs: a family of metagenomically discovered marine anion-conducting and intensely desensitizing channelrhodopsins. <i>Nature Communications</i> , 2019, 10, 3315.	12.8	56
1513	Computer-aided re-engineering of nonribosomal peptide and polyketide biosynthetic assembly lines. <i>Natural Product Reports</i> , 2019, 36, 1249-1261.	10.3	35
1514	Combining genome-wide and transcriptome-wide analyses reveal the evolutionary conservation and functional diversity of aquaporins in cotton. <i>BMC Genomics</i> , 2019, 20, 538.	2.8	20
1515	Draft genome sequence of cauliflower ( <i>Brassica oleracea</i> L. var. <i>botrytis</i> ) provides new insights into the C genome in <i>Brassica</i> species. <i>Horticulture Research</i> , 2019, 6, 82.	6.3	53
1516	Characterization and analysis of the transcriptome in <i>Gymnocypris selincuoensis</i> on the Qinghai-Tibetan Plateau using single-molecule long-read sequencing and RNA-seq. <i>DNA Research</i> , 2019, 26, 353-363.	3.4	31
1517	Particle Migration and Clogging in Porous Media: A Convergent Flow Microfluidics Study. <i>Journal of Geophysical Research: Solid Earth</i> , 2019, 124, 9495-9504.	3.4	56
1518	DnaJ molecules as potential effectors in <i>Meloidogyne arenaria</i> . An unexplored group of proteins in plant parasitic nematodes. <i>Communicative and Integrative Biology</i> , 2019, 12, 151-161.	1.4	5
1519	Occurrence of Ordered and Disordered Structural Elements in Postsynaptic Proteins Supports Optimization for Interaction Diversity. <i>Entropy</i> , 2019, 21, 761.	2.2	6
1520	Insights revealed by the co-crystal structure of the <i>Saccharomyces cerevisiae</i> histidine phosphotransfer protein Ypd1 and the receiver domain of its downstream response regulator Ssk1. <i>Protein Science</i> , 2019, 28, 2099-2111.	7.6	5
1521	Remote homology searches identify bacterial homologues of eukaryotic lipid transfer proteins, including Chorein-N domains in TamB and AsmA and Mdm31p. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 43.	2.0	35
1522	Protease-associated import systems are widespread in Gram-negative bacteria. <i>PLoS Genetics</i> , 2019, 15, e1008435.	3.5	15
1523	An Overview of Genes From <i>Cyberlindnera americana</i> , a Symbiont Yeast Isolated From the Gut of the Bark Beetle <i>Dendroctonus rhizophagus</i> (Curculionidae: Scolytinae), Involved in the Detoxification Process Using Genome and Transcriptome Data. <i>Frontiers in Microbiology</i> , 2019, 10, 2180.	3.5	11
1524	The complete chloroplast genome of sweet tea ( <i>Lithocarpus polystachyus</i> ). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 2489-2490.	0.4	5
1525	ProtDec-LTR3.0: Protein Remote Homology Detection by Incorporating Profile-Based Features Into Learning to Rank. <i>IEEE Access</i> , 2019, 7, 102499-102507.	4.2	41
1526	Comparative Study of Gut Microbiota in Wild and Captive Giant Pandas ( <i>Ailuropoda melanoleuca</i> ). <i>Genes</i> , 2019, 10, 827.	2.4	69
1527	Extensive Tandem Duplication Events Drive the Expansion of the C1q-Domain-Containing Gene Family in Bivalves. <i>Marine Drugs</i> , 2019, 17, 583.	4.6	33
1528	PacBio single-molecule long-read sequencing shed new light on the complexity of the <i>Carex breviculmis</i> transcriptome. <i>BMC Genomics</i> , 2019, 20, 789.	2.8	25

#	ARTICLE	IF	CITATIONS
1529	Dissecting the Genome-Wide Evolution and Function of R2R3-MYB Transcription Factor Family in <i>Rosa chinensis</i> . <i>Genes</i> , 2019, 10, 823.	2.4	14
1530	Species-wide Metabolic Interaction Network for Understanding Natural Lignocellulose Digestion in Termite Gut Microbiota. <i>Scientific Reports</i> , 2019, 9, 16329.	3.3	28
1531	Genome-wide identification and characterization, phylogenetic comparison and expression profiles of SPL transcription factor family in <i>B. juncea</i> (Cruciferae). <i>PLoS ONE</i> , 2019, 14, e0224704.	2.5	5
1532	Pomegranate PLAC8 family. <i>Acta Horticulturae</i> , 2019, , 35-40.	0.2	1
1533	PDBe: improved findability of macromolecular structure data in the PDB. <i>Nucleic Acids Research</i> , 2020, 48, D335-D343.	14.5	86
1534	Diverse cell junctions with unique molecular composition in tissues of a sponge (Porifera). <i>EvoDevo</i> , 2019, 10, 26.	3.2	16
1535	The structure of the bacterial iron- catecholate transporter Fiu suggests that it imports substrates via a two-step mechanism. <i>Journal of Biological Chemistry</i> , 2019, 294, 19523-19534.	3.4	22
1536	Genome-wide characterization and evolutionary analysis of heat shock transcription factors (HSFs) to reveal their potential role under abiotic stresses in radish ( <i>Raphanus sativus</i> L.). <i>BMC Genomics</i> , 2019, 20, 772.	2.8	23
1537	Active Fungal Communities in Asymptomatic <i>Eucalyptus grandis</i> Stems Differ between a Susceptible and Resistant Clone. <i>Microorganisms</i> , 2019, 7, 375.	3.6	6
1538	Genome-Wide Analysis of NAC Gene Family in <i>Betula pendula</i> . <i>Forests</i> , 2019, 10, 741.	2.1	44
1539	A Sequence-Indexed <i>Mutator</i> Insertional Library for Maize Functional Genomics Study. <i>Plant Physiology</i> , 2019, 181, 1404-1414.	4.8	28
1540	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chi- like protein tail- fibre. <i>Molecular Microbiology</i> , 2019, 112, 1831-1846.	2.5	24
1541	High-throughput DNA sequencing technologies for water and wastewater analysis. <i>Science Progress</i> , 2019, 102, 351-376.	1.9	16
1542	Metatranscriptomic and metabolite profiling reveals vertical heterogeneity within a <i>Zygnema</i> green algal mat from Svalbard (High Arctic). <i>Environmental Microbiology</i> , 2019, 21, 4283-4299.	3.8	31
1543	Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. <i>Microbiome</i> , 2019, 7, 119.	11.1	65
1544	Characterization of VQ motif-containing protein family and their expression patterns under phytohormones and abiotic stresses in melon ( <i>Cucumis melo</i> L.). <i>Plant Growth Regulation</i> , 2019, 89, 273-285.	3.4	8
1545	De novo transcriptome assembly for four species of crustose coralline algae and analysis of unique orthologous genes. <i>Scientific Reports</i> , 2019, 9, 12611.	3.3	10
1546	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	11.1	65

#	ARTICLE	IF	CITATIONS
1547	Persistent metagenomic signatures of early-life hospitalization and antibiotic treatment in the infant gut microbiota and resistome. <i>Nature Microbiology</i> , 2019, 4, 2285-2297.	13.3	191
1548	Genome-wide analysis of cotton C2H2-zinc finger transcription factor family and their expression analysis during fiber development. <i>BMC Plant Biology</i> , 2019, 19, 400.	3.6	27
1549	High-Throughput RNA Sequencing Reveals NDUFC2-AS lncRNA Promotes Adipogenic Differentiation in Chinese Buffalo ( <i>Bubalus bubalis</i> L). <i>Genes</i> , 2019, 10, 689.	2.4	32
1550	Comparative study of excretory–secretory proteins released by <i>Schistosoma mansoni</i> -resistant, susceptible and naïve <i>Biomphalaria glabrata</i> . <i>Parasites and Vectors</i> , 2019, 12, 452.	2.5	19
1551	Bulked segregant analysis RNA-seq (BSR-Seq) validated a stem resistance locus in <i>Aegilops umbellulata</i> , a wild relative of wheat. <i>PLoS ONE</i> , 2019, 14, e0215492.	2.5	25
1552	Up-regulation of a homeodomain-leucine zipper gene HD-1 contributes to trichome initiation and development in cotton. <i>Journal of Integrative Agriculture</i> , 2019, 18, 361-371.	3.5	8
1553	MbnH is a diheme MauG-like protein associated with microbial copper homeostasis. <i>Journal of Biological Chemistry</i> , 2019, 294, 16141-16151.	3.4	6
1554	The RabGAP Gene Family in Tomato ( <i>Solanum lycopersicum</i> ) and Wild Relatives: Identification, Interaction Networks, and Transcriptional Analysis during Plant Development and in Response to Salt Stress. <i>Genes</i> , 2019, 10, 638.	2.4	10
1555	The Effect of Blue Light on the Production of Citrinin in <i>Monascus purpureus</i> M9 by Regulating the mraox Gene through lncRNA AOANCR. <i>Toxins</i> , 2019, 11, 536.	3.4	18
1556	A novel transcriptome-derived SNPs array for tench ( <i>Tinca tinca</i> L.). <i>PLoS ONE</i> , 2019, 14, e0213992.	2.5	3
1557	Effects of Essential Oil Citral on the Growth, Mycotoxin Biosynthesis and Transcriptomic Profile of <i>Alternaria alternata</i> . <i>Toxins</i> , 2019, 11, 553.	3.4	45
1558	Horizontal and vertical integrative analysis methods for mental disorders omics data. <i>Scientific Reports</i> , 2019, 9, 13430.	3.3	5
1559	Cold Acclimation Improves the Desiccation Stress Resilience of Polar Strains of <i>Klebsormidium</i> (Streptophyta). <i>Frontiers in Microbiology</i> , 2019, 10, 1730.	3.5	15
1560	Genome-Wide Analysis of Cotton Auxin Early Response Gene Families and Their Roles in Somatic Embryogenesis. <i>Genes</i> , 2019, 10, 730.	2.4	18
1561	The pH optimum of soil exoenzymes adapt to long term changes in soil pH. <i>Soil Biology and Biochemistry</i> , 2019, 138, 107601.	8.8	73
1562	Cadherin switch marks germ layer formation in the diploblastic sea anemone <i>Nematostella vectensis</i> . <i>Development (Cambridge)</i> , 2019, 146, .	2.5	14
1563	Identification and evolutionary characterization of salt-responsive transcription factors in the succulent halophyte <i>Suaeda fruticosa</i> . <i>PLoS ONE</i> , 2019, 14, e0222940.	2.5	9
1564	Protein fold recognition based on multi-view modeling. <i>Bioinformatics</i> , 2019, 35, 2982-2990.	4.1	70

#	ARTICLE	IF	CITATIONS
1565	Extent and Origins of Functional Diversity in a Subfamily of Glycoside Hydrolases. <i>Journal of Molecular Biology</i> , 2019, 431, 1217-1233.	4.2	13
1566	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	13.3	141
1567	Systematic domain-based aggregation of protein structures highlights DNA-, RNA- and other ligand-binding positions. <i>Nucleic Acids Research</i> , 2019, 47, 582-593.	14.5	16
1568	NBS-Encoding Genes in <i>Brassica napus</i> Evolved Rapidly After Allopolyploidization and Co-localize With Known Disease Resistance Loci. <i>Frontiers in Plant Science</i> , 2019, 10, 26.	3.6	27
1569	Genome-wide characterization and expression profiling of SWEET genes in cabbage ( <i>Brassica oleracea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 93.	2.8	51
1570	Comparative analysis of two sister <i>Erythrophleum</i> species (Leguminosae) reveal contrasting transcriptome-wide responses to early drought stress. <i>Gene</i> , 2019, 694, 50-62.	2.2	2
1571	The Role of the CopA Copper Efflux System in <i>Acinetobacter baumannii</i> Virulence. <i>International Journal of Molecular Sciences</i> , 2019, 20, 575.	4.1	35
1572	Newly Discovered Occurrences and Gene Tree of the Extracellular Globins and Linker Chains from the Giant Hexagonal Bilayer Hemoglobin in Metazoans. <i>Genome Biology and Evolution</i> , 2019, 11, 597-612.	2.5	12
1573	Triplet-pore structure of a highly divergent TOM complex of hydrogenosomes in <i>Trichomonas vaginalis</i> . <i>PLoS Biology</i> , 2019, 17, e3000098.	5.6	33
1574	Genome-Wide Identification and Expression Profiling of Sugar Transporter Protein (STP) Family Genes in Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> L.) Reveals their Involvement in Clubroot Disease Responses. <i>Genes</i> , 2019, 10, 71.	2.4	29
1575	Metabolic diversity within the globally abundant Marine Group II Euryarchaea offers insight into ecological patterns. <i>Nature Communications</i> , 2019, 10, 271.	12.8	66
1576	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
1577	The Hsp70 Gene Family in <i>Boleophthalmus pectinirostris</i> : Genome-Wide Identification and Expression Analysis under High Ammonia Stress. <i>Animals</i> , 2019, 9, 36.	2.3	12
1578	Plant Aquaporins: Diversity, Evolution and Biotechnological Applications. <i>Current Protein and Peptide Science</i> , 2019, 20, 368-395.	1.4	42
1579	Gut virome of mammals and birds reveals high genetic diversity of the family Microviridae. <i>Virus Evolution</i> , 2019, 5, vez013.	4.9	37
1580	Amino Acid Residues Î²139, Î²189, and Î²319 Modulate ADP-Inhibition in <i>Escherichia coli</i> H <sup>+</sup> -FOF1-ATP Synthase. <i>Biochemistry (Moscow)</i> , 2019, 84, 407-415.	1.5	4
1581	Diversity of circular RNAs and RNA ligases in archaeal cells. <i>Biochimie</i> , 2019, 164, 37-44.	2.6	6
1582	Metatranscriptomics of the Hu sheep rumen microbiome reveals novel cellulases. <i>Biotechnology for Biofuels</i> , 2019, 12, 153.	6.2	42

#	ARTICLE	IF	CITATIONS
1583	Embryonic development of a parthenogenetic vertebrate, the mourning gecko ( <i>Lepidodactylus</i> ) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	1.8	19
1584	Genomic analysis and lactose transporter expression in <i>Kluyveromyces marxianus</i> CCT 7735. <i>Fungal Biology</i> , 2019, 123, 687-697.	2.5	4
1585	Metaproteomics: Sample Preparation and Methodological Considerations. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1073, 187-215.	1.6	26
1586	Mosaic origin of the eukaryotic kinetochore. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12873-12882.	7.1	76
1587	The Transcriptome Landscape of Walnut Interspecies Hybrid ( <i>Juglans hindsii</i> Å— <i>Juglans regia</i> ) and Regulation of Cambial Activity in Relation to Grafting. <i>Frontiers in Genetics</i> , 2019, 10, 577.	2.3	9
1588	Emerging Sample Treatments in Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2019, , .	1.6	6
1589	Evolutionary Analyses Reveal Diverged Patterns of SQUAMOSA Promoter Binding Protein-Like (SPL) Gene Family in <i>Oryza</i> Genus. <i>Frontiers in Plant Science</i> , 2019, 10, 565.	3.6	37
1590	De novo transcriptome assembly of a facultative parasitic nematode <i>Pelodera</i> (syn. <i>Rhabditis</i> ) <i>strongyloides</i> . <i>Gene</i> , 2019, 710, 30-38.	2.2	3
1591	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	2.5	27
1592	Leaf Transcriptome Assembly of <i>Protium copal</i> (Burseraceae) and Annotation of Terpene Biosynthetic Genes. <i>Genes</i> , 2019, 10, 392.	2.4	6
1593	The complete genome of <i>Rachiplusia nu</i> nucleopolyhedrovirus (RanuNPV) and the identification of a baculoviral CPD-photolyase homolog. <i>Virology</i> , 2019, 534, 64-71.	2.4	8
1594	In-depth proteomic characterization of <i>Schistosoma haematobium</i> : Towards the development of new tools for elimination. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007362.	3.0	31
1595	The isoprenoid alcohol pathway, a synthetic route for isoprenoid biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12810-12815.	7.1	108
1596	ANASTASIA: An Automated Metagenomic Analysis Pipeline for Novel Enzyme Discovery Exploiting Next Generation Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 469.	2.3	21
1597	Long Noncoding RNA: Genomics and Relevance to Physiology. , 2019, 9, 933-946.		25
1598	A haplotype-resolved draft genome of the European sardine ( <i>Sardina pilchardus</i> ). <i>GigaScience</i> , 2019, 8, .	6.4	14
1599	Genome-wide identification, characterization and expression analysis of the non-specific lipid transfer proteins in potato. <i>BMC Genomics</i> , 2019, 20, 375.	2.8	21
1600	AutoMLST: an automated web server for generating multi-locus species trees highlighting natural product potential. <i>Nucleic Acids Research</i> , 2019, 47, W276-W282.	14.5	286



#	ARTICLE	IF	CITATIONS
1601	Biological and molecular characterization of a bacteriophage infecting <i>Xanthomonas campestris</i> pv. <i>campestris</i> , isolated from brassica fields. <i>Archives of Virology</i> , 2019, 164, 1857-1862.	2.1	6
1602	Large-Scale Genomics Reveals the Genetic Characteristics of Seven Species and Importance of Phylogenetic Distance for Estimating Pan-Genome Size. <i>Frontiers in Microbiology</i> , 2019, 10, 834.	3.5	48
1603	Genome-Wide Identification of WRKY Genes and Their Response to Cold Stress in <i>Coffea canephora</i> . <i>Forests</i> , 2019, 10, 335.	2.1	15
1604	Prediction of pathogenicity genes involved in adaptation to a lupin host in the fungal pathogens <i>Botrytis cinerea</i> and <i>Sclerotinia sclerotiorum</i> via comparative genomics. <i>BMC Genomics</i> , 2019, 20, 385.	2.8	11
1605	ARGA, a pipeline for primer evaluation on antibiotic resistance genes. <i>Environment International</i> , 2019, 128, 137-145.	10.0	14
1606	Investigation of evolutionary and expressional relationships in the function of the leucine-rich repeat receptor-like protein kinase gene family (LRR-RLK) in the radish ( <i>Raphanus sativus</i> L.). <i>Scientific Reports</i> , 2019, 9, 6937.	3.3	26
1607	Diversification of cytokinin phosphotransfer signaling genes in <i>Medicago truncatula</i> and other legume genomes. <i>BMC Genomics</i> , 2019, 20, 373.	2.8	14
1608	GenDiS database update with improved approach and features to recognize homologous sequences of protein domain superfamilies. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	0
1609	Biosynthesis of methyl (E)-cinnamate in the liverwort <i>Conocephalum salebrosum</i> and evolution of cinnamic acid methyltransferase. <i>Phytochemistry</i> , 2019, 164, 50-59.	2.9	7
1610	A core set of venom proteins is released by entomopathogenic nematodes in the genus <i>Steinernema</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007626.	4.7	58
1611	Genome-wide analysis of HSP70 family genes in cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> ) reveals their involvement in floral development. <i>BMC Genomics</i> , 2019, 20, 369.	2.8	16
1612	An <i>Entamoeba</i> -Specific Mitosomal Membrane Protein with Potential Association to the Golgi Apparatus. <i>Genes</i> , 2019, 10, 367.	2.4	7
1613	The conservation and functionality of the oxygen-sensing enzyme Factor Inhibiting HIF (FIH) in non-vertebrates. <i>PLoS ONE</i> , 2019, 14, e0216134.	2.5	7
1614	Computational Characterization of the mtORF of Pocilloporid Corals: Insights into Protein Structure and Function in Stylophora Lineages from Contrasting Environments. <i>Genes</i> , 2019, 10, 324.	2.4	5
1615	De Novo Transcriptome Assembly and Functional Annotation in Five Species of Bats. <i>Scientific Reports</i> , 2019, 9, 6222.	3.3	23
1616	Evaluation of Phage Therapy in the Context of <i>Enterococcus faecalis</i> and Its Associated Diseases. <i>Viruses</i> , 2019, 11, 366.	3.3	55
1617	Genome-wide and functional analyses of tyrosine kinase-like family genes reveal potential roles in development and virulence in mosquito pathogen <i>Pythium guiyangense</i> . <i>Fungal Genetics and Biology</i> , 2019, 130, 11-18.	2.1	7
1618	Protein Structure-Guided Hidden Markov Models (HMMs) as A Powerful Method in the Detection of Ancestral Endogenous Viral Elements. <i>Viruses</i> , 2019, 11, 320.	3.3	7

#	ARTICLE	IF	CITATIONS
1619	Computational identification of prion-like RNA-binding proteins that form liquid phase-separated condensates. <i>Bioinformatics</i> , 2019, 35, 4617-4623.	4.1	45
1620	Retrosynthetic design of metabolic pathways to chemicals not found in nature. <i>Current Opinion in Systems Biology</i> , 2019, 14, 82-107.	2.6	84
1621	Genome analysis of <i>Paenibacillus polymyxa</i> A18 gives insights into the features associated with its adaptation to the termite gut environment. <i>Scientific Reports</i> , 2019, 9, 6091.	3.3	16
1622	Protein tertiary structure modeling driven by deep learning and contact distance prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1165-1178.	2.6	149
1623	Novel lineage-specific transmembrane $\alpha$ -barrel proteins in the endoplasmic reticulum of <i>Entamoeba histolytica</i> . <i>FEBS Journal</i> , 2019, 286, 3416-3432.	4.7	4
1624	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	6.4	88
1625	Comparative analysis of the root and leaf transcriptomes in <i>Chelidonium majus</i> L.. <i>PLoS ONE</i> , 2019, 14, e0215165.	2.5	13
1626	The role of C-terminal extensions in controlling ECF $\sigma$ factor activity in the widely conserved groups ECF41 and ECF42. <i>Molecular Microbiology</i> , 2019, 112, 498-514.	2.5	19
1627	Genomic Analyses of <i>Bifidobacterium moukalabense</i> Reveal Adaptations to Frugivore/Folivore Feeding Behavior. <i>Microorganisms</i> , 2019, 7, 99.	3.6	6
1628	Broad-specificity GH131 $\alpha$ -glucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019, 21, 2724-2739.	3.8	18
1629	New insights into the origin and evolution of $\alpha$ -amylase genes in green plants. <i>Scientific Reports</i> , 2019, 9, 4929.	3.3	14
1630	Structures in multiple conformations reveal distinct transition metal and proton pathways in an Nrap transporter. <i>ELife</i> , 2019, 8, .	6.0	50
1631	Functional Characterization of OXYL, A SghC1qDC LacNAc-specific Lectin from The Crinoid Feather Star <i>Anneissia Japonica</i> . <i>Marine Drugs</i> , 2019, 17, 136.	4.6	11
1632	The Molecular Basis of Freshwater Adaptation in Prawns: Insights from Comparative Transcriptomics of Three <i>Macrobrachium</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 1002-1018.	2.5	23
1633	The transcriptome of the veiled chameleon ( <i>Chamaeleo calyptratus</i> ): A resource for studying the evolution and development of vertebrates. <i>Developmental Dynamics</i> , 2019, 248, 702-708.	1.8	26
1634	The Draft Genome of an Octocoral, <i>Dendronephthya gigantea</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 949-953.	2.5	44
1635	A matter of background: DNA repair pathways as a possible cause for the sparse distribution of CRISPR-Cas systems in bacteria. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180088.	4.0	30
1636	Essentials of Bioinformatics, Volume I. , 2019, , .		8

#	ARTICLE	IF	CITATIONS
1637	Molecular evolution of Pr1 proteases depicts ongoing diversification in <i>Metarhizium</i> spp. <i>Molecular Genetics and Genomics</i> , 2019, 294, 901-917.	2.1	8
1638	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	1.0	3
1639	A hybrid <i>de novo</i> assembly of the sea pansy ( <i>Renilla muelleri</i> ) genome. <i>GigaScience</i> , 2019, 8, .	6.4	27
1640	The intrinsic dimension of protein sequence evolution. <i>PLoS Computational Biology</i> , 2019, 15, e1006767.	3.2	19
1641	Adaptation of the Human Gut Microbiota Metabolic Network During the First Year After Birth. <i>Frontiers in Microbiology</i> , 2019, 10, 848.	3.5	11
1642	Selection pressure causes differentiation of the SPL gene family in the Juglandaceae. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1037-1048.	2.1	6
1643	Following the Evolutionary Track of a Highly Specific <i>Arginine Oxidase</i> by Reconstruction and Biochemical Analysis of Ancestral and Native Enzymes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	19
1644	TriPepSVM: <i>de novo</i> prediction of RNA-binding proteins based on short amino acid motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4406-4417.	14.5	44
1645	Protein Structure Annotations. , 2019, , 201-234.		5
1646	The SPB-Box Transcription Factor AaSPL2 Positively Regulates Artemisinin Biosynthesis in <i>Artemisia annua</i> L.. <i>Frontiers in Plant Science</i> , 2019, 10, 409.	3.6	25
1647	De Novo Plant Transcriptome Assembly and Annotation Using Illumina RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2019, 1933, 265-275.	0.9	9
1648	Genome-wide identification and abiotic stress-responsive pattern of heat shock transcription factor family in <i>Triticum aestivum</i> L.. <i>BMC Genomics</i> , 2019, 20, 257.	2.8	70
1649	Genomic analysis of the aggressive tree pathogen <i>Ceratocystis albifundus</i> . <i>Fungal Biology</i> , 2019, 123, 351-363.	2.5	11
1650	Pathway and Gene Discovery from Natural Hosts and Organisms. <i>Methods in Molecular Biology</i> , 2019, 1927, 1-9.	0.9	1
1651	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. <i>Water Research</i> , 2019, 155, 275-287.	11.3	77
1652	Genome-Wide Identification and Analysis of High-Copy-Number LTR Retrotransposons in Asian Pears. <i>Genes</i> , 2019, 10, 156.	2.4	4
1653	Structure–function characterization of an insecticidal protein GNIP1Aa, a member of an MACPF and Î2-tripod families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2897-2906.	7.1	19
1654	PDZ Domains Across the Microbial World: Molecular Link to the Proteases, Stress Response, and Protein Synthesis. <i>Genome Biology and Evolution</i> , 2019, 11, 644-659.	2.5	12

#	ARTICLE	IF	CITATIONS
1655	Extensive Reduction of the Nuclear Pore Complex in Nucleomorphs. <i>Genome Biology and Evolution</i> , 2019, 11, 678-687.	2.5	4
1656	Genome-wide analysis of the NAC transcription factor family in Tartary buckwheat ( <i>Fagopyrum</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 10	2.8	90
1657	Land-plant Phylogenomic and Pomegranate Transcriptomic Analyses Reveal an Evolutionary Scenario of CYP75 Genes Subsequent to Whole Genome Duplications. <i>Journal of Plant Biology</i> , 2019, 62, 48-60.	2.1	14
1658	Host Specificity of the <i>Dickeya</i> Bacteriophage PP35 Is Directed by a Tail Spike Interaction With Bacterial O-Antigen, Enabling the Infection of Alternative Non-pathogenic Bacterial Host. <i>Frontiers in Microbiology</i> , 2018, 9, 3288.	3.5	28
1659	Study on aquaporins of <i>Setaria italica</i> suggests the involvement of SiPIP3;1 and SiSIP1;1 in abiotic stress response. <i>Functional and Integrative Genomics</i> , 2019, 19, 587-596.	3.5	23
1660	LM11-like and KNOX1 genes coordinately regulate plant leaf development in dicotyledons. <i>Plant Molecular Biology</i> , 2019, 99, 449-460.	3.9	17
1661	Shift in <i>Bacillus</i> sp. JR3 esterase LipJ activity profile after addition of essential residues from family I.5 thermophilic lipases. <i>Biochemical Engineering Journal</i> , 2019, 144, 166-176.	3.6	2
1662	Linking gene expression and oenological traits: Comparison between <i>Torulaspora delbrueckii</i> and <i>Saccharomyces cerevisiae</i> strains. <i>International Journal of Food Microbiology</i> , 2019, 294, 42-49.	4.7	27
1663	Evolution and functional divergence of MADS-box genes in <i>Pyrus</i> . <i>Scientific Reports</i> , 2019, 9, 1266.	3.3	15
1664	The tyrosine transporter of <i>Toxoplasma gondii</i> is a member of the newly defined apicomplexan amino acid transporter (ApiAT) family. <i>PLoS Pathogens</i> , 2019, 15, e1007577.	4.7	39
1665	Angiosperm-Wide and Family-Level Analyses of AP2/ERF Genes Reveal Differential Retention and Sequence Divergence After Whole-Genome Duplication. <i>Frontiers in Plant Science</i> , 2019, 10, 196.	3.6	42
1666	Evolution of cnidarian <i>trans</i>-defensins: Sequence, structure and exploration of chemical space. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 551-560.	2.6	20
1667	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. <i>Microbiome</i> , 2019, 7, 26.	11.1	60
1668	Next generation sequencing from <i>Hepatozoon canis</i> (Apicomplexa: Coccidia: Adeleorina): Complete apicoplast genome and multiple mitochondrion-associated sequences. <i>International Journal for Parasitology</i> , 2019, 49, 375-387.	3.1	25
1669	Near-Complete Genome Sequence of a Human Pegivirus Variant Isolated from a Hepatitis E Virus-Infected Patient. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
1670	Carbohydrate catabolic capability of a <i>Flavobacteriia</i> bacterium isolated from hadal water. <i>Systematic and Applied Microbiology</i> , 2019, 42, 263-274.	2.8	25
1671	Comparative analysis of seven types of superoxide dismutases for their ability to respond to oxidative stress in <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2019, 9, 2170.	3.3	24
1672	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. <i>Cell Reports</i> , 2019, 26, 2078-2087.e3.	6.4	36

#	ARTICLE	IF	CITATIONS
1673	A combined computational strategy of sequence and structural analysis predicts the existence of a functional eicosanoid pathway in <i>Drosophila melanogaster</i> . PLoS ONE, 2019, 14, e0211897.	2.5	25
1674	Analysis of Predicted Host-Parasite Interactomes Reveals Commonalities and Specificities Related to Parasitic Lifestyle and Tissues Tropism. Frontiers in Immunology, 2019, 10, 212.	4.8	34
1675	The Genome Sequence of the Eastern Woodchuck ( <i>Marmota monax</i> ) – A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	1.8	13
1676	Protein fold recognition model based on cubic lattice. International Journal of Data Mining and Bioinformatics, 2019, 22, 75.	0.1	0
1677	IslandCafe: Compositional Anomaly and Feature Enrichment Assessment for Delineation of Genomic Islands. G3: Genes, Genomes, Genetics, 2019, 9, 3273-3285.	1.8	13
1678	Functional Multigenomic Screening of Human-Associated Bacteria for NF- $\kappa$ B-Inducing Bioactive Effectors. MBio, 2019, 10, .	4.1	8
1679	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. MBio, 2019, 10, .	4.1	19
1681	Characterization of Core Microbiomes and Functional Profiles of Mesophilic Anaerobic Digesters Fed With <i>Chlorella vulgaris</i> Green Microalgae and Maize Silage. Frontiers in Energy Research, 2019, 7, .	2.3	19
1682	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
1683	Genome-Wide Analysis of Cell Cycle-Regulating Genes in the Symbiotic Dinoflagellate <i>Breviolum minutum</i> . G3: Genes, Genomes, Genetics, 2019, 9, 3843-3853.	1.8	3
1684	A Benchmark for Homomeric Enzyme Active Site Structure Prediction Highlights the Importance of Accurate Modeling of Protein Symmetry. ACS Omega, 2019, 4, 22356-22362.	3.5	1
1685	A New Lineage of <i>Cryptococcus gattii</i> (VGV) Discovered in the Central Zambezi Miombo Woodlands. MBio, 2019, 10, .	4.1	66
1686	Evolutionary balance between LRR domain loss and young NBS-LRR genes production governs disease resistance in <i>Arachis hypogaea</i> cv. Tifrunner. BMC Genomics, 2019, 20, 844.	2.8	30
1687	Transcriptomic analysis of $\beta$ -synuclein knockdown after T3 spinal cord injury in rats. BMC Genomics, 2019, 20, 851.	2.8	6
1688	Genome-Wide Analysis of the DYW Subgroup PPR Gene Family and Identification of GmPPR4 Responses to Drought Stress. International Journal of Molecular Sciences, 2019, 20, 5667.	4.1	26
1689	Alien domains shaped the modular structure of plant NLR proteins. Genome Biology and Evolution, 2019, 11, 3466-3477.	2.5	21
1690	Genome-Wide Identification and Characterization of FBA Gene Family in Polyploid Crop <i>Brassica napus</i> . International Journal of Molecular Sciences, 2019, 20, 5749.	4.1	14
1691	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	3.3	19

#	ARTICLE	IF	CITATIONS
1692	A Comparison of the Maximum Entropy Principle Across Biological Spatial Scales. <i>Entropy</i> , 2019, 21, 1009.	2.2	13
1693	The first complete chloroplast genome of <i>Quercus coccinea</i> (Scarlet Oak) and its phylogenetic position within Fagaceae. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3634-3635.	0.4	6
1694	The complete chloroplast genome of <i>Paris polyphylla</i> var. <i>chinensis</i> , an endemic medicinal herb in China. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3888-3889.	0.4	1
1695	Novel findings to the biosynthetic pathway of magnoflorine and taspine through transcriptomic and metabolomic analysis of <i>Croton draco</i> (Euphorbiaceae). <i>BMC Plant Biology</i> , 2019, 19, 560.	3.6	7
1696	The transcriptomic signature of low aggression in honey bees resembles a response to infection. <i>BMC Genomics</i> , 2019, 20, 1029.	2.8	11
1697	The de novo transcriptome of workers head of the higher group termite <i>Globitermes sulphureus</i> Haviland (Blattodea: Termitidae). <i>Heliyon</i> , 2019, 5, e02969.	3.2	0
1698	The complex evolutionary history of sulfoxide synthase in ovothiol biosynthesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191812.	2.6	19
1699	Identification and Expression Analysis of the NAC Gene Family in <i>Coffea canephora</i> . <i>Agronomy</i> , 2019, 9, 670.	3.0	19
1700	PMBD: a Comprehensive Plastics Microbial Biodegradation Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	81
1701	PacBio Long-Read Sequencing Reveals the Transcriptomic Complexity and Aux/IAA Gene Evolution in <i>Gnetum</i> (Gnetales). <i>Forests</i> , 2019, 10, 1043.	2.1	6
1702	<i>Trochodendron aralioides</i> , the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. <i>GigaScience</i> , 2019, 8, .	6.4	20
1703	Organ transcriptomes of the lucinid clam <i>Loripes orbiculatus</i> (Poli, 1791) provide insights into their specialised roles in the biology of a chemosymbiotic bivalve. <i>BMC Genomics</i> , 2019, 20, 820.	2.8	13
1704	Whole Genome Re-sequencing Reveals Natural Variation and Adaptive Evolution of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2792.	3.5	39
1705	Decrypting tubby-like protein gene family of multiple functions in starch root crop cassava. <i>AoB PLANTS</i> , 2019, 11, plz075.	2.3	8
1706	Microbial Community Rearrangements in Power-to-Biomethane Reactors Employing Mesophilic Biogas Digestate. <i>Frontiers in Energy Research</i> , 2019, 7, .	2.3	19
1707	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo ( <i>Phyllostachys violascens</i> ). <i>BMC Bioinformatics</i> , 2019, 20, 687.	2.6	14
1708	Variability of mitochondrial ORFans hints at possible differences in the system of doubly uniparental inheritance of mitochondria among families of freshwater mussels (Bivalvia: Unionida). <i>BMC Evolutionary Biology</i> , 2019, 19, 229.	3.2	18
1709	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53

#	ARTICLE	IF	CITATIONS
1710	New Genus Fibrolongavirus in Siphoviridae Phages of <i>Staphylococcus pseudintermedius</i> . <i>Viruses</i> , 2019, 11, 1143.	3.3	6
1711	Comparative genomics study reveals Red Sea <i>Bacillus</i> with characteristics associated with potential microbial cell factories (MCFs). <i>Scientific Reports</i> , 2019, 9, 19254.	3.3	6
1712	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25900-25908.	7.1	165
1713	The Chalcone Isomerase Family in Cotton: Whole-Genome Bioinformatic and Expression Analyses of the <i>Gossypium barbadense</i> L. Response to <i>Fusarium</i> Wilt Infection. <i>Genes</i> , 2019, 10, 1006.	2.4	13
1714	Emission and biosynthesis of volatile terpenoids from the plasmodial slime mold <i>Physarum polycephalum</i> . <i>Beilstein Journal of Organic Chemistry</i> , 2019, 15, 2872-2880.	2.2	4
1715	Secretory RING finger proteins function as effectors in a grapevine galling insect. <i>BMC Genomics</i> , 2019, 20, 923.	2.8	15
1716	Programmed Cell Death in <i>Neurospora crassa</i> Is Controlled by the Allorecognition Determinant <i>rcd-1</i> . <i>Genetics</i> , 2019, 213, 1387-1400.	2.9	32
1717	Modeling the Architecture of Depolymerase-Containing Receptor Binding Proteins in <i>Klebsiella</i> Phages. <i>Frontiers in Microbiology</i> , 2019, 10, 2649.	3.5	76
1718	Characterization and Functional Divergence of a Novel DUF668 Gene Family in Rice Based on Comprehensive Expression Patterns. <i>Genes</i> , 2019, 10, 980.	2.4	17
1719	Bioinformatics Analysis of the Lipxygenase Gene Family in Radish ( <i>Raphanus sativus</i> ) and Functional Characterization in Response to Abiotic and Biotic Stresses. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6095.	4.1	17
1720	Mitochondrial genomes of the early land plant lineage liverworts (Marchantiophyta): conserved genome structure, and ongoing low frequency recombination. <i>BMC Genomics</i> , 2019, 20, 953.	2.8	21
1721	Transcriptomic Evidence of Adaptive Evolution of the Epiphytic Fern <i>Asplenium nidus</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-9.	1.6	15
1722	Comparative analysis of five <i>Mucor</i> species transcriptomes. <i>Genomics</i> , 2019, 111, 1306-1314.	2.9	14
1723	Planktonic Marine Archaea. <i>Annual Review of Marine Science</i> , 2019, 11, 131-158.	11.6	129
1724	Lateral Gene Transfer Shapes the Distribution of RuBisCO among Candidate Phyla Radiation Bacteria and DPANN Archaea. <i>Molecular Biology and Evolution</i> , 2019, 36, 435-446.	8.9	54
1725	Terpene Biosynthesis in Red Algae Is Catalyzed by Microbial Type But Not Typical Plant Terpene Synthases. <i>Plant Physiology</i> , 2019, 179, 382-390.	4.8	40
1726	RNA interference-mediated knockdown of eye coloration genes in the western tarnished plant bug ( <i>Lygus hesperus</i> Knight). <i>Archives of Insect Biochemistry and Physiology</i> , 2019, 100, e21527.	1.5	19
1727	Computational Design of Stable and Soluble Biocatalysts. <i>ACS Catalysis</i> , 2019, 9, 1033-1054.	11.2	87



#	ARTICLE	IF	CITATIONS
1728	Comparative transcriptome analysis identifies genes associated with papilla development in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 255-263.	1.0	4
1729	Expansion and Diversification of MFS Transporters in <i>Kluyveromyces marxianus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3330.	3.5	17
1730	Transcriptome-wide analysis of <i>Chlorella</i> reveals auxin-induced carotenogenesis pathway in green microalgae. <i>Algal Research</i> , 2019, 37, 320-335.	4.6	25
1731	Genome-wide identification and characterization of laccase gene family in <i>Citrus sinensis</i> . <i>Gene</i> , 2019, 689, 114-123.	2.2	37
1732	Prediction of the intestinal resistome by a three-dimensional structure-based method. <i>Nature Microbiology</i> , 2019, 4, 112-123.	13.3	129
1733	Dissecting the Genomic Diversification of Late Embryogenesis Abundant (LEA) Protein Gene Families in Plants. <i>Genome Biology and Evolution</i> , 2019, 11, 459-471.	2.5	102
1734	DIP-2 suppresses ectopic neurite sprouting and axonal regeneration in mature neurons. <i>Journal of Cell Biology</i> , 2019, 218, 125-133.	5.2	23
1735	An important resource for understanding bio-adhesion mechanisms: Cement gland transcriptomes of two goose barnacles, <i>Pollicipes pollicipes</i> and <i>Lepas anatifera</i> (Cirripedia, Thoracica). <i>Marine Genomics</i> , 2019, 45, 16-20.	1.1	11
1736	Refined template selection and combination algorithm significantly improves template-based modeling accuracy. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950006.	0.8	13
1737	The Evolutionary Traceability of a Protein. <i>Genome Biology and Evolution</i> , 2019, 11, 531-545.	2.5	23
1738	Cystic Fibrosis-Associated <i>Stenotrophomonas maltophilia</i> Strain-Specific Adaptations and Responses to pH. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	11
1739	Plant-specific ribosome biogenesis factors in <i>Arabidopsis thaliana</i> with essential function in rRNA processing. <i>Nucleic Acids Research</i> , 2019, 47, 1880-1895.	14.5	47
1740	Characterization of novel lignocellulose-degrading enzymes from the porcupine microbiome using synthetic metagenomics. <i>PLoS ONE</i> , 2019, 14, e0209221.	2.5	20
1741	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee ( <i>Halictidae</i> : <i>Nomia melanderi</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	1.8	19
1742	Building Bridges Between Structural and Network-Based Systems Biology. <i>Molecular Biotechnology</i> , 2019, 61, 221-229.	2.4	10
1743	MMseqs2 desktop and local web server app for fast, interactive sequence searches. <i>Bioinformatics</i> , 2019, 35, 2856-2858.	4.1	321
1744	A Real-Time Multiplex PCR Assay for Detection of <i>Elizabethkingia</i> Species and Differentiation between <i>Elizabethkingia anophelis</i> and <i>E. meningoseptica</i> . <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	6
1745	Gene expression changes elicited by a parasitic B chromosome in the grasshopper <i>Eyprepocnemis plorans</i> are consistent with its phenotypic effects. <i>Chromosoma</i> , 2019, 128, 53-67.	2.2	15

#	ARTICLE	IF	CITATIONS
1746	Long-term investigation of microbial community composition and transcription patterns in a biogas plant undergoing ammonia crisis. <i>Microbial Biotechnology</i> , 2019, 12, 305-323.	4.2	25
1747	Identification and expression analysis of phosphatidyl ethanolamine-binding protein (PEBP) gene family in cotton. <i>Genomics</i> , 2019, 111, 1373-1380.	2.9	17
1748	A Composite Approach to Protein Tertiary Structure Prediction: Hidden Markov Model Based on Lattice. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 899-918.	1.9	4
1749	The genome of the jellyfish <i>Aurelia</i> and the evolution of animal complexity. <i>Nature Ecology and Evolution</i> , 2019, 3, 96-104.	7.8	86
1750	ConDo: protein domain boundary prediction using coevolutionary information. <i>Bioinformatics</i> , 2019, 35, 2411-2417.	4.1	19
1751	Identification and comprehensive analysis of the characteristics and roles of leucine-rich repeat receptor-like protein kinase (LRR-RLK) genes in <i>Sedum alfredii</i> Hance responding to cadmium stress. <i>Ecotoxicology and Environmental Safety</i> , 2019, 167, 95-106.	6.0	16
1752	Genome-wide identification and analysis of the evolution and expression patterns of the GATA transcription factors in three species of <i>Gossypium</i> genus. <i>Gene</i> , 2019, 680, 72-83.	2.2	25
1753	Bacterial contributions to delignification and lignocellulose degradation in forest soils with metagenomic and quantitative stable isotope probing. <i>ISME Journal</i> , 2019, 13, 413-429.	9.8	246
1754	MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. <i>Briefings in Bioinformatics</i> , 2019, 20, 1160-1166.	6.5	4,864
1755	Protein Remote Homology Detection and Fold Recognition Based on Sequence-Order Frequency Matrix. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 292-300.	3.0	21
1756	An account of <i>in silico</i> identification tools of secreted effector proteins in bacteria and future challenges. <i>Briefings in Bioinformatics</i> , 2019, 20, 110-129.	6.5	22
1757	ProtDet-CCH: Protein Remote Homology Detection by Combining Long Short-Term Memory and Ranking Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1203-1210.	3.0	30
1758	HMMCAS: A Web Tool for the Identification and Domain Annotations of CAS Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1313-1315.	3.0	43
1759	Molecular cloning and comparative analysis of transcripts encoding chemosensory proteins from two plant bugs, <i>Lygus lineolaris</i> and <i>Lygus hesperus</i> . <i>Insect Science</i> , 2020, 27, 404-424.	3.0	5
1760	Genes coding for LysM domains in the dermatophyte <i>Trichophyton rubrum</i> : A transcription analysis. <i>Medical Mycology</i> , 2020, 58, 372-379.	0.7	13
1761	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	5.6	89
1762	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree ( <i>Moringa oleifera</i> ). <i>Genomics</i> , 2020, 112, 621-628.	2.9	22
1764	Collection of antimicrobial peptides database and its derivatives: Applications and beyond. <i>Protein Science</i> , 2020, 29, 36-42.	7.6	82

#	ARTICLE	IF	CITATIONS
1765	Genome-wide identification, characterization, and expression analysis of nucleotide-binding leucine-rich repeats gene family under environmental stresses in tea ( <i>Camellia sinensis</i> ). <i>Genomics</i> , 2020, 112, 1351-1362.	2.9	7
1766	Getting to Know Your Neighbor: Protein Structure Prediction Comes of Age with Contextual Machine Learning. <i>Journal of Computational Biology</i> , 2020, 27, 796-814.	1.6	15
1767	A xylan-degrading thermophilic and obligate anaerobe <i>Xylanivirga thermophila</i> gen. nov., sp. nov., isolated from an anammox dominant wastewater treatment plant, and proposal of <i>Xylanivirgaceae</i> fam. nov.. <i>Anaerobe</i> , 2020, 61, 102075.	2.1	10
1768	DEEPCON: protein contact prediction using dilated convolutional neural networks with dropout. <i>Bioinformatics</i> , 2020, 36, 470-477.	4.1	40
1769	Transcriptome analysis of <i>Aconitum carmichaelii</i> and exploration of the salsolinol biosynthetic pathway. <i>FÄ-toterapÄ-ÄÇ</i> , 2020, 140, 104412.	2.2	7
1770	Protein Structural Information and Evolutionary Landscape by In Vitro Evolution. <i>Molecular Biology and Evolution</i> , 2020, 37, 1179-1192.	8.9	24
1771	Diversity, dynamics and effects of long terminal repeat retrotransposons in the model grass <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2020, 227, 1736-1748.	7.3	33
1772	Evolutionarily Conserved Interactions within the Pore Domain of Acid-Sensing Ion Channels. <i>Biophysical Journal</i> , 2020, 118, 861-872.	0.5	9
1773	Artificial intelligence in bioinformatics. , 2020, , 217-237.		4
1774	Diversity and Expression Patterns of MADS-Box Genes in <i>Gnetum luofuense</i> “Implications for Functional Diversity and Evolution. <i>Tropical Plant Biology</i> , 2020, 13, 36-49.	1.9	8
1775	Insight into the relationship between S-lignin and fiber quality based on multiple research methods. <i>Plant Physiology and Biochemistry</i> , 2020, 147, 251-261.	5.8	6
1776	Nonspecific expression of fertilization genes in the crown“ofÄ-thorns <i>Acanthaster cf. solaris</i> : Unexpected evidence of hermaphroditism in a coral reef predator. <i>Molecular Ecology</i> , 2020, 29, 363-379.	3.9	10
1777	<i>Fusarium virguliform</i> “ <i>e</i> “ Transcriptional Plasticity Is Revealed by Host Colonization of Maize versus Soybean. <i>Plant Cell</i> , 2020, 32, 336-351.	6.6	28
1778	Fold-LTR-TCP: protein fold recognition based on triadic closure principle. <i>Briefings in Bioinformatics</i> , 2020, 21, 2185-2193.	6.5	56
1779	Genome“wide analysis of the Chinese sturgeon <i>sox</i> “ gene family: identification, characterisation and expression profiles of different tissues. <i>Journal of Fish Biology</i> , 2020, 96, 175-184.	1.6	13
1780	Genome-wide identification, characterisation and expression profile analysis of DEAD-box family genes in sweet potato wild ancestor <i>Ipomoea trifida</i> under abiotic stresses. <i>Genes and Genomics</i> , 2020, 42, 325-335.	1.4	20
1781	Genome-Wide Identification and Characterization of the Mitochondrial Transcription Termination Factors (mTERFs) in <i>Capsicum annuum</i> L.. <i>International Journal of Molecular Sciences</i> , 2020, 21, 269.	4.1	26
1782	Genome“wide identification, characterization, and expression analysis of GDSL-type esterases/lipases gene family in relation to grape berry ripening. <i>Scientia Horticulturae</i> , 2020, 264, 109162.	3.6	26

#	ARTICLE	IF	CITATIONS
1783	PreDSLpmo: A neural network-based prediction tool for functional annotation of lytic polysaccharide monooxygenases. <i>Journal of Biotechnology</i> , 2020, 308, 148-155.	3.8	0
1784	A jumbo phage that forms a nucleus-like structure evades CRISPR-Cas DNA targeting but is vulnerable to type III RNA-based immunity. <i>Nature Microbiology</i> , 2020, 5, 48-55.	13.3	123
1785	Identification and functional characterization of the astacidin family of proline-rich host defence peptides (PcAst) from the red swamp crayfish ( <i>Procambarus clarkii</i> , Girard 1852). <i>Developmental and Comparative Immunology</i> , 2020, 105, 103574.	2.3	12
1786	RemeDB: Tool for Rapid Prediction of Enzymes Involved in Bioremediation from High-Throughput Metagenome Data Sets. <i>Journal of Computational Biology</i> , 2020, 27, 1020-1029.	1.6	22
1787	Structural Mechanism of Regioselectivity in an Unusual Bacterial Acyl-CoA Dehydrogenase. <i>Journal of the American Chemical Society</i> , 2020, 142, 835-846.	13.7	9
1788	Inferring RPW8-NLRs' evolution patterns in seed plants: case study in <i>Vitis vinifera</i> . <i>Planta</i> , 2020, 251, 32.	3.2	13
1789	Cultivation and functional characterization of 79 planctomycetes uncovers their unique biology. <i>Nature Microbiology</i> , 2020, 5, 126-140.	13.3	164
1790	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	13.3	75
1791	eCAMI: simultaneous classification and motif identification for enzyme annotation. <i>Bioinformatics</i> , 2020, 36, 2068-2075.	4.1	27
1792	Drivers of metabolic diversification: how dynamic genomic neighbourhoods generate new biosynthetic pathways in the Brassicaceae. <i>New Phytologist</i> , 2020, 227, 1109-1123.	7.3	49
1793	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
1794	Comprehensive transcriptome analysis of faba bean in response to vernalization. <i>Planta</i> , 2020, 251, 22.	3.2	10
1795	Stable cellulase immobilized on graphene oxide@CMC-g-poly(AMPS-co-AAm) hydrogel for enhanced enzymatic hydrolysis of lignocellulosic biomass. <i>Carbohydrate Polymers</i> , 2020, 230, 115661.	10.2	55
1796	Graph Theory-Based Sequence Descriptors as Remote Homology Predictors. <i>Biomolecules</i> , 2020, 10, 26.	4.0	13
1797	Genome-wide identification and expression analysis of the CLC superfamily genes in tea plants ( <i>Camellia sinensis</i> ). <i>Functional and Integrative Genomics</i> , 2020, 20, 497-508.	3.5	12
1798	Identification of MYB Transcription Factors Regulating Theanine Biosynthesis in Tea Plant Using Omics-Based Gene Coexpression Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 918-926.	5.2	20
1799	A chromosome-scale reference genome of trifoliate orange ( <i>Poncirus trifoliata</i> ) provides insights into disease resistance, cold tolerance and genome evolution in <i>Citrus</i> . <i>Plant Journal</i> , 2020, 104, 1215-1232.	5.7	56
1800	Functional and Structural Analysis of Predicted Proteins Obtained from <i>Homo sapiens</i> Minisatellite 33.15-Tagged Transcript pAKT-45 Variants. <i>BioMed Research International</i> , 2020, 2020, 1-9.	1.9	1

#	ARTICLE	IF	CITATIONS
1801	Deltaproteobacteria and Spirochaetes-Like Bacteria Are Abundant Putative Mercury Methylators in Oxygen-Deficient Water and Marine Particles in the Baltic Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 574080.	3.5	33
1802	The use of consensus sequence information to engineer stability and activity in proteins. <i>Methods in Enzymology</i> , 2020, 643, 149-179.	1.0	23
1803	Genome-wide identification of NF-YA gene family in cotton and the positive role of GhNF-YA10 and GhNF-YA23 in salt tolerance. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 2103-2115.	7.5	12
1804	Alternative Splicing Enhances the Transcriptome Complexity of <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 578100.	3.6	14
1805	The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , 2020, 28, 724-740.e8.	11.0	352
1806	Hidden in plain sight: Systematic investigation of Leucine-rich repeat containing genes unveil the their regulatory network in response to <i>Fusarium</i> wilt in tung tree. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1759-1767.	7.5	10
1807	<i>Chlorella vulgaris</i> and Its Phycosphere in Wastewater: Microalgae-Bacteria Interactions During Nutrient Removal. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 557572.	4.1	34
1808	Molecular and structural analysis of central transport channel in complex with Nup93 of nuclear pore complex. <i>Protein Science</i> , 2020, 29, 2510-2527.	7.6	5
1809	A Need for Improved Cellulase Identification from Metagenomic Sequence Data. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	2
1810	Linking omics and ecology to dissect interactions between the apple proliferation phytoplasma and its psyllid vector <i>Cacopsylla melanoneura</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 127, 103474.	2.7	5
1811	The Chromosome Level Genome and Genome-wide Association Study for the Agronomic Traits of <i>Panax Notoginseng</i> . <i>IScience</i> , 2020, 23, 101538.	4.1	34
1812	Genome-Wide Analysis of OPR Family Genes in Cotton Identified a Role for GhOPR9 in <i>Verticillium dahliae</i> Resistance. <i>Genes</i> , 2020, 11, 1134.	2.4	18
1813	Molecular Evolution and Expansion of the KUP Family in the Allopolyploid Cotton Species <i>Gossypium hirsutum</i> and <i>Gossypium barbadense</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 545042.	3.6	3
1814	NADPH oxidases and the evolution of plant salinity tolerance. <i>Plant, Cell and Environment</i> , 2020, 43, 2957-2968.	5.7	49
1815	Identification and effect of Zf-AD-containing C2H2 zinc finger genes on BmNPV replication in the silkworm ( <i>Bombyx mori</i> ). <i>Pesticide Biochemistry and Physiology</i> , 2020, 170, 104678.	3.6	0
1816	NST- and SND-subgroup NAC proteins coordinately act to regulate secondary cell wall formation in cotton. <i>Plant Science</i> , 2020, 301, 110657.	3.6	15
1817	Identification of chalcone synthase genes and their expression patterns reveal pollen abortion in cotton. <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 3691-3699.	3.8	15
1818	Genome-wide identification and expression analysis of the MYB transcription factor in Japanese plum ( <i>Prunus salicina</i> ). <i>Genomics</i> , 2020, 112, 4875-4886.	2.9	25

#	ARTICLE	IF	CITATIONS
1819	Comprehensive multiomics analysis reveals key roles of NACs in plant growth and development and its environmental adaption mechanism by regulating metabolite pathways. <i>Genomics</i> , 2020, 112, 4897-4911.	2.9	6
1820	Boosting the accuracy of protein secondary structure prediction through nearest neighbor search and method hybridization. <i>Bioinformatics</i> , 2020, 36, i317-i325.	4.1	8
1821	PyMod 3: a complete suite for structural bioinformatics in PyMOL. <i>Bioinformatics</i> , 2021, 37, 1471-1472.	4.1	73
1822	CerealsDBâ€”new tools for the analysis of the wheat genome: update 2020. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	16
1823	Early Metazoan Origin and Multiple Losses of a Novel Clade of RIM Presynaptic Calcium Channel Scaffolding Protein Homologs. <i>Genome Biology and Evolution</i> , 2020, 12, 1217-1239.	2.5	7
1824	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	2.5	29
1825	Shared up-regulation and contrasting down-regulation of gene expression distinguish desiccation-tolerant from intolerant green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17438-17445.	7.1	22
1826	Computational identification of receptor-like kinases â€œRLKâ€ and receptor-like proteins â€œRLPâ€ in legumes. <i>BMC Genomics</i> , 2020, 21, 459.	2.8	16
1827	The combination of artificial intelligence and systems biology for intelligent vaccine design. <i>Expert Opinion on Drug Discovery</i> , 2020, 15, 1267-1281.	5.0	26
1828	Identification and characterization of putative ovarian lincRNAs in dairy goats treated for repeated estrous synchronization. <i>Animal Reproduction Science</i> , 2020, 221, 106537.	1.5	0
1829	De novo transcriptome analysis of high growth rate <i>Pyropia yezoensis</i> (Bangiales, Rhodophyta) mutant with high utilization of nitrogen. <i>Acta Botanica Croatica</i> , 2020, 79, 201-211.	0.7	4
1830	CoryneRegNet 7, the reference database and analysis platform for corynebacterial gene regulatory networks. <i>Scientific Data</i> , 2020, 7, 142.	5.3	22
1831	Liver transcriptome resources of four commercially exploited teleost species. <i>Scientific Data</i> , 2020, 7, 214.	5.3	4
1832	Genome-wide identification and expression analysis of lipoxygenase genes in Tartary buckwheat. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 273-286.	1.3	7
1833	Bioinformatic tools to understand structure and function of plant proteins. , 2020, , 69-93.		2
1834	Whole-Genome Sequencing and Bioinformatic Analysis of Environmental, Agricultural, and Human <i>Campylobacter jejuni</i> Isolates From East Tennessee. <i>Frontiers in Microbiology</i> , 2020, 11, 571064.	3.5	7
1835	A full-length transcriptome and gene expression analysis reveal genes and molecular elements expressed during seed development in <i>Gnetum luofuense</i> . <i>BMC Plant Biology</i> , 2020, 20, 531.	3.6	9
1836	ReFold-MAP: Protein remote homology detection and fold recognition based on features extracted from profiles. <i>Analytical Biochemistry</i> , 2020, 611, 114013.	2.4	3



#	ARTICLE	IF	CITATIONS
1837	Discovery and comparative genomic analysis of elk circovirus (ElkCV), a novel circovirus species and the first reported from a cervid host. <i>Scientific Reports</i> , 2020, 10, 19548.	3.3	17
1838	Identifying Genes Involved in Alkaloid Biosynthesis in <i>Vinca minor</i> through Transcriptomics and Gene Co-Expression Analysis. <i>Biomolecules</i> , 2020, 10, 1595.	4.0	12
1839	The Tetracentron genome provides insight into the early evolution of eudicots and the formation of vessel elements. <i>Genome Biology</i> , 2020, 21, 291.	8.8	23
1840	Bacteriophages vB_Sen-TO17 and vB_Sen-E22, Newly Isolated Viruses from Chicken Feces, Specific for Several <i>Salmonella enterica</i> Strains. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8821.	4.1	13
1841	Expression profiling of MADS-box gene family revealed its role in vegetative development and stem ripening in <i>S. spontaneum</i> . <i>Scientific Reports</i> , 2020, 10, 20536.	3.3	10
1842	Identification, evolution, expression, and docking studies of fatty acid desaturase genes in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2020, 21, 778.	2.8	31
1843	Genome-wide analysis of PHD finger gene family and identification of potential miRNA and their PHD finger gene specific targets in <i>Oryza sativa indica</i> . <i>Non-coding RNA Research</i> , 2020, 5, 191-200.	4.6	2
1844	Sequence Analysis and Structure Prediction of SARS-CoV-2 Accessory Proteins 9b and ORF14: Evolutionary Analysis Indicates Close Relatedness to Bat Coronavirus. <i>BioMed Research International</i> , 2020, 2020, 1-13.	1.9	27
1845	Coevolutionary Analysis Reveals a Conserved Dual Binding Interface between Extracytoplasmic Function If Factors and Class I Anti-If Factors. <i>MSystems</i> , 2020, 5, .	3.8	2
1846	The regulatory pathways of distinct flowering characteristics in Chinese jujube. <i>Horticulture Research</i> , 2020, 7, 123.	6.3	16
1847	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	14.5	410
1848	Undinarchaeota illuminate DPANN phylogeny and the impact of gene transfer on archaeal evolution. <i>Nature Communications</i> , 2020, 11, 3939.	12.8	102
1849	Molecular characterization of a fungal gasdermin-like protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18600-18607.	7.1	50
1850	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in <i>Giardia</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 3525-3549.	8.9	9
1851	Identification and Bioinformatic Analysis of the GmDOG1-Like Family in Soybean and Investigation of Their Expression in Response to Gibberellic Acid and Absciscic Acid. <i>Plants</i> , 2020, 9, 937.	3.5	3
1852	In-silico analysis of cucumber ( <i>Cucumis sativus</i> L.) Genome for WRKY transcription factors and cis-acting elements. <i>Computational Biology and Chemistry</i> , 2020, 85, 107212.	2.3	11
1853	Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. <i>Bioinformatics</i> , 2020, 36, 3975-3981.	4.1	2
1854	lncRNA_Mdeep: An Alignment-Free Predictor for Distinguishing Long Non-Coding RNAs from Protein-Coding Transcripts by Multimodal Deep Learning. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5222.	4.1	12



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1855	De novo assembly and characterization of transcriptome in the medicinal plant <i>Euphorbia jolkini</i> . <i>Genes and Genomics</i> , 2020, 42, 1011-1021.	1.4	3
1856	Transcriptomic comparison reveals modifications in gene expression, photosynthesis, and cell wall in woody plant as responses to external pH changes. <i>Ecotoxicology and Environmental Safety</i> , 2020, 203, 111007.	6.0	9
1857	High-Quality Resolution of the Outbreak-Related Zika Virus Genome and Discovery of New Viruses Using Ion Torrent-Based Metatranscriptomics. <i>Viruses</i> , 2020, 12, 782.	3.3	5
1858	Genome-Wide Identification and Expression Analysis of MAPK and MAPKK Gene Family in Pomegranate ( <i>Punica Granatum</i> L.). <i>Agronomy</i> , 2020, 10, 1015.	3.0	0
1859	Genome-Wide Characterization and Expression Analysis of NHX Gene Family under Salinity Stress in <i>Gossypium barbadense</i> and Its Comparison with <i>Gossypium hirsutum</i> . <i>Genes</i> , 2020, 11, 803.	2.4	22
1860	The alcohol dehydrogenase gene family in sugarcane and its involvement in cold stress regulation. <i>BMC Genomics</i> , 2020, 21, 521.	2.8	57
1861	The Spruce Genome. <i>Compendium of Plant Genomes</i> , 2020, , .	0.5	0
1862	Genome-wide identification and characterization of HSP70 gene family in four species of cotton. <i>Genomics</i> , 2020, 112, 4442-4453.	2.9	12
1863	Transcriptome alterations of field-evolved resistance in <i>Pectinophora gossypiella</i> against Bt Bollgard II cotton in India. <i>Journal of Applied Entomology</i> , 2020, 144, 929-940.	1.8	2
1864	<i>Schistosoma haematobium</i> Extracellular Vesicle Proteins Confer Protection in a Heterologous Model of Schistosomiasis. <i>Vaccines</i> , 2020, 8, 416.	4.4	27
1865	The sugar transporter system of strawberry: genome-wide identification and expression correlation with fruit soluble sugar-related traits in a <i>Fragaria</i> – <i>Ananassa</i> germplasm collection. <i>Horticulture Research</i> , 2020, 7, 132.	6.3	24
1866	Transcriptional Response of Osmolyte Synthetic Pathways and Membrane Transporters in a Euryhaline Diatom During Long-term Acclimation to a Salinity Gradient. <i>Journal of Phycology</i> , 2020, 56, 1712-1728.	2.3	16
1867	Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus <i>Friedmanniomyces endolithicus</i> . <i>Fungal Biology</i> , 2020, 124, 458-467.	2.5	23
1868	Genome-wide screening of the classical cadherin gene family and cadherin-1 expression response infected with <i>Streptococcus agalactiae</i> in Nile tilapia ( <i>Oreochromis niloticus</i> ). <i>Aquaculture Reports</i> , 2020, 17, 100393.	1.7	2
1869	De novo transcriptome assembly and functional annotation for Y-organs of the blue crab ( <i>Callinectes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T. <i>Endocrinology</i> , 2020, 298, 113567.	1.8	7
1870	Transcriptomic Analysis of Four Cerianthid (Cnidaria, Ceriantharia) Venoms. <i>Marine Drugs</i> , 2020, 18, 413.	4.6	20
1871	Identification and Expression Analysis of Strigolactone Biosynthetic and Signaling Genes in Response to Salt and Alkaline Stresses in Soybean ( <i>Glycine max</i> ). <i>DNA and Cell Biology</i> , 2020, 39, 1850-1861.	1.9	14
1872	Comparative transcriptome analysis of high-growth and wild-type strains of <i>Pyropia yezoensis</i> . <i>Acta Botanica Croatica</i> , 2020, 79, 148-156.	0.7	5

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1873	Genome-wide identification of ATP binding cassette (ABC) transporter and heavy metal associated (HMA) gene families in flax ( <i>Linum usitatissimum</i> L.). <i>BMC Genomics</i> , 2020, 21, 722.	2.8	42
1874	Identification of Neuropeptides and Their Receptors in the Ectoparasitoid, <i>Habrobracon hebetor</i> . <i>Frontiers in Physiology</i> , 2020, 11, 575655.	2.8	10
1875	The Developmental Transcriptome of <i>Aedes albopictus</i> , a Major Worldwide Human Disease Vector. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1051-1062.	1.8	30
1876	Transcriptomic data on the transgenerational exposure of the keystone amphipod <i>Gammarus locusta</i> to simvastatin. <i>Data in Brief</i> , 2020, 32, 106248.	1.0	7
1877	An Expanded Genetic Code Enables Trimethylamine Metabolism in Human Gut Bacteria. <i>MSystems</i> , 2020, 5, .	3.8	22
1878	CryoEM structure of the type IVa pilus secretin required for natural competence in <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 5080.	12.8	21
1879	Formation and diversification of a paradigm biosynthetic gene cluster in plants. <i>Nature Communications</i> , 2020, 11, 5354.	12.8	50
1880	Complete genome sequence of a novel lytic phage infecting <i>Aeromonas hydrophila</i> , an infectious agent in striped catfish ( <i>Pangasianodon hypophthalmus</i> ). <i>Archives of Virology</i> , 2020, 165, 2973-2977.	2.1	15
1881	Genome sequence of segmented filamentous bacteria present in the human intestine. <i>Communications Biology</i> , 2020, 3, 485.	4.4	27
1882	Genome-wide transcriptome and proteome profiles indicate an active role of alternative splicing during de-etiolation of maize seedlings. <i>Planta</i> , 2020, 252, 60.	3.2	0
1883	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	2.8	45
1884	Genome-Scale Metabolic Model of the Human Pathogen <i>Candida albicans</i> : A Promising Platform for Drug Target Prediction. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 171.	3.5	16
1885	Characterization of vB_StuS_MMMA13, a Newly Discovered Bacteriophage Infecting the Agar-Degrading Species <i>Sphingomonas turrivirgatae</i> . <i>Viruses</i> , 2020, 12, 894.	3.3	2
1886	Genome-wide identification and expression patterns analysis of the RPD3/HDA1 gene family in cotton. <i>BMC Genomics</i> , 2020, 21, 643.	2.8	11
1887	Comprehensive identification and analysis of DELLA genes throughout the plant kingdom. <i>BMC Plant Biology</i> , 2020, 20, 372.	3.6	10
1888	Characteristics of a Series of Three Bacteriophages Infecting <i>Salmonella enterica</i> Strains. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6152.	4.1	21
1889	Identification of a Metagenome-Assembled Genome of an Uncultured <i>Methyloceanibacter</i> sp. Strain Acquired from an Activated Sludge System Used for Landfill Leachate Treatment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
1890	Genome-wide characterization and expression profiling of MAPK cascade genes in <i>Salvia miltiorrhiza</i> reveals the function of SmMAPK3 and SmMAPK1 in secondary metabolism. <i>BMC Genomics</i> , 2020, 21, 630.	2.8	9

#	ARTICLE	IF	CITATIONS
1891	Characterization of the leaf rust responsive ARF genes in wheat ( <i>Triticum aestivum</i> L.). <i>Plant Cell Reports</i> , 2020, 39, 1639-1654.	5.6	8
1892	Genome-Wide Characterization, Evolution, and Expression Analysis of the Leucine-Rich Repeat Receptor-Like Protein Kinase (LRR-RLK) Gene Family in <i>Medicago truncatula</i> . <i>Life</i> , 2020, 10, 176.	2.4	9
1893	Evolution of isoprenyl diphosphate synthase-like terpene synthases in fungi. <i>Scientific Reports</i> , 2020, 10, 14944.	3.3	14
1894	Genome-wide identification and characterization of DCL, AGO and RDR gene families in <i>Saccharum spontaneum</i> . <i>Scientific Reports</i> , 2020, 10, 13202.	3.3	23
1895	FASTQINS and ANUBIS: two bioinformatic tools to explore facts and artifacts in transposon sequencing and essentiality studies. <i>Nucleic Acids Research</i> , 2020, 48, e102-e102.	14.5	15
1896	ARDEP, a Rapid Degenerate Primer Design Pipeline Based on k-mers for Amplicon Microbiome Studies. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 5958.	2.6	4
1897	SelfAT-Fold: protein fold recognition based on residue-based and motif-based self-attention networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, PP, 1-1.	3.0	10
1898	Genome-Wide Identification and Capsaicinoid Biosynthesis-Related Expression Analysis of the R2R3-MYB Gene Family in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2020, 11, 598183.	2.3	23
1899	Isolation, Identification, and Complete Genome Assembly of an Endophytic <i>Bacillus velezensis</i> YB-130, Potential Biocontrol Agent Against <i>Fusarium graminearum</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 598285.	3.5	38
1900	Identification, Phylogeny, and Comparative Expression of the Lipxygenase Gene Family of the Aquatic Duckweed, <i>Spirodela polyrhiza</i> , during Growth and in Response to Methyl Jasmonate and Salt. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9527.	4.1	13
1901	Characterization of Prodiginine Pathway in Marine Sponge-Associated <i>Pseudoalteromonas</i> sp. PPB1 in Hilo, Hawai'i. <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	3.9	1
1902	Immunoproteomic Analysis Reveals Novel Candidate Antigens for the Diagnosis of Paracoccidioidomycosis Due to <i>Paracoccidioides lutzii</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 357.	3.5	19
1903	Genome-Wide Analysis of the Cyclin Gene Family and Their Expression Profile in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9430.	4.1	13
1904	Characterization of Metagenome-Assembled Genomes and Carbohydrate-Degrading Genes in the Gut Microbiota of Tibetan Pig. <i>Frontiers in Microbiology</i> , 2020, 11, 595066.	3.5	34
1905	Genome-wide identification and expression analysis of the CLC gene family in pomegranate ( <i>Punica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.6	12
1906	Identification and functional characterization of ABCC transporters for Cd tolerance and accumulation in <i>Sedum alfredii</i> Hance. <i>Scientific Reports</i> , 2020, 10, 20928.	3.3	14
1907	Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. <i>BMC Biology</i> , 2020, 18, 139.	3.8	17
1908	An Earliest Endosymbiont, <i>Wolbachia massiliensis</i> sp. nov., Strain PL13 from the Bed Bug ( <i>Cimex</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	4.1	23

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1909	The Transcriptome of <i>Cunninghamia lanceolata</i> male/female cone reveal the association between MIKC MADS-box genes and reproductive organs development. <i>BMC Plant Biology</i> , 2020, 20, 508.	3.6	15
1910	Characterization of the Topological Features of Catalytic Sites in Protein Coevolution Networks*. <i>Chinese Physics Letters</i> , 2020, 37, 068701.	3.3	2
1911	Identification and Expression Analysis of Sugar Transporter Gene Family in <i>Aspergillus oryzae</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-15.	1.6	6
1912	Hemiptera phylogenomic resources: Tree-based orthology prediction and conserved exon identification. <i>Molecular Ecology Resources</i> , 2020, 20, 1346-1360.	4.8	5
1913	A Review of Deep Learning Methods for Antibodies. <i>Antibodies</i> , 2020, 9, 12.	2.5	40
1914	Genome-Wide Identification and Characterization of Gene Families in <i>Arachis</i> : Methods and Strategies. <i>Frontiers in Genetics</i> , 2020, 11, 525.	2.3	9
1915	Chromosome-level assembly of the melon thrips genome yields insights into evolution of a sap-sucking lifestyle and pesticide resistance. <i>Molecular Ecology Resources</i> , 2020, 20, 1110-1125.	4.8	31
1916	Cloning, molecular and functional characterization by overexpression in <i>Arabidopsis</i> of MAPKK genes from grapevine ( <i>Vitis vinifera</i> ). <i>BMC Plant Biology</i> , 2020, 20, 194.	3.6	9
1917	Genomic Identification, Evolution, and Expression Analysis of Collagen Genes Family in Water Buffalo during Lactation. <i>Genes</i> , 2020, 11, 515.	2.4	11
1918	Review: Long non-coding RNA in livestock. <i>Animal</i> , 2020, 14, 2003-2013.	3.3	31
1919	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. <i>Plant Physiology</i> , 2020, 183, 399-413.	4.8	40
1920	The Bioinformatic and In Vitro Studies of <i>Clostridioides Difficile</i> Aminopeptidase M24 Revealed the Immunoreactive KKGIK Peptide. <i>Cells</i> , 2020, 9, 1146.	4.1	2
1921	Classification and functional analyses of putative virulence factors of <i>Mycobacterium tuberculosis</i> : A combined sequence and structure based study. <i>Computational Biology and Chemistry</i> , 2020, 87, 107270.	2.3	0
1922	The Kernel Size-Related Quantitative Trait Locus <i>qKW9</i> Encodes a Pentatricopeptide Repeat Protein That Affects Photosynthesis and Grain Filling. <i>Plant Physiology</i> , 2020, 183, 1696-1709.	4.8	29
1923	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	1.9	34
1924	Genome-centric microbiome analysis reveals solid retention time (SRT)-shaped species interactions and niche differentiation in food waste and sludge co-digesters. <i>Water Research</i> , 2020, 181, 115858.	11.3	37
1925	Dynamics of the transcriptional landscape during human fetal testis and ovary development. <i>Human Reproduction</i> , 2020, 35, 1099-1119.	0.9	22
1926	Predicting host taxonomic information from viral genomes: A comparison of feature representations. <i>PLoS Computational Biology</i> , 2020, 16, e1007894.	3.2	31

#	ARTICLE	IF	CITATIONS
1927	Engineered triply orthogonal pyrrolysyl-tRNA synthetase/tRNA pairs enable the genetic encoding of three distinct non-canonical amino acids. <i>Nature Chemistry</i> , 2020, 12, 535-544.	13.6	93
1928	Improved bacterial recombineering by parallelized protein discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13689-13698.	7.1	82
1929	Metagenomics reveals impact of geography and acute diarrheal disease on the Central Indian human gut microbiome. <i>Gut Microbes</i> , 2020, 12, 1752605.	9.8	22
1930	A Clone Resource of <i>Magnaporthe oryzae</i> Effectors That Share Sequence and Structural Similarities Across Host-Specific Lineages. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1032-1035.	2.6	20
1931	Genome-wide characterization of the abscisic acid-, stress- and ripening-induced (ASR) gene family in wheat ( <i>Triticum aestivum</i> L.). <i>Biological Research</i> , 2020, 53, 23.	3.4	20
1932	Screening and functional identification of lncRNAs in antler mesenchymal and cartilage tissues using high-throughput sequencing. <i>Scientific Reports</i> , 2020, 10, 9492.	3.3	5
1933	Pheromone biosynthetic pathway and chemoreception proteins in sex pheromone gland of <i>Eogystia hippophaecolus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 35, 100702.	1.0	1
1934	Higher-order Markov models for metagenomic sequence classification. <i>Bioinformatics</i> , 2020, 36, 4130-4136.	4.1	6
1935	Draft genomes of two outcrossing wild rice, <i>Oryza rufipogon</i> and <i>O. longistaminata</i> , reveal genomic features associated with mating-system evolution. <i>Plant Direct</i> , 2020, 4, e00232.	1.9	9
1936	Pattern recognition receptors in grass carp <i>Ctenopharyngodon idella</i> : II. Organization and expression analysis of NOD-like receptors. <i>Developmental and Comparative Immunology</i> , 2020, 110, 103734.	2.3	17
1937	CRISPRcasIdentifier: Machine learning for accurate identification and classification of CRISPR-Cas systems. <i>GigaScience</i> , 2020, 9, .	6.4	31
1938	Importance of <i>Defluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	3.6	13
1939	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	4.6	13
1940	Disequilibrium evolution of the Fructose-1,6-bisphosphatase gene family leads to their functional biodiversity in <i>Gossypium</i> species. <i>BMC Genomics</i> , 2020, 21, 379.	2.8	13
1941	A cotton $\beta$ -1,3-/4-fucosyltransferase-encoding gene, FucT4, plays an important role in cell elongation and is significantly associated with fiber quality. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1141-1153.	2.1	3
1942	The nuclear and mitochondrial genomes of <i>Friesemelitta varia</i> – a highly eusocial stingless bee (Meliponini) with a permanently sterile worker caste. <i>BMC Genomics</i> , 2020, 21, 386.	2.8	15
1943	Basic Helix-Loop-Helix (bHLH) transcription factor family in Yellow horn ( <i>Xanthoceras sorbifolia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10 patterns. <i>International Journal of Biological Macromolecules</i> , 2020, 160, 711-723.	7.5	17
1944	An evolutionarily conserved motif is required for Plasmodesmata-located protein 5 to regulate cell-to-cell movement. <i>Communications Biology</i> , 2020, 3, 291.	4.4	15

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1945	Transcriptome Analysis of Maternal Gene Transcripts in Unfertilized Eggs of <i>Misgurnus anguillicaudatus</i> and Identification of Immune-Related Maternal Genes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3872.	4.1	4
1946	Identification of a chitosanase from the marine metagenome and its molecular improvement based on evolution data. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6647-6657.	3.6	7
1947	RNA Pol II Length and Disorder Enable Cooperative Scaling of Transcriptional Bursting. <i>Molecular Cell</i> , 2020, 79, 207-220.e8.	9.7	32
1948	Shifting evolutionary sands: transcriptome characterization of the <i>Aptostichus atomarius</i> species complex. <i>BMC Evolutionary Biology</i> , 2020, 20, 68.	3.2	1
1949	The Complete Chloroplast Genome Sequencing and Comparative Analysis of Reed Canary Grass ( <i>Phalaris arundinacea</i> ) and Hardinggrass ( <i>P. aquatica</i> ). <i>Plants</i> , 2020, 9, 748.	3.5	9
1950	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	2.3	13
1951	Genome-wide analysis of the U-box E3 ubiquitin ligase enzyme gene family in tomato. <i>Scientific Reports</i> , 2020, 10, 9581.	3.3	40
1952	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	3.5	48
1953	A case study of salivary microbiome in smokers and non-smokers in Hungary: analysis by shotgun metagenome sequencing. <i>Journal of Oral Microbiology</i> , 2020, 12, 1773067.	2.7	18
1954	Metabolic Engineering Strategies in Diatoms Reveal Unique Phenotypes and Genetic Configurations With Implications for Algal Genetics and Synthetic Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 513.	4.1	26
1955	Diversity and Evolutionary Dynamics of Antiphage Defense Systems in <i>Ralstonia solanacearum</i> Species Complex. <i>Frontiers in Microbiology</i> , 2020, 11, 961.	3.5	11
1956	Genomic Origin and Diversification of the Glucosinolate MAM Locus. <i>Frontiers in Plant Science</i> , 2020, 11, 711.	3.6	10
1957	<i>Clostridioides difficile</i> Senses and Hijacks Host Heme for Incorporation into an Oxidative Stress Defense System. <i>Cell Host and Microbe</i> , 2020, 28, 411-421.e6.	11.0	36
1958	Characterization and Analysis of the Full-Length Transcriptomes of Multiple Organs in <i>Pseudotaxus chienii</i> (W.C.Cheng) W.C.Cheng. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4305.	4.1	4
1959	Genome mining and sequence analysis of chemosensory soluble proteins in arthropods. <i>Methods in Enzymology</i> , 2020, 642, 1-20.	1.0	5
1960	Evolution of Two Ubiquitin-like System of Autophagy in Orchid. <i>Horticultural Plant Journal</i> , 2020, 6, 321-334.	5.0	6
1961	NAC Family Transcription Factors in Carrot: Genomic and Transcriptomic Analysis and Responses to Abiotic Stresses. <i>DNA and Cell Biology</i> , 2020, 39, 816-827.	1.9	7
1962	Genome-wide identification and expression analysis of WRKY transcription factors in pearl millet ( <i>Pennisetum glaucum</i> ) under dehydration and salinity stress. <i>BMC Genomics</i> , 2020, 21, 231.	2.8	56



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1963	Mechanism of Antibacterial Activity of <i>Bacillus amyloliquefaciens</i> C-1 Lipopeptide toward Anaerobic <i>Clostridium difficile</i> . <i>BioMed Research International</i> , 2020, 2020, 1-12.	1.9	23
1964	Portal of Juglandaceae: A comprehensive platform for Juglandaceae study. <i>Horticulture Research</i> , 2020, 7, 35.	6.3	22
1965	A novel thermostable cellulase cocktail enhances lignocellulosic bioconversion and biorefining in a broad range of pH. <i>International Journal of Biological Macromolecules</i> , 2020, 154, 349-360.	7.5	47
1966	Insights Into the Function of the NuA4 Complex in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 125.	3.6	21
1967	Comparison of Viromes in Ticks from Different Domestic Animals in China. <i>Virologica Sinica</i> , 2020, 35, 398-406.	3.0	15
1968	COST1 regulates autophagy to control plant drought tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7482-7493.	7.1	71
1969	Genome-Scale Identification, in Silico Characterization and Interaction Study Between Wheat SNARE and NPSN Gene Families Involved in Vesicular Transport. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2492-2501.	3.0	8
1970	Characterization of the Gh4CL gene family reveals a role of Gh4CL7 in drought tolerance. <i>BMC Plant Biology</i> , 2020, 20, 125.	3.6	40
1971	Genome Sequence and Comparative Analysis of <i>Colletotrichum gloeosporioides</i> Isolated from <i>Liriodendron</i> Leaves. <i>Phytopathology</i> , 2020, 110, 1260-1269.	2.2	13
1972	Transcriptome Analysis of the Cytokinin Response in <i>Medicago truncatula</i> . <i>Journal of Plant Biology</i> , 2020, 63, 189-202.	2.1	2
1973	The chromosome-scale assembly of the willow genome provides insight into Salicaceae genome evolution. <i>Horticulture Research</i> , 2020, 7, 45.	6.3	35
1974	Genome-Wide Identification and Evolutionary Analysis of the Fruit-Weight 2.2-Like Gene Family in Polyploid Oilseed Rape ( <i>Brassica napus</i> L.). <i>DNA and Cell Biology</i> , 2020, 39, 766-782.	1.9	3
1975	Transcriptomic analysis of the mode of action of the candidate anti-fouling compound di(1H-indol-3-yl)methane (DIM) on a marine biofouling species, the bryozoan <i>Bugula neritina</i> . <i>Marine Pollution Bulletin</i> , 2020, 152, 110904.	5.0	3
1976	The Cytochrome P450 Monooxygenase Inventory of Grapevine ( <i>Vitis vinifera</i> L.): Genome-Wide Identification, Evolutionary Characterization and Expression Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 44.	2.3	35
1977	First Genome of the Brown Alga <i>Undaria pinnatifida</i> : Chromosome-Level Assembly Using PacBio and Hi-C Technologies. <i>Frontiers in Genetics</i> , 2020, 11, 140.	2.3	39
1978	Genome-wide characterization and expression analyses of the auxin/indole-3-acetic acid (Aux/IAA) gene family in barley ( <i>Hordeum vulgare</i> L.). <i>Scientific Reports</i> , 2020, 10, 10242.	3.3	15
1979	Genome-Wide Identification, Evolution, and Expression of GDSL-Type Esterase/Lipase Gene Family in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 726.	3.6	47
1980	Genome-wide analysis and comparison of the DNA-binding one zinc finger gene family in diploid and tetraploid cotton ( <i>Gossypium</i> ). <i>PLoS ONE</i> , 2020, 15, e0235317.	2.5	6



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1981	Genome-wide Identification and Expression Analysis of TALE Gene Family in Pomegranate ( <i>Punica</i> ) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	3.0	8
1982	Microbial succession during the transition from active to inactive stages of deep-sea hydrothermal vent sulfide chimneys. <i>Microbiome</i> , 2020, 8, 102.	11.1	62
1983	A bacterial cytidine deaminase toxin enables CRISPR-free mitochondrial base editing. <i>Nature</i> , 2020, 583, 631-637.	27.8	409
1984	Functional analysis of RXLR effectors from the New Zealand kauri dieback pathogen <i>Phytophthora agathidicida</i>. <i>Molecular Plant Pathology</i> , 2020, 21, 1131-1148.	4.2	13
1985	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. <i>Cell Host and Microbe</i> , 2020, 28, 380-389.e9.	11.0	51
1986	The Gut Microbiota in Prediabetes and Diabetes: A Population-Based Cross-Sectional Study. <i>Cell Metabolism</i> , 2020, 32, 379-390.e3.	16.2	233
1987	Comparative study of the SBP-box gene family in rice siblings. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	2
1988	Improved reconstruction and comparative analysis of chromosome 12 to rectify Mis-assemblies in <i>Gossypium arboreum</i> . <i>BMC Genomics</i> , 2020, 21, 470.	2.8	0
1989	Pervasive duplication, biased molecular evolution and comprehensive functional analysis of the PP2C family in <i>Glycine max</i> . <i>BMC Genomics</i> , 2020, 21, 465.	2.8	9
1990	The auxin response factor gene family in wheat ( <i>Triticum aestivum</i> L.): Genome-wide identification, characterization and expression analyses in response to leaf rust. <i>South African Journal of Botany</i> , 2021, 140, 312-325.	2.5	13
1991	MetaRibo-Seq measures translation in microbiomes. <i>Nature Communications</i> , 2020, 11, 3268.	12.8	30
1992	Evolutionary History of the Globin Gene Family in Annelids. <i>Genome Biology and Evolution</i> , 2020, 12, 1719-1733.	2.5	8
1993	Signatures of adaptation to a monocot host in the plantâ€parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	5.7	9
1994	Complete transcriptome assembly and annotation of a critically important amphipod species in freshwater ecotoxicological risk assessment: <i>Gammarus fossarum</i> . <i>Environment International</i> , 2020, 137, 105319.	10.0	8
1995	Transcriptome-Wide Identification, Evolutionary Analysis, and GA Stress Response of the GRAS Gene Family in <i>Panax ginseng</i> C. A. Meyer. <i>Plants</i> , 2020, 9, 190.	3.5	13
1996	Systematic identification of long intergenic non-coding RNAs expressed in bovine oocytes. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 13.	3.3	11
1997	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	10.3	112
1998	Analysis of two Mexican <i>Pectobacterium brasiliense</i> strains reveals an inverted relationship between c-di-GMP levels with exopolysaccharide production and swarming motility. <i>Microbiological Research</i> , 2020, 235, 126427.	5.3	7

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1999	Genome-Wide Identification of the Auxin Response Factor (ARF) Gene Family and Their Expression Analysis during Flower Development of <i>Osmanthus fragrans</i> . <i>Forests</i> , 2020, 11, 245.	2.1	10
2000	Toward the Mechanistic Understanding of Enzymatic CO <sub>2</sub> Reduction. <i>ACS Catalysis</i> , 2020, 10, 3844-3856.	11.2	76
2001	Genome-wide annotation, comparison and functional genomics of carbohydrate-active enzymes in legumes infecting <i>Fusarium oxysporum</i> formae speciales. <i>Mycology</i> , 2020, 11, 56-70.	4.4	12
2002	Origin and Evolution of Polycyclic Triterpene Synthesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1925-1941.	8.9	38
2003	Genome-wide analysis of a putative lipid transfer protein LTP_2 gene family reveals CsLTP_2 genes involved in response of cucumber against root-knot nematode ( <i>Meloidogyne incognita</i> ). <i>Genome</i> , 2020, 63, 225-238.	2.0	11
2004	Characterizing ciguatoxin (CTX)- and Non-CTX-producing strains of <i>Gambierdiscus balechii</i> using comparative transcriptomics. <i>Science of the Total Environment</i> , 2020, 717, 137184.	8.0	12
2005	Genome of <i>Tripterygium wilfordii</i> and identification of cytochrome P450 involved in triptolide biosynthesis. <i>Nature Communications</i> , 2020, 11, 971.	12.8	103
2006	Genome-wide identification, phylogeny, and expression analysis of the <i>CA</i> gene family in tomato. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 70-83.	1.3	5
2007	De novo Transcriptome Reveals Gene Changes in the Development of the Endosperm Chalazal Haustorium in <i>Taxillus chinensis</i> (DC.) Danser. <i>BioMed Research International</i> , 2020, 2020, 1-12.	1.9	8
2008	Genome-Wide Profiling and Phylogenetic Analysis of the SWEET Sugar Transporter Gene Family in Walnut and Their Lack of Responsiveness to <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1251.	4.1	17
2009	Assembly-free single-molecule sequencing recovers complete virus genomes from natural microbial communities. <i>Genome Research</i> , 2020, 30, 437-446.	5.5	80
2010	Passion Fruit Green Spot Virus Genome Harbors a New Orphan ORF and Highlights the Flexibility of the 5'-End of the RNA2 Segment Across Cileviruses. <i>Frontiers in Microbiology</i> , 2020, 11, 206.	3.5	41
2011	Hookworms Evade Host Immunity by Secreting a Deoxyribonuclease to Degrade Neutrophil Extracellular Traps. <i>Cell Host and Microbe</i> , 2020, 27, 277-289.e6.	11.0	53
2012	TRPA1 modulates noxious odor responses in <i>Lygus hesperus</i> . <i>Journal of Insect Physiology</i> , 2020, 122, 104038.	2.0	6
2013	Comprehensive phylogenomic analysis of ERF genes in sorghum provides clues to the evolution of gene functions and redundancy among gene family members. <i>3 Biotech</i> , 2020, 10, 139.	2.2	16
2014	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , 2020, 18, 12.	3.8	95
2015	Structural Insights into the Unique Activation Mechanisms of a Non-classical Calpain and Its Disease-Causing Variants. <i>Cell Reports</i> , 2020, 30, 881-892.e5.	6.4	17
2016	Trimethylamine-N-Oxide Postprandial Response in Plasma and Urine Is Lower After Fermented Compared to Non-Fermented Dairy Consumption in Healthy Adults. <i>Nutrients</i> , 2020, 12, 234.	4.1	27

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2017	Tentacle Transcriptomes of the Speckled Anemone ( <i>Actiniaria: Actiniidae: Oulactis</i> sp.): Venom-Related Components and Their Domain Structure. <i>Marine Biotechnology</i> , 2020, 22, 207-219.	2.4	19
2018	Transcriptional regulation by $\gamma$ factor phosphorylation in bacteria. <i>Nature Microbiology</i> , 2020, 5, 395-406.	13.3	17
2019	The mirid bug <i>Apolygus lucorum</i> deploys a glutathione peroxidase as a candidate effector to enhance plant susceptibility. <i>Journal of Experimental Botany</i> , 2020, 71, 2701-2712.	4.8	30
2020	Protein Fold Recognition by Combining Support Vector Machines and Pairwise Sequence Similarity Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2008-2016.	3.0	13
2021	Critiquing Protein Family Classification Models Using Sufficient Input Subsets. <i>Journal of Computational Biology</i> , 2020, 27, 1219-1231.	1.6	7
2022	Genome-Based Comparison of All Species of the Genus <i>Moorella</i> , and Status of the Species <i>Moorella thermoacetica</i> and <i>Moorella thermoautotrophica</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 3070.	3.5	12
2023	Highly efficient production of chitooligosaccharides by enzymes mined directly from the marine metagenome. <i>Carbohydrate Polymers</i> , 2020, 234, 115909.	10.2	23
2024	Plant Mitochondrial Carriers: Molecular Gatekeepers That Help to Regulate Plant Central Carbon Metabolism. <i>Plants</i> , 2020, 9, 117.	3.5	23
2025	De Novo Transcriptome Identifies Olfactory Genes in <i>Diachasmimorpha longicaudata</i> (Ashmead). <i>Genes</i> , 2020, 11, 144.	2.4	8
2026	Computationally Aided Discovery of LysEFm5 Variants with Improved Catalytic Activity and Stability. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	2
2027	Genome-Wide Identification, Expression Profile of the TIFY Gene Family in <i>Brassica oleracea</i> var. capitata, and Their Divergent Response to Various Pathogen Infections and Phytohormone Treatments. <i>Genes</i> , 2020, 11, 127.	2.4	31
2028	Draft Genome of the Asian Buffalo Leech <i>Hirudinaria manillensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1321.	2.3	11
2029	Genome Sequence Resource of <i>Magnaporthe oryzae</i> Laboratory Strain 2539. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1029-1031.	2.6	2
2030	Advances in Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , 2020, , .	1.3	0
2031	XynDZ5: A New Thermostable GH10 Xylanase. <i>Frontiers in Microbiology</i> , 2020, 11, 545.	3.5	20
2032	Atypical <i>Salmonella enterica</i> Serovars in Murine and Human Macrophage Infection Models. <i>Infection and Immunity</i> , 2020, 88, .	2.2	6
2033	GrAPFI: predicting enzymatic function of proteins from domain similarity graphs. <i>BMC Bioinformatics</i> , 2020, 21, 168.	2.6	8
2034	Genome-wide identification and expression analysis of the NAC transcription factor family in tomato ( <i>Solanum lycopersicum</i> ) during aluminum stress. <i>BMC Genomics</i> , 2020, 21, 288.	2.8	81

#	ARTICLE	IF	CITATIONS
2035	Bioinformatics approaches applied in pan-genomics and their challenges. , 2020, , 43-64.		1
2036	Dissociation between the critical role of ClpB of <i>Francisella tularensis</i> for the heat shock response and the DnaK interaction and its important role for efficient type VI secretion and bacterial virulence. <i>PLoS Pathogens</i> , 2020, 16, e1008466.	4.7	10
2037	Transcriptome analysis revealed cadmium accumulation mechanisms in hyperaccumulator <i>Siegesbeckia orientalis</i> L.. <i>Environmental Science and Pollution Research</i> , 2020, 27, 18853-18865.	5.3	12
2038	Identification, expression and miRNA targeting of auxin response factor genes related to phyllody in the witchesâ€™ broom disease of jujube. <i>Gene</i> , 2020, 746, 144656.	2.2	15
2039	Genome-wide characterization of two-component system (TCS) genes in melon ( <i>Cucumis melo</i> L.). <i>Plant Physiology and Biochemistry</i> , 2020, 151, 197-213.	5.8	15
2040	The transcriptome of the newt <i>Cynops orientalis</i> provides new insights into evolution and function of sexual gene networks in sarcopterygians. <i>Scientific Reports</i> , 2020, 10, 5445.	3.3	11
2041	SMRT sequencing of the <i>Oryza rufipogon</i> genome reveals the genomic basis of rice adaptation. <i>Communications Biology</i> , 2020, 3, 167.	4.4	20
2042	De Novo Transcriptome Assembly and Annotation of Liver and Brain Tissues of Common Brushtail Possums ( <i>Trichosurus vulpecula</i> ) in New Zealand: Transcriptome Diversity after Decades of Population Control. <i>Genes</i> , 2020, 11, 436.	2.4	8
2043	No More Tears: Mining Sequencing Data for Novel Bt Cry Toxins with CryProcessor. <i>Toxins</i> , 2020, 12, 204.	3.4	19
2044	Comparative Metatranscriptomics of Periodontitis Supports a Common Polymicrobial Shift in Metabolic Function and Identifies Novel Putative Disease-Associated ncRNAs. <i>Frontiers in Microbiology</i> , 2020, 11, 482.	3.5	16
2045	PHYCI_587572: An RxLR Effector Gene and New Biomarker in A Recombinase Polymerase Amplification Assay for Rapid Detection of <i>Phytophthora cinnamomi</i> . <i>Forests</i> , 2020, 11, 306.	2.1	12
2046	Genome mining as a biotechnological tool for the discovery of novel marine natural products. <i>Critical Reviews in Biotechnology</i> , 2020, 40, 571-589.	9.0	26
2047	Pyrene biodegradation and its potential pathway involving <i>Roseobacter</i> clade bacteria. <i>International Biodeterioration and Biodegradation</i> , 2020, 150, 104961.	3.9	28
2048	Gene expression differences between abalone that are susceptible and resilient to a simulated heat wave event. <i>Aquaculture</i> , 2020, 526, 735317.	3.5	7
2049	Dataset for the combined transcriptome assembly of <i>M. oleifera</i> and functional annotation. <i>Data in Brief</i> , 2020, 30, 105416.	1.0	4
2050	Identification and Characterization of a DmoB Flavin Oxidoreductase from a Putative Two-Component DMS <i>C</i> -Monooxygenase. <i>ACS Omega</i> , 2020, 5, 9830-9838.	3.5	1
2051	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog ( <i>Canis lupus</i> ) Tj ETQq0.0.0 rgBT /Overlock 1	6.4	47
2052	Transcriptomic analysis of polyketide synthases in a highly ciguatoxic dinoflagellate, <i>Gambierdiscus polynesiensis</i> and low toxicity <i>Gambierdiscus pacificus</i> , from French Polynesia. <i>PLoS ONE</i> , 2020, 15, e0231400.	2.5	14

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2053	<i>De Novo</i> Assembly of a High-Quality Reference Genome for the Horned Lark (<i>Eremophila</i>). <i>ETQq0 0 0 rgBT /Overlqck 10 Tf 5</i>	1.8	10
2054	Protein Fold Recognition Based on Auto-Weighted Multi-view Graph Embedding Learning Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1-1.	3.0	7
2055	Probing the Mobilome: Discoveries in the Dynamic Microbiome. <i>Trends in Microbiology</i> , 2021, 29, 158-170.	7.7	41
2056	Isolation and characterization of Salt Overly Sensitive family genes in spinach. <i>Physiologia Plantarum</i> , 2021, 171, 520-532.	5.2	20
2057	PL-search: a profile-link-based search method for protein remote homology detection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
2058	Genome-wide identification and expression analysis of the B-box gene family in peach fruit during postharvest cold storage and subsequent shelf life. <i>Postharvest Biology and Technology</i> , 2021, 172, 111387.	6.0	6
2059	Phylogenetic and ion-response analyses reveal a relationship between gene expansion and functional divergence in the Ca <sup>2+</sup> /cation antiporter family in Angiosperms. <i>Plant Molecular Biology</i> , 2021, 105, 303-320.	3.9	7
2060	Comprehensive analysis of polygalacturonase genes offers new insights into their origin and functional evolution in land plants. <i>Genomics</i> , 2021, 113, 1096-1108.	2.9	8
2061	Plant DNA barcoding necessitates marker-specific efforts to establish more comprehensive reference databases. <i>Genome</i> , 2021, 64, 265-298.	2.0	20
2062	High quality genome of <i>Erigeron breviscapus</i> provides a reference for herbal plants in Asteraceae. <i>Molecular Ecology Resources</i> , 2021, 21, 153-169.	4.8	21
2063	A chromosome-level genome assembly of the woolly apple aphid, <i>Eriosoma lanigerum</i> Hausmann (Hemiptera: Aphididae). <i>Molecular Ecology Resources</i> , 2021, 21, 316-326.	4.8	28
2064	Acidobacteria are active and abundant members of diverse atmospheric H <sub>2</sub> -oxidizing communities detected in temperate soils. <i>ISME Journal</i> , 2021, 15, 363-376.	9.8	23
2065	Molecular characterization and modeling study of the Podr1 gene and genome-scale identification of whole ATP-binding cassette (ABC) transporters in <i>Penicillium occitanis</i> . <i>Genomics</i> , 2021, 113, 795-811.	2.9	3
2066	Genomic screening and molecular dynamics simulations of <scp>cyanovirinâ€N</scp> homologs from cyanobacteria phylum. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 322-329.	2.6	1
2067	Methionine aminopeptidases with short sequence inserts within the catalytic domain are differentially inhibited: Structural and biochemical studies of three proteins from <i>Vibrio</i> spp.. <i>European Journal of Medicinal Chemistry</i> , 2021, 209, 112883.	5.5	3
2068	Application of the immobilized enzyme on magnetic graphene oxide nano-carrier as a versatile bi-functional tool for efficient removal of dye from water. <i>Bioresource Technology</i> , 2021, 319, 124228.	9.6	73
2069	Expression of a Brassica napus metal transport protein (BnMTP3) in <i>Arabidopsis thaliana</i> confers tolerance to Zn and Mn. <i>Plant Science</i> , 2021, 304, 110754.	3.6	20
2070	Marine <i>Dadabacteria</i> exhibit genome streamlining and phototrophy-driven niche partitioning. <i>ISME Journal</i> , 2021, 15, 1248-1256.	9.8	39

#	ARTICLE	IF	CITATIONS
2071	A multilayered cross-species analysis of GRAS transcription factors uncovered their functional networks in plant adaptation to the environment. <i>Journal of Advanced Research</i> , 2021, 29, 191-205.	9.5	10
2072	A novel wheat ASR gene, TaASR2D, enhances drought tolerance in <i>Brachypodium distachyon</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 159, 400-414.	5.8	10
2073	Dynamics of microbial stress responses driven by abiotic changes along a temporal gradient in Deception Island, Maritime Antarctica. <i>Science of the Total Environment</i> , 2021, 758, 143671.	8.0	9
2074	Probing periodontal microbial dark matter using metataxonomics and metagenomics. <i>Periodontology</i> 2000, 2021, 85, 12-27.	13.4	16
2075	Genome-Wide Analysis of Heat Shock Transcription Factors in <i>Ziziphus jujuba</i> Identifies Potential Candidates for Crop Improvement Under Abiotic Stress. <i>Applied Biochemistry and Biotechnology</i> , 2021, 193, 1023-1041.	2.9	6
2076	Conservative route to genome compaction in a miniature annelid. <i>Nature Ecology and Evolution</i> , 2021, 5, 231-242.	7.8	51
2077	Machine learning for metabolic engineering: A review. <i>Metabolic Engineering</i> , 2021, 63, 34-60.	7.0	135
2078	Multiple Sequence Alignment for Large Heterogeneous Datasets Using SATĀ©, PASTA, and UPP. <i>Methods in Molecular Biology</i> , 2021, 2231, 99-119.	0.9	1
2079	CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021, 49, e20-e20.	14.5	44
2080	Genome-wide analysis of the MADS-Box gene family in <i>Chrysanthemum</i> . <i>Computational Biology and Chemistry</i> , 2021, 90, 107424.	2.3	26
2081	Long-range correlation and critical fluctuations in coevolution networks of protein sequences. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2021, 562, 125339.	2.6	5
2082	Genome-wide identification of polar auxin transporter gene families reveals a possible new polar auxin flow in inverted cuttings of <i>Populus yunnanensis</i> . <i>Gene</i> , 2021, 772, 145349.	2.2	2
2083	Mining germplasm panels and phenotypic datasets to identify loci for resistance to <i>Phytophthora sojae</i> in soybean. <i>Plant Genome</i> , 2021, 14, e20063.	2.8	13
2084	A biaryl-linked tripeptide from <i>Planomonospora</i> reveals a widespread class of minimal RiPP gene clusters. <i>Cell Chemical Biology</i> , 2021, 28, 733-739.e4.	5.2	47
2085	Cyanorak v2.1: a scalable information system dedicated to the visualization and expert curation of marine and brackish picocyanobacteria genomes. <i>Nucleic Acids Research</i> , 2021, 49, D667-D676.	14.5	38
2086	Comparative genomics highlights the importance of drug efflux transporters during evolution of mycoparasitism in <i>Clonostachys</i> subgenus <i>Bionectria</i> (Fungi, Ascomycota, Hypocreales). <i>Evolutionary Applications</i> , 2021, 14, 476-497.	3.1	19
2087	Chromosome-level genome of the peach fruit moth <i>Carposina sasakii</i> (Lepidoptera: Carposinidae) provides a resource for evolutionary studies on moths. <i>Molecular Ecology Resources</i> , 2021, 21, 834-848.	4.8	25
2088	Molecular characterization of western corn rootworm pyrethroid resistance. <i>Pest Management Science</i> , 2021, 77, 860-868.	3.4	5



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2089	Analysis of insect nuclear small heat shock proteins and interacting proteins. Cell Stress and Chaperones, 2021, 26, 265-274.	2.9	5
2090	Long-Term Waterlogging as Factor Contributing to Hypoxia Stress Tolerance Enhancement in Cucumber: Comparative Transcriptome Analysis of Waterlogging Sensitive and Tolerant Accessions. Genes, 2021, 12, 189.	2.4	27
2091	Computational Modeling of RdRp Inhibitors for the Development of Drugs against Novel Coronavirus (nCoV). Methods in Pharmacology and Toxicology, 2021, , 541.	0.2	0
2092	Genome-wide identification and expression pattern of alkaline/neutral invertase gene family in <i>Dendrobium catenatum</i> . Biotechnology and Biotechnological Equipment, 2021, 35, 527-537.	1.3	4
2093	In silico tertiary structure prediction and evolutionary analysis of two DNA-binding proteins (DBP-1) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 1075-1086.	1.5	1
2094	Bioinformatics: new tools and applications in life science and personalized medicine. Applied Microbiology and Biotechnology, 2021, 105, 937-951.	3.6	14
2096	Expansion and re-classification of the extracytoplasmic function (ECF) Ĩf factor family. Nucleic Acids Research, 2021, 49, 986-1005.	14.5	32
2097	Genome-wide identification and analysis of cystatin family genes in Sorghum ( <i>Sorghum</i> bicolor) Tj ETQq1 1 0.784314.3gBT /Over	2.0	14
2098	Putative Novel Effector Genes Revealed by the Genomic Analysis of the Phytopathogenic Fungus <i>Fusarium oxysporum</i> f. sp. <i>physali</i> (Foph) That Infects Cape Gooseberry Plants. Frontiers in Microbiology, 2020, 11, 593915.	3.5	8
2099	Microbial niche differentiation explains nitrite oxidation in marine oxygen minimum zones. ISME Journal, 2021, 15, 1317-1329.	9.8	28
2100	De novo genome assembly of the potent medicinal plant <i>Rehmannia glutinosa</i> using nanopore technology. Computational and Structural Biotechnology Journal, 2021, 19, 3954-3963.	4.1	26
2101	Molecular and Structural Evolution of Cytochrome P450 Aromatase. International Journal of Molecular Sciences, 2021, 22, 631.	4.1	14
2102	Bridging Themes: Short Protein Segments Found in Different Architectures. Molecular Biology and Evolution, 2021, 38, 2191-2208.	8.9	32
2103	Mind the mushroom: natural product biosynthetic genes and enzymes of Basidiomycota. Natural Product Reports, 2021, 38, 702-722.	10.3	54
2104	Universal and taxon-specific trends in protein sequences as a function of age. Elife, 2021, 10, .	6.0	20
2105	A Predictive Approach to Infer the Activity and Natural Variation of Retrotransposon Families in Plants. Methods in Molecular Biology, 2021, 2250, 1-14.	0.9	7
2106	Wood transcriptome analysis of <i>Pinus densiflora</i> identifies genes critical for secondary cell wall formation and NAC transcription factors involved in tracheid formation. Tree Physiology, 2021, 41, 1289-1305.	3.1	13
2107	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. Nature Microbiology, 2021, 6, 354-365.	13.3	109



#	ARTICLE	IF	CITATIONS
2108	Unraveling the roles of the reductant and free copper ions in LPMO kinetics. <i>Biotechnology for Biofuels</i> , 2021, 14, 28.	6.2	62
2109	Computational Approaches in Identifying Long Non-coding RNA. , 2021, , 487-505.		0
2110	Functional Genomics of Teak. <i>Compendium of Plant Genomes</i> , 2021, , 253-265.	0.5	1
2111	Full-Length Transcriptome Analysis of Four Different Tissues of <i>Cephalotaxus oliveri</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 787.	4.1	16
2112	UDP-Glucose Dehydrogenases: Identification, Expression, and Function Analyses in Upland Cotton ( <i>Gossypium hirsutum</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 597890.	2.3	5
2113	Transposable Elements and Teleost Migratory Behaviour. <i>International Journal of Molecular Sciences</i> , 2021, 22, 602.	4.1	9
2115	Crystal structure of steroid reductase SRD5A reveals conserved steroid reduction mechanism. <i>Nature Communications</i> , 2021, 12, 449.	12.8	23
2116	Positive selection analysis reveals the deep-sea adaptation of a hadal sea cucumber ( <i>Paelopatides</i> sp.) to the Mariana Trench. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 266-281.	1.3	9
2117	Propedia: a database for proteinâ€‘peptide identification based on a hybrid clustering algorithm. <i>BMC Bioinformatics</i> , 2021, 22, 1.	2.6	261
2118	A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Lecture Notes in Computer Science</i> , 2021, , 116-126.	1.3	0
2119	Seasonal shifts in the gut microbiome indicate plastic responses to diet in wild geladas. <i>Microbiome</i> , 2021, 9, 26.	11.1	105
2120	RNA-sequencing indicates high hemocyanin expression as a key strategy for cold adaptation in the Antarctic amphipod <i>Eusirus</i> cf. <i>giganteus</i> clade g3. <i>Biocell</i> , 2021, 45, 1611-1619.	0.7	5
2121	Role of Computational Biology in Sustainable Development of Agriculture. , 2021, , 53-69.		0
2122	An efficient protein homology detection approach based on seq2seq model and ranking. <i>Biotechnology and Biotechnological Equipment</i> , 2021, 35, 633-640.	1.3	3
2123	Comparative Genomics, from the Annotated Genome to Valuable Biological Information: A Case Study. <i>Methods in Molecular Biology</i> , 2021, 2242, 91-112.	0.9	0
2124	Identification and Downstream Analyses of Domains Amplified in Plant Genomes: The Case of StAR-Related Lipid Transfer (START) Domains in Rice. <i>Methods in Molecular Biology</i> , 2021, 2238, 325-338.	0.9	1
2125	Polymorphism of genetic ambigrams. <i>Virus Evolution</i> , 2021, 7, veab038.	4.9	5
2127	The enzymology of oxazolone and thioamide synthesis in methanobactin. <i>Methods in Enzymology</i> , 2021, 656, 341-373.	1.0	3

#	ARTICLE	IF	CITATIONS
2128	White pupae phenotype of tephritids is caused by parallel mutations of a MFS transporter. <i>Nature Communications</i> , 2021, 12, 491.	12.8	25
2129	<i>Rhodnius prolixus</i> uses the peptidoglycan recognition receptor rpPGRP-LC/LA to detect Gram-negative bacteria and activate the IMD pathway. <i>Current Research in Insect Science</i> , 2021, 1, 100006.	1.7	11
2130	Genome-wide identification, characterization and transcriptional profiling of NHX-type (Na <sup>+</sup> /H <sup>+</sup> ) antiporters under salinity stress in soybean. <i>3 Biotech</i> , 2021, 11, 16.	2.2	19
2131	Pleiotropic function of the SQUAMOSA PROMOTER-BINDING PROTEIN-LIKE gene TaSPL14 in wheat plant architecture. <i>Planta</i> , 2021, 253, 44.	3.2	26
2132	Characterization and functional analysis of phytoene synthase gene family in tobacco. <i>BMC Plant Biology</i> , 2021, 21, 32.	3.6	18
2133	Online Genomic Resources and Bioinformatics Tools Available for Epigenetics and Non-coding RNA. , 2021, , 306-328.		0
2134	Genomic analyses of Biston suppressaria nucleopolyhedrovirus: a viral isolate obtained from the tea looper caterpillar, Biston suppressaria (Guenée, 1857). <i>Brazilian Journal of Microbiology</i> , 2021, 52, 219-227.	2.0	2
2135	Genome-wide identification and characterization of NBS-encoding genes in <i>Raphanus sativus</i> L. and their roles related to <i>Fusarium oxysporum</i> resistance. <i>BMC Plant Biology</i> , 2021, 21, 47.	3.6	18
2136	Genomes of Diverse Isolates of <i>Prochlorococcus</i> High-Light-Adapted Clade II in the Western Pacific Ocean. <i>Frontiers in Marine Science</i> , 2021, 7, .	2.5	1
2138	Genome wide identification and expression analysis of pepper C2H2 zinc finger transcription factors in response to anthracnose pathogen <i>Colletotrichum truncatum</i> . <i>3 Biotech</i> , 2021, 11, 118.	2.2	9
2139	Genome-wide search and structural and functional analyses for late embryogenesis-abundant (LEA) gene family in poplar. <i>BMC Plant Biology</i> , 2021, 21, 110.	3.6	18
2140	Protuberances are organized distinct regions of long-term callus: histological and transcriptomic analyses in kiwifruit. <i>Plant Cell Reports</i> , 2021, 40, 637-665.	5.6	6
2141	Identification of a solo acylhomoserine lactone synthase from the myxobacterium <i>Archangium gephyra</i> . <i>Scientific Reports</i> , 2021, 11, 3018.	3.3	4
2142	Evolution, expression and functional analysis of cultivated allotetraploid cotton DIR genes. <i>BMC Plant Biology</i> , 2021, 21, 89.	3.6	13
2144	Synthetic Biology and Computer-Based Frameworks for Antimicrobial Peptide Discovery. <i>ACS Nano</i> , 2021, 15, 2143-2164.	14.6	51
2145	Glycine acylation and trafficking of a new class of bacterial lipoprotein by a composite secretion system. <i>ELife</i> , 2021, 10, .	6.0	7
2147	Molecular characterization of SIATG18f in response to Tomato leaf curl New Delhi virus infection in tomato and development of a CAPS marker for leaf curl disease tolerance. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1463-1474.	3.6	14
2150	Genome-wide characterization of the hyperaccumulator <i>Sedum alfredii</i> F-box family under cadmium stress. <i>Scientific Reports</i> , 2021, 11, 3023.	3.3	3

#	ARTICLE	IF	CITATIONS
2151	Gene function adjustment for carbohydrate metabolism and enrichment of rumen microbiota with antibiotic resistance genes during subacute rumen acidosis induced by a high-grain diet in lactating dairy cows. <i>Journal of Dairy Science</i> , 2021, 104, 2087-2105.	3.4	24
2152	Genome-Wide Characterization of HSP90 Gene Family in Cucumber and Their Potential Roles in Response to Abiotic and Biotic Stresses. <i>Frontiers in Genetics</i> , 2021, 12, 584886.	2.3	9
2153	A Novel Singleton Giant Phage Yong-XC31 Lytic to the Pyropia Pathogen <i>Vibrio mediterranei</i> . <i>Applied Sciences (Switzerland)</i> , 2021, 11, 1602.	2.5	4
2154	Genome sequences of <i>Tropheus moorii</i> and <i>Petrochromis trewavasae</i> , two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. <i>Scientific Reports</i> , 2021, 11, 4309.	3.3	4
2155	Genome-Wide Identification and Characterization of bHLH Transcription Factors Related to Anthocyanin Biosynthesis in Red Walnut ( <i>Juglans regia</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 632509.	2.3	23
2156	Genome-Wide Identification and Evolutionary Analysis of AOMT Gene Family in Pomegranate ( <i>Punica</i> ) Tj ETQq1 1 0.784314 rgBT / Over	3.0	4
2157	Insights into the diversification of subclade IVa bHLH transcription factors in Fabaceae. <i>BMC Plant Biology</i> , 2021, 21, 109.	3.6	1
2159	Developing Innolysins Against <i>Campylobacter jejuni</i> Using a Novel Prophage Receptor-Binding Protein. <i>Frontiers in Microbiology</i> , 2021, 12, 619028.	3.5	24
2160	Ecological Specialization and Evolutionary Reticulation in Extant Hyaenidae. <i>Molecular Biology and Evolution</i> , 2021, 38, 3884-3897.	8.9	15
2161	The legume information system and associated online genomic resources. , 2021, 3, e74.		12
2162	Comparative Genomic Analysis of <i>Mycobacteriaceae</i> Reveals Horizontal Gene Transfer-Mediated Evolution of the CRISPR-Cas System in the <i>Mycobacterium tuberculosis</i> Complex. <i>MSystems</i> , 2021, 6, .	3.8	11
2163	Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. <i>Plant Physiology</i> , 2021, 186, 420-433.	4.8	16
2164	A Single Nucleotide Mutation in a GLUTAMATE RECEPTOR-LIKE Gene Confers Resistance to Fusarium Wilt in <i>Gossypium hirsutum</i> . <i>Advanced Science</i> , 2021, 8, 2002723.	11.2	37
2165	Insights into triterpene synthesis and unsaturated fatty-acid accumulation provided by chromosomal-level genome analysis of <i>Akebia trifoliata</i> subsp. <i>australis</i> . <i>Horticulture Research</i> , 2021, 8, 33.	6.3	23
2166	Jasmonate and abscisic acid-activated AaGSW1-AaTCP15/AaORA transcriptional cascade promotes artemisinin biosynthesis in <i>Artemisia annua</i> . <i>Plant Biotechnology Journal</i> , 2021, 19, 1412-1428.	8.3	45
2167	Genome-wide identification and expression profiling of chitinase genes in tea ( <i>Camellia sinensis</i> (L.) O.) Tj ETQq1 1 0.784314 rgBT / Over	3.1	16
2170	Deciphering the transcriptomic regulation of heat stress responses in <i>Nothofagus pumilio</i> . <i>PLoS ONE</i> , 2021, 16, e0246615.	2.5	6
2172	Genomic-Wide Analysis of the PLC Family and Detection of GmPL-PLC7 Responses to Drought and Salt Stresses in Soybean. <i>Frontiers in Plant Science</i> , 2021, 12, 631470.	3.6	15

#	ARTICLE	IF	CITATIONS
2174	Comparative transcriptomic analysis reveals the cold acclimation during chilling stress in sensitive and resistant passion fruit ( <i>Passiflora edulis</i> ) cultivars. PeerJ, 2021, 9, e10977.	2.0	9
2176	Integrating structure-based machine learning and co-evolution to investigate specificity in plant sesquiterpene synthases. PLoS Computational Biology, 2021, 17, e1008197.	3.2	11
2177	Comparative Analyses of Full-Length Transcriptomes Reveal Gnetum luofuense Stem Developmental Dynamics. Frontiers in Genetics, 2021, 12, 615284.	2.3	8
2178	Phylogeny and evolution of <i>Lasiopodomys</i> in subfamily Arvicolinae based on mitochondrial genomics. PeerJ, 2021, 9, e10850.	2.0	7
2179	Genome-wide identification and expression analysis of the Brassica oleracea L. chitin-binding genes and response to pathogens infections. Planta, 2021, 253, 80.	3.2	9
2180	Additional description and genome analyses of Caenorhabditis auriculariae representing the basal lineage of genus Caenorhabditis. Scientific Reports, 2021, 11, 6720.	3.3	10
2181	Dynamic transcriptome analysis identifies genes related to fatty acid biosynthesis in the seeds of Prunus pedunculata Pall. BMC Plant Biology, 2021, 21, 152.	3.6	2
2182	Genome-Wide Identification of WRKY Gene Family and Expression Analysis under Abiotic Stress in Barley. Agronomy, 2021, 11, 521.	3.0	18
2183	Sulfate transport mutants affect hydrogen sulfide and sulfite production during alcoholic fermentation. Yeast, 2021, 38, 367-381.	1.7	8
2184	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, Harpalus pensylvanicus. Journal of Chemical Ecology, 2021, 47, 334-349.	1.8	0
2185	Adaptation and convergence in circadian-related genes in Iberian freshwater fish. BMC Ecology and Evolution, 2021, 21, 38.	1.6	3
2187	Toward Characterising the Cellular 3D-Proteome. Frontiers in Bioinformatics, 2021, 1, .	2.1	3
2188	Genome-wide identification, characterization, and expression analysis of the NAC transcription factor family in orchardgrass (Dactylis glomerata L.). BMC Genomics, 2021, 22, 178.	2.8	21
2189	A Roadmap for Genome-Based Phage Taxonomy. Viruses, 2021, 13, 506.	3.3	268
2190	Genome-wide identification and expression profiling of basic leucine zipper transcription factors following abiotic stresses in potato (Solanum tuberosum L.). PLoS ONE, 2021, 16, e0247864.	2.5	9
2192	Genome-wide identification of superoxide dismutase gene families and their expression patterns under low-temperature, salt and osmotic stresses in watermelon and melon. 3 Biotech, 2021, 11, 194.	2.2	8
2193	Common Oral Medications Lead to Prophage Induction in Bacterial Isolates from the Human Gut. Viruses, 2021, 13, 455.	3.3	35
2194	Chromosome-level reference genome of the sour sop ( <i>Annona muricata</i> ): A new resource for Magnoliid research and tropical pomology. Molecular Ecology Resources, 2021, 21, 1608-1619.	4.8	18

#	ARTICLE	IF	CITATIONS
2195	Transcriptomic Diversity in the Livers of South African Sardines Participating in the Annual Sardine Run. <i>Genes</i> , 2021, 12, 368.	2.4	2
2196	A Comprehensive Phylogenetic Analysis of the Serpin Superfamily. <i>Molecular Biology and Evolution</i> , 2021, 38, 2915-2929.	8.9	39
2197	Systematic investigation and expression profiles of the GbR2R3-MYB transcription factor family in ginkgo ( <i>Ginkgo biloba</i> L.). <i>International Journal of Biological Macromolecules</i> , 2021, 172, 250-262.	7.5	23
2198	Molecular Characterization, Gene Evolution and Expression Analysis of the F-Box Gene Family in Tomato ( <i>Solanum lycopersicum</i> ). <i>Genes</i> , 2021, 12, 417.	2.4	10
2199	Genome-wide characterization and expression profiling of EIN3/EIL family genes in <i>Zea mays</i> . <i>Plant Gene</i> , 2021, 25, 100270.	2.3	8
2200	The genome of <i>Magnolia biondii</i> Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. <i>Horticulture Research</i> , 2021, 8, 38.	6.3	32
2202	Metagenomic Insights Into Functional and Taxonomic Compositions of an Activated Sludge Microbial Community Treating Leachate of a Completed Landfill: A Pathway-Based Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 640848.	3.5	2
2203	Single individual structural variant detection uncovers widespread hemizyosity in molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200153.	4.0	19
2204	Toxin-antitoxin RNA pairs safeguard CRISPR-Cas systems. <i>Science</i> , 2021, 372, .	12.6	55
2205	Phylogenomic Analyses of Nucleotide-Sugar Biosynthetic and Interconverting Enzymes Illuminate Cell Wall Composition in Fungi. <i>MBio</i> , 2021, 12, .	4.1	4
2206	A Superfamily-wide Activity Atlas of Serine Hydrolases in <i>Drosophila melanogaster</i> . <i>Biochemistry</i> , 2021, 60, 1312-1324.	2.5	18
2207	Prevalence of antibiotic resistance genes and bacterial pathogens along the soil-mangrove root continuum. <i>Journal of Hazardous Materials</i> , 2021, 408, 124985.	12.4	27
2208	Structure-based phylogeny identifies avoralstat as a TMPRSS2 inhibitor that prevents SARS-CoV-2 infection in mice. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	24
2209	Neofunctionalization of a polyploidization-activated cotton long intergenic non-coding RNA <i>DAN1</i> during drought stress regulation. <i>Plant Physiology</i> , 2021, 186, 2152-2168.	4.8	27
2212	Microbial community characterization of shrimp survivors to AHPND challenge test treated with an effective shrimp probiotic ( <i>Vibrio diabolis</i> ). <i>Microbiome</i> , 2021, 9, 88.	11.1	36
2213	A multi-omics approach to lignocellulolytic enzyme discovery reveals a new ligninase activity from <i>Parascedosporium putredinis</i> NO1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
2215	Genomic-, phenotypic-, and toxicity-based safety assessment and probiotic potency of <i>Bacillus coagulans</i> IDCC 1201 isolated from green malt. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, 48, .	3.0	14
2216	Genome-wide identification and expression analysis of the plant specific LIM genes in <i>Gossypium arboreum</i> under phytohormone, salt and pathogen stress. <i>Scientific Reports</i> , 2021, 11, 9177.	3.3	4

#	ARTICLE	IF	CITATIONS
2217	Shared ancestry of core-histone subunits and non-histone plant proteins containing the Histone Fold Motif (HFM). <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2140001.	0.8	2
2219	Transcriptome-based metabolic profiling of flavonoids in <i>Agave lechuguilla</i> waste biomass. <i>Plant Science</i> , 2021, 305, 110748.	3.6	12
2220	Genome-wide identification, evolutionary relationship and expression analysis of AGO, DCL and RDR family genes in tea. <i>Scientific Reports</i> , 2021, 11, 8679.	3.3	11
2221	Genome-wide identification, evolution, and transcriptome-based expression profiling analysis of suppressors of cytokine signaling (SOCS) in grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Aquaculture</i> , 2021, 536, 736484.	3.5	3
2222	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. <i>Microorganisms</i> , 2021, 9, 841.	3.6	36
2223	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .	12.6	91
2225	An Alternative and Conserved Cell Wall Enzyme That Can Substitute for the Lipid II Synthase MurG. <i>MBio</i> , 2021, 12, .	4.1	6
2226	Pathogenic missense protein variants affect different functional pathways and proteomic features than healthy population variants. <i>PLoS Biology</i> , 2021, 19, e3001207.	5.6	13
2227	Integration of early disease-resistance phenotyping, histological characterization, and transcriptome sequencing reveals insights into downy mildew resistance in <i>impatiens</i> . <i>Horticulture Research</i> , 2021, 8, 108.	6.3	5
2228	Advances in Genomics-Based Breeding of Barley: Molecular Tools and Genomic Databases. <i>Agronomy</i> , 2021, 11, 894.	3.0	23
2229	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. <i>Molecular Systems Biology</i> , 2021, 17, e9880.	7.2	33
2230	The Significance of Genotypic Diversity in Coral Competitive Interaction: A Transcriptomic Perspective. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	1
2231	Rengasvirus, a Circular Replication-Associated Protein-Encoding Single-Stranded DNA Virus-Related Genome That Is a Common Contaminant in Metagenomic Data. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
2232	Genome-wide identification and phylogenetic relationships of the Hsp70 gene family of <i>Aegilops tauschii</i> , wild emmer wheat ( <i>Triticum dicoccoides</i> ) and bread wheat ( <i>Triticum aestivum</i> ). <i>3 Biotech</i> , 2021, 11, 301.	2.2	6
2233	Population transcriptomic sequencing reveals allopatric divergence and local adaptation in <i>Pseudotaxus chienii</i> (Taxaceae). <i>BMC Genomics</i> , 2021, 22, 388.	2.8	11
2234	<i>Bremerella alba</i> sp. nov., a novel planctomycete isolated from the surface of the macroalga <i>Fucus spiralis</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126189.	2.8	14
2235	Mechanism of MRX inhibition by Rif2 at telomeres. <i>Nature Communications</i> , 2021, 12, 2763.	12.8	22
2236	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	12.6	128

#	ARTICLE	IF	CITATIONS
2237	Revealing the developmental dynamics in male strobilus transcriptome of <i>Gnetum luofuense</i> using nanopore sequencing technology. <i>Scientific Reports</i> , 2021, 11, 10516.	3.3	6
2238	MyCLADE: a multi-source domain annotation server for sequence functional exploration. <i>Nucleic Acids Research</i> , 2021, 49, W452-W458.	14.5	2
2239	Ketogenic diet-mediated steroid metabolism reprogramming improves the immune microenvironment and myelin growth in spinal cord injury rats according to gene and co-expression network analyses. <i>Aging</i> , 2021, 13, 12973-12995.	3.1	7
2240	Comprehensive genome-wide identification, characterization, and expression profiling of MATE gene family in <i>Nicotiana tabacum</i> . <i>Gene</i> , 2021, 783, 145554.	2.2	12
2241	The <i>Trypanosoma brucei</i> subpellicular microtubule array is organized into functionally discrete subdomains defined by microtubule associated proteins. <i>PLoS Pathogens</i> , 2021, 17, e1009588.	4.7	13
2243	Genome-resolved metagenomics suggests a mutualistic relationship between <i>Mycoplasma</i> and salmonid hosts. <i>Communications Biology</i> , 2021, 4, 579.	4.4	55
2244	Covariation of the Fecal Microbiome with Diet in Nonpasserine Birds. <i>MSphere</i> , 2021, 6, .	2.9	22
2245	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. <i>Gastroenterology</i> , 2021, 160, 2089-2102.e12.	1.3	45
2246	Polysaccharide utilization loci-driven enzyme discovery reveals BD-FAE: a bifunctional feruloyl and acetyl xylan esterase active on complex natural xylans. <i>Biotechnology for Biofuels</i> , 2021, 14, 127.	6.2	10
2247	Aux/IAA and ARF Gene Families in <i>Salix suchowensis</i> : Identification, Evolution, and Dynamic Transcriptome Profiling During the Plant Growth Process. <i>Frontiers in Plant Science</i> , 2021, 12, 666310.	3.6	12
2248	Absence of CG methylation alters the long noncoding transcriptome landscape in multiple species. <i>FEBS Letters</i> , 2021, 595, 1734-1747.	2.8	4
2249	RiPPMiner-Genome: A Web Resource for Automated Prediction of Crosslinked Chemical Structures of RiPPs by Genome Mining. <i>Journal of Molecular Biology</i> , 2021, 433, 166887.	4.2	19
2251	Gene Ontology Meta Annotator for Plants (GOMAP). <i>Plant Methods</i> , 2021, 17, 54.	4.3	21
2252	Microbiomes in supragingival biofilms and saliva of adolescents with gingivitis and gingival health. <i>Oral Diseases</i> , 2022, 28, 2000-2014.	3.0	7
2253	Genome-wide analysis of the serine carboxypeptidase-like protein family in <i>Triticum aestivum</i> reveals TaSCPL184-6D is involved in abiotic stress response. <i>BMC Genomics</i> , 2021, 22, 350.	2.8	24
2254	Analysis of diverse eukaryotes suggests the existence of an ancestral mitochondrial apparatus derived from the bacterial type II secretion system. <i>Nature Communications</i> , 2021, 12, 2947.	12.8	19
2255	Protein Structure Prediction: Conventional and Deep Learning Perspectives. <i>Protein Journal</i> , 2021, 40, 522-544.	1.6	36
2257	Genome-wide identification and analysis of cytokinin dehydrogenase/oxidase (CKX) family genes in <i>Brassica oleracea</i> L. reveals their involvement in response to <i>Plasmodiophora brassicae</i> infections. <i>Horticultural Plant Journal</i> , 2022, 8, 68-80.	5.0	15



#	ARTICLE	IF	CITATIONS
2258	Anaerobic Sulfur Oxidation Underlies Adaptation of a Chemosynthetic Symbiont to Oxic-Anoxic Interfaces. <i>MSystems</i> , 2021, 6, e0118620.	3.8	10
2259	Genome-wide in silico identification and characterization of sodium-proton (Na <sup>+</sup> /H <sup>+</sup> ) antiporters in <i>Indica</i> rice. <i>Plant Gene</i> , 2021, 26, 100280.	2.3	9
2260	Degradation of ester linkages in rice straw components by <i>Sphingobium</i> species recovered from the sea bottom using a non- $\alpha$ -secretory tannase family I $\alpha$ /I $\beta$ hydrolase. <i>Environmental Microbiology</i> , 2021, 23, 4151-4167.	3.8	0
2261	Low nitrogen availability inhibits the phosphorus starvation response in maize ( <i>Zea mays</i> ssp. <i>mays</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 259.	3.6	16
2263	Transcriptome analysis during early regeneration of <i>Lumbriculus variegatus</i> . <i>Gene Reports</i> , 2021, 23, 101050.	0.8	7
2264	A hierarchical deep learning based approach for multi-functional enzyme classification. <i>Protein Science</i> , 2021, 30, 1935-1945.	7.6	8
2265	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	8.3	50
2266	SIRT6 transcriptionally regulates fatty acid transport by suppressing PPAR $\gamma$ <sup>3</sup> . <i>Cell Reports</i> , 2021, 35, 109190.	6.4	35
2267	Genome-Wide Identification and Genetic Variations of the Starch Synthase Gene Family in Rice. <i>Plants</i> , 2021, 10, 1154.	3.5	12
2269	<i>Acinetobacter baumannii</i> Fatty Acid Desaturases Facilitate Survival in Distinct Environments. <i>ACS Infectious Diseases</i> , 2021, 7, 2221-2228.	3.8	9
2270	Tentacle Morphological Variation Coincides with Differential Expression of Toxins in Sea Anemones. <i>Toxins</i> , 2021, 13, 452.	3.4	12
2271	Arabinogalactan-proteins from non-coniferous gymnosperms have unusual structural features. <i>Carbohydrate Polymers</i> , 2021, 261, 117831.	10.2	11
2272	Assessing Biosynthetic Gene Cluster Diversity of Specialized Metabolites in the Conserved Gut Symbionts of Herbivorous Turtle Ants. <i>Frontiers in Microbiology</i> , 2021, 12, 678100.	3.5	10
2274	<i>RAPID</i> omics v2.0: going deeper and wider in the prediction of protein-RNA interactions. <i>Nucleic Acids Research</i> , 2021, 49, W72-W79.	14.5	79
2275	Genome-wide identification and expression analysis of LBD transcription factor genes in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>BMC Plant Biology</i> , 2021, 21, 296.	3.6	24
2276	MULTICOM2 open-source protein structure prediction system powered by deep learning and distance prediction. <i>Scientific Reports</i> , 2021, 11, 13155.	3.3	0
2278	How Deep Learning Tools Can Help Protein Engineers Find Good Sequences. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6440-6450.	2.6	7
2279	The Pleistocene species pump past its prime: Evidence from European butterfly sister species. <i>Molecular Ecology</i> , 2021, 30, 3575-3589.	3.9	35

#	ARTICLE	IF	CITATIONS
2282	Copper binding by a unique family of metalloproteins is dependent on kynurenine formation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	8
2283	Chromosome-Scale Genome Assembly of the Resurrection Plant <i>Acanthochlamys bracteata</i> (Velloziaceae). Genome Biology and Evolution, 2021, 13, .	2.5	6
2284	Comparative analyses of transcriptional responses of <i>Dectes texanus</i> LeConte (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 T 11448.	3.3	6
2285	Nutrient Loading and Viral Memory Drive Accumulation of Restriction Modification Systems in Bloom-Forming Cyanobacteria. MBio, 2021, 12, e0087321.	4.1	7
2287	Learning the protein language: Evolution, structure, and function. Cell Systems, 2021, 12, 654-669.e3.	6.2	194
2288	Genome-wide characterization, evolution, and expression profiling of FBA gene family in response to light treatments and abiotic stress in <i>Nicotiana tabacum</i> . Plant Signaling and Behavior, 2021, 16, 1938442.	2.4	6
2289	Differential responses of anthers of stress tolerant and sensitive wheat cultivars to high temperature stress. Planta, 2021, 254, 4.	3.2	14
2290	Trajectories of Homoeolog-Specific Expression in Allotetraploid <i>Tragopogon castellanus</i> Populations of Independent Origins. Frontiers in Plant Science, 2021, 12, 679047.	3.6	3
2291	Exploring Codon Adjustment Strategies towards Escherichia coli-Based Production of Viral Proteins Encoded by HTH1, a Novel Prophage of the Marine Bacterium <i>Hypnocyclicus thermotrophus</i> . Viruses, 2021, 13, 1215.	3.3	3
2292	Genome-Wide Identification of Soybean ABC Transporters Relate to Aluminum Toxicity. International Journal of Molecular Sciences, 2021, 22, 6556.	4.1	19
2293	MiMiC: a bioinformatic approach for generation of synthetic communities from metagenomes. Microbial Biotechnology, 2021, 14, 1757-1770.	4.2	12
2294	S2L-PSIBLAST: a supervised two-layer search framework based on PSI-BLAST for protein remote homology detection. Bioinformatics, 2021, 37, 4321-4327.	4.1	7
2295	Interkingdom Gut Microbiome and Resistome of the Cockroach <i>Blattella germanica</i> . MSystems, 2021, 6, .	3.8	13
2296	Development and Interrogation of a Transcriptomic Resource for the Giant Triton Snail ( <i>Charonia</i> Tj ETQq1 1 0.784314 rgBT /Overlock 2.4 6	2.4	6
2297	Genome-wide identification and expression analysis of the bHLH transcription factor family and its response to abiotic stress in sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. BMC Genomics, 2021, 22, 415.	2.8	29
2298	Comprehensive analysis of structural, functional, and evolutionary dynamics of Leucine Rich Repeats-RLKs in <i>Thinopyrum elongatum</i> . International Journal of Biological Macromolecules, 2021, 183, 513-527.	7.5	14
2299	Computational and Synthetic Biology Approaches for the Biosynthesis of Antiviral and Anticancer Terpenoids from <i>Bacillus subtilis</i> . Medicinal Chemistry, 2022, 18, 307-322.	1.5	1
2301	Genome wide identification, classification and functional characterization of heat shock transcription factors in cultivated and ancestral cottons ( <i>Gossypium</i> spp.). International Journal of Biological Macromolecules, 2021, 182, 1507-1527.	7.5	11

#	ARTICLE	IF	CITATIONS
2302	Genome-wide identification of heat shock transcription factors and potential role in regulation of antioxidant response under hot water and glycine betaine treatments in cold-stored peaches. Journal of the Science of Food and Agriculture, 2022, 102, 628-643.	3.5	10
2303	Genome-Wide Identification and Expression Analysis of the Î²-Amylase Gene Family in <i>Chenopodium quinoa</i> . DNA and Cell Biology, 2021, 40, 936-948.	1.9	4
2304	<i>Lysobacter enzymogenes</i> antagonizes soilborne bacteria using the type IV secretion system. Environmental Microbiology, 2021, 23, 4673-4688.	3.8	18
2305	Generation of Self-Inhibitory Recombinant Viral Hemorrhagic Septicemia Virus (VHSV) by Insertion of Viral P Gene-Targeting Artificial MicroRNA into Viral Genome and Effect of Dicer Gene Knockout on the Recombinant VHSV Replication. Marine Biotechnology, 2021, 23, 546-559.	2.4	3
2306	Characterization of a member of the CEACAM protein family as a novel marker of proton pump-rich ionocytes on the zebrafish epidermis. PLoS ONE, 2021, 16, e0254533.	2.5	5
2307	Biosynthetic potential of uncultured Antarctic soil bacteria revealed through long-read metagenomic sequencing. ISME Journal, 2022, 16, 101-111.	9.8	40
2308	Improving protein tertiary structure prediction by deep learning and distance prediction in CASP14. Proteins: Structure, Function and Bioinformatics, 2022, 90, 58-72.	2.6	18
2309	Genome-wide Identification and Expression Analysis of NAC Transcription Factor Family Genes during Fruit and Kernel Development in Siberian Apricot. Journal of the American Society for Horticultural Science, 2021, 146, 276-285.	1.0	2
2310	Pathogenic and Indigenous Denitrifying Bacteria are Transcriptionally Active and Key Multi-Antibiotic-Resistant Players in Wastewater Treatment Plants. Environmental Science & Technology, 2021, 55, 10862-10874.	10.0	60
2312	Structural and evolutionary exploration of the IL-3 family and its alpha subunit receptors. Amino Acids, 2021, 53, 1211-1227.	2.7	3
2313	Unveiling the keratinolytic transcriptome of the black carpet beetle ( <i>Attagenus unicolor</i> ) for sustainable poultry feather recycling. Applied Microbiology and Biotechnology, 2021, 105, 5577-5587.	3.6	1
2314	Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily. Cell, 2021, 184, 3660-3673.e18.	28.9	58
2315	<i>Curv virga aplysinae</i> gen. nov., sp. nov., a marine bacterium isolated from the sea sponge <i>Aplysina fistularis</i> . International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	8
2316	Chromosomal-scale genome assembly of <i>Eleutherococcus senticosus</i> provides insights into chromosome evolution in Araliaceae. Molecular Ecology Resources, 2021, 21, 2204-2220.	4.8	10
2317	Structural basis of the membrane intramolecular transacylase reaction responsible for lyso-form lipoprotein synthesis. Nature Communications, 2021, 12, 4254.	12.8	6
2318	The chromosome-level reference genome assembly for <i>Dendrobium officinale</i> and its utility of functional genomics research and molecular breeding study. Acta Pharmaceutica Sinica B, 2021, 11, 2080-2092.	12.0	54
2319	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. Frontiers in Plant Science, 2021, 12, 668623.	3.6	18
2320	Holocene life and microbiome profiling in ancient tropical Lake Chalco, Mexico. Scientific Reports, 2021, 11, 13848.	3.3	8

#	ARTICLE	IF	CITATIONS
2322	The complete mitochondrial genome of <i>Cycas debaoensis</i> revealed unexpected static evolution in gymnosperm species. <i>PLoS ONE</i> , 2021, 16, e0255091.	2.5	6
2323	Parallel functional reduction in the mitochondria of apicomplexan parasites. <i>Current Biology</i> , 2021, 31, 2920-2928.e4.	3.9	26
2324	Complete genome sequence and phylogenomic analysis of the first N4-like lytic bacteriophage vB_Ppp_A38 (fA38) infecting <i>Pectobacterium parmentieri</i> . <i>European Journal of Plant Pathology</i> , 2021, 161, 483-489.	1.7	2
2325	Draft genome of <i>Puya raimondii</i> (Bromeliaceae), the Queen of the Andes. <i>Genomics</i> , 2021, 113, 2537-2546.	2.9	4
2326	Metatranscriptomic Analysis of Bacterial Communities on Laundered Textiles: A Pilot Case Study. <i>Microorganisms</i> , 2021, 9, 1591.	3.6	5
2327	<i>Serendipita</i> Fungi Modulate the Switchgrass Root Transcriptome to Circumvent Host Defenses and Establish a Symbiotic Relationship. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1128-1142.	2.6	6
2328	Genome-Wide Analysis and Functional Characterization of the UDP-Glycosyltransferase Family in Grapes. <i>Horticulturae</i> , 2021, 7, 204.	2.8	11
2329	De novo transcriptome analysis of white teak ( <i>Gmelina arborea</i> Roxb) wood reveals critical genes involved in xylem development and secondary metabolism. <i>BMC Genomics</i> , 2021, 22, 494.	2.8	1
2330	Genome-wide analysis and expression patterns of lipid phospholipid phospholipase gene family in <i>Brassica napus</i> L.. <i>BMC Genomics</i> , 2021, 22, 548.	2.8	13
2331	A phylogeny-aware approach reveals unexpected venom components in divergent lineages of cone snails. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211017.	2.6	7
2332	Genome-wide identification, expression analysis, and functional study of the GRAS transcription factor family and its response to abiotic stress in sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. <i>BMC Genomics</i> , 2021, 22, 509.	2.8	28
2333	CASPredict: a web service for identifying Cas proteins. <i>PeerJ</i> , 2021, 9, e11887.	2.0	8
2334	Metabolic Adaptations to Marine Environments: Molecular Diversity and Evolution of Ovothiol Biosynthesis in Bacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	9
2335	Transcriptional profiling analysis of susceptible and resistant strains of <i>Anticarsia gemmatalis</i> and their response to <i>Bacillus thuringiensis</i> . <i>Genomics</i> , 2021, 113, 2264-2275.	2.9	8
2336	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. <i>ISME Journal</i> , 2022, 16, 307-320.	9.8	71
2337	Diverse evolutionary origins of microbial [4 + 2]-cyclases in natural product biosynthesis. <i>International Journal of Biological Macromolecules</i> , 2021, 182, 154-161.	7.5	3
2338	Genome-wide identification of the MIOX gene family and their expression profile in cotton development and response to abiotic stress. <i>PLoS ONE</i> , 2021, 16, e0254111.	2.5	9
2339	Metabolic potential and survival strategies of microbial communities across extreme temperature gradients on Deception Island volcano, Antarctica. <i>Environmental Microbiology</i> , 2021, 23, 4054-4073.	3.8	7

#	ARTICLE	IF	CITATIONS
2340	Genetic and phylogenetic analysis of dissimilatory iodate-reducing bacteria identifies potential niches across the world's oceans. ISME Journal, 2022, 16, 38-49.	9.8	21
2341	An Ecological Basis for Dual Genetic Code Expansion in Marine Deltaproteobacteria. Frontiers in Microbiology, 2021, 12, 680620.	3.5	4
2342	Transporter characterisation reveals aminoethylphosphonate mineralisation as a key step in the marine phosphorus redox cycle. Nature Communications, 2021, 12, 4554.	12.8	21
2343	The Novel Sequence Distance Measuring Algorithm Based on Optimal Transport and Cross-Attention Mechanism. Shock and Vibration, 2021, 2021, 1-10.	0.6	1
2344	DiTing: A Pipeline to Infer and Compare Biogeochemical Pathways From Metagenomic and Metatranscriptomic Data. Frontiers in Microbiology, 2021, 12, 698286.	3.5	21
2345	Functional diversity of isoprenoid lipids in <i>Methylobacterium extorquens</i> PA1. Molecular Microbiology, 2021, 116, 1064-1078.	2.5	12
2346	The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. Microorganisms, 2021, 9, 1704.	3.6	5
2347	A New Contact Killing Toxin Permeabilizes Cells and Belongs to a Broadly Distributed Protein Family. MSphere, 2021, 6, e0031821.	2.9	5
2348	Pan-Genome of Novel <i>Pantoea stewartii</i> subsp. <i>indologenes</i> Reveals Genes Involved in Onion Pathogenicity and Evidence of Lateral Gene Transfer. Microorganisms, 2021, 9, 1761.	3.6	5
2349	Genome-wide analysis of HECT E3 ubiquitin ligase gene family in <i>Solanum lycopersicum</i> . Scientific Reports, 2021, 11, 15891.	3.3	10
2350	High-Quality Complete Genome Resource of Pathogenic Bacterium <i>Pectobacterium atrosepticum</i> Strain Green1 Isolated from Potato ( <i>Solanum tuberosum</i> L.) in Greenland. Molecular Plant-Microbe Interactions, 2021, 34, 1328-1333.	2.6	0
2351	Genome-wide identification and analysis of the heat shock transcription factor family in moso bamboo ( <i>Phyllostachys edulis</i> ). Scientific Reports, 2021, 11, 16492.	3.3	23
2353	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. Microbial Genomics, 2021, 7, .	2.0	9
2354	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. Frontiers in Microbiology, 2021, 12, 666558.	3.5	8
2355	Hb adaptation to hypoxia in high-altitude fishes: Fresh evidence from schizothoracinae fishes in the Qinghai-Tibetan Plateau. International Journal of Biological Macromolecules, 2021, 185, 471-484.	7.5	8
2356	Captive Common Marmosets ( <i>Callithrix jacchus</i> ) Are Colonized throughout Their Lives by a Community of <i>Bifidobacterium</i> Species with Species-Specific Genomic Content That Can Support Adaptation to Distinct Metabolic Niches. MBio, 2021, 12, e0115321.	4.1	8
2357	Data on the first functionally-annotated de novo transcriptome assembly for North American flying squirrels (genus <i>Glaucomys</i> ). Data in Brief, 2021, 37, 107267.	1.0	1
2358	ViralFP: A Web Application of Viral Fusion Proteins. Frontiers in Medical Technology, 2021, 3, 722392.	2.5	2

#	ARTICLE	IF	CITATIONS
2360	Does Differential Receptor Distribution Underlie Variable Responses to a Neuropeptide in the Lobster Cardiac System?. International Journal of Molecular Sciences, 2021, 22, 8703.	4.1	0
2361	Genome-wide identification and function analysis of HMAD gene family in cotton ( <i>Gossypium</i> spp.). BMC Plant Biology, 2021, 21, 386.	3.6	4
2362	Diatoms and Plants Acyl-CoA:lysophosphatidylcholine Acyltransferases (LPCATs) Exhibit Diverse Substrate Specificity and Biochemical Properties. International Journal of Molecular Sciences, 2021, 22, 9056.	4.1	6
2363	Full-length transcriptome analysis of <i>Spodoptera frugiperda</i> larval brain reveals detoxification genes. PeerJ, 2021, 9, e12069.	2.0	6
2364	Genomic divergence and differential gene expression between crustacean ecotypes across a marine thermal gradient. Marine Genomics, 2021, 58, 100847.	1.1	1
2365	Identification of C2H2 subfamily ZAT genes in <i>Gossypium</i> species reveals GhZAT34 and GhZAT79 enhanced salt tolerance in <i>Arabidopsis</i> and cotton. International Journal of Biological Macromolecules, 2021, 184, 967-980.	7.5	18
2366	Characterization and comparative analysis of transcriptional profiles of porcine colostrum and mature milk at different parities. BMC Genomic Data, 2021, 22, 25.	1.7	3
2367	Genome-wide detection and classification of terpene synthase genes in <i>Aquilaria agallochum</i> . Physiology and Molecular Biology of Plants, 2021, 27, 1711-1729.	3.1	10
2368	Diverse Bacteriophages Infecting the Bacterial Striped Catfish Pathogen <i>Edwardsiella ictaluri</i> . Microorganisms, 2021, 9, 1830.	3.6	2
2370	Molecular characteristics of <i>S-RNase</i> alleles as the determinant of self-incompatibility in the style of <i>Fragaria viridis</i> . Horticulture Research, 2021, 8, 185.	6.3	17
2371	Genome Analysis of <i>Phytophthora nicotianae</i> JM01 Provides Insights into Its Pathogenicity Mechanisms. Plants, 2021, 10, 1620.	3.5	4
2372	Genome-wide identification and expression analysis revealed cinnamyl alcohol dehydrogenase genes correlated with fruit-firmness in strawberry1. Journal of Berry Research, 2021, 11, 447-464.	1.4	6
2373	Genome-Wide Identification, Phylogenetic and Expression Pattern Analysis of GATA Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). Plants, 2021, 10, 1626.	3.5	11
2375	<i>Schumannella soli</i> sp. nov., a novel actinomycete isolated from mangrove soil by in situ cultivation. Antonie Van Leeuwenhoek, 2021, 114, 1657-1667.	1.7	7
2376	High-quality evergreen azalea genome reveals tandem duplication-facilitated low-altitude adaptability and floral scent evolution. Plant Biotechnology Journal, 2021, 19, 2544-2560.	8.3	35
2377	Genome wide analysis of IQD gene family in diploid and tetraploid species of cotton ( <i>Gossypium</i> spp.). International Journal of Biological Macromolecules, 2021, 184, 1035-1061.	7.5	7
2378	Analyses of open-access multi-omics data sets reveal genetic and expression characteristics of maize <i>ZmCCT</i> family genes. AoB PLANTS, 2021, 13, plab048.	2.3	1
2379	Comparison of gene expression in the red imported fire ant ( <i>Solenopsis invicta</i> ) under different temperature conditions. Scientific Reports, 2021, 11, 16476.	3.3	8



#	ARTICLE	IF	CITATIONS
2380	JA signal-mediated immunity of <i>Dendrobium catenatum</i> to necrotrophic Southern Blight pathogen. <i>BMC Plant Biology</i> , 2021, 21, 360.	3.6	9
2381	Enzyme engineering and <i>in vivo</i> testing of a formate reduction pathway. <i>Synthetic Biology</i> , 2021, 6, ysab020.	2.2	7
2382	Evolution of pectin synthesis relevant galacturonosyltransferase gene family and its expression during cotton fiber development. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	3
2383	The DUF221 domain-containing (DDP) genes identification and expression analysis in tomato under abiotic and phytohormone stress. <i>GM Crops and Food</i> , 2021, 12, 586-599.	3.8	5
2384	Comprehensive analysis of KCS gene family in Citrinae reveals the involvement of CsKCS2 and CsKCS11 in fruit cuticular wax synthesis at ripening. <i>Plant Science</i> , 2021, 310, 110972.	3.6	18
2385	FunOrder: A robust and semi-automated method for the identification of essential biosynthetic genes through computational molecular co-evolution. <i>PLoS Computational Biology</i> , 2021, 17, e1009372.	3.2	9
2387	In silico integrative analysis for the characterization of LYT1 a unique protein of <i>Trypanosoma cruzi</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-7.	3.5	0
2388	Functional characterization of a cellulose synthase, CtCESA1, from the marine red alga <i>Calliarthron tuberculatum</i> (Corallinales). <i>Journal of Experimental Botany</i> , 2021, , .	4.8	4
2389	Depletion of a <i>Toxoplasma</i> porin leads to defects in mitochondrial morphology and contacts with the endoplasmic reticulum. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	17
2390	Key <i>auxin response factor</i> (ARF) genes constraining wheat tillering of mutant <i>dmc</i> . <i>PeerJ</i> , 2021, 9, e12221.	2.0	10
2391	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	2.9	34
2392	Cyclic nucleotide gated channel genes (CNGCs) in Rosaceae: genome-wide annotation, evolution and the roles on Valsa canker resistance. <i>Plant Cell Reports</i> , 2021, 40, 2369-2382.	5.6	10
2394	Up-regulation of apoptotic- and cell survival-related gene pathways following exposures of western corn rootworm to <i>B. thuringiensis</i> crystalline pesticidal proteins in transgenic maize roots. <i>BMC Genomics</i> , 2021, 22, 639.	2.8	4
2395	Genome-Wide Identification and Analysis of the Metallothionein Genes in <i>Oryza</i> Genus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9651.	4.1	8
2396	Genomic Analyses of <i>Penicillium</i> Species Have Revealed Patulin and Citrinin Gene Clusters and Novel Loci Involved in Oxylipin Production. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 743.	3.5	6
2398	Prokaryotic viruses impact functional microorganisms in nutrient removal and carbon cycle in wastewater treatment plants. <i>Nature Communications</i> , 2021, 12, 5398.	12.8	49
2399	Genome-wide identification and transcriptome-based expression profiling of the <i>Sox</i> gene family in the spinyhead croaker ( <i>Collichthys lucidus</i> ). <i>Journal of Fish Biology</i> , 2022, 100, 15-24.	1.6	4
2400	De Novo Transcriptome Assembly, Functional Annotation, and Transcriptome Dynamics Analyses Reveal Stress Tolerance Genes in Mangrove Tree ( <i>Bruguiera gymnorhiza</i> ). <i>International Journal of Molecular Sciences</i> , 2021, 22, 9874.	4.1	3



#	ARTICLE	IF	CITATIONS
2401	Large-scale gene gains and losses molded the NLR defense arsenal during the Cucurbita evolution. <i>Planta</i> , 2021, 254, 82.	3.2	6
2402	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	8.3	18
2403	De novo transcriptome assembly, polymorphic SSR markers development and population genetics analyses for southern corn rust ( <i>Puccinia polysora</i> ). <i>Scientific Reports</i> , 2021, 11, 18029.	3.3	3
2404	Proteomic Tools for the Analysis of Proteins. <i>Methods in Molecular Biology</i> , 2022, 2364, 363-425.	0.9	1
2405	Genomics-informed insights into microbial degradation of N,N-dimethylformamide. <i>International Biodeterioration and Biodegradation</i> , 2021, 163, 105283.	3.9	10
2406	Genome-Wide Identification and Expression Analysis of AP2/EREBP Transcription Factors in Litchi ( <i>Litchi chinensis</i> Sonn.). <i>Tropical Plant Biology</i> , 2021, 14, 381.	1.9	0
2408	High-Quality Complete Genome Resource of Plant-Pathogenic Bacterium <i>Dickeya solani</i> IPO 2019, Isolated from <i>Hyacinthus orientalis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1088-1092.	2.6	1
2409	Characterization of Annexin gene family and functional analysis of RsANN1a involved in heat tolerance in radish ( <i>Raphanus sativus</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2027-2041.	3.1	9
2410	Mechanistic insights into the success of xenobiotic degraders resolved from metagenomes of microbial enrichment cultures. <i>Journal of Hazardous Materials</i> , 2021, 418, 126384.	12.4	10
2412	Genome-Wide Identification and Evolutionary Analysis of the SRO Gene Family in Tomato. <i>Frontiers in Genetics</i> , 2021, 12, 753638.	2.3	10
2413	PASS: Protein Annotation Surveillance Site for Protein Annotation Using Homologous Clusters, NLP, and Sequence Similarity Networks. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	0
2414	Full-length transcriptome analysis and identification of transcript structures in <i>Eimeria necatrix</i> from different developmental stages by single-molecule real-time sequencing. <i>Parasites and Vectors</i> , 2021, 14, 502.	2.5	6
2416	The time course of molecular acclimation to seawater in a euryhaline fish. <i>Scientific Reports</i> , 2021, 11, 18127.	3.3	9
2417	StAR-Related Lipid Transfer (START) Domains Across the Rice Pangenome Reveal How Ontogeny Recapitulated Selection Pressures During Rice Domestication. <i>Frontiers in Genetics</i> , 2021, 12, 737194.	2.3	2
2418	Genome-wide identification and molecular evolution analysis of the heat shock transcription factor (HSF) gene family in four diploid and two allopolyploid <i>Gossypium</i> species. <i>Genomics</i> , 2021, 113, 3112-3127.	2.9	13
2420	When homologous sequences meet structural decoys: Accurate contact prediction by $\langle \text{tFold} \rangle$ in $\langle \text{CASP14} \rangle$ ( $\langle \text{tFold} \rangle$ for $\langle \text{CASP14} \rangle$ contact) Tj ETQq1 1 0.78414 rgB4 Overlook	2.1	1
2421	Full-length sequencing of <i>Ginkgo biloba</i> L. reveals the synthesis of terpenoids during seed development. <i>Industrial Crops and Products</i> , 2021, 170, 113714.	5.2	10
2422	Sesquiterpene biosynthesis in a leafy liverwort <i>Radula lindenbergiana</i> Gottsche ex C. Hartm. <i>Phytochemistry</i> , 2021, 190, 112847.	2.9	5

#	ARTICLE	IF	CITATIONS
2423	Genome-wide identification and analysis of promising GDSL-type lipases related to gummy stem blight resistance in watermelon ( <i>Citrullus lanatus</i> ). <i>Scientia Horticulturae</i> , 2021, 289, 110461.	3.6	4
2424	Strain-level multiomics analysis reveals significant variation in cheeses from different regions. <i>LWT - Food Science and Technology</i> , 2021, 151, 112043.	5.2	17
2425	Testes morphology and the identification of transcripts of the hormonal pathways of the velvetbean caterpillar <i>Anticarsia gemmatilis</i> Hübner, 1818 (Lepidoptera: Erebidæ). <i>Arthropod Structure and Development</i> , 2021, 65, 101111.	1.4	1
2426	Identification of a novel circovirus in blood sample of giant pandas ( <i>Ailuropoda melanoleuca</i> ). <i>Infection, Genetics and Evolution</i> , 2021, 95, 105077.	2.3	4
2427	Polyketide synthase genes and molecular trade-offs in the ichthyotoxic species <i>Prymnesium parvum</i> . <i>Science of the Total Environment</i> , 2021, 795, 148878.	8.0	10
2428	Identification of grape H3K4 genes and their expression profiles during grape fruit ripening and postharvest ROS treatment. <i>Genomics</i> , 2021, 113, 3793-3803.	2.9	2
2429	Genome-wide analysis of the MADS-box gene family in <i>Rhododendron hainanense</i> Merr. and expression analysis under heat and waterlogging stresses. <i>Industrial Crops and Products</i> , 2021, 172, 114007.	5.2	20
2430	A haploid diamondback moth ( <i>Plutella xylostella</i> L.) genome assembly resolves 31 chromosomes and identifies a diamide resistance mutation. <i>Insect Biochemistry and Molecular Biology</i> , 2021, 138, 103622.	2.7	19
2431	Biosynthesis and emission of methyl hexanoate, the major constituent of floral scent of a night-blooming water lily <i>Victoria cruziana</i> . <i>Phytochemistry</i> , 2021, 191, 112899.	2.9	4
2432	Identification of novel membrane proteins for improved lignocellulose conversion. <i>Current Opinion in Biotechnology</i> , 2022, 73, 198-204.	6.6	2
2433	Exploring the global metagenome for plastic-degrading enzymes. <i>Methods in Enzymology</i> , 2021, 648, 137-157.	1.0	16
2435	Predicted Structural Variability of <i>Mycobacterium tuberculosis</i> PPE18 Protein With Immunological Implications Among Clinical Strains. <i>Frontiers in Microbiology</i> , 2020, 11, 595312.	3.5	4
2436	Pearl Sac Gene Expression Profiles Associated With Pearl Attributes in the Silver-Lip Pearl Oyster, <i>Pinctada maxima</i> . <i>Frontiers in Genetics</i> , 2020, 11, 597459.	2.3	11
2437	Multi-responses of O-methyltransferase genes to salt stress and fiber development of <i>Gossypium</i> species. <i>BMC Plant Biology</i> , 2021, 21, 37.	3.6	16
2438	Mapping genomes by using bioinformatics data and tools. , 2021, , 245-278.		3
2439	Heat shock protein 70 (Hsp70) and heat shock transcription factor (Hsf) gene families in <i>Cynoglossus semilaevis</i> : genome-wide identification and correlation analysis in response to low salinity stress. <i>Marine and Freshwater Research</i> , 2021, 72, 1132.	1.3	2
2440	Comprehensive identification and expression analysis of. <i>Functional Plant Biology</i> , 2021, 48, 1039-1052.	2.1	8
2441	Comprehensive analysis of full-length transcriptomes of <i>Schizothorax prenanti</i> by single-molecule long-read sequencing. <i>Genomics</i> , 2022, 114, 456-464.	2.9	14

#	ARTICLE	IF	CITATIONS
2443	Genome-Wide Mining of Disease Resistance Gene Analogs Using Conserved Domains. <i>Methods in Molecular Biology</i> , 2020, 2107, 365-375.	0.9	1
2444	The Clustal Omega Multiple Alignment Package. <i>Methods in Molecular Biology</i> , 2021, 2231, 3-16.	0.9	144
2445	Large-Scale Multiple Sequence Alignment and Phylogeny Estimation. <i>Computational Biology</i> , 2013, , 85-146.	0.2	14
2446	The MULTICOM Protein Tertiary Structure Prediction System. <i>Methods in Molecular Biology</i> , 2014, 1137, 29-41.	0.9	8
2447	De Novo Membrane Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2015, 1215, 331-350.	0.9	7
2448	Fundamentals of Comparative Genome Analysis in <i>Caenorhabditis</i> Nematodes. <i>Methods in Molecular Biology</i> , 2015, 1327, 11-21.	0.9	3
2449	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2016, 1374, 293-337.	0.9	7
2450	HMMs in Protein Fold Classification. <i>Methods in Molecular Biology</i> , 2017, 1552, 13-27.	0.9	2
2451	Coevolutionary Analysis of Protein Sequences for Molecular Modeling. <i>Methods in Molecular Biology</i> , 2019, 2022, 379-397.	0.9	7
2452	Clustal Omega, Accurate Alignment of Very Large Numbers of Sequences. <i>Methods in Molecular Biology</i> , 2014, 1079, 105-116.	0.9	980
2453	Deducing Intracellular Distributions of Metabolic Pathways from Genomic Data. <i>Methods in Molecular Biology</i> , 2014, 1083, 187-211.	0.9	12
2454	Exploiting Complex Protein Domain Networks for Protein Function Annotation. <i>Studies in Computational Intelligence</i> , 2019, , 598-610.	0.9	7
2455	The Statistical Analysis of Protein Domain Family Distributions via Jaccard Entropy Measures. , 2020, , 169-207.		3
2456	<i>Pochonia chlamydosporia</i> : Multitrophic Lifestyles Explained by a Versatile Genome. , 2017, , 197-207.		7
2457	OWL-DL Domain-Models as Abstract Workflows. <i>Lecture Notes in Computer Science</i> , 2012, , 56-66.	1.3	6
2458	A recombinant infectious bronchitis virus from a chicken with a spike gene closely related to that of a turkey coronavirus. <i>Archives of Virology</i> , 2020, 165, 703-707.	2.1	19
2459	Systematic analysis of the OFP genes in six Rosaceae genomes and their roles in stress response in Chinese pear ( <i>Pyrus bretschneideri</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2085-2094.	3.1	8
2460	Transcriptome analysis in <i>Parhyale hawaiiensis</i> reveal sex-specific responses to AgNP and AgCl exposure. <i>Environmental Pollution</i> , 2020, 260, 113963.	7.5	13

#	ARTICLE	IF	CITATIONS
2461	Transcriptome profiling of the floral buds and discovery of genes related to sex-differentiation in the dioecious cucurbit <i>Coccinia grandis</i> (L.) Voigt. <i>Gene</i> , 2017, 626, 395-406.	2.2	20
2462	The identification of an R2R3-MYB transcription factor involved in regulating anthocyanin biosynthesis in <i>Primulina swinglei</i> flowers. <i>Gene</i> , 2020, 752, 144788.	2.2	17
2463	Global Analysis of Gene Expression Profiles Provides Novel Insights into the Development and Evolution of the Large Crustacean <i>Eriocheir sinensis</i> . <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 443-454.	6.9	5
2464	Structural insights into Î²-1,3-glucan cleavage by a glycoside hydrolase family. <i>Nature Chemical Biology</i> , 2020, 16, 920-929.	8.0	19
2465	MicroRNA and mRNA interactions coordinate the immune response in non-lethal heat stressed <i>Litopenaeus vannamei</i> against AHPND-causing <i>Vibrio parahaemolyticus</i> . <i>Scientific Reports</i> , 2020, 10, 787.	3.3	19
2466	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. <i>Scientific Data</i> , 2018, 5, 180114.	5.3	26
2467	<i>Mycena</i> genomes resolve the evolution of fungal bioluminescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31267-31277.	7.1	30
2468	LAMPA, Large Multidomain Protein Annotator, and its application to RNA virus polyproteins. <i>Bioinformatics</i> , 2020, 36, 2731-2739.	4.1	7
2469	HECNet: a hierarchical approach to enzyme function classification using a Siamese Triplet Network. <i>Bioinformatics</i> , 2020, 36, 4583-4589.	4.1	19
2470	Evolutionary and Comparative Analysis of Bacterial Nonhomologous End Joining Repair. <i>Genome Biology and Evolution</i> , 2020, 12, 2450-2466.	2.5	19
2471	Phylogenomics Identifies a New Major Subgroup of Apicomplexans, Marosporida <i>class nov.</i> , with Extreme Apicoplast Genome Reduction. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	23
2472	OUP accepted manuscript. <i>Virus Evolution</i> , 2020, 6, veaa007.	4.9	34
2473	Fatty acid bioconversion in harpacticoid copepods in a changing environment: a transcriptomic approach. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190645.	4.0	26
2474	<i>Limnoglobus roseus</i> gen. nov., sp. nov., a novel freshwater planctomycete with a giant genome from the family Gemmataceae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1240-1249.	1.7	30
2475	<i>Fulvivirga aurantia</i> sp. nov. and <i>Xanthovirga aplysinae</i> gen. nov., sp. nov., marine bacteria isolated from the sponge <i>Aplysina fistularis</i> , and emended description of the genus <i>Fulvivirga</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2766-2781.	1.7	26
2476	<i>Sporofaciens musculi</i> gen. nov., sp. nov., a novel bacterium isolated from the caecum of an obese mouse. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	15
2477	The complete replicons of 16 <i>Ensifer meliloti</i> strains offer insights into intra- and inter-replicon gene transfer, transposon-associated loci, and repeat elements. <i>Microbial Genomics</i> , 2018, 4, .	2.0	21
2478	Assessing the impact, genomics and evolution of type II secretion across a large, medically important genus: the <i>Legionella</i> type II secretion paradigm. <i>Microbial Genomics</i> , 2019, 5, .	2.0	26

#	ARTICLE	IF	CITATIONS
2479	Comparative genome analysis of <i>Lactobacillus mudanjiangensis</i> , an understudied member of the <i>Lactobacillus plantarum</i> group. <i>Microbial Genomics</i> , 2019, 5, .	2.0	9
2480	An assessment of genome annotation coverage across the bacterial tree of life. <i>Microbial Genomics</i> , 2020, 6, .	2.0	55
2481	Arterivirus nsp12 versus the coronavirus nsp16 2â€²-O-methyltransferase: comparison of the C-terminal cleavage products of two nidovirus pp1ab polyproteins. <i>Journal of General Virology</i> , 2015, 96, 2643-2655.	2.9	14
2581	Aligning biological sequences by exploiting residue conservation and coevolution. <i>Physical Review E</i> , 2020, 102, 062409.	2.1	12
2582	The <i>Parauncinula polyspora</i> Draft Genome Provides Insights into Patterns of Gene Erosion and Genome Expansion in Powdery Mildew Fungi. <i>MBio</i> , 2019, 10, .	4.1	18
2583	Genome-wide analyses of cassava Pathogenesis-related (PR) gene families reveal core transcriptome responses to whitefly infestation, salicylic acid and jasmonic acid. <i>BMC Genomics</i> , 2020, 21, 93.	2.8	41
2584	Role of diversity-generating retroelements for regulatory pathway tuning in cyanobacteria. <i>BMC Genomics</i> , 2020, 21, 664.	2.8	13
2585	An Aggregation-defective Mutant of <i>Methanothermobacter</i> sp. CaT2 Reveals Unique Protein-dependent Aggregation. <i>Microbes and Environments</i> , 2019, 34, 244-251.	1.6	3
2586	A TALE of shrimps: Genome-wide survey of homeobox genes in 120 species from diverse crustacean taxa. <i>F1000Research</i> , 2018, 7, 71.	1.6	2
2587	Comparative genomic analysis of crustacean hyperglycemic hormone (CHH) neuropeptide genes across diverse crustacean species. <i>F1000Research</i> , 2018, 7, 100.	1.6	7
2588	Independent accretion of TIM22 complex subunits in the animal and fungal lineages. <i>F1000Research</i> , 2020, 9, 1060.	1.6	7
2589	The ubiquitous and ancient ER membrane protein complex (EMC): tether or not?. <i>F1000Research</i> , 2015, 4, 624.	1.6	75
2590	The ubiquitous and ancient ER membrane protein complex (EMC): tether or not?. <i>F1000Research</i> , 2015, 4, 624.	1.6	63
2591	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004182.	3.2	97
2592	Learning causal networks with latent variables from multivariate information in genomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005662.	3.2	28
2593	Differential Protein Expression in the Hemolymph of <i>Bithynia siamensis goniomphalos</i> Infected with <i>Opisthorchis viverrini</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005104.	3.0	12
2594	Symbiodinium Transcriptomes: Genome Insights into the Dinoflagellate Symbionts of Reef-Building Corals. <i>PLoS ONE</i> , 2012, 7, e35269.	2.5	221
2595	RNA-Seq Analysis of the <i>Sclerotinia homoeocarpa</i> â€œ Creeping Bentgrass Pathosystem. <i>PLoS ONE</i> , 2012, 7, e41150.	2.5	33

#	ARTICLE	IF	CITATIONS
2596	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	2.5	42
2597	ThioFinder: A Web-Based Tool for the Identification of Thiopeptide Gene Clusters in DNA Sequences. PLoS ONE, 2012, 7, e45878.	2.5	51
2598	Metagenomic Analysis of the Microbiota from the Crop of an Invasive Snail Reveals a Rich Reservoir of Novel Genes. PLoS ONE, 2012, 7, e48505.	2.5	62
2599	Comparative Genomic and Phylogenetic Approaches to Characterize the Role of Genetic Recombination in Mycobacterial Evolution. PLoS ONE, 2012, 7, e50070.	2.5	17
2600	Biochemical and Mutational Analysis of a Novel Nicotinamidase from <i>Oceanobacillus iheyensis</i> HTE831. PLoS ONE, 2013, 8, e56727.	2.5	16
2601	Analysis of the Protein Phosphotome of <i>Entamoeba histolytica</i> Reveals an Intricate Phosphorylation Network. PLoS ONE, 2013, 8, e78714.	2.5	10
2602	Snf2 Family Gene Distribution in Higher Plant Genomes Reveals DRD1 Expansion and Diversification in the Tomato Genome. PLoS ONE, 2013, 8, e81147.	2.5	9
2603	Sequencing and De Novo Assembly of the Transcriptome of the Glassy-Winged Sharpshooter ( <i>Homalodisca vitripennis</i> ). PLoS ONE, 2013, 8, e81681.	2.5	15
2604	Structure-Function Features of a Mycoplasma Glycolipid Synthase Derived from Structural Data Integration, Molecular Simulations, and Mutational Analysis. PLoS ONE, 2013, 8, e81990.	2.5	10
2605	New Insights into the Phylogeny and Molecular Classification of Nicotinamide Mononucleotide Deamidases. PLoS ONE, 2013, 8, e82705.	2.5	7
2606	Bioinformatics Analysis of Bacterial Annexins – Putative Ancestral Relatives of Eukaryotic Annexins. PLoS ONE, 2014, 9, e85428.	2.5	14
2607	Analyses of Hypomethylated Oil Palm Gene Space. PLoS ONE, 2014, 9, e86728.	2.5	26
2608	Screening Suitable Reference Genes for Normalization in Reverse Transcription Quantitative Real-Time PCR Analysis in Melon. PLoS ONE, 2014, 9, e87197.	2.5	69
2609	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. PLoS ONE, 2014, 9, e87353.	2.5	79
2610	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. PLoS ONE, 2014, 9, e90574.	2.5	86
2611	Identification of Suitable Reference Genes for Gene Expression Normalization in qRT-PCR Analysis in Watermelon. PLoS ONE, 2014, 9, e90612.	2.5	174
2612	A 14.7 kDa Protein from <i>Francisella tularensis</i> subsp. <i>novicida</i> (Named FTN_1133), Involved in the Response to Oxidative Stress Induced by Organic Peroxides, Is Not Endowed with Thiol-Dependent Peroxidase Activity. PLoS ONE, 2014, 9, e99492.	2.5	8
2613	Genome-Wide Analysis of the NADK Gene Family in Plants. PLoS ONE, 2014, 9, e101051.	2.5	37



#	ARTICLE	IF	CITATIONS
2614	Large-Scale Phylogenetic Classification of Fungal Chitin Synthases and Identification of a Putative Cell-Wall Metabolism Gene Cluster in <i>Aspergillus</i> Genomes. PLoS ONE, 2014, 9, e104920.	2.5	18
2615	Transcriptome-Based Identification of ABC Transporters in the Western Tarnished Plant Bug <i>Lygus hesperus</i> . PLoS ONE, 2014, 9, e113046.	2.5	48
2616	The Search for Therapeutic Bacteriophages Uncovers One New Subfamily and Two New Genera of Pseudomonas-Infecting Myoviridae. PLoS ONE, 2015, 10, e0117163.	2.5	33
2617	Transcriptome Sequencing and Positive Selected Genes Analysis of <i>Bombyx mandarina</i> . PLoS ONE, 2015, 10, e0122837.	2.5	25
2618	New Perspectives on Microbial Community Distortion after Whole-Genome Amplification. PLoS ONE, 2015, 10, e0124158.	2.5	35
2619	Characterization of the Newly Isolated Lytic Bacteriophages KTN6 and KT28 and Their Efficacy against <i>Pseudomonas aeruginosa</i> Biofilm. PLoS ONE, 2015, 10, e0127603.	2.5	69
2620	An Evolutionary View on Disulfide Bond Connectivities Prediction Using Phylogenetic Trees and a Simple Cysteine Mutation Model. PLoS ONE, 2015, 10, e0131792.	2.5	11
2621	Phylogenetic Co-Occurrence of ExoR, ExoS, and ChvI, Components of the RSI Bacterial Invasion Switch, Suggests a Key Adaptive Mechanism Regulating the Transition between Free-Living and Host-Invasive Phases in Rhizobiales. PLoS ONE, 2015, 10, e0135655.	2.5	23
2622	Genome Sequence of African Swine Fever Virus BA71, the Virulent Parental Strain of the Nonpathogenic and Tissue-Culture Adapted BA71V. PLoS ONE, 2015, 10, e0142889.	2.5	69
2623	Comprehensive Analysis of the COBRA-Like (COBL) Gene Family in <i>Gossypium</i> Identifies Two COBLs Potentially Associated with Fiber Quality. PLoS ONE, 2015, 10, e0145725.	2.5	40
2624	Towards Plant Species Identification in Complex Samples: A Bioinformatics Pipeline for the Identification of Novel Nuclear Barcode Candidates. PLoS ONE, 2016, 11, e0147692.	2.5	8
2625	Inter-Protein Sequence Co-Evolution Predicts Known Physical Interactions in Bacterial Ribosomes and the Trp Operon. PLoS ONE, 2016, 11, e0149166.	2.5	58
2626	Enhancement of DNaseI Salt Tolerance by Mimicking the Domain Structure of DNase from an Extremely Halotolerant Bacterium <i>Thioalkalivibrio</i> sp. K90mix. PLoS ONE, 2016, 11, e0150404.	2.5	5
2627	Evolution of Pentameric Ligand-Gated Ion Channels: Pro-Loop Receptors. PLoS ONE, 2016, 11, e0151934.	2.5	84
2628	Genome-Wide Identification of the Transcription Factors Involved in Citrus Fruit Ripening from the Transcriptomes of a Late-Ripening Sweet Orange Mutant and Its Wild Type. PLoS ONE, 2016, 11, e0154330.	2.5	25
2629	Alternative Isoform Analysis of Ttc8 Expression in the Rat Pineal Gland Using a Multi-Platform Sequencing Approach Reveals Neural Regulation. PLoS ONE, 2016, 11, e0163590.	2.5	8
2630	Molecular Models for the Core Components of the Flagellar Type-III Secretion Complex. PLoS ONE, 2016, 11, e0164047.	2.5	14
2631	Intraspecific Variation and Phylogenetic Relationships Are Revealed by ITS1 Secondary Structure Analysis and Single-Nucleotide Polymorphism in <i>Ganoderma lucidum</i> . PLoS ONE, 2017, 12, e0169042.	2.5	14



#	ARTICLE	IF	CITATIONS
2632	Comparative analysis of NBS-LRR genes and their response to <i>Aspergillus flavus</i> in <i>Arachis</i> . PLoS ONE, 2017, 12, e0171181.	2.5	50
2633	Domestication drive the changes of immune and digestive system of Eurasian perch ( <i>Perca fluviatilis</i> ). PLoS ONE, 2017, 12, e0172903.	2.5	12
2634	Genome-wide analysis of rice dehydrin gene family: Its evolutionary conservedness and expression pattern in response to PEG induced dehydration stress. PLoS ONE, 2017, 12, e0176399.	2.5	54
2635	The antenna transcriptome changes in mosquito <i>Anopheles sinensis</i> , pre- and post- blood meal. PLoS ONE, 2017, 12, e0181399.	2.5	17
2636	Differential transcriptome analysis reveals genes related to cold tolerance in seabuckthorn carpenter moth, <i>Eogystia hippophaecolus</i> . PLoS ONE, 2017, 12, e0187105.	2.5	26
2637	Abundance and co-occurrence of extracellular capsules increase environmental breadth: Implications for the emergence of pathogens. PLoS Pathogens, 2017, 13, e1006525.	4.7	62
2638	Beyond the sea: <i>Crepidula atrasolea</i> as a spiralian model system. International Journal of Developmental Biology, 2017, 61, 479-493.	0.6	13
2639	Genome-wide identification and expression analysis of the $\alpha$ -amylase genes strongly associated with fruit development, ripening, and abiotic stress response in two banana cultivars. Frontiers of Agricultural Science and Engineering, 2016, 3, 346.	1.4	18
2640	LTRpred: de novo annotation of intact retrotransposons. Journal of Open Source Software, 2020, 5, 2170.	4.6	17
2642	An Overview of Computational Tools of Nucleic Acid Binding Site Prediction for Site-specific Proteins and Nucleases. Protein and Peptide Letters, 2020, 27, 370-384.	0.9	2
2643	Development and Application of Computational Methods in Phage Display Technology. Current Medicinal Chemistry, 2020, 26, 7672-7693.	2.4	13
2644	Current Advances in the Identification and Characterization of Putative Drug and Vaccine Targets in the Bacterial Genomes. Current Topics in Medicinal Chemistry, 2015, 16, 1040-1069.	2.1	35
2645	Relevance of Machine Learning Techniques and Various Protein Features in Protein Fold Classification: A Review. Current Bioinformatics, 2019, 14, 688-697.	1.5	17
2646	Paleovirology: The Study of Endogenous Viral Elements. , 2016, , 273-292.		7
2647	Re-annotation of the genome sequence of <i>Helicobacter pylori</i> 26695. Journal of Integrative Bioinformatics, 2013, 10, 233.	1.5	16
2648	Definitive Assignment by Multigenome Analysis of the Gammaproteobacterial Genus <i>Thermithiobacillus</i> to the Class Acidithiobacillia. Polish Journal of Microbiology, 2014, 63, 245-247.	1.7	8
2649	Methanesulfonate supports growth as the sole sulfur source for the marine diatom <i>Thalassiosira pseudonana</i> NCMA 1335. Aquatic Microbial Ecology, 2017, 78, 177-185.	1.8	2
2650	Cycloheximide-Producing <i>Streptomyces</i> Associated With <i>Xyleborinus saxesenii</i> and <i>Xyleborus affinis</i> Fungus-Farming Ambrosia Beetles. Frontiers in Microbiology, 2020, 11, 562140.	3.5	22

#	ARTICLE	IF	CITATIONS
2651	Urbanization and Waterborne Pathogen Emergence in Low-Income Countries: Where and How to Conduct Surveys?. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 480.	2.6	14
2652	Genetic Diversity of Serine Protease Inhibitors in Myxozoan (Cnidaria, Myxozoa) Fish Parasites. <i>Microorganisms</i> , 2020, 8, 1502.	3.6	10
2653	Genomic Insight into <i>Pediococcus acidilactici</i> HN9, a Potential Probiotic Strain Isolated from the Traditional Thai-Style Fermented Beef Nhang. <i>Microorganisms</i> , 2021, 9, 50.	3.6	18
2654	Biodefense Oriented Genomic-Based Pathogen Classification Systems: Challenges and Opportunities. <i>Journal of Bioterrorism &amp; Biodefense</i> , 2012, 03, 1000113.	0.1	7
2655	RNAi technology targeting <i>Pb</i> and <i>GP</i> 43 and <i>Pb</i> and <i>P</i> 27 in <i>Paracoccidioides brasiliensis</i> . <i>Open Journal of Genetics</i> , 2013, 03, 1-8.	0.1	2
2656	Identification and expression analysis of YABBY family genes associated with fruit shape in tomato ( <i>Solanum lycopersicum</i> L.). <i>Genetics and Molecular Research</i> , 2015, 14, 7079-7091.	0.2	26
2657	Genome-Wide Analysis of Type VI System Clusters and Effectors in <i>Burkholderia</i> Species. <i>Plant Pathology Journal</i> , 2018, 34, 11-22.	1.7	20
2658	Genome-wide Identification, Classification, and Expression Analysis of the Receptor-Like Protein Family in Tomato. <i>Plant Pathology Journal</i> , 2018, 34, 435-444.	1.7	34
2659	SFannotation: A Simple and Fast Protein Function Annotation System. <i>Genomics and Informatics</i> , 2014, 12, 76.	0.8	1
2660	Data enabled prediction analysis assigns folate/biopterin transporter (BT1) family to 36 hypothetical membrane proteins in <i>Leishmania donovani</i> . <i>Bioinformatics</i> , 2019, 15, 697-708.	0.5	2
2661	Decoding the vital segments in human ATP-dependent RNA helicase. <i>Bioinformatics</i> , 2020, 16, 160-170.	0.5	7
2663	Cell-cycle dependent phosphorylation of yeast pericentrin regulates $\gamma$ -TuSC-mediated microtubule nucleation. <i>ELife</i> , 2014, 3, e02208.	6.0	84
2664	Punctuated evolution and transitional hybrid network in an ancestral cell cycle of fungi. <i>ELife</i> , 2016, 5, .	6.0	52
2665	Residue proximity information and protein model discrimination using saturation-suppressor mutagenesis. <i>ELife</i> , 2015, 4, .	6.0	34
2666	The magnesium transporter A is activated by cardiolipin and is highly sensitive to free magnesium in vitro. <i>ELife</i> , 2016, 5, .	6.0	40
2667	Constitutive scaffolding of multiple Wnt enhanceosome components by Legless/BCL9. <i>ELife</i> , 2017, 6, .	6.0	69
2668	Multiple short windows of calcium-dependent protein kinase 4 activity coordinate distinct cell cycle events during <i>Plasmodium</i> gametogenesis. <i>ELife</i> , 2017, 6, .	6.0	62
2669	Structural relationship between the putative hair cell mechanotransduction channel TMC1 and TMEM16 proteins. <i>ELife</i> , 2018, 7, .	6.0	84

#	ARTICLE	IF	CITATIONS
2670	Functional metagenomics-guided discovery of potent Cas9 inhibitors in the human microbiome. ELife, 2019, 8, .	6.0	56
2671	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. ELife, 2020, 9, .	6.0	27
2672	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. ELife, 2020, 9, .	6.0	25
2673	The identification of immune genes in the milk transcriptome of the Tasmanian devil ( <i>Sarcophilus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	16
2674	RNA-Seq of the Caribbean reef-building coral <i>Orbicella faveolata</i> (Scleractinia-Merulinidae) under bleaching and disease stress expands models of coral innate immunity. PeerJ, 2016, 4, e1616.	2.0	56
2675	<i>De novo</i> genome assembly of <i>Geosmithia morbida</i> , the causal agent of thousand cankers disease. PeerJ, 2016, 4, e1952.	2.0	9
2676	The genome and transcriptome of <i>Phalaenopsis</i> yield insights into floral organ development and flowering regulation. PeerJ, 2016, 4, e2017.	2.0	39
2677	SigmodD: a user-friendly tool for improving bacterial genome annotation through analysis of transcription control signals. PeerJ, 2016, 4, e2056.	2.0	10
2678	A comparative in-silico analysis of autophagy proteins in ciliates. PeerJ, 2017, 5, e2878.	2.0	11
2679	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquillettii</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. PeerJ, 2017, 5, e2951.	2.0	23
2680	Evolutionary and functional implications of hypervariable loci within the skin virome. PeerJ, 2017, 5, e2959.	2.0	28
2681	Candidate genes that have facilitated freshwater adaptation by palaemonid prawns in the genus <i>Macrobrachium</i> : identification and expression validation in a model species ( <i>M.</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	30
2682	Genome-wide analysis of WRKY transcription factors in wheat ( <i>Triticum aestivum</i> L.) and differential expression under water deficit condition. PeerJ, 2017, 5, e3232.	2.0	97
2683	Accumulation and expression of multiple antibiotic resistance genes in <i>Arcobacter cryaerophilus</i> that thrives in sewage. PeerJ, 2017, 5, e3269.	2.0	29
2684	290 metagenome-assembled genomes from the Mediterranean Sea: a resource for marine microbiology. PeerJ, 2017, 5, e3558.	2.0	71
2685	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. PeerJ, 2017, 5, e3702.	2.0	16
2686	The <i>Legionella pneumophila</i> effector Lpg1137 is a homologue of mitochondrial SLC25 carrier proteins, not of known serine proteases. PeerJ, 2017, 5, e3849.	2.0	2
2687	Codominant grasses differ in gene expression under experimental climate extremes in native tallgrass prairie. PeerJ, 2018, 6, e4394.	2.0	7

#	ARTICLE	IF	CITATIONS
2688	Sexually dimorphic venom proteins in long-jawed orb-weaving spiders (<i>Tetragnatha</i>) comprise novel gene families. PeerJ, 2018, 6, e4691.	2.0	21
2689	Tackling critical parameters in metazoan meta-barcoding experiments: a preliminary study based on <i>coxI</i> DNA barcode. PeerJ, 2018, 6, e4845.	2.0	6
2690	Venomix: a simple bioinformatic pipeline for identifying and characterizing toxin gene candidates from transcriptomic data. PeerJ, 2018, 6, e5361.	2.0	18
2691	Complete paternally inherited mitogenomes of two freshwater mussels <i>Unio pictorum</i> and <i>Sinanodonta woodiana</i> (Bivalvia: Unionidae). PeerJ, 2018, 6, e5573.	2.0	11
2692	Genome-wide identification and expression profile analysis of the <i>Hsp20</i> gene family in Barley (<i>Hordeum vulgare</i> L.). PeerJ, 2019, 7, e6832.	2.0	23
2693	Plastome sequences help to improve the systematic position of trinerved <i>Lindera</i> species in the family Lauraceae. PeerJ, 2019, 7, e7662.	2.0	21
2694	Systematic analysis of NAC transcription factors in <i>Gossypium barbadense</i> uncovers their roles in response to Verticillium wilt. PeerJ, 2019, 7, e7995.	2.0	11
2695	Genome-wide identification and characterization of the soybean SOD family during alkaline stress. PeerJ, 2020, 8, e8457.	2.0	16
2696	Genome-wide identification and characterization of TCP family genes in <i>Brassica juncea</i> var. tumida. PeerJ, 2020, 8, e9130.	2.0	11
2697	Genome-wide analysis of the C3H zinc finger family reveals its functions in salt stress responses of <i>Pyrus betulaefolia</i>. PeerJ, 2020, 8, e9328.	2.0	16
2698	PhylomeDB V5: an expanding repository for genome-wide catalogues of annotated gene phylogenies. Nucleic Acids Research, 2022, 50, D1062-D1068.	14.5	30
2699	Functions predict horizontal gene transfer and the emergence of antibiotic resistance. Science Advances, 2021, 7, eabj5056.	10.3	44
2700	The novel anti-CRISPR AcrIIA22 relieves DNA torsion in target plasmids and impairs SpyCas9 activity. PLoS Biology, 2021, 19, e3001428.	5.6	13
2701	Genomic and Transcriptomic Insight of Giant Sclerotium Formation of Wood-Decay Fungi. Frontiers in Microbiology, 2021, 12, 746121.	3.5	7
2702	Taxonomy-aware, sequence similarity ranking reliably predicts phageâ€“host relationships. BMC Biology, 2021, 19, 223.	3.8	16
2703	Discovery and characterization of a novel Dyp-type peroxidase from a marine actinobacterium isolated from Trondheim fjord, Norway. Journal of Inorganic Biochemistry, 2022, 226, 111651.	3.5	8
2705	Genome sequencing of turmeric provides evolutionary insights into its medicinal properties. Communications Biology, 2021, 4, 1193.	4.4	23
2706	Genome-Wide Identification and Bioinformatics Analysis of Auxin Response Factor Genes in Highbush Blueberry. Horticulturae, 2021, 7, 403.	2.8	5

#	ARTICLE	IF	CITATIONS
2707	Genome-wide identification and expression profile analysis of trihelix transcription factor family genes in response to abiotic stress in sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. <i>BMC Genomics</i> , 2021, 22, 738.	2.8	17
2708	Genome-Wide Identification and Characterization of Polygalacturonase Gene Family in Maize ( <i>Zea mays</i> ) Tj ETQq1 1 0.784314 rgBT /Ov 4.1 14	4.1	14
2709	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9Âyears. <i>Microbiome</i> , 2021, 9, 199.	11.1	33
2710	A bacterial membrane sculpting protein with BAR domain-like activity. <i>ELife</i> , 2021, 10, .	6.0	6
2711	The Adaptive Evolution and Gigantism Mechanisms of the Hadal â€œSupergiantâ€•Amphipod <i>Alicella gigantea</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	4
2712	Genome-Wide Identification of LRR-RLK Family in <i>Saccharum</i> and Expression Analysis in Response to Biotic and Abiotic Stress. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1632-1651.	2.4	10
2714	Novel Phage-Derived Depolymerase with Activity against <i>Proteus mirabilis</i> Biofilms. <i>Microorganisms</i> , 2021, 9, 2172.	3.6	16
2715	Transcriptome-wide characterization and functional analysis of Xyloglucan endo-transglycosylase/hydrolase (XTH) gene family of <i>Salicornia europaea</i> L. under salinity and drought stress. <i>BMC Plant Biology</i> , 2021, 21, 491.	3.6	18
2716	Genomic analysis of the polyamine biosynthesis pathway in duckweed <i>Spirodela polyrhiza</i> L.: presence of the arginine decarboxylase pathway, absence of the ornithine decarboxylase pathway, and response to abiotic stresses. <i>Planta</i> , 2021, 254, 108.	3.2	6
2717	Genome-Wide Identification and Expression Analysis of AP2/ERF Transcription Factor Related to Drought Stress in Cultivated Peanut ( <i>Arachis hypogaea</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 750761.	2.3	21
2718	Comparative RNA-Seq Analyses of <i>Solenopsis japonica</i> (Hymenoptera: Formicidae) Reveal Gene in Response to Cold Stress. <i>Genes</i> , 2021, 12, 1610.	2.4	10
2719	App-SpaM: phylogenetic placement of short reads without sequence alignment. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	5
2720	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. <i>IScience</i> , 2021, 24, 103324.	4.1	25
2721	MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples. <i>Journal of Computational Biology</i> , 2021, 28, 1063-1074.	1.6	2
2722	bHLH Transcription Factors Undergo Alternative Splicing During Cold Acclimation in a Eucalyptus hybrid. <i>Plant Molecular Biology Reporter</i> , 0, , 1.	1.8	2
2723	The Bioinformatics Virtual Coordination Network: An Open-Source and Interactive Learning Environment. <i>Frontiers in Education</i> , 2021, 6, .	2.1	2
2724	Metagenome-Assembled Genomes from Monte Cristo Cave (Diamantina, Brazil) Reveal Prokaryotic Lineages As Functional Models for Life on Mars. <i>Astrobiology</i> , 2021, , .	3.0	4
2725	Genome-wide analysis of <i>Claviceps paspali</i> : insights into the secretome of the main species causing ergot disease in <i>Paspalum</i> spp. <i>BMC Genomics</i> , 2021, 22, 766.	2.8	1

#	ARTICLE	IF	CITATIONS
2727	Insights into the evolution and hypoglycemic metabolite biosynthesis of autotetraploid <i>Cyclocarya paliurus</i> by combining genomic, transcriptomic and metabolomic analyses. <i>Industrial Crops and Products</i> , 2021, 173, 114154.	5.2	13
2731	From Genomes to Protein Functions. <i>SpringerBriefs in Systems Biology</i> , 2013, , 3-17.	0.3	0
2732	Functional Annotation. <i>Chapman &amp; Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , .	0.1	0
2733	Analysis Pipelines for Next- Generation Sequencing Data. <i>Chapman &amp; Hall/CRC Mathematical and Computational Biology Series</i> , 2012, , .	0.1	0
2734	Sequence Homology Handling. <i>Computational Biology</i> , 2013, , 301-334.	0.2	1
2735	Status of Research on Insertion and Deletion Variations in the Human Population. <i>Computational Biology</i> , 2013, , 173-181.	0.2	0
2736	LncRNA Research Resources. <i>Materials and Methods</i> , 0, 3, .	0.0	0
2738	Setting up a Meta-Threading Pipeline for High-Throughput Structural Bioinformatics: eThread Software Distribution, Walkthrough and Resource Profiling. <i>Journal of Computer Science and Systems Biology</i> , 2013, 06, .	0.0	3
2739	Analysis of Biological Sequences. , 2014, , 249-253.		0
2740	Transparent Incremental Updates for Genomics Data Analysis Pipelines. <i>Lecture Notes in Computer Science</i> , 2014, , 311-320.	1.3	5
2742	Neurodegenerative Diseases: Phenome to Genome Analysis. <i>MOJ Proteomics &amp; Bioinformatics</i> , 2014, 2, .	0.1	2
2743	Atlas of the Open Reading Frames in Human Diseases: Dark Matter of the Human Genome. <i>MOJ Proteomics &amp; Bioinformatics</i> , 2015, 2, .	0.1	1
2746	Characterization of gibberellin 2-oxidase isoforms in coconut ( <i>Cocos nucifera</i> L.). <i>Journal of Plantation Crops</i> , 2015, 43, .	0.0	0
2748	Systematic Determination of Transcription Factor DNA-Binding Specificities in Yeast. <i>Methods in Molecular Biology</i> , 2016, 1361, 203-225.	0.9	0
2750	Characterization of pyrethroid resistance in the western corn rootworm<i>Diabrotica virgifera virgifera</i> LeConte. , 2016, , .		0
2756	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. , 2016, , 137-165.		0
2758	A Computational Model for Predicting RNase H Domain of Retrovirus. <i>PLoS ONE</i> , 2016, 11, e0161913.	2.5	4
2763	Discriminative Motif Elicitation via Maximization of Statistical Overrepresentation. <i>Lecture Notes in Computer Science</i> , 2017, , 501-512.	1.3	0

#	ARTICLE	IF	CITATIONS
2766	Finding Genes. , 2017, , 127-141.		0
2779	Characterization of a hypothetical protein YVRE from <i>Bacillus subtilis</i> indicates its key role as glucono-lactonase in pentose phosphate pathway and glucose metabolism. <i>Bioinformation</i> , 2017, 13, 430-438.	0.5	2
2783	<i>Streptococcus azizii</i> sp. nov., isolated from naïve weanling mice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 5032-5037.	1.7	5
2784	Herramientas bioinformáticas usadas en el estudio de enzimas fenoloxidasas del género <i>Pleurotus</i> . <i>Mexican Journal of Biotechnology</i> , 2018, 3, 95-118.	0.3	0
2786	AutoModel: A Client-Server Tool for Intuitive and Interactive Homology Modeling of Protein-Ligand Complexes. <i>Lecture Notes in Computer Science</i> , 2018, , 78-89.	1.3	1
2787	The Transcriptome of <i>Paraphelidium Tribonemae</i> Illuminates the Ancestry of Fungi and Opisthosporidia. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2809	Genomics Approach to Identify the Cause of the Missing Omega-5 Gliadin Protein in O-Free Wheat. <i>Plant Breeding and Biotechnology</i> , 2018, 6, 413-425.	0.9	4
2813	Bacterial Pan-Genomics. , 2019, , 21-38.		6
2814	Application of Genomics to Understand the Pathogenic Microbial Diversity. , 2019, , 49-82.		0
2827	Genome-wide identification and expression profiling of the C2H2-type zinc finger protein genes in the silkworm <i>Bombyx mori</i> . <i>PeerJ</i> , 2019, 7, e7222.	2.0	6
2831	Annotation of a hypothetical protein coding gene PAS_chr2-2_0152 containing Lysine Methyl transferase SMYD domain from <i>Komagataella phaffii</i> GS115. <i>Bioinformation</i> , 2019, 15, 542-547.	0.5	0
2840	Exploring Toxin Evolution: Venom Protein Transcript Sequencing and Transcriptome-Guided High-Throughput Proteomics. <i>Methods in Molecular Biology</i> , 2020, 2068, 97-127.	0.9	3
2846	Factors influencing estimates of coordinate error for molecular replacement. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 19-27.	2.3	6
2854	Whole genome sequence and comparative genome analyses of multi-resistant <i>Staphylococcus warneri</i> GD01 isolated from a diseased pig in China. <i>PLoS ONE</i> , 2020, 15, e0233363.	2.5	4
2860	Questing functions and structures of hypothetical proteins from <i>Campylobacter jejuni</i> : a computer-aided approach. <i>Bioscience Reports</i> , 2020, 40, .	2.4	6
2869	Comparison of gut viral communities in diarrhoea and healthy dairy calves. <i>Journal of General Virology</i> , 2021, 102, .	2.9	5
2870	Comparative RNA-Seq Analysis Reveals Potentially Resistance-Related Genes in Response to Bacterial Canker of Tomato. <i>Genes</i> , 2021, 12, 1745.	2.4	5
2871	Genome-wide identification, classification, and expression analysis of the JmjC domain-containing histone demethylase gene family in birch. <i>BMC Genomics</i> , 2021, 22, 772.	2.8	10



#	ARTICLE	IF	CITATIONS
2872	Genome-wide identification and expression analysis of the bHLH transcription factor family and its response to abiotic stress in foxtail millet ( <i>Setaria italica</i> L.). BMC Genomics, 2021, 22, 778.	2.8	10
2876	TportHMM: Predicting the substrate class of transmembrane transport proteins using profile Hidden Markov Models. , 2020, , .		2
2877	SKP1-like protein, CrSKP1-e, interacts with pollen-specific F-box proteins and assembles into SCF-type E3 complex in “Wuzishatangju” ( <i>Citrus reticulata</i> Blanco) pollen. PeerJ, 2020, 8, e10578.	2.0	6
2882	A Novel Algorithm for Training Hidden Markov Models with Positive and Negative Examples. , 2020, , .		2
2883	Genome analysis of <i>Plectus murrayi</i> , a nematode from continental Antarctica. G3: Genes, Genomes, Genetics, 2021, 11, 1-9.	1.8	4
2888	Comparative Analyses and Phylogenetic Relationships between <i>Cryptomeria fortunei</i> and Related Species Based on Complete Chloroplast Genomes. Phyton, 2020, 89, 957-986.	0.7	1
2889	Comparative in Silico Studies for the Molecular Basis of Lepidopteran Insect Pests Bio-Control Using Insect’s Own Enzymes. Learning and Analytics in Intelligent Systems, 2020, , 55-64.	0.6	0
2892	Use Chou’s 5-Steps Rule to Predict Remote Homology Proteins by Merging Grey Incidence Analysis and Domain Similarity Analysis. Natural Science, 2020, 12, 181-198.	0.4	23
2893	Venom Gland Peptides of Arthropods from the Brazilian Cerrado Biome Unveiled by Transcriptome Analysis. Lecture Notes in Computer Science, 2020, , 48-57.	1.3	0
2894	Bioinformatics Analysis of Plant Cell Wall Evolution. Methods in Molecular Biology, 2020, 2149, 483-502.	0.9	0
2896	In silico detection tools to identify fungal secondary metabolites and their biosynthetic gene clusters. , 2020, , 23-35.		0
2897	The Terpene Synthase Gene Family in Norway Spruce. Compendium of Plant Genomes, 2020, , 177-192.	0.5	2
2901	Identification and characterization of the glycoside hydrolase family 18 genes from the entomopathogenic fungus <i>Isaria cicadae</i> genome. Canadian Journal of Microbiology, 2020, 66, 274-287.	1.7	3
2902	The crystal structure of the TonB-dependent transporter YncD reveals a positively charged substrate-binding site. Acta Crystallographica Section D: Structural Biology, 2020, 76, 484-495.	2.3	8
2904	Tomato COI gene family identification and expression under abiotic and phytohormone stress. Journal of Genetics, 2021, 100, 1.	0.7	1
2905	Real-time monitoring of <i>Pseudomonas aeruginosa</i> biofilm growth dynamics and persister cells’ eradication. Emerging Microbes and Infections, 2021, 10, 2062-2075.	6.5	21
2906	Transcriptomic Profile of the Cockle <i>Cerastoderma edule</i> Exposed to Seasonal Diarrhetic Shellfish Toxin Contamination. Toxins, 2021, 13, 784.	3.4	3
2907	Genome-wide investigation of the GRAS transcription factor family in foxtail millet ( <i>Setaria italica</i> L.). BMC Plant Biology, 2021, 21, 508.	3.6	19

#	ARTICLE	IF	CITATIONS
2908	Computationally Reconstructed Interactome of Bradyrhizobium diazoefficiens USDA110 Reveals Novel Functional Modules and Protein Hubs for Symbiotic Nitrogen Fixation. International Journal of Molecular Sciences, 2021, 22, 11907.	4.1	0
2909	Genome-wide identification and expression analysis of the xyloglucan endotransglucosylase/hydrolase gene family in poplar. BMC Genomics, 2021, 22, 804.	2.8	20
2910	Transcriptome profiling reveals the developmental regulation of NaCl-treated Forcipomyia taiwana eggs. BMC Genomics, 2021, 22, 792.	2.8	2
2911	Proteogenomic discovery of sORF-encoded peptides associated with bacterial virulence in Yersinia pestis. Communications Biology, 2021, 4, 1248.	4.4	10
2913	Interactions of the Intracellular Bacterium <i>Cardinium</i> with Its Host, the House Dust Mite <i>Dermatophagoides farinae</i> , Based on Gene Expression Data. MSystems, 2021, 6, e0091621.	3.8	7
2914	The First De Novo Transcriptome Assembly and Transcriptomic Dynamics of the Mangrove Tree <i>Rhizophora stylosa</i> Griff. (Rhizophoraceae). International Journal of Molecular Sciences, 2021, 22, 11964.	4.1	5
2915	Genome-wide analysis of Dof transcription factors and their response to cold stress in rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.8	11
2925	<i>Arthrobacter mobilis</i> sp. nov., a novel actinobacterium isolated from Cholistan desert soil. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5445-5452.	1.7	14
2927	Transcriptome-sequencing analyses reveal flower color formation in <i>Strelitzia reginae</i> . Biologia Plantarum, 0, 64, 717-724.	1.9	0
2928	Genome-wide identification of Hsp70/110 genes in rainbow trout and their regulated expression in response to heat stress. PeerJ, 2020, 8, e10022.	2.0	19
2934	Identifying Evolutionary Origins of Repeat Domains in Protein Families. , 2020, , .		0
2935	Predicting protein secondary structure by an ensemble through feature-based accuracy estimation. , 2020, , .		1
2936	Identification of L-asparaginases from <i>Streptomyces</i> strains with competitive activity and immunogenic profiles: a bioinformatic approach. PeerJ, 2020, 8, e10276.	2.0	6
2937	A comprehensive survey of the aldehyde dehydrogenase gene superfamily in <i>Saccharum</i> and the role of ScALDH2B-1 in the stress response. Environmental and Experimental Botany, 2022, 194, 104725.	4.2	11
2938	Characterization of the sugarcane MYC gene family and the negative regulatory role of ShMYC4 in response to pathogen stress. Industrial Crops and Products, 2022, 176, 114292.	5.2	10
2940	Utilization Efficiency of Human Milk Oligosaccharides by Human-Associated <i>Akkermansia</i> Is Strain Dependent. Applied and Environmental Microbiology, 2022, 88, AEM0148721.	3.1	29
2941	Evolutionary and expression dynamics of LRR-RLKs and functional establishment of KLAVER homolog in shoot mediated regulation of AON in chickpea symbiosis. Genomics, 2021, 113, 4313-4326.	2.9	10
2942	Virome in Fecal Samples From Wild Giant Pandas ( <i>Ailuropoda Melanoleuca</i> ). Frontiers in Veterinary Science, 2021, 8, 767494.	2.2	4

#	ARTICLE	IF	CITATIONS
2943	In silico analysis and expression profiling of S-domain receptor-like kinases (SD-RLKs) under different abiotic stresses in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2021, 22, 817.	2.8	6
2944	The Many Faces of Lipids in Genome Stability (and How to Unmask Them). <i>International Journal of Molecular Sciences</i> , 2021, 22, 12930.	4.1	8
2945	Identification of Raf-Like Kinases B Subfamily Genes in <i>Gossypium</i> Species Revealed GhRAF42 Enhanced Salt Tolerance in Cotton. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12649.	4.1	3
2948	Genome-Wide Identification, Characterization, and Expression Analysis of DDE_Tnp_4 Family Genes in <i>Eriochloa sinensis</i> . <i>Antibiotics</i> , 2021, 10, 1430.	3.7	2
2950	The copper-linked <i>Escherichia coli</i> AZY operon: Structure, metal binding, and a possible physiological role in copper delivery. <i>Journal of Biological Chemistry</i> , 2022, 298, 101445.	3.4	1
2951	Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. <i>ISME Journal</i> , 2022, 16, 1074-1085.	9.8	25
2952	Evolution of polarity protein BASL and the capacity for stomatal lineage asymmetric divisions. <i>Current Biology</i> , 2022, 32, 329-337.e5.	3.9	16
2953	Genome-wide identification of Gramineae histone modification genes and their potential roles in regulating wheat and maize growth and stress responses. <i>BMC Plant Biology</i> , 2021, 21, 543.	3.6	8
2954	Oxygen-deficient water zones in the Baltic Sea promote uncharacterized Hg methylating microorganisms in underlying sediments. <i>Limnology and Oceanography</i> , 2022, 67, 135-146.	3.1	15
2955	Venoms for all occasions: The functional toxin profiles of different anatomical regions in sea anemones are related to their ecological function. <i>Molecular Ecology</i> , 2022, 31, 866-883.	3.9	21
2956	Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. <i>Communications Biology</i> , 2021, 4, 1320.	4.4	13
2957	MADS-box transcription factors determine the duration of temporary winter dormancy in closely related evergreen and deciduous <i>Iris</i> spp.. <i>Journal of Experimental Botany</i> , 2022, 73, 1429-1449.	4.8	6
2958	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2022, 109, 7-22.	5.7	17
2959	Toward the Heterologous Biosynthesis of Plant Natural Products: Gene Discovery and Characterization. <i>ACS Synthetic Biology</i> , 2021, 10, 2784-2795.	3.8	12
2960	Identification and characterization of a novel bocaparvovirus in tufted deer ( <i>Elaphodus cephalophus</i> ) in China. <i>Archives of Virology</i> , 2022, 167, 201-206.	2.1	2
2961	Alcohol Acyltransferase Is Involved in the Biosynthesis of C6 Esters in Apricot ( <i>Prunus armeniaca</i> L.) Fruit. <i>Frontiers in Plant Science</i> , 2021, 12, 763139.	3.6	4
2962	Selective Sweeps and Polygenic Adaptation Drive Local Adaptation along Moisture and Temperature Gradients in Natural Populations of Coast Redwood and Giant Sequoia. <i>Genes</i> , 2021, 12, 1826.	2.4	7
2964	Integrated transcriptome and small RNA sequencing analyses reveal a drought stress response network in <i>Sophora tonkinensis</i> . <i>BMC Plant Biology</i> , 2021, 21, 566.	3.6	4

#	ARTICLE	IF	CITATIONS
2965	Integrative Transcriptomics and Proteomics Analyses to Reveal the Developmental Regulation of <i>Metorchis orientalis</i> : A Neglected Trematode With Potential Carcinogenic Implications. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 783662.	3.9	1
2966	Genome-Wide Identification and Gene Expression Analysis of Acyl-Activating Enzymes Superfamily in Tomato ( <i>Solanum lycopersicum</i> ) Under Aluminum Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 754147.	3.6	10
2967	A draft genome sequence of the common, or spectacled caiman <i>Caiman crocodilus</i> . <i>F1000Research</i> , 0, 10, 1230.	1.6	0
2969	The Chemosensory Transcriptome of a Diving Beetle. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	1
2970	Proteomic Approaches to Understand Plant Response to Abiotic Stresses. , 2021, , 351-383.		2
2972	LNCRI: Long Non-Coding RNA Identifier in Multiple Species. <i>IEEE Access</i> , 2021, 9, 167219-167228.	4.2	2
2974	Genome-Wide Identification of R2R3-MYB Transcription Factors: Discovery of a “Dual-Function” Regulator of Gypenoside and Flavonol Biosynthesis in <i>Gynostemma pentaphyllum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 796248.	3.6	6
2975	Exploiting protein family and protein network data to identify novel drug targets for bladder cancer. <i>Oncotarget</i> , 2022, 13, 105-117.	1.8	2
2976	Structural Identification of Metalloproteomes in Marine Diatoms, an Efficient Algae Model in Toxic Metals Bioremediation. <i>Molecules</i> , 2022, 27, 378.	3.8	10
2977	Profiling Signal Transduction in Global Marine Biofilms. <i>Frontiers in Microbiology</i> , 2021, 12, 768926.	3.5	9
2978	Genome-wide identification and expression analysis of the coronatine-insensitive 1 (COI1) gene family in response to biotic and abiotic stresses in <i>Saccharum</i> . <i>BMC Genomics</i> , 2022, 23, 38.	2.8	4
2979	Genomic Analyses of <i>Pediococcus pentosaceus</i> ST65ACC, a Bacteriocinogenic Strain Isolated from Artisanal Raw-Milk Cheese. <i>Probiotics and Antimicrobial Proteins</i> , 2023, 15, 630-645.	3.9	7
2980	Genomic Identification, Evolution, and Expression Analysis of Bromodomain Genes Family in Buffalo. <i>Genes</i> , 2022, 13, 103.	2.4	1
2981	Transcriptomic profiling of watermelon ( ) provides insights into male flowers development. <i>Journal of Integrative Agriculture</i> , 2022, 21, 407-421.	3.5	4
2982	Gene cluster from plant to microbes: Their role in genome architecture, organism's development, specialized metabolism and drug discovery. <i>Biochimie</i> , 2022, 193, 1-15.	2.6	4
2983	Genome-wide identification and expression analysis of GDSL esterase/lipase genes in tomato. <i>Journal of Integrative Agriculture</i> , 2022, 21, 389-406.	3.5	7
2984	Proteomic characterization of pilot scale hot-water extracts from the industrial carrageenan red seaweed <i>Eucheuma denticulatum</i> . <i>Algal Research</i> , 2022, 62, 102619.	4.6	11
2985	Gene Regulatory Networks Shape Developmental Plasticity of Root Cell Types Under Water Extremes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1

#	ARTICLE	IF	CITATIONS
2987	Chromosome-Level Genome Assembly Provides New Insights into Genome Evolution and Tuberous Root Formation of <i>Potentilla anserina</i> . <i>Genes</i> , 2021, 12, 1993.	2.4	8
2988	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. <i>Horticulture Research</i> , 2022, 9, .	6.3	10
2989	Actinoporin-like Proteins Are Widely Distributed in the Phylum Porifera. <i>Marine Drugs</i> , 2022, 20, 74.	4.6	2
2990	Metagenomic analysis of viral community in the Yangtze River expands known eukaryotic and prokaryotic virus diversity in freshwater. <i>Virologica Sinica</i> , 2022, 37, 60-69.	3.0	13
2991	A Micrarchaeon Isolate Is Covered by a Proteinaceous S-Layer. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0155321.	3.1	4
2994	Evolution and Stress Responses of CLO Genes and Potential Function of the GhCLO06 Gene in Salt Resistance of Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 801239.	3.6	3
2995	Comparative genome analysis of plant ascomycete fungal pathogens with different lifestyles reveals distinctive virulence strategies. <i>BMC Genomics</i> , 2022, 23, 34.	2.8	13
2997	Comparative transcriptomics reveal tissue level specialization towards diet in prickleback fishes. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2022, 192, 275-295.	1.5	10
2998	Learning protein fitness models from evolutionary and assay-labeled data. <i>Nature Biotechnology</i> , 2022, 40, 1114-1122.	17.5	90
2999	Refining the domain architecture model of the replication origin firing factor Treslin/TICRR. <i>Life Science Alliance</i> , 2022, 5, e202101088.	2.8	7
3000	Quantitative Insights into the Contribution of Nematocysts to the Adaptive Success of Cnidarians Based on Proteomic Analysis. <i>Biology</i> , 2022, 11, 91.	2.8	2
3001	Finding and Characterizing Repeats in Plant Genomes. <i>Methods in Molecular Biology</i> , 2022, 2443, 327-385.	0.9	2
3002	Hsp60/10 and sHsp families of heat shock protein genes in rainbow trout ( <i>Oncorhynchus mykiss</i> ) and their expression under heat stress. <i>Aquaculture International</i> , 2022, 30, 1-18.	2.2	2
3003	Whole Genome Sequence of an Edible Mushroom <i>Stropharia rugosoannulata</i> (Daqiugaigu). <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 99.	3.5	14
3004	ASPIRER: a new computational approach for identifying non-classical secreted proteins based on deep learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	11
3005	Cation/Proton Antiporter Genes in Tomato: Genomic Characterization, Expression Profiling, and Co-Localization with Salt Stress-Related QTLs. <i>Agronomy</i> , 2022, 12, 245.	3.0	6
3006	Optimized splitting of mixed-species RNA sequencing data. <i>Journal of Bioinformatics and Computational Biology</i> , 2022, 20, 2250001.	0.8	1
3007	Genome-Wide Identification of JRL Genes in Moso Bamboo and Their Expression Profiles in Response to Multiple Hormones and Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2021, 12, 809666.	3.6	4

#	ARTICLE	IF	CITATIONS
3008	Differential Transcriptome Analysis Reveals Genes Related to Low- and High-Temperature Stress in the Fall Armyworm, <i>Spodoptera frugiperda</i> . <i>Frontiers in Physiology</i> , 2021, 12, 827077.	2.8	11
3009	A computational method for predicting nucleocapsid protein in retroviruses. <i>Scientific Reports</i> , 2022, 12, 524.	3.3	0
3010	Starch content changes and metabolism-related gene regulation of Chinese cabbage synergistically induced by <i>Plasmodiophora brassicae</i> infection. <i>Horticulture Research</i> , 2022, 9, .	6.3	12
3011	Genome-wide identification of auxin response factor (ARF) gene family and the miR160-ARF18-mediated response to salt stress in peanut ( <i>Arachis hypogaea</i> L.). <i>Genomics</i> , 2022, 114, 171-184.	2.9	30
3012	Genome-Wide Characterization and Abiotic Stresses Expression Analysis of Annexin Family Genes in Poplar. <i>International Journal of Molecular Sciences</i> , 2022, 23, 515.	4.1	3
3013	The Linker Region Promotes Activity and Binding Efficiency of Modular LPMO towards Polymeric Substrate. <i>Microbiology Spectrum</i> , 2022, 10, e0269721.	3.0	11
3014	Characterizing the oral and distal gut microbiota of the threatened southern sea otter ( <i>Enhydra</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.0	7
3015	RdRp-based sensitive taxonomic classification of RNA viruses for metagenomic data. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	1
3016	<i>PERCC1</i> , a new member of the <i>Yap/TAZ</i> / <i>FAM181</i> transcriptional co-regulator family. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	2
3017	Inferring the genetic responses to acute drought stress across an ecological gradient. <i>BMC Genomics</i> , 2022, 23, 3.	2.8	2
3018	De Novo Transcriptome of <i>Mammillaria bombycina</i> (Cactaceae) under In Vitro Conditions and Identification of Glyoxalase Genes. <i>Plants</i> , 2022, 11, 399.	3.5	0
3019	Molecular characterization of Zn(II)2Cys6 cluster gene family and their association with pathogenicity of the onion basal rot pathogen, <i>Fusarium oxysporum</i> f. sp. <i>cepae</i> . <i>Physiological and Molecular Plant Pathology</i> , 2022, 117, 101782.	2.5	1
3020	Genome-Wide Identification and Co-Expression Analysis of ARF and IAA Family Genes in <i>Euscaphis konishii</i> : Potential Regulators of Triterpenoids and Anthocyanin Biosynthesis. <i>Frontiers in Genetics</i> , 2021, 12, 737293.	2.3	1
3021	Insight into the symbiotic lifestyle of DPANN archaea revealed by cultivation and genome analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	30
3022	<i>Latilactobacillus fragifolii</i> sp. nov., isolated from leaves of a strawberry plant ( <i>Fragaria x ananassa</i> ). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	7
3023	Genome-Wide Identification and Comparative Analysis of WRKY Transcription Factors Related to Momilactone Biosynthesis in <i>Calohyphnum plumiforme</i> . <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	2.2	3
3024	Genome-wide identification and expression analysis of the bZIP gene family in silver birch ( <i>Betula</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	4
3025	Characterization of a Group of UDP-Glycosyltransferases Involved in the Biosynthesis of Triterpenoid Saponins of <i>Panax notoginseng</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 770-779.	3.8	16



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3026	Genome-wide identification of C2H2-type zinc finger gene family members and their expression during abiotic stress responses in orchardgrass ( <i>Dactylis glomerata</i> ). <i>Genome</i> , 2022, 65, 189-203.	2.0	3
3027	Identification of the Cesa Subfamily and Functional Analysis of GhMCesA35 in <i>Gossypium hirsutum</i> L.. <i>Genes</i> , 2022, 13, 292.	2.4	4
3028	Assessment of Hydrocarbon Degradation Potential in Microbial Communities in Arctic Sea Ice. <i>Microorganisms</i> , 2022, 10, 328.	3.6	13
3029	Functional and genomic comparative study of the bitter taste receptor family TAS2R: Insight into the role of human TAS2R5. <i>FASEB Journal</i> , 2022, 36, e22175.	0.5	4
3030	Genome-wide identification and expression analysis of the Hsp gene superfamily in Asian long-horned beetle ( <i>Anoplophora glabripennis</i> ). <i>International Journal of Biological Macromolecules</i> , 2022, 200, 583-592.	7.5	9
3032	TransPi€a comprehensive TRanscriptome ANALysiS Pipeline for <i>de novo</i> transcriptome assembly. <i>Molecular Ecology Resources</i> , 2022, 22, 2070-2086.	4.8	14
3033	Identification of Peanut Aux/IAA Genes and Functional Prediction during Seed Development and Maturation. <i>Plants</i> , 2022, 11, 472.	3.5	4
3034	Giant sponge grounds of Central Arctic seamounts are associated with extinct seep life. <i>Nature Communications</i> , 2022, 13, 638.	12.8	22
3035	<i>De Novo</i> Biosynthesis of Oleanane-Type Ginsenosides in <i>Saccharomyces cerevisiae</i> Using Two Types of Glycosyltransferases from <i>Panax ginseng</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 2231-2240.	5.2	14
3036	The genome of the rice variety LTH provides insight into its universal susceptibility mechanism to worldwide rice blast fungal strains. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1012-1026.	4.1	16
3037	Hot spots-making directed evolution easier. <i>Biotechnology Advances</i> , 2022, 56, 107926.	11.7	35
3038	Genome-Wide Analysis of U-box E3 Ubiquitin Ligase Family in Response to ABA Treatment in <i>Salvia miltiorrhiza</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 829447.	3.6	5
3040	Inflammation and convergent placenta gene co-option contributed to a novel reproductive tissue. <i>Current Biology</i> , 2022, 32, 715-724.e4.	3.9	8
3041	First Multi-Organ Full-Length Transcriptome of Tree Fern <i>Alsophila spinulosa</i> Highlights the Stress-Resistant and Light-Adapted Genes. <i>Frontiers in Genetics</i> , 2021, 12, 784546.	2.3	4
3042	Long-Range PCR Reveals the Genetic Cargo of IncP-1 Plasmids in the Complex Microbial Community of an On-Farm Biopurification System Treating Pesticide-Contaminated Wastewater. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0164821.	3.1	1
3043	First Insights into the Repertoire of Secretory Lectins in Rotifers. <i>Marine Drugs</i> , 2022, 20, 130.	4.6	7
3045	<i>In silico</i> Analysis of the Entire <i>P. glaucum</i> Genome Identifies Regulatory Genes of the bZIP Family Modulated in Response Pathways to Water Stress. <i>American Journal of Plant Sciences</i> , 2022, 13, 277-293.	0.8	2
3046	Genomics of Climate Adaptation in <i>Pinus Lambertiana</i> . <i>Compendium of Plant Genomes</i> , 2022, , 51-65.	0.5	1



#	ARTICLE	IF	CITATIONS
3047	A Five-Fold Expansion of the Global RNA Virome Reveals Multiple New Clades of RNA Bacteriophages. SSRN Electronic Journal, 0, , .	0.4	4
3048	Genome-wide identification of CAMTA gene family members in rice ( <i>Oryza sativa</i> L.) and in silico study on their versatility in respect to gene expression and promoter structure. Functional and Integrative Genomics, 2022, 22, 193-214.	3.5	9
3049	Comparison of Gut Viral Communities in Atopic Dermatitis and Healthy Children. Frontiers in Medicine, 2022, 9, 835467.	2.6	4
3050	Gut Virome of the World's Highest-Elevation Lizard Species ( <i>Phrynocephalus erythrurus</i> ) and Tj ETQq1 10.784314 rgBT /Ov 3.0 12	3.0	12
3052	Comparative analysis of differential gene expression indicates divergence in ontogenetic strategies of leaves in two conifer genera. Ecology and Evolution, 2022, 12, e8611.	1.9	3
3053	A holistic genome dataset of bacteria, archaea and viruses of the Pearl River estuary. Scientific Data, 2022, 9, 49.	5.3	12
3054	Dynamic Expression, Differential Regulation and Functional Diversity of the CNGC Family Genes in Cotton. International Journal of Molecular Sciences, 2022, 23, 2041.	4.1	8
3055	Understanding the biomass conversion processes of bovine gut microbiota through community-wide metabolic interaction network. Bioresource Technology Reports, 2022, 17, 100989.	2.7	0
3056	Time-resolved and multi-tissue RNAseq provides new insights on the immune responses of European eels following infection with <i>Aeromonas hydrophila</i> . 2022, 1, 100003.		3
3057	Genome-Wide Characterization and Anthocyanin-Related Expression Analysis of the B-BOX Gene Family in <i>Capsicum annuum</i> L.. Frontiers in Genetics, 2022, 13, 847328.	2.3	6
3058	Genomic Analysis of Molecular Bacterial Mechanisms of Resistance to Phage Infection. Frontiers in Microbiology, 2021, 12, 784949.	3.5	13
3059	Using deep learning to annotate the protein universe. Nature Biotechnology, 2022, 40, 932-937.	17.5	133
3060	Sexual Crossing, Chromosome-Level Genome Sequences, and Comparative Genomic Analyses for the Medicinal Mushroom <i>Taiwanofungus camphoratus</i> (Syn. <i>Antrodia cinnamomea</i> ) Tj ETQq0 0 0 rgBT 40 10 40 10 50 2	10	40
3061	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. ELife, 2022, 11, .	6.0	43
3062	Transkingdom Analysis of the Female Reproductive Tract Reveals Bacteriophages form Communities. Viruses, 2022, 14, 430.	3.3	10
3064	Extended characterisation of five archival tick-borne viruses provides insights for virus discovery in Australian ticks. Parasites and Vectors, 2022, 15, 59.	2.5	2
3066	NRD: Nicotiana Resistance Database, a Comprehensive Platform of Stress Tolerance in Nicotiana. Agronomy, 2022, 12, 508.	3.0	0
3067	Genome-Wide Analysis of the Gene Structure, Expression and Protein Interactions of the Peach ( <i>Prunus persica</i> ) TIFY Gene Family. Frontiers in Plant Science, 2022, 13, 792802.	3.6	11

#	ARTICLE	IF	CITATIONS
3068	METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. <i>Microbiome</i> , 2022, 10, 33.	11.1	168
3069	Genome-wide identification, phylogenetic and expression pattern analysis of MADS-box family genes in foxtail millet ( <i>Setaria italica</i> ). <i>Scientific Reports</i> , 2022, 12, 4979.	3.3	12
3070	Genome-wide identification and comparative analysis of lipocalin families in Lepidoptera with an emphasis on <i>Bombyx mori</i> . <i>Insect Science</i> , 2022, , .	3.0	1
3071	In silico evaluation of a targeted metaproteomics strategy for broad screening of cellulolytic enzyme capacities in anaerobic microbiome bioreactors. , 2022, 15, 32.		3
3073	Pan-Genome Analysis of <i>Delftia tsuruhatensis</i> Reveals Important Traits Concerning the Genetic Diversity, Pathogenicity, and Biotechnological Properties of the Species. <i>Microbiology Spectrum</i> , 2022, 10, e0207221.	3.0	13
3074	Pervasive occurrence of splice-site-creating mutations and their possible involvement in genetic disorders. <i>Npj Genomic Medicine</i> , 2022, 7, 22.	3.8	3
3076	Systematic identification and expression profiles of the BAHD superfamily acyltransferases in barley ( <i>Hordeum vulgare</i> ). <i>Scientific Reports</i> , 2022, 12, 5063.	3.3	5
3078	Heat Shock Protein 20 Gene Superfamilies in Red Algae: Evolutionary and Functional Diversities. <i>Frontiers in Plant Science</i> , 2022, 13, 817852.	3.6	6
3079	Functional and Phylogenetic Characterization of Bacteria in Bovine Rumen Using Fractionation of Ruminal Fluid. <i>Frontiers in Microbiology</i> , 2022, 13, 813002.	3.5	8
3081	Protein dynamics developments for the large scale and cryoEM: case study of <i>ProDy</i> 2.0. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 399-409.	2.3	7
3082	Transcriptome analysis of the bivalve <i>Placuna placenta</i> mantle reveals potential biomineralization-related genes. <i>Scientific Reports</i> , 2022, 12, 4743.	3.3	6
3083	Genome-wide identification, characterisation, and expression of C3HC4-type RING finger gene family in <i>Capsicum annuum</i> L. <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 603-614.	1.9	3
3084	Pan-Genome Analysis Reveals the Abundant Gene Presence/Absence Variations Among Different Varieties of Melon and Their Influence on Traits. <i>Frontiers in Plant Science</i> , 2022, 13, 835496.	3.6	8
3085	Genomic Fishing and Data Processing for Molecular Evolution Research. <i>Methods and Protocols</i> , 2022, 5, 26.	2.0	4
3086	Chromosome-Level Genome Assembly of <i>Bupleurum chinense</i> DC Provides Insights Into the Saikosaponin Biosynthesis. <i>Frontiers in Genetics</i> , 2022, 13, 878431.	2.3	0
3087	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. <i>Communications Biology</i> , 2022, 5, 247.	4.4	3
3088	The APAF1_C/WD40 repeat domain-encoding gene from the sea lettuce <i>Ulva mutabilis</i> sheds light on the evolution of NB-ARC domain-containing proteins in green plants. <i>Planta</i> , 2022, 255, 76.	3.2	5
3089	Structural Domains of CIF3 Required for Interaction with Cytokinesis Regulatory Proteins and for Cytokinesis Initiation in <i>Trypanosoma brucei</i> . <i>MSphere</i> , 2022, 7, e0004722.	2.9	3

#	ARTICLE	IF	CITATIONS
3091	Genome-Wide Identification, Evolution and Expression Analysis of the Glutathione S-Transferase Supergene Family in Euphorbiaceae. <i>Frontiers in Plant Science</i> , 2022, 13, 808279.	3.6	3
3092	EnsembleFam: towards more accurate protein family prediction in the twilight zone. <i>BMC Bioinformatics</i> , 2022, 23, 90.	2.6	3
3093	Efficient Exploration of Sequence Space by Sequence-Guided Protein Engineering and Design. <i>Biochemistry</i> , 2023, 62, 210-220.	2.5	11
3094	Tissue-Specific Expression of the Terpene Synthase Family Genes in <i>Rosa chinensis</i> and Effect of Abiotic Stress Conditions. <i>Genes</i> , 2022, 13, 547.	2.4	11
3096	High transcriptome plasticity drives phosphate starvation responses in tomato. <i>Stress Biology</i> , 2022, 2, 1.	3.1	4
3097	Unifying the known and unknown microbial coding sequence space. <i>ELife</i> , 2022, 11, .	6.0	41
3098	HIV-1 infections with multiple founders associate with the development of neutralization breadth. <i>PLoS Pathogens</i> , 2022, 18, e1010369.	4.7	5
3099	Comparative analysis of the kinomes of <i>Plasmodium falciparum</i> , <i>Plasmodium vivax</i> and their host <i>Homo sapiens</i> . <i>BMC Genomics</i> , 2022, 23, 237.	2.8	9
3100	Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. <i>Nature Ecology and Evolution</i> , 2022, 6, 630-643.	7.8	13
3101	Genome-wide identification of glutathione S-transferase gene family members in tea plant ( <i>Camellia</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Macromolecules</i> , 2022, 205, 749-760.	7.5	17
3102	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
3103	The importance of biofilm formation for cultivation of a <i>Micrarchaeon</i> and its interactions with its <i>Thermoplasmatales</i> host. <i>Nature Communications</i> , 2022, 13, 1735.	12.8	12
3104	Dissection of valine-glutamine genes and their responses to drought stress in <i>Arachis hypogaea</i> cv. Tifrunner. <i>Functional and Integrative Genomics</i> , 2022, , 1.	3.5	3
3105	A chromosome-scale genome assembly of the Mongolian oak ( <i>Quercus mongolica</i> ). <i>Molecular Ecology Resources</i> , 2022, 22, 2396-2410.	4.8	25
3106	The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. <i>BMC Plant Biology</i> , 2022, 22, 179.	3.6	13
3108	Genome-wide survey of the GATA gene family in camptothecin-producing plant <i>Ophiorrhiza pumila</i> . <i>BMC Genomics</i> , 2022, 23, 256.	2.8	9
3109	Two defence systems eliminate plasmids from seventh pandemic <i>Vibrio cholerae</i> . <i>Nature</i> , 2022, 604, 323-329.	27.8	69
3110	Genome-Wide Identification of TLP Gene Family and Their Roles in <i>Carya cathayensis</i> Sarg in Response to <i>Botryosphaeria dothidea</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 849043.	3.6	2

#	ARTICLE	IF	CITATIONS
3111	Conformational Variation in Enzyme Catalysis: A Structural Study on Catalytic Residues. Journal of Molecular Biology, 2022, 434, 167517.	4.2	17
3112	Description and genome analysis of <i>Luteimonas viscosa</i> sp. nov., a novel bacterium isolated from soil of a sunflower field. Antonie Van Leeuwenhoek, 2022, 115, 749-760.	1.7	2
3113	Genome-wide identification and characterization of bZIP gene family and cloning of candidate genes for anthocyanin biosynthesis in pomegranate ( <i>Punica granatum</i> ). BMC Plant Biology, 2022, 22, 170.	3.6	17
3114	Identification of Differentially Expressed Genes Reveal Conserved Mechanisms in the Rice-Magnaporthe oryzae Interaction. Frontiers in Plant Science, 2022, 13, 723356.	3.6	2
3115	Genome-wide identification and low-salinity stress analysis of the Hsp70 gene family in swimming crab ( <i>Portunus trituberculatus</i> ). International Journal of Biological Macromolecules, 2022, 208, 126-135.	7.5	13
3116	Phylogenetic analysis of PP2C proteins and interactive proteins analyze of BjuPP2C52 in Brassica juncea. Plant Physiology and Biochemistry, 2022, 179, 25-31.	5.8	2
3117	Metabolome and whole transcriptome analyses reveal the molecular mechanisms underlying terpenoids biosynthesis in <i>Sapindus mukorossi</i> fruits. Industrial Crops and Products, 2022, 181, 114810.	5.2	5
3118	Knowledge-Based Unfolded State Model for Protein Design. Methods in Molecular Biology, 2022, 2405, 403-424.	0.9	0
3119	Full Issue PDF. Molecular Plant-Microbe Interactions, 2021, 34, 1228-1333.	2.6	0
3120	Hydrogen bonds meet self-attention: all you need for protein structure embedding. , 2021, , .		3
3121	Deep Conservation of Histone Variants in Thermococcales Archaea. Genome Biology and Evolution, 2022, 14, .	2.5	6
3123	Analyses of Lysin-motif Receptor-like Kinase (LysM-RLK) Gene Family in Allotetraploid Brassica napus L. and Its Progenitor Species: An In Silico Study. Cells, 2022, 11, 37.	4.1	8
3124	Advances in Biosynthesis of Natural Products from Marine Microorganisms. Microorganisms, 2021, 9, 2551.	3.6	11
3125	GDS: A Genomic Database for Strawberries ( <i>Fragaria</i> spp.). Horticulturae, 2022, 8, 41.	2.8	4
3126	Co-cultivation of the anaerobic fungus <i>Caecomyces churrovis</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. Biotechnology for Biofuels, 2021, 14, 234.	6.2	21
3128	The microbial gbu gene cluster links cardiovascular disease risk associated with red meat consumption to microbiota l-carnitine catabolism. Nature Microbiology, 2022, 7, 73-86.	13.3	36
3129	Investigating the OXA Variants of ESKAPE Pathogens. Antibiotics, 2021, 10, 1539.	3.7	7
3131	A Beginner's Guide on Integrating *Omics Approaches to Study Marine Microbial Communities: Details and Discussions From Sample Collection to Bioinformatics Analysis. Frontiers in Marine Science, 2021, 8, .	2.5	2

#	ARTICLE	IF	CITATIONS
3133	Unlocking the bacterial contact-dependent antibacterial activity to engineer a biocontrol alliance of two species from natural incompatibility to artificial compatibility. <i>Stress Biology</i> , 2021, 1, 1.	3.1	4
3134	Genome-Wide Identification and Characterization of Caffeic Acid O-Methyltransferase Gene Family in Soybean. <i>Plants</i> , 2021, 10, 2816.	3.5	13
3135	Hoyosella laciisalsi sp. nov., a halotolerant actinobacterium isolated from the Lake Gudzhirganskoe. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	6
3136	Marine Fungi. <i>The Microbiomes of Humans, Animals, Plants, and the Environment</i> , 2022, , 243-295.	0.6	4
3137	Linear plasmids in Klebsiella and other Enterobacteriaceae. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
3138	Genome-wide identification and evolution of interleukins and their potential roles in response to CCRV and Aeromonas hydrophila challenge in grass carp (Ctenopharyngodon idella). <i>Aquaculture</i> , 2022, 556, 738266.	3.5	1
3140	R2R3-MYB gene family: Genome-wide identification provides insight to improve the content of proanthocyanidins in Trifolium repens. <i>Gene</i> , 2022, , 146523.	2.2	3
3143	Integrative Analysis of Nanopore and Illumina Sequencing Reveals Alternative Splicing Complexity in Pig Longissimus Dorsi Muscle. <i>Frontiers in Genetics</i> , 2022, 13, 877646.	2.3	7
3144	Origin and early evolution of the plant terpene synthase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2100361119.	7.1	48
3145	Sexual morph specialisation in a trioecious nematode balances opposing selective forces. <i>Scientific Reports</i> , 2022, 12, 6402.	3.3	3
3146	Whole-Genome-Based Web Genomic Resource for Water Buffalo (Bubalus bubalis). <i>Frontiers in Genetics</i> , 2022, 13, 809741.	2.3	4
3147	Identification and Characterization of SOG1 (Suppressor of Gamma Response 1) Homologues in Plants Using Data Mining Resources and Gene Expression Profiling. <i>Genes</i> , 2022, 13, 667.	2.4	4
3148	Virome in the cloaca of wild and breeding birds revealed a diversity of significant viruses. <i>Microbiome</i> , 2022, 10, 60.	11.1	32
3473	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. <i>Journal of Molecular Biology</i> , 2022, 434, 167579.	4.2	22
3474	Deletion and tandem duplications of biosynthetic genes drive the diversity of triterpenoids in Aralia elata. <i>Nature Communications</i> , 2022, 13, 2224.	12.8	34
3475	Molecular evolutionary analysis of the <scp>SM</scp> and <scp>SNARE</scp> vesicle fusion machinery in ciliates shows concurrent expansions in late secretory machinery. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12919.	1.7	4
3476	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. <i>Environmental Microbiomes</i> , 2022, 17, 19.	5.0	6
3477	Managing and Documenting Legacy Scientific Workflows. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 277.	1.5	2

#	ARTICLE	IF	CITATIONS
3478	Genome Mining Shows Ubiquitous Presence and Extensive Diversity of Toxin-Antitoxin Systems in <i>Pseudomonas syringae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 815911.	3.5	5
3479	Profiles of Natural and Designed Protein-Like Sequences Effectively Bridge Protein Sequence Gaps: Implications in Distant Homology Detection. <i>Methods in Molecular Biology</i> , 2022, 2449, 149-167.	0.9	2
3480	Bioinformatics-assisted multiomics approaches to improve the agronomic traits in cotton. , 2022, , 233-251.		1
3481	Enhanced Cultured Diversity of the Mouse Gut Microbiota Enables Custom-Made Synthetic Communities. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
3482	Transcriptome Analysis Reveals the Molecular Response to Salinity Challenge in Larvae of the Giant Freshwater Prawn <i>Macrobrachium rosenbergii</i> . <i>Frontiers in Physiology</i> , 2022, 13, 885035.	2.8	1
3483	Comprehensive Profiling of Tubby-Like Proteins in Soybean and Roles of the GmTLP8 Gene in Abiotic Stress Responses. <i>Frontiers in Plant Science</i> , 2022, 13, 844545.	3.6	10
3484	Genome-Wide Identification and Expression Analysis of LBD Transcription Factor Genes in Passion Fruit ( <i>Passiflora edulis</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 4700.	4.1	15
3485	Identification and Biosynthesis of Pro-Inflammatory Sulfonolipids from an Opportunistic Pathogen <i>Chryseobacterium gleum</i> . <i>ACS Chemical Biology</i> , 2022, 17, 1197-1206.	3.4	12
3486	Bacterial-type ferroxidase tunes iron-dependent phosphate sensing during Arabidopsis root development. <i>Current Biology</i> , 2022, 32, 2189-2205.e6.	3.9	16
3487	Transcriptomic Insights into the Diversity and Evolution of Myxozoa (Cnidaria, Endocnidozoa) Toxin-like Proteins. <i>Marine Drugs</i> , 2022, 20, 291.	4.6	2
3488	Transcriptome and Metabolome Analysis of the Synthesis Pathways of Allelochemicals in <i>Eupatorium adenophorum</i> . <i>ACS Omega</i> , 2022, 7, 16803-16816.	3.5	1
3489	Whole-Transcriptome Analysis Reveals Long Noncoding RNAs Involved in Female Floral Development of Hickory ( <i>Carya cathayensis</i> Sarg.). <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	2
3490	Genome-Wide Identification of the SAMS Gene Family in Upland Cotton ( <i>Gossypium hirsutum</i> L.) and Expression Analysis in Drought Stress Treatments. <i>Genes</i> , 2022, 13, 860.	2.4	2
3491	Gene regulatory networks shape developmental plasticity of root cell types under water extremes in rice. <i>Developmental Cell</i> , 2022, 57, 1177-1192.e6.	7.0	27
3492	Tolypocladamide H and the Proposed Tolypocladamide NRPS in <i>Tolypocladium</i> Species. <i>Journal of Natural Products</i> , 2022, 85, 1363-1373.	3.0	10
3493	Cryptic Genes for Interbacterial Antagonism Distinguish <i>Rickettsia</i> Species Infecting Blacklegged Ticks From Other <i>Rickettsia</i> Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 880813.	3.9	8
3494	A comparative study indicates vertical inheritance and horizontal gene transfer of arsenic resistance-related genes in eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2022, 173, 107479.	2.7	4
3495	Complete Genome Sequence of Enterobacter Phage vB_EcRAM-01, a New <i>Pseudotevenvirus</i> against the Enterobacter cloacae Complex. <i>Microbiology Resource Announcements</i> , 2022, , e0004522.	0.6	0

#	ARTICLE	IF	CITATIONS
3496	Highly transmissible cytoplasmic incompatibility by the extracellular insect symbiont <i>Spiroplasma</i> . <i>IScience</i> , 2022, 25, 104335.	4.1	20
3497	Impacts of food waste to sludge ratios on microbial dynamics and functional traits in thermophilic digesters. <i>Water Research</i> , 2022, 219, 118590.	11.3	4
3498	Reconstruction of full-length LINE-1 progenitors from ancestral genomes. <i>Genetics</i> , 2022, 221, .	2.9	6
3499	The Mantle Transcriptome of <i>Chamelea gallina</i> (Mollusca: Bivalvia) and Shell Biomineralization. <i>Animals</i> , 2022, 12, 1196.	2.3	1
3500	Inferring antibiotic susceptibility from metagenomic data: dream or reality?. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1225-1229.	6.0	3
3501	Genomic features of the polyphagous cotton leafworm <i>Spodoptera littoralis</i> . <i>BMC Genomics</i> , 2022, 23, 353.	2.8	2
3502	Allorecognition genes drive reproductive isolation in <i>Podospora anserina</i> . <i>Nature Ecology and Evolution</i> , 2022, 6, 910-923.	7.8	15
3503	Evaluating metagenomic assembly approaches for biome-specific gene catalogues. <i>Microbiome</i> , 2022, 10, 72.	11.1	18
3504	Rapid evolution of T2/S-RNase genes in <i>Fragaria</i> linked to multiple transitions from self-incompatibility to self-compatibility. <i>Plant Diversity</i> , 2023, 45, 219-228.	3.7	3
3505	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
3506	Diacylglycerol, PKC and MAPK signaling initiate tubeworm metamorphosis in response to bacteria. <i>Developmental Biology</i> , 2022, 487, 99-109.	2.0	7
3508	WITCH: Improved Multiple Sequence Alignment Through Weighted Consensus Hidden Markov Model Alignment. <i>Journal of Computational Biology</i> , 2022, , .	1.6	10
3509	Distinct gene clusters drive formation of ferrosome organelles in bacteria. <i>Nature</i> , 2022, 606, 160-164.	27.8	15
3510	Chromosome-level assembly, annotation and phylome of <i>Pelobates cultripes</i> , the western spadefoot toad. <i>DNA Research</i> , 2022, 29, .	3.4	1
3511	Genome-wide identification of sugar transporter gene family in Brassicaceae crops and an expression analysis in the radish. <i>BMC Plant Biology</i> , 2022, 22, 245.	3.6	1
3512	TFK1, a basal body transition fibre protein that is essential for cytokinesis in <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2022, 135, .	2.0	1
3515	Gene Co-expression Network and Regression Analysis Identify the Transcriptomic, Physiological, and Biochemical Indicators of the Response of Alpine Woody Plant <i>Rhododendron rex</i> to Drought Stress. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
3516	Whole-genome sequencing uncovers the structural and transcriptomic landscape of hexaploid wheat/ <i>Ambylopyrum muticum</i> introgression lines. <i>Plant Biotechnology Journal</i> , 2023, 21, 482-496.	8.3	10



#	ARTICLE	IF	CITATIONS
3517	HDACs Gene Family Analysis of Eight Rosaceae Genomes Reveals the Genomic Marker of Cold Stress in <i>Prunus mume</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 5957.	4.1	7
3518	Ancient Origins of Cytoskeletal Crosstalk: Spectraplakins-like Proteins Precede the Emergence of Cortical Microtubule Stabilization Complexes as Crosslinkers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5594.	4.1	3
3520	Role of plant growth-promoting rhizobacteria in boosting the phytoremediation of stressed soils: Opportunities, challenges, and prospects. <i>Chemosphere</i> , 2022, 303, 134954.	8.2	68
3521	In silico identification of <i>Theileria parva</i> surface proteins. <i>Cell Surface</i> , 2022, 8, 100078.	3.0	0
3522	Antibiotics-Induced Transfer of Resistance Genes and Emergence of New Resistant Bacteria in Red Swamp Crayfish Guts and Culture Sediments. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3524	Genome-Wide Identification and Functional Differentiation of Fatty Acid Desaturase Genes in <i>Olea europaea</i> L.. <i>Plants</i> , 2022, 11, 1415.	3.5	2
3525	Genome-Wide Identification, Characterization, and Expression Profiling Analysis of SPL Gene Family during the Inflorescence Development in <i>Trifolium repens</i> . <i>Genes</i> , 2022, 13, 900.	2.4	4
3528	Identification and relative expression analysis of CaFRK gene family in pepper. <i>3 Biotech</i> , 2022, 12, .	2.2	2
3529	Combinatorial assembly and optimisation of designer cellulosomes: a galactomannan case study. , 2022, 15, .		4
3530	Anti-CRISPR prediction using deep learning reveals an inhibitor of Cas13b nucleases. <i>Molecular Cell</i> , 2022, 82, 2714-2726.e4.	9.7	17
3531	UDP-glucose pyrophosphorylase: genome-wide identification, expression and functional analyses in <i>Gossypium hirsutum</i> . <i>PeerJ</i> , 0, 10, e13460.	2.0	2
3533	Conservation and Divergence of Phosphoenolpyruvate Carboxylase Gene Family in Cotton. <i>Plants</i> , 2022, 11, 1482.	3.5	1
3534	Metagenomic assembled plasmids of the human microbiome vary across disease cohorts. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
3535	Ecogenomics sheds light on diverse lifestyle strategies in freshwater CPR. <i>Microbiome</i> , 2022, 10, .	11.1	22
3536	Species-Specific Gene Expansion of the Cellulose synthase Gene Superfamily in the Orchidaceae Family and Functional Divergence of Mannan Synthesis-Related Genes in <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
3539	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014, 14, 329.	3.6	0
3541	Gut transcriptome of two bark beetle species stimulated with the same kairomones reveals molecular differences in detoxification pathways. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3080-3095.	4.1	5
3542	Contrastive learning on protein embeddings enlightens midnight zone. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	38

#	ARTICLE	IF	CITATIONS
3543	Targeted Large-Scale Genome Mining and Candidate Prioritization for Natural Product Discovery. <i>Marine Drugs</i> , 2022, 20, 398.	4.6	13
3544	Genome-Wide Characterization of Superoxide Dismutase (SOD) Genes in <i>Daucus carota</i> : Novel Insights Into Structure, Expression, and Binding Interaction With Hydrogen Peroxide (H <sub>2</sub> O <sub>2</sub> ) Under Abiotic Stress Condition. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	13
3545	Mechanistic insights into the key marine dimethylsulfoniopropionate synthesis enzyme DsyB/DSYB. , 2022, 1, 114-130.		5
3546	Using population selection and sequencing to characterize natural variation of starvation resistance in <i>Caenorhabditis elegans</i> . <i>ELife</i> , 0, 11, .	6.0	4
3547	A light-sensing system in the common ancestor of the fungi. <i>Current Biology</i> , 2022, 32, 3146-3153.e3.	3.9	13
3548	Plant pan-genomics: recent advances, new challenges, and roads ahead. <i>Journal of Genetics and Genomics</i> , 2022, 49, 833-846.	3.9	27
3549	Global leaf and root transcriptome in response to cadmium reveals tolerance mechanisms in <i>Arundo donax</i> L. <i>BMC Genomics</i> , 2022, 23, .	2.8	7
3550	Evolutionary Divergence and <i>Radula</i> Diversification in Two Ecomorphs from an Adaptive Radiation of Freshwater Snails. <i>Genes</i> , 2022, 13, 1029.	2.4	3
3551	DeepPhageTP: a convolutional neural network framework for identifying phage-specific proteins from metagenomic sequencing data. <i>PeerJ</i> , 0, 10, e13404.	2.0	3
3552	Machine learning/molecular dynamic protein structure prediction approach to investigate the protein conformational ensemble. <i>Scientific Reports</i> , 2022, 12, .	3.3	11
3553	Characterization of the genome and silk-gland transcriptomes of Darwin's bark spider ( <i>Caerostris</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 T	2.5	8
3555	Complete genome sequence and phylogenetic analysis of medicinal plant <i>Abrus cantoniensis</i> for evolutionary research and germplasm utilization. <i>Plant Genome</i> , 0, , .	2.8	2
3556	Gene Transfer Agents in Bacterial Endosymbionts of Microbial Eukaryotes. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	8
3557	Cloning and Functional Analysis of NtMYB9 in Jinzhanyintai™ of <i>Narcissus tazetta</i> var. <i>chinensis</i> . <i>Horticulturae</i> , 2022, 8, 528.	2.8	1
3558	Genome-Wide Identification and Analysis of the Class III Peroxidase Gene Family in Tobacco ( <i>Nicotiana</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 T	2.3	9
3559	Cellular RNA Targets of Cold Shock Proteins CspC and CspE and Their Importance for Serum Resistance in Septicemic <i>Escherichia coli</i> . <i>MSystems</i> , 2022, 7, .	3.8	11
3560	Identification of aluminum-activated malate transporters (ALMT) family genes in hydrangea and functional characterization of HmALMT5/9/11 under aluminum stress. <i>PeerJ</i> , 0, 10, e13620.	2.0	3
3561	Structure-Functional Characteristics of the Svx Protein The Virulence Factor of the Phytopathogenic Bacterium <i>Pectobacterium atrosepticum</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6914.	4.1	5

#	ARTICLE	IF	CITATION
3562	Structural and functional analysis of a resistance gene and resistance gene analogs in local cultivars of Ipomoea batatas Lam. from Barbados. Physiological and Molecular Plant Pathology, 2022, 120, 101855.	2.5	0
3563	Discovery of deoxyribonuclease II-like proteins in bacteria. Molecular Phylogenetics and Evolution, 2022, 174, 107554.	2.7	0
3564	Microbial metabolic routes in metagenome assembled genomes are mirrored by the mass balance of polycyclic aromatic hydrocarbons in a high altitude lake. Environmental Pollution, 2022, 308, 119592.	7.5	0
3565	Genome assembly provided new insights into the Cinnamomum burmannii evolution and D-borneol biosynthesis differences between chemotypes. Industrial Crops and Products, 2022, 186, 115181.	5.2	6
3567	Taxonomically Restricted Genes Are Associated With Responses to Biotic and Abiotic Stresses in Sugarcane (Saccharum spp.). Frontiers in Plant Science, 0, 13, .	3.6	3
3568	Marine Microeukaryote Metatranscriptomics: Sample Processing and Bioinformatic Workflow Recommendations for Ecological Applications. Frontiers in Marine Science, 0, 9, .	2.5	8
3569	Long-read-based draft genome sequence of Indian black gram IPUâ€™94â€™1 â€“ Uttaraâ€™™: Insights into disease resistance and seed storage protein genes. Plant Genome, 2022, 15, .	2.8	3
3570	Genome-Wide Evolutionary Analysis of Putative Non-Specific Herbicide Resistance Genes and Compilation of Core Promoters between Monocots and Dicots. Genes, 2022, 13, 1171.	2.4	5
3571	Evaluation and Genome Analysis of Bacillus subtilis YB-04 as a Potential Biocontrol Agent Against Fusarium Wilt and Growth Promotion Agent of Cucumber. Frontiers in Microbiology, 0, 13, .	3.5	16
3572	Protective Effects of Cinnamaldehyde on the Oxidative Stress, Inflammatory Response, and Apoptosis in the Hepatocytes of Salmonella Gallinarum-Challenged Young Chicks. Oxidative Medicine and Cellular Longevity, 2022, 2022, 1-21.	4.0	3
3573	Deciphering polymorphism in 61,157 Escherichia coli genomes via epistatic sequence landscapes. Nature Communications, 2022, 13, .	12.8	6
3574	Comparative phylogeny and evolutionary analysis of Dicer-like protein family in two plant monophyletic lineages. Journal of Genetic Engineering and Biotechnology, 2022, 20, 103.	3.3	0
3575	Transcriptome Analysis of Soursop (Annona muricata L.) Fruit under Postharvest Storage Identifies Genes Families Involved in Ripening. Plants, 2022, 11, 1798.	3.5	3
3576	Identification of a Putative CodY Regulon in the Gram-Negative Phylum Synergistetes. International Journal of Molecular Sciences, 2022, 23, 7911.	4.1	0
3577	Many dissimilar NusG protein domains switch between Î±-helix and Î²-sheet folds. Nature Communications, 2022, 13, .	12.8	20
3579	Transcriptome of the coralline alga Calliarthron tuberculosum (Corallinales, Rhodophyta) reveals convergent evolution of a partial lignin biosynthesis pathway. PLoS ONE, 2022, 17, e0266892.	2.5	4
3580	A consensus protocol for the recovery of mercury methylation genes from metagenomes. Molecular Ecology Resources, 2023, 23, 190-204.	4.8	10
3581	Deep-Sea Sediments from the Southern Gulf of Mexico Harbor a Wide Diversity of PKS I Genes. Antibiotics, 2022, 11, 887.	3.7	0

#	ARTICLE	IF	CITATIONS
3582	Structurally derived universal mechanism for the catalytic cycle of the tail-anchored targeting factor Get3. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 820-830.	8.2	7
3583	Characterization of the <i>WRKY</i> gene family reveals its contribution to the adaptability of almond (<i>Prunus dulcis</i>). <i>PeerJ</i> , 0, 10, e13491.	2.0	5
3584	Genome-Wide Analysis of CqCrRLK1L and CqRALF Gene Families in <i>Chenopodium quinoa</i> and Their Roles in Salt Stress Response. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
3585	Biomimetic generation of the strongest known biomaterial found in limpet tooth. <i>Nature Communications</i> , 2022, 13, .	12.8	5
3586	Genome-wide identification, phylogenetic analysis, and expression profiles of trihelix transcription factor family genes in quinoa ( <i>Chenopodium quinoa</i> Willd.) under abiotic stress conditions. <i>BMC Genomics</i> , 2022, 23, .	2.8	8
3587	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. <i>Antibiotics</i> , 2022, 11, 952.	3.7	10
3588	The clove ( <i>Syzygium aromaticum</i> ) genome provides insights into the eugenol biosynthesis pathway. <i>Communications Biology</i> , 2022, 5, .	4.4	6
3589	Wide distribution of the <i>sad</i> gene cluster for subâ€terminal oxidation in alkane utilizers. <i>Environmental Microbiology</i> , 2022, 24, 6307-6319.	3.8	6
3590	Identifying potential flavonoid biosynthesis regulator in <i>Zanthoxylum bungeanum</i> Maxim. by genome-wide characterization of the MYB transcription factor gene family. <i>Journal of Integrative Agriculture</i> , 2022, 21, 1997-2018.	3.5	6
3591	The PH Domain and C-Terminal polyD Motif of Phafin2 Exhibit a Unique Concurrence in Animals. <i>Membranes</i> , 2022, 12, 696.	3.0	1
3592	Emerging Computational Approaches for Antimicrobial Peptide Discovery. <i>Antibiotics</i> , 2022, 11, 936.	3.7	12
3593	Origins, genomic structure and copy number variation of snake venom myotoxins. <i>Toxicon</i> , 2022, 216, 92-106.	1.6	5
3594	Evaluation and redesign of the primers for detecting nitrogen cycling genes in environments. <i>Methods in Ecology and Evolution</i> , 2022, 13, 1976-1989.	5.2	6
3595	Pan-genome analysis of three main Chinese chestnut varieties. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
3596	Molecular Characterization of TGF-Beta Gene Family in Buffalo to Identify Gene Duplication and Functional Mutations. <i>Genes</i> , 2022, 13, 1302.	2.4	7
3597	Genome-Wide Identification and Characterization of RNA/DNA Differences Associated with <i>Fusarium graminearum</i> Infection in Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7982.	4.1	2
3598	A unique class of Zn <sup>2+</sup> -binding serine-based PBPs underlies cephalosporin resistance and sporogenesis in <i>Clostridioides difficile</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	9
3599	Genome-Wide Identification and Expression Pattern Analysis of the TCP Gene Family in Radish ( <i>Raphanus sativus</i> L.). <i>Horticulturae</i> , 2022, 8, 656.	2.8	1

#	ARTICLE	IF	CITATIONS
3600	MRG Chip: A High-Throughput qPCR-Based Tool for Assessment of the Heavy Metal(loid) Resistome. <i>Environmental Science &amp; Technology</i> , 2022, 56, 10656-10667.	10.0	10
3601	Modulating co-translational protein folding by rational design and ribosome engineering. <i>Nature Communications</i> , 2022, 13, .	12.8	12
3602	A temporal view of the water kefir microbiota and flavour attributes. <i>Innovative Food Science and Emerging Technologies</i> , 2022, 80, 103084.	5.6	15
3604	Comparative Genomic Characterization of Insulin-Like Growth Factor Binding Proteins in Cattle and Buffalo. <i>BioMed Research International</i> , 2022, 2022, 1-15.	1.9	4
3605	Structured hierarchical models for probabilistic inference from perturbation screening data. <i>Annals of Applied Statistics</i> , 2022, 16, .	1.1	0
3607	Genome of the hoverfly <i>Eupeodes corollae</i> provides insights into the evolution of predation and pollination in insects. <i>BMC Biology</i> , 2022, 20, .	3.8	6
3608	Genome-wide identification and characterization of GATA family genes in wheat. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	14
3609	Characterization and Functional Implications of the Nonexpressor of Pathogenesis-Related Genes 1 (NPR1) in <i>Saccharum</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 7984.	4.1	3
3611	A fat body transcriptome analysis of the immune responses of <i>Rhodnius prolixus</i> to artificial infections with bacteria. <i>Parasites and Vectors</i> , 2022, 15, .	2.5	2
3612	Genome-wide identification and expression analysis of the SINAC gene family in tomato based on a high-quality genome. <i>Horticulture Environment and Biotechnology</i> , 0, , .	2.1	0
3613	Genome-wide analysis of the Thaumatin-like gene family in Qingke ( <i>Hordeum vulgare</i> L. var. nudum) uncovers candidates involved in plant defense against biotic and abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
3614	Vexitoxins: conotoxin-like venom peptides from predatory gastropods of the genus <i>Vexillum</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	2.6	4
3617	The gill transcriptome of threatened European freshwater mussels. <i>Scientific Data</i> , 2022, 9, .	5.3	10
3618	Effect of a Stannous Fluoride Dentifrice on Biofilm Composition, Gene Expression and Biomechanical Properties. <i>Microorganisms</i> , 2022, 10, 1691.	3.6	6
3619	Comparative Genomics of Mortierellaceae Provides Insights into Lipid Metabolism: Two Novel Types of Fatty Acid Synthase. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 891.	3.5	4
3620	CRISPRCasStack: a stacking strategy-based ensemble learning framework for accurate identification of Cas proteins. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
3621	Identification of early quassinoid biosynthesis in the invasive tree of heaven ( <i>Ailanthus altissima</i> ) confirms evolutionary origin from protolimonoids. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	12
3623	Identification of OSCA gene family in <i>Solanum habrochaites</i> and its function analysis under stress. <i>BMC Genomics</i> , 2022, 23, .	2.8	9

#	ARTICLE	IF	CITATIONS
3624	Genome-wide identification and expression analysis of the cucumber PP2C gene family. BMC Genomics, 2022, 23, .	2.8	11
3625	The chromosome-level holly ( <i>Ilex latifolia</i> ) genome reveals key enzymes in triterpenoid saponin biosynthesis and fruit color change. Frontiers in Plant Science, 0, 13, .	3.6	7
3627	Insights into Evolutionary, Genomic, and Biogeographic Characterizations of <i>Chryseobacterium nepalense</i> Represented by a Polyvinyl Alcohol-Degrading Bacterium, AC3. Microbiology Spectrum, 2022, 10, .	3.0	1
3629	Genome-wide characterization of laccase gene family in <i>Schizophyllum commune</i> 20R-7-F01, isolated from deep sediment 2 km below the seafloor. Frontiers in Microbiology, 0, 13, .	3.5	2
3632	Genome-wide characterization and expression analysis of <i>bHLH</i> gene family in physic nut ( <i>Jatropha curcas</i> L.). PeerJ, 0, 10, e13786.	2.0	4
3633	Genomes from Uncultivated Pelagiphages Reveal Multiple Phylogenetic Clades Exhibiting Extensive Auxiliary Metabolic Genes and Cross-Family Multigene Transfers. MSystems, 2022, 7, .	3.8	4
3634	A taxonomic note on the genus <i>Prevotella</i> : Description of four novel genera and emended description of the genera <i>Hallella</i> and <i>Xylanibacter</i> . Systematic and Applied Microbiology, 2022, 45, 126354.	2.8	23
3635	Pathogenesis-related protein-4 (PR-4) gene family in Qingke ( <i>Hordeum vulgare</i> L. var. <i>nudum</i> ): genome-wide identification, structural analysis and expression profile under stresses. Molecular Biology Reports, 2022, 49, 9397-9408.	2.3	5
3636	Bacterial species metabolic interaction network for deciphering the lignocellulolytic system in fungal cultivating termite gut microbiota. BioSystems, 2022, 221, 104763.	2.0	2
3638	In silico structural homology modeling and functional characterization of <i>Mycoplasma gallisepticum</i> variable lipoprotein hemagglutinin proteins. Frontiers in Veterinary Science, 0, 9, .	2.2	0
3639	Mass spectrometry of short peptides reveals common features of metazoan peptidergic neurons. Nature Ecology and Evolution, 2022, 6, 1438-1448.	7.8	20
3640	Genome-wide analysis of the G-box regulating factors protein family reveals its roles in response to <i>Sclerotinia sclerotiorum</i> infection in rapeseed ( <i>Brassica napus</i> L.). Frontiers in Plant Science, 0, 13, .	3.6	1
3641	The chromosome-level genome of <i>Gypsophila paniculata</i> reveals the molecular mechanism of floral development and ethylene insensitivity. Horticulture Research, 2022, 9, .	6.3	5
3642	Genome-Wide Identification and Analysis of the Growth-Regulating Factor Family in <i>Zanthoxylum armatum</i> DC and Functional Analysis of ZaGRF6 in Leaf Size and Longevity Regulation. International Journal of Molecular Sciences, 2022, 23, 9043.	4.1	2
3643	Transcriptome-guided annotation and functional classification of long non-coding RNAs in <i>Arabidopsis thaliana</i> . Scientific Reports, 2022, 12, .	3.3	8
3644	Phylotranscriptomics reveals the reticulate evolutionary history of a widespread diatom species complex. Journal of Phycology, 2022, 58, 643-656.	2.3	8
3646	Similar protein segments shared between domains of different evolutionary lineages. Protein Science, 2022, 31, .	7.6	8
3647	Dynamain-Related Proteins Enhance Tomato Immunity by Mediating Pattern Recognition Receptor Trafficking. Membranes, 2022, 12, 760.	3.0	3

#	ARTICLE	IF	CITATIONS
3648	The nearly complete assembly of the <i>Cercis chinensis</i> genome and Fabaceae phylogenomic studies provide insights into new gene evolution. <i>Plant Communications</i> , 2023, 4, 100422.	7.7	4
3649	BoGDB: An integrative genomic database for <i>Brassica oleracea</i> L. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3650	Individuality and ethnicity eclipse a short-term dietary intervention in shaping microbiomes and viromes. <i>PLoS Biology</i> , 2022, 20, e3001758.	5.6	8
3651	Exploring the medicinally important secondary metabolites landscape through the lens of transcriptome data in fenugreek ( <i>Trigonella foenum graecum</i> L.). <i>Scientific Reports</i> , 2022, 12, .	3.3	9
3652	Genome-Wide Identification and Expression Analysis of Eggplant DIR Gene Family in Response to Biotic and Abiotic Stresses. <i>Horticulturae</i> , 2022, 8, 732.	2.8	4
3653	Advanced genes expression pattern greatly contributes to divergence in <i>Verticillium</i> wilt resistance between <i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3654	A different transcriptional landscape sheds light on Russian sturgeon ( <i>Acipenser gueldenstaedtii</i> ) mechanisms to cope with bacterial infection and chronic heat stress. <i>Fish and Shellfish Immunology</i> , 2022, 128, 505-522.	3.6	5
3655	Analysis of <i>Crassostrea gasar</i> transcriptome reveals candidate genes involved in metal metabolism. <i>Chemosphere</i> , 2022, 307, 136009.	8.2	3
3659	A chromosome-level genome assembly of the highly heterozygous sea urchin <i>Echinometra</i> sp. EZ reveals adaptation in the regulatory regions of stress response genes. <i>Genome Biology and Evolution</i> , 0, , .	2.5	1
3662	<i>PTC2</i> region genotypes counteract <i>Biomphalaria glabrata</i> population differences between M-line and BS90 in resistance to infection by <i>Schistosoma mansoni</i> . <i>PeerJ</i> , 0, 10, e13971.	2.0	4
3664	Genome sequencing and comparative analysis of <i>Ficus benghalensis</i> and <i>Ficus religiosa</i> species reveal evolutionary mechanisms of longevity. <i>IScience</i> , 2022, 25, 105100.	4.1	12
3665	Genome-wide identification and characterization of the fatty acid desaturase gene family in <i>Vanilla planifolia</i> . <i>South African Journal of Botany</i> , 2022, 150, 813-820.	2.5	0
3666	The first transcriptome dataset of roselle ( <i>Hibiscus sabdariffa</i> L.) calyces during maturation. <i>Data in Brief</i> , 2022, 45, 108613.	1.0	0
3667	Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. <i>Methods in Molecular Biology</i> , 2022, , 137-165.	0.9	1
3668	ContactLib-ATT: A Structure-Based Search Engine for Homologous Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 3421-3429.	3.0	1
3669	Virtual screening techniques in pharmaceutical research. , 2022, , 89-128.		0
3670	Domain Structure Classifications. , 2022, , 1-16.		0
3671	Monotreme-specific conserved putative proteins derived from retroviral reverse transcriptase. <i>Virus Evolution</i> , 2022, 8, .	4.9	3



#	ARTICLE	IF	CITATIONS
3672	Variational Autoencoders and Evolutionary Algorithms for Targeted Novel Enzyme Design. , 2022, , .		0
3674	Genome architecture and diverged selection shaping pattern of genomic differentiation in wild barley. <i>Plant Biotechnology Journal</i> , 2023, 21, 46-62.	8.3	7
3675	Genome-wide identification of wheat ABC1K gene family and functional dissection of TaABC1K3 and TaABC1K6 involved in drought tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
3676	Genome-Wide Identification and Expression Analysis of the PIN Auxin Transporter Gene Family in <i>Zanthoxylum armatum</i> DC. <i>Agriculture (Switzerland)</i> , 2022, 12, 1318.	3.1	2
3678	Genome-wide analysis of the acyl-coenzyme A synthetase family and their association with the formation of goat milk flavour. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
3679	Combined transcriptomic and proteomic analysis reveals multiple pathways involved in self-pollen tube development and the potential roles of FviYABBY1 in self-incompatibility in <i>Fragaria viridis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
3680	Toward the Complete Functional Characterization of a Minimal Bacterial Proteome. <i>Journal of Physical Chemistry B</i> , 2022, 126, 6820-6834.	2.6	8
3681	Integration of Microalgaeâ€Based Wastewater Bioremediationâ€Biorefinery Process to Promote Circular Bioeconomy and Sustainability: A Review. <i>Clean - Soil, Air, Water</i> , 2023, 51, .	1.1	1
3682	Expansion of the global RNA virome reveals diverse clades of bacteriophages. <i>Cell</i> , 2022, 185, 4023-4037.e18.	28.9	96
3684	Genome-Wide Identification of Histone Modification (HM) Gene Family and Their Expression Patterns Under Abiotic Stress and Different Developmental Stages of Tea ( <i>Camellia assamica</i> ). <i>Journal of Plant Growth Regulation</i> , 2023, 42, 2960-2982.	5.1	2
3685	The non-glycosylated protein of <i>Toxocara canis</i> MUC-1 interacts with proteins of murine macrophages. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010734.	3.0	2
3686	Functional divergence of GLP genes between <i>G. barbadense</i> and <i>G. hirsutum</i> in response to <i>Verticillium dahliae</i> infection. <i>Genomics</i> , 2022, 114, 110470.	2.9	3
3687	Comprehensive Genome-Wide Analysis of Wnt Gene Family and Expression Profiling during Limb Regeneration in <i>Portunus trituberculatus</i> . <i>Fishes</i> , 2022, 7, 258.	1.7	3
3688	Genome-Wide Identification and Analysis of the MADS-Box Gene Family in Almond Reveal Its Expression Features in Different Flowering Periods. <i>Genes</i> , 2022, 13, 1764.	2.4	1
3689	Genome-wide identification and adaptive evolution of CesA/Csl superfamily among species with different life forms in Orchidaceae. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3691	Hybrid metagenome assemblies link carbohydrate structure with function in the human gut microbiome. <i>Communications Biology</i> , 2022, 5, .	4.4	4
3692	Insights of auxin signaling F-box genes in wheat ( <i>Triticum aestivum</i> L.) and their dynamic expression during the leaf rust infection. <i>Protoplasma</i> , 2023, 260, 723-739.	2.1	2
3693	A high-quality chromosome-level genome assembly of the bivalve mollusk <i>Mactra veneriformis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	3

#	ARTICLE	IF	CITATIONS
3694	CLADE 2.0: Evolution-Driven Cluster Learning-Assisted Directed Evolution. Journal of Chemical Information and Modeling, 2022, 62, 4629-4641.	5.4	8
3695	Comprehensive analysis of pathogen-responsive wheat NAC transcription factors: new candidates for crop improvement. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	6
3696	Meta-transcriptomics reveals potential virus transfer between <i>Aedes communis</i> mosquitoes and their parasitic water mites. Virus Evolution, 0, , .	4.9	0
3699	Expression and estrogen regulation of G protein-coupled estrogen receptor in human glioblastoma cells. Oncology Letters, 2022, 24, .	1.8	6
3700	Molecular advances to study the function, evolution and spectral tuning of arthropod visual opsins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, .	4.0	14
3701	Comprehensive phylogenetic analysis of the ribonucleotide reductase family reveals an ancestral clade. ELife, 0, 11, .	6.0	9
3703	Lactobacillus supports Clostridiales to restrict gut colonization by multidrug-resistant Enterobacteriaceae. Nature Communications, 2022, 13, .	12.8	22
3704	PacBio single molecule real-time sequencing of a full-length transcriptome of the greenfin horse-faced filefish <i>Thamnaconus modestus</i> . Frontiers in Marine Science, 0, 9, .	2.5	0
3705	Chromosome-scale assemblies of <i>Acanthamoeba castellanii</i> genomes provide insights into <i>Legionella pneumophila</i> infection-related chromatin reorganization. Genome Research, 2022, 32, 1698-1710.	5.5	13
3706	Complete Genome Sequence of a Novel <i>Lactobacillus paracasei</i> TK1501 and Its Application in the Biosynthesis of Isoflavone Aglycones. Foods, 2022, 11, 2807.	4.3	3
3708	Prevalence and mobility of integrative and conjugative elements within a <i>Streptomyces</i> natural population. Frontiers in Microbiology, 0, 13, .	3.5	3
3710	Host and gut bacteria share metabolic pathways for anti-cancer drug metabolism. Nature Microbiology, 2022, 7, 1605-1620.	13.3	28
3711	Omics data unveil early molecular response underlying limb regeneration in the Chinese mitten crab, <i>Eriocheir sinensis</i> . Science Advances, 2022, 8, .	10.3	9
3712	Genome-Wide Investigation and Characterization of SWEET Gene Family with Focus on Their Evolution and Expression during Hormone and Abiotic Stress Response in Maize. Genes, 2022, 13, 1682.	2.4	8
3713	Antagonistic potential of <i>Trichoderma</i> as a biocontrol agent against <i>Sclerotinia asari</i> . Frontiers in Microbiology, 0, 13, .	3.5	3
3714	In silico prediction methods of self-interacting proteins: an empirical and academic survey. Frontiers of Computer Science, 2023, 17, .	2.4	0
3715	GR0P: A genomic information repository for oilplants. Frontiers in Plant Science, 0, 13, .	3.6	0
3716	Comparative Genomic Characterization of Relaxin Peptide Family in Cattle and Buffalo. BioMed Research International, 2022, 2022, 1-11.	1.9	1

#	ARTICLE	IF	CITATIONS
3717	Microbiome-phage interactions in inflammatory bowel disease. <i>Clinical Microbiology and Infection</i> , 2023, 29, 682-688.	6.0	10
3718	<i>De novo</i> genome assembly of the medicinal plant <i>Gentiana macrophylla</i> provides insights into the genomic evolution and biosynthesis of iridoids. <i>DNA Research</i> , 2022, 29, .	3.4	10
3719	Systematic and functional analysis of non-specific lipid transfer protein family genes in sugarcane under <i>Xanthomonas albilineans</i> infection and salicylic acid treatment. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
3720	Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. <i>Cell Host and Microbe</i> , 2022, 30, 1630-1645.e25.	11.0	26
3721	Identification of long non-coding RNAs involved in floral scent of <i>Rosa hybrida</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7
3723	The <i>Vinca minor</i> genome highlights conserved evolutionary traits in monoterpene indole alkaloid synthesis. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	1.8	5
3724	Genome-wide identification and analysis of LOX genes in soybean cultivar ‘Zhonghuang 13’. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	1
3725	Carbon fixation pathways across the bacterial and archaeal tree of life. , 2022, 1, .		12
3726	Genome-wide identification of the auxin response factor (ARF) gene family in <i>Magnolia sieboldii</i> and functional analysis of MsARF5. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	6
3727	Transcriptome analysis identifies TODL as a novel lncRNA associated with proliferation, differentiation, and tumorigenesis in liposarcoma through FOXM1. <i>Pharmacological Research</i> , 2022, 185, 106462.	7.1	9
3728	Identification of epigenetic histone modifications and analysis of histone lysine methyltransferases in <i>Alexandrium pacificum</i> . <i>Harmful Algae</i> , 2022, 119, 102323.	4.8	5
3729	ChALKBH10 negatively regulates salt tolerance in cotton. <i>Plant Physiology and Biochemistry</i> , 2022, 192, 87-100.	5.8	6
3730	Mining of the CULLIN E3 ubiquitin ligase genes in the whole genome of <i>Salvia miltiorrhiza</i> . <i>Current Research in Food Science</i> , 2022, 5, 1760-1768.	5.8	3
3731	Identification of Dof Transcription Factors in the Genome of <i>Rosa chinensis</i> . <i>Journal of the American Society for Horticultural Science</i> , 2022, 147, 239-248.	1.0	0
3732	Enrofloxacin-induced transfer of multiple-antibiotic resistance genes and emergence of novel resistant bacteria in red swamp crayfish guts and pond sediments. <i>Journal of Hazardous Materials</i> , 2023, 443, 130261.	12.4	14
3733	Comparative transcriptome profiling and weighted gene co-expression network analysis to identify core genes in maize ( <i>Zea mays</i> L.) silks infected by multiple fungi. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
3734	Genome-Wide Analysis of the Almond AP2/ERF Superfamily and Its Functional Prediction during Dormancy in Response to Freezing Stress. <i>Biology</i> , 2022, 11, 1520.	2.8	5
3735	Genome Assembly of the Medicinal Plant <i>Voacanga thouarsii</i> . <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	4

#	ARTICLE	IF	CITATIONS
3736	Molecular Characterization of bHLH Transcription Factor Family in Rose ( <i>Rosa chinensis</i> Jacq.) under <i>Botrytis cinerea</i> Infection. <i>Horticulturae</i> , 2022, 8, 989.	2.8	3
3737	Uncovering Pseudogenes and Intergenic Protein-coding Sequences in <i>TriTryps</i> ™ Genomes. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	2
3738	A Genome Sequence Assembly of the Phototactic and Optogenetic Model Fungus <i>Blastocladiella emersonii</i> Reveals a Diversified Nucleotide-Cyclase Repertoire. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
3739	Genome-wide identification and expression profiling of WUSCHEL-related homeobox (WOX) genes confer their roles in somatic embryogenesis, growth and abiotic stresses in banana. <i>3 Biotech</i> , 2022, 12, .	2.2	4
3742	Genome-Wide Identification, Evolution, and Expression Pattern Analysis of the GATA Gene Family in Tartary Buckwheat ( <i>Fagopyrum tataricum</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 12434.	4.1	8
3743	Creating De Novo Overlapped Genes. <i>Methods in Molecular Biology</i> , 2023, , 95-120.	0.9	2
3744	Expansion and Neofunctionalization of Actinoporin-like Genes in Mediterranean Mussel ( <i>Mytilus</i> ) Tj ETQq0 0 0 rgBT /Overlpc 10 Tf 5	2.5	1
3745	Predicted landscape of <scp>RETINOBLASTOMAâ€RELATED LxCxE</scp> â€mediated interactions across the Chloroplastida. <i>Plant Journal</i> , 0, , .	5.7	1
3746	The PET-Degrading Potential of Global Metagenomes: From In Silico Mining to Active Enzymes. <i>Methods in Molecular Biology</i> , 2023, , 139-151.	0.9	1
3748	Metabolic, fibrotic and splicing pathways are all altered in Emery-Dreifuss muscular dystrophy spectrum patients to differing degrees. <i>Human Molecular Genetics</i> , 2023, 32, 1010-1031.	2.9	1
3749	EpichloÃ« seed transmission efficiency is influenced by plant defense response mechanisms. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
3750	The first transcriptomic analyses of fruits and cladodes for comparison between three species of <i>Opuntia</i> . <i>Genetic Resources and Crop Evolution</i> , 0, , .	1.6	0
3751	Draft genome of the bluefin tuna blood fluke, <i>Cardicola forsteri</i> . <i>PLoS ONE</i> , 2022, 17, e0276287.	2.5	0
3753	Comparative genomics and pangenomics of vancomycin-resistant and susceptible <i>Enterococcus faecium</i> from Irish hospitals. <i>Journal of Medical Microbiology</i> , 2022, 71, .	1.8	4
3754	<i>In Silico</i> Characterization of <i>bla</i> <sub>NDM</sub> -Harboring Conjugative Plasmids in <i>Acinetobacter</i> Species. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	2
3755	Genome sequence of the entomopathogenic <i>Serratia entomophila</i> isolate 626 and characterisation of the species specific itaconate degradation pathway. <i>BMC Genomics</i> , 2022, 23, .	2.8	4
3756	A contiguous <i>de novo</i> genome assembly of sugar beet EL10 ( <i>Beta vulgaris&lt;/i&gt; L.). <i>DNA Research</i>, 2023, 30, .</i>	3.4	15
3757	Genome-wide characterization of DcHsp90 gene family in carnation ( <i>Dianthus caryophyllus</i> L.) and functional analysis of DcHsp90-6 in heat tolerance. <i>Protoplasma</i> , 2023, 260, 807-819.	2.1	2

#	ARTICLE	IF	CITATIONS
3758	Synthetic Biology Meets Machine Learning. <i>Methods in Molecular Biology</i> , 2023, , 21-39.	0.9	2
3759	Pan-Genome Analysis Reveals Functional Divergences in Gut-Restricted <i>Gilliamella</i> and <i>Snodgrassella</i> . <i>Bioengineering</i> , 2022, 9, 544.	3.5	5
3762	Multi-Organ Transcriptome Response of Lumpfish ( <i>Cyclopterus lumpus</i> ) to <i>Aeromonas salmonicida</i> Subspecies <i>salmonicida</i> Systemic Infection. <i>Microorganisms</i> , 2022, 10, 2113.	3.6	6
3763	Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464.	7.7	6
3764	A new family of CRISPR-Cas type V nucleases with CasPAM recognition. <i>EMBO Reports</i> , 2022, 23, .	4.5	10
3765	Integrated Analysis of Transcriptome and microRNA Profile Reveals the Toxicity of Euphorbia Factors toward Human Colon Adenocarcinoma Cell Line Caco-2. <i>Molecules</i> , 2022, 27, 6931.	3.8	2
3766	Towards rational computational peptide design. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	11
3768	Nutrient regulation of lipochitooligosaccharide recognition in plants via NSP1 and NSP2. <i>Nature Communications</i> , 2022, 13, .	12.8	18
3769	AP2/ERF genes associated with superfast fig ( <i>Ficus carica</i> L.) fruit ripening. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
3771	Genome-Wide Identification of Auxin-Responsive GH3 Gene Family in <i>Saccharum</i> and the Expression of ScGH3-1 in Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12750.	4.1	6
3772	Assessment of the Generalization Abilities of Machine-Learning Scoring Functions for Structure-Based Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 5485-5502.	5.4	11
3775	Behavioral and transcriptomic changes in butenolide treated larvae of the cosmopolitan fouling bryozoan <i>Bugulina</i> ( <i>Bugula</i> ) <i>neritina</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	0
3777	Genome-Wide Identification and Expression Analysis of AMT and NRT Gene Family in Pecan ( <i>Carya</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 Sciences, 2022, 23, 13314.	4.1	4
3778	Genome-wide identification and expression analysis of MIKCC genes in rose provide insight into their effects on flower development. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
3779	Molecular phenotyping uncovers differences in basic housekeeping functions among closely related species of hares ( <i>Lepus</i> spp., Lagomorpha: Leporidae). <i>Molecular Ecology</i> , 2023, 32, 4097-4117.	3.9	3
3780	Transcriptome analysis of flathead grey mullet ( <i>Mugil cephalus</i> ) ovarian development induced by recombinant gonadotropin hormones. <i>Frontiers in Physiology</i> , 0, 13, .	2.8	0
3781	The dynamics of lncRNAs transcription in interspecific F1 allotriploid hybrids between Brassica species. <i>Genomics</i> , 2022, 114, 110505.	2.9	3
3782	Deep into the Apoplast: Grapevine and <i>Plasmopara viticola</i> Proteomes Reveal the Secret Beneath Host and Pathogen Communication at 6 h After Contact. <i>Phytopathology</i> , 2023, 113, 893-903.	2.2	2

#	ARTICLE	IF	CITATIONS
3783	Can <i>Artemia franciscana</i> produce essential fatty acids? Unveiling the capacity of brine shrimp to biosynthesise long-chain polyunsaturated fatty acids. <i>Aquaculture</i> , 2023, 563, 738869.	3.5	7
3784	The Sour sop Genome ( <i>Annona muricata</i> L., Annonaceae). <i>Compendium of Plant Genomes</i> , 2022, , 149-174.	0.5	0
3785	SecReT6 update: a comprehensive resource of bacterial Type VI Secretion Systems. <i>Science China Life Sciences</i> , 2023, 66, 626-634.	4.9	24
3786	Genome-wide analysis of zinc finger-homeodomain (ZF-HD) transcription factors in diploid and tetraploid cotton. <i>Functional and Integrative Genomics</i> , 2022, 22, 1269-1281.	3.5	4
3787	A Comprehensive Analysis of the DUF4228 Gene Family in <i>Gossypium</i> Reveals the Role of GhDUF4228-67 in Salt Tolerance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13542.	4.1	2
3789	Genome-wide identification of WD40 superfamily in <i>Cerasus humilis</i> and functional characteristics of ChTTG1. <i>International Journal of Biological Macromolecules</i> , 2023, 225, 376-388.	7.5	3
3790	Bioinformatics analysis and function prediction of NBS-LRR gene family in <i>Broussonetia papyrifera</i> . <i>Biotechnology Letters</i> , 2023, 45, 13-31.	2.2	1
3791	Genome-wide identification of exon extension/shrinkage events induced by splice-site-creating mutations. <i>RNA Biology</i> , 2022, 19, 1143-1152.	3.1	0
3792	Genome-Wide Identification and In Silico Analysis of ZF-HD Transcription Factor Genes in <i>Zea mays</i> L.. <i>Genes</i> , 2022, 13, 2112.	2.4	6
3793	The Innovative Informatics Approaches of High-Throughput Technologies in Livestock: Spearheading the Sustainability and Resiliency of Agrigenomics Research. <i>Life</i> , 2022, 12, 1893.	2.4	0
3795	Nearest neighbor search on embeddings rapidly identifies distant protein relations. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	13
3796	Anaerobic mercury methylators inhabit sinking particles of oxic water columns. <i>Water Research</i> , 2023, 229, 119368.	11.3	5
3797	Light response of <i>Vibrio parahaemolyticus</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	1
3798	The Peach ( <i>Prunus persica</i> ) CBL and CIPK Family Genes: Protein Interaction Profiling and Expression Analysis in Response to Various Abiotic Stresses. <i>Plants</i> , 2022, 11, 3001.	3.5	2
3799	Novel Insights into Anthocyanin Synthesis in the Calyx of Roselle Using Integrated Transcriptomic and Metabolomic Analyses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13908.	4.1	3
3800	Genome-wide identification and characterization profile of phosphatidyl ethanolamine-binding protein family genes in carrot. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
3801	Viral community-wide auxiliary metabolic genes differ by lifestyles, habitats, and hosts. <i>Microbiome</i> , 2022, 10, .	11.1	35
3802	<i>GmFtsH25</i> overexpression increases soybean seed yield by enhancing photosynthesis and photosynthates. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1026-1040.	8.5	7

#	ARTICLE	IF	CITATIONS
3803	Genomic remnants of ancestral methanogenesis and hydrogenotrophy in Archaea drive anaerobic carbon cycling. <i>Science Advances</i> , 2022, 8, .	10.3	17
3804	Gotta Go Slow: Two Evolutionarily Distinct Annelids Retain a Common Hedgehog Pathway Composition, Outlining Its Pan-Bilateria Core. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14312.	4.1	0
3805	Heterotrophic denitrification: An overlooked factor that contributes to nitrogen removal in n-DAMO mixed culture. <i>Environmental Research</i> , 2023, 216, 114802.	7.5	4
3807	Identification and Characterization of ZF-HD Genes in Response to Abscissic Acid and Abiotic Stresses in Maize. <i>Phyton</i> , 2023, 92, 707-723.	0.7	0
3808	Molecular evolution and structural analyses of proteins involved in metabolic pathways of volatile organic compounds in <i>Petunia hybrida</i> (Solanaceae). <i>Genetics and Molecular Biology</i> , 2023, 46, .	1.3	0
3809	Transcriptomics-based Analysis of the Response of Sugar Content in Litchi Pulp to Foliar Calcium Fertilizer Treatment. <i>Journal of the American Society for Horticultural Science</i> , 2023, 148, 9-20.	1.0	0
3810	Distribution and phylogeny of mercury methylation, demethylation, and reduction genes in the Seto Inland Sea of Japan. <i>Marine Pollution Bulletin</i> , 2023, 186, 114381.	5.0	2
3811	Pyrite-enhanced Sludge Digestion via Stimulation of Direct Interspecies Electron Transfer between Syntrophic Propionate- and Sulfur-oxidizing Bacteria and Methanogens: Genome-centric Metagenomics Evidence. <i>Chemical Engineering Journal</i> , 2023, 456, 141089.	12.7	15
3812	Chromosomal-level genome and multi-omics dataset provides new insights into leaf pigmentation in <i>Acer palmatum</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 227, 93-104.	7.5	4
3813	<i>Trypanosoma evansi</i> secretome carries potential biomarkers for Surra diagnosis. <i>Journal of Proteomics</i> , 2023, 272, 104789.	2.4	2
3814	The allene oxide synthase gene family in sugarcane and its involvement in disease resistance. <i>Industrial Crops and Products</i> , 2023, 192, 116136.	5.2	9
3815	Genome-wide characterization of the common bean kinome: Catalog and insights into expression patterns and genetic organization. <i>Gene</i> , 2023, 855, 147127.	2.2	3
3816	BacARscan: an <i>in silico</i> resource to discern diversity in antibiotic resistance genes. <i>Biology Methods and Protocols</i> , 2022, 7, .	2.2	0
3817	GPU-accelerated and pipelined methylation calling. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	0
3818	Gene transcriptional profiles in gonads of <i>Bacillus</i> taxa (Phasmida) with different cytological mechanisms of automictic parthenogenesis. <i>Zoological Letters</i> , 2022, 8, .	1.3	0
3819	Expanding known viral diversity in plants: virome of 161 species alongside an ancient canal. <i>Environmental Microbiomes</i> , 2022, 17, .	5.0	4
3820	AnnotaPipeline: An integrated tool to annotate eukaryotic proteins using multi-omics data. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
3822	Marine bacteroidetes use a conserved enzymatic cascade to digest diatom $\beta$ -mannan. <i>ISME Journal</i> , 2023, 17, 276-285.	9.8	5



#	ARTICLE	IF	CITATIONS
3823	Deep-sea sediment metagenome from Bay of Bengal reveals distinct microbial diversity and functional significance. <i>Genomics</i> , 2022, 114, 110524.	2.9	9
3824	Genome-wide identification and analysis of LEA_2 gene family in alfalfa ( <i>Medicago sativa</i> L.) under aluminum stress. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
3825	Tandem repeats structure of gel-forming mucin domains could be revealed by SMRT sequencing data. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
3826	Non-cyanobacterial diazotrophs: global diversity, distribution, ecophysiology, and activity in marine waters. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	8.6	11
3827	Comparative genomics reveals insight into the evolutionary origin of massively scrambled genomes. <i>ELife</i> , 0, 11, .	6.0	5
3828	Genome-wide identification and expression analysis of the SPL transcription factor family and its response to abiotic stress in Quinoa ( <i>Chenopodium quinoa</i> ). <i>BMC Genomics</i> , 2022, 23, .	2.8	11
3829	High-resolution reconstruction of a Jumbo-bacteriophage infecting capsulated bacteria using hyperbranched tail fibers. <i>Nature Communications</i> , 2022, 13, .	12.8	12
3830	Sequence-specific capture and concentration of viral RNA by type III CRISPR system enhances diagnostic. <i>Nature Communications</i> , 2022, 13, .	12.8	8
3831	PPDP: A Data Portal of Paris polyphylla for Polyphyllin Biosynthesis and Germplasm Resource Exploration. <i>Diversity</i> , 2022, 14, 1057.	1.7	1
3832	Gene Loss may have Shaped the Cnidarian and Bilaterian Hox and ParaHox Complement. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	5
3833	Systematic evaluation of genome-wide metabolic landscapes in lactic acid bacteria reveals diet- and strain-specific probiotic idiosyncrasies. <i>Cell Reports</i> , 2022, 41, 111735.	6.4	8
3834	High Level of Interaction between Phages and Bacteria in an Artisanal Raw Milk Cheese Microbial Community. <i>MSystems</i> , 2023, 8, .	3.8	5
3835	Genome-Wide Characterization and Expression Profiling of NBS-LRR-Encoding Gene Family in Radish ( <i>Raphanus sativus</i> L.). <i>Horticulturae</i> , 2022, 8, 1164.	2.8	0
3837	An in-planta comparative study of <i>Plasmopara viticola</i> proteome reveals different infection strategies towards susceptible and Rpv3-mediated resistance hosts. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
3838	An updated version of the Madagascar periwinkle genome. <i>F1000Research</i> , 0, 11, 1541.	1.6	6
3839	Bioinformatics study of the DNA and RNA viruses infecting plants and bacteria that could potentially affect animals and humans. <i>Current Bioinformatics</i> , 2022, 18, .	1.5	0
3840	AcaFinder: Genome Mining for Anti-CRISPR-Associated Genes. <i>MSystems</i> , 2022, 7, .	3.8	4
3841	The squalene route to C30 carotenoid biosynthesis and the origins of carotenoid biosynthetic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	10

#	ARTICLE	IF	CITATIONS
3843	Genome-Wide Analysis of Wheat GATA Transcription Factor Genes Reveals Their Molecular Evolutionary Characteristics and Involvement in Salt and Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 27.	4.1	10
3844	Genome-Wide Identification and Expression Analysis of Kinesin Family in Barley ( <i>Hordeum vulgare</i> ). <i>Genes</i> , 2022, 13, 2376.	2.4	2
3845	Transcriptome profiling of two <i>Moringa</i> species and insights into their antihyperglycemic activity. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	2
3846	Pharokka: a fast scalable bacteriophage annotation tool. <i>Bioinformatics</i> , 2023, 39, .	4.1	53
3847	Transcriptome Analysis on the Underlying Physiological Mechanism of Calcium and Magnesium Resolving “Sugar Receding” in “Feizixiao”™ Litchi Pulp. <i>Horticulturae</i> , 2022, 8, 1197.	2.8	0
3848	Genomic Analysis of <i>Pseudomonas asiatica</i> JP233: An Efficient Phosphate-Solubilizing Bacterium. <i>Genes</i> , 2022, 13, 2290.	2.4	1
3849	Genome-wide identification and characterization of <i>NHL</i> gene family in response to alkaline stress, ABA and MEJA treatments in wild soybean ( <i>Glycine soja</i> ). <i>PeerJ</i> , 0, 10, e14451.	2.0	4
3850	Genome-wide identification, characterization, and genetic diversity of CCR gene family in <i>Dalbergia odorifera</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
3851	GhCDPK60 positively regulates drought stress tolerance in both transgenic <i>Arabidopsis</i> and cotton by regulating proline content and ROS level. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
3852	In Silico Genome-Wide Mining and Analysis of Terpene Synthase Gene Family in <i>Hevea Brasiliensis</i> . <i>Biochemical Genetics</i> , 2023, 61, 1185-1209.	1.7	1
3853	Identification of Seven Additional Genome Segments of Grapevine-Associated Jivivirus 1. <i>Viruses</i> , 2023, 15, 39.	3.3	0
3854	iORbase: A database for the prediction of the structures and functions of insect olfactory receptors. <i>Insect Science</i> , 2023, 30, 1245-1254.	3.0	2
3855	Microbiome-mediated fructose depletion restricts murine gut colonization by vancomycin-resistant <i>Enterococcus</i> . <i>Nature Communications</i> , 2022, 13, .	12.8	8
3856	Identification, classification, and expression profile analysis of heat shock transcription factor gene family in <i>Salvia miltiorrhiza</i> . <i>PeerJ</i> , 0, 10, e14464.	2.0	1
3857	Mapping the FtsQBL divisome components in bacterial NTD pathogens as potential drug targets. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
3858	Whole genome resource and genetic analysis of <i>Magnaporthe oryzae</i> from two field isolates in northeast China. <i>Molecular Plant-Microbe Interactions</i> , 0, , .	2.6	0
3859	Transcriptome profiling reveals the underlying mechanism of grape post-harvest pathogen <i>Penicillium olsonii</i> against the metabolites of <i>Bacillus velezensis</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
3860	Comprehensive Analysis of the lncRNA-miRNA-mRNA Regulatory Network for Intramuscular Fat in Pigs. <i>Genes</i> , 2023, 14, 168.	2.4	4

#	ARTICLE	IF	CITATIONS
3861	Bioinformatic Approaches for Characterizing Molecular Structure and Function of Food Proteins. Annual Review of Food Science and Technology, 2023, 14, 203-224.	9.9	3
3862	MYB Transcription Factor Family in Pearl Millet: Genome-Wide Identification, Evolutionary Progression and Expression Analysis under Abiotic Stress and Phytohormone Treatments. Plants, 2023, 12, 355.	3.5	10
3863	Characterization and Analysis of the Full-Length Transcriptome Provide Insights into Fruit Quality Formation in Kiwifruit Cultivar Actinidia arguta cv. Qinzuyu. Agronomy, 2023, 13, 143.	3.0	0
3864	Early origin and evolution of the FtsZ/tubulin protein family. Frontiers in Microbiology, 0, 13, .	3.5	3
3865	Genome-wide identification of acyl-CoA binding proteins and possible functional prediction in legumes. Frontiers in Genetics, 0, 13, .	2.3	2
3866	Genome-wide association and RNA-seq analyses identify loci for pod orientation in rapeseed (Brassica) Tj ETQq1 1 0.784314 rgBT /Overl	3.6	6
3867	Potential for mercury methylation by Asgard archaea in mangrove sediments. ISME Journal, 2023, 17, 478-485.	9.8	6
3868	Deciphering basic and key traits of antibiotic resistome in influent and effluent of hospital wastewater treatment systems. Water Research, 2023, 231, 119614.	11.3	23
3869	In silico analysis of NAC gene family in the mangrove plant Avicennia marina provides clues for adaptation to intertidal habitats. Plant Molecular Biology, 2023, 111, 393-413.	3.9	2
3870	The <i>Aphelenchoides</i> genomes reveal substantial horizontal gene transfers in the last common ancestor of free-living and major plant-parasitic nematodes. Molecular Ecology Resources, 2023, 23, 905-919.	4.8	2
3871	Stem transcriptome screen for selection in wild and cultivated pitahaya (<i>Selenicereus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 342 Td (	2.0	1
3872	The functional analysis of sugar transporter proteins in sugar accumulation and pollen tube growth in pummelo (Citrus grandis). Frontiers in Plant Science, 0, 13, .	3.6	0
3873	Transformer-based deep learning for predicting protein properties in the life sciences. ELife, 0, 12, .	6.0	29
3874	Identification of PLATZ genes in Malus and expression characteristics of MdPLATZs in response to drought and ABA stresses. Frontiers in Plant Science, 0, 13, .	3.6	5
3875	Diversity of viral communities in faecal samples of farmed red foxes. Heliyon, 2023, 9, e12826.	3.2	0
3876	Genome-wide identification, evolution, and expression analysis of carbonic anhydrases genes in soybean (Glycine max). Functional and Integrative Genomics, 2023, 23, .	3.5	1
3877	Î²-LacFamPred: An online tool for prediction and classification of Î²-lactamase class, subclass, and family. Frontiers in Microbiology, 0, 13, .	3.5	0
3878	In Silico Analysis of a Drosophila Parasitoid Venom Peptide Reveals Prevalence of the Cationic Polar Cation Clip Motif in Knottin Proteins. Pathogens, 2023, 12, 143.	2.8	1

#	ARTICLE	IF	CITATIONS
3879	Nuclear Genome Sequence and Gene Expression of an Intracellular Fungal Endophyte Stimulating the Growth of Cranberry Plants. <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 126.	3.5	2
3880	Metabolic Sensing of Extracytoplasmic Copper Availability via Translational Control by a Nascent Exported Protein. <i>MBio</i> , 2023, 14, .	4.1	2
3881	Auxin- and pH-induced guttation in <i>Phycomyces</i> sporangiophores: relation between guttation and diminished elongation growth. <i>Protoplasma</i> , 0, , .	2.1	0
3882	Genomic survey of NPF and NRT2 transporter gene families in five inbred maize lines and their responses to pathogens infection. <i>Genomics</i> , 2023, 115, 110555.	2.9	1
3883	Genome-Wide Identification and Analysis of the MAPK and MAPKK Gene Families in Potato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.0	0
3884	In silico detection and characterization of novel virulence proteins of the emerging poultry pathogen <i>Gallibacterium anatis</i> . <i>Genomics and Informatics</i> , 2022, 20, e41.	0.8	1
3885	Variation in heat shock protein 40 kDa relates to divergence in thermotolerance among cryptic rotifer species. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
3886	Genome-Wide Investigation of the CBL-CIPK Gene Family in Oil Persimmon: Evolution, Function and Expression Analysis during Development and Stress. <i>Horticulturae</i> , 2023, 9, 30.	2.8	0
3887	Mapping the early life gut microbiome in neonates with critical congenital heart disease: multiomics insights and implications for host metabolic and immunological health. <i>Microbiome</i> , 2022, 10, .	11.1	14
3889	Genome-wide characterization of the PP2C gene family in peanut ( <i>Arachis hypogaea</i> L.) and the identification of candidate genes involved in salinity-stress response. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	8
3891	Genome-Wide Identification, Characterization, and Expression Analysis of the U-Box Gene Family in <i>Punica granatum</i> L.. <i>Agronomy</i> , 2023, 13, 332.	3.0	1
3893	Genome-wide identification and characterization of exapted transposable elements in the large genome of sunflower ( <i>Helianthus annuus</i> L.). <i>Plant Journal</i> , 2023, 113, 734-748.	5.7	3
3894	Do mitochondria use efflux pumps to protect their ribosomes from antibiotics?. <i>Microbiology (United)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.8	1
3895	Revisiting chloroplast genomic landscape and annotation towards comparative chloroplast genomes of Rhamnaceae. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	8
3896	Deciphering the Genetic Basis of Silkworm Cocoon Colors Provides New Insights into Biological Coloration and Phenotypic Diversification. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	5
3898	A conserved motif suggests a common origin for a group of proteins involved in the cell division of Gram-positive bacteria. <i>PLoS ONE</i> , 2023, 18, e0273136.	2.5	1
3899	Using evolutionary data to make sense of macromolecules with a "coface" lifted "ConSurf. <i>Protein Science</i> , 2023, 32, .	7.6	73
3900	Antimicrobial high molecular weight pectin polysaccharides production from diverse citrus peels using a novel PL10 family pectate lyase. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123457.	7.5	2

#	ARTICLE	IF	CITATIONS
3901	Killer Knots: Molecular Evolution of Inhibitor Cystine Knot Toxins in Wandering Spiders (Araneae:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.4	4
3902	Coevolution and smFRET Enhances Conformation Sampling and FRET Experimental Design in Tandem PDZ1â€“2 Proteins. Journal of Physical Chemistry B, 2023, 127, 884-898.	2.6	2
3903	Leveraging comparative genomics to uncover alien genes in bacterial genomes. Microbial Genomics, 2023, 9, .	2.0	4
3905	Deciphering evolutionary dynamics of WRKY genes in Arachis species. BMC Genomics, 2023, 24, .	2.8	5
3906	Impact of meltwater flow intensity on the spatiotemporal heterogeneity of microbial mats in the McMurdo Dry Valleys, Antarctica. ISME Communications, 2023, 3, .	4.2	3
3907	Independent Innexin Radiation Shaped Signaling in Ctenophores. Molecular Biology and Evolution, 2023, 40, .	8.9	2
3910	A novel chemogenomic discovery platform identifies bioactive hits with rapid bactericidal activity against Mycobacteroides Abscessus. Tuberculosis, 2023, 139, 102317.	1.9	0
3911	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. Journal of Advanced Research, 2024, 56, 15-29.	9.5	3
3913	Identification of PAL Gene in Purple Cabbage and Functional Analysis Related to Anthocyanin Synthesis. Horticulturae, 2023, 9, 469.	2.8	1
3914	PHOSPHORUSâ€“STARVATION TOLERANCE 1 (OsPSTOL1) is prevalent in upland rice and enhances root growth and hastens low phosphate signaling in wheat. Plant, Cell and Environment, 2023, 46, 2187-2205.	5.7	3
3915	Genome-wide identification of the ABA receptor PYL gene family and expression analysis in Prunus avium L.. Scientia Horticulturae, 2023, 313, 111919.	3.6	5
3916	The H3K79 methylase DOT1, unreported in photosynthetic plants, exists in Alexandrium pacificum and participates in its growth regulation. Marine Pollution Bulletin, 2023, 190, 114867.	5.0	1
3917	Genome-wide investigation of aquaporin genes in Corchorus spp and their role in organ development and abiotic stress tolerance. Plant Gene, 2023, 34, 100410.	2.3	2
3918	Genome-resolving metagenomics reveals wild western capercaillies (Tetrao urogallus) as avian hosts for antibiotic-resistance bacteria and their interactions with the gut-virome community. Microbiological Research, 2023, 271, 127372.	5.3	1
3919	Evolution of cox2 introns in angiosperm mitochondria and efficient splicing of an elongated cox2i691 intron. Gene, 2023, 869, 147393.	2.2	0
3920	Organelle genomes of Indigofera amblyantha and Indigofera pseudotinctoria: comparative genome analysis, and intracellular gene transfer. Industrial Crops and Products, 2023, 198, 116674.	5.2	2
3921	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. Nature Communications, 2023, 14, .	12.8	10
3922	Identification and characterization of ABC proteins in an important rice insect pest, Cnaphalocrocis medinalis unveil their response to Cry1C toxin. International Journal of Biological Macromolecules, 2023, 237, 123949.	7.5	1

#	ARTICLE	IF	CITATIONS
3923	Insights into identifying resistance genes for cold and disease stresses through chromosome-level reference genome analyses of <i>Poncirus polyandra</i> . <i>Genomics</i> , 2023, 115, 110617.	2.9	1
3924	The <i>Populus koreana</i> genome provides insights into the biosynthesis of plant aroma. <i>Industrial Crops and Products</i> , 2023, 197, 116453.	5.2	1
3927	Genome-wide characterization, phylogenetic and expression analysis of Histone gene family in cucumber ( <i>Cucumis sativus</i> L.). <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123401.	7.5	3
3928	Genome-wide Transcriptome Analysis Reveals the Gene Regulatory Network in Star Fruit Flower Blooming. <i>Tropical Plant Biology</i> , 2023, 16, 1-11.	1.9	0
3929	Genome-wide identification, evolution and expression analysis of bone morphogenetic protein (BMP) gene family in chinese soft-shell turtle ( <i>Pelodiscus sinensis</i> ). <i>Frontiers in Genetics</i> , 0, 14, .	2.3	4
3933	KinFams: De-Novo Classification of Protein Kinases Using CATH Functional Units. <i>Biomolecules</i> , 2023, 13, 277.	4.0	3
3934	The complete chloroplast genome of <i>Hibiscus syriacus</i> using long-read sequencing: Comparative analysis to examine the evolution of the tribe Hibisceae. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
3935	Parvovirus dark matter in the cloaca of wild birds. <i>GigaScience</i> , 2022, 12, .	6.4	4
3937	The rubber tree kinome: Genome-wide characterization and insights into coexpression patterns associated with abiotic stress responses. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2
3939	Genome-wide identification and expression analysis of the cotton patatin-related phospholipase A genes and response to stress tolerance. <i>Planta</i> , 2023, 257, .	3.2	4
3940	The Bcl-2-associated athanogene gene family in tobacco ( <i>Nicotiana tabacum</i> ) and the function of NtBAG5 in leaf senescence. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
3941	Uncovering a Complex Virome Associated with the Cacao Pathogens <i>Ceratocystis cacaofunesta</i> and <i>Ceratocystis fimbriata</i> . <i>Pathogens</i> , 2023, 12, 287.	2.8	3
3942	Single-cell amplified genomes reveal most streamlined free-living marine bacteria. <i>Environmental Microbiology</i> , 2023, 25, 1136-1154.	3.8	5
3945	Genome-wide identification and analysis of the evolution and expression pattern of the <i>HVA22</i> gene family in three wild species of tomatoes. <i>PeerJ</i> , 0, 11, e14844.	2.0	1
3946	Uncovering the involvement of DoDELLA1-interacting proteins in development by characterizing the DoDELLA gene family in <i>Dendrobium officinale</i> . <i>BMC Plant Biology</i> , 2023, 23, .	3.6	1
3947	Dataset of 143 metagenome-assembled genomes from the Arctic and Atlantic Oceans, including 21 for eukaryotic organisms. <i>Data in Brief</i> , 2023, 47, 108990.	1.0	1
3948	Genome analysis and genomic comparison of a fungal cultivar of the nonsocial weevil <i>Euops chinensis</i> reveals its plant decomposition and protective roles in fungus-farming mutualism. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
3949	Co-diversification of an intestinal <i>Mycoplasma</i> and its salmonid host. <i>ISME Journal</i> , 2023, 17, 682-692.	9.8	14

#	ARTICLE	IF	CITATIONS
3950	A subfamily classification to choreograph the diverse activities within glycoside hydrolase family 31. <i>Journal of Biological Chemistry</i> , 2023, 299, 103038.	3.4	6
3951	The Antidepressant Sertraline Affects Cell Signaling and Metabolism in <i>Trichophyton rubrum</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 275.	3.5	1
3952	Genome-wide identification and analysis of the molecular evolution and expression of type-A response regulator genes in <i>Populus deltoids</i> . <i>Industrial Crops and Products</i> , 2023, 194, 116336.	5.2	1
3953	Genome-Wide Analysis of SIMILAR TO RCD ONE (SRO) Family Revealed Their Roles in Abiotic Stress in Poplar. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4146.	4.1	5
3954	Genome-wide identification of the fibrillin gene family in chickpea ( <i>Cicer arietinum</i> L.) and its response to drought stress. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123757.	7.5	1
3955	Genome-Wide Identification and Abiotic Stress Response Analysis of PP2C Gene Family in Woodland and Pineapple Strawberries. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4049.	4.1	6
3956	Genome-wide identification and analysis of the SUPPRESSOR of MAX2 1-LIKE gene family and its interaction with DWARF14 in poplar. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	4
3957	Genome-wide identification and characterization of the lettuce GASA family in response to abiotic stresses. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	0
3958	Field plus lab experiments help identify freezing tolerance and associated genes in subtropical evergreen broadleaf trees: A case study of <i>Camellia oleifera</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
3959	The wealth of shared resources: Improving molecular taxonomy using eDNA and public databases. <i>Zoologica Scripta</i> , 2023, 52, 226-234.	1.7	3
3960	A novel and diverse group of Candidatus Patescibacteria from bathypelagic Lake Baikal revealed through long-read metagenomics. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	2
3961	Roadmap to the study of gene and protein phylogeny and evolution—A practical guide. <i>PLoS ONE</i> , 2023, 18, e0279597.	2.5	4
3962	Improved global protein homolog detection with major gains in function identification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	15
3964	In silico approaches for the quest of the novel enzymes. , 2023, , 65-78.		1
3966	Pan-Chromosome and Comparative Analysis of <i>Agrobacterium fabrum</i> Reveal Important Traits Concerning the Genetic Diversity, Evolutionary Dynamics, and Niche Adaptation of the Species. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
3967	Data-driven design of orthogonal protein-protein interactions. <i>Science Signaling</i> , 2023, 16, .	3.6	0
3968	Differences in heat tolerance, water use efficiency and growth among Douglas-fir families and varieties evidenced by GWAS and common garden studies. <i>AoB PLANTS</i> , 2023, 15, .	2.3	2
3970	PSnpBind-ML: predicting the effect of binding site mutations on protein-ligand binding affinity. <i>Journal of Cheminformatics</i> , 2023, 15, .	6.1	2



#	ARTICLE	IF	CITATIONS
3971	Substantial viral and bacterial diversity at the bat–tick interface. <i>Microbial Genomics</i> , 2023, 9, .	2.0	2
3972	Genome-wide characterization of R2R3-MYB gene family in <i>Santalum album</i> and their expression analysis under cold stress. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2
3973	Cryo-EM structure of gas vesicles for buoyancy-controlled motility. <i>Cell</i> , 2023, 186, 975-986.e13.	28.9	16
3974	Exploring microbial functional biodiversity at the protein family level—From metagenomic sequence reads to annotated protein clusters. <i>Frontiers in Bioinformatics</i> , 0, 3, .	2.1	2
3975	Structural and Functional Classification of G-Quadruplex Families within the Human Genome. <i>Genes</i> , 2023, 14, 645.	2.4	2
3976	Discovery and comparative genomic analysis of a novel equine anellovirus, representing the first complete Mutorquevirus genome. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
3977	Transposon-derived transcription factors across metazoans. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	2
3979	Abundance and composition of particles and their attached microbiomes along an Atlantic Meridional Transect. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	4
3980	Genome-wide identification, expression profile and evolutionary relationships of TPS genes in the neotropical fruit tree species <i>Psidium cattleianum</i> . <i>Scientific Reports</i> , 2023, 13, .	3.3	1
3981	WITCH-NG: efficient and accurate alignment of datasets with sequence length heterogeneity. <i>Bioinformatics Advances</i> , 2023, 3, .	2.4	2
3983	Genome-Wide Identification and Analysis of NBS-LRR-Encoding Genes in Mungbean ( <i>Vigna radiata</i> L.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> <i>Journal of Plant Growth Regulation</i> , 2023, 42, 6667-6680.	5.1	4
3984	Purriato is a conserved small open reading frame gene that interacts with the CASA pathway to regulate muscle homeostasis and epithelial tissue growth in <i>Drosophila</i> . <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	0
3985	Changes in community structures and functions of the gut microbiomes of deep-sea cold seep mussels during in situ transplantation experiment. <i>Animal Microbiome</i> , 2023, 5, .	3.8	2
3986	Accurate prediction by AlphaFold2 for ligand binding in a reductive dehalogenase and implications for PFAS (per- and polyfluoroalkyl substance) biodegradation. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
3988	Plastid Genome Assembly Using Long-read data. <i>Molecular Ecology Resources</i> , 2023, 23, 1442-1457.	4.8	4
3990	Genome-wide characterization of ubiquitin-conjugating enzyme gene family explores its genetic effects on the oil content and yield of <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
3991	Current challenges in designer cellulosome engineering. <i>Applied Microbiology and Biotechnology</i> , 2023, 107, 2755-2770.	3.6	4
3992	Genome-centric metagenomics reveals the host-driven dynamics and ecological role of CPR bacteria in an activated sludge system. <i>Microbiome</i> , 2023, 11, .	11.1	11

#	ARTICLE	IF	CITATIONS
3993	Transposable Element Interactions Shape the Ecology of the Deer Mouse Genome. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	6
3994	Differential Retention of Pfam Domains Contributes to Long-term Evolutionary Trends. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
3995	Potential Auxiliary Metabolic Capabilities and Activities Reveal Biochemical Impacts of Viruses in Municipal Wastewater Treatment Plants. <i>Environmental Science &amp; Technology</i> , 2023, 57, 5485-5498.	10.0	9
3996	Recovery of metagenomic data from the <i>Aedes aegypti</i> microbiome using a reproducible snakemake pipeline: MINUUR. <i>Wellcome Open Research</i> , 0, 8, 131.	1.8	1
3997	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. <i>PLoS Computational Biology</i> , 2023, 19, e1010966.	3.2	0
3998	Gram-positive anaerobic cocci guard skin homeostasis by regulating host-defense mechanisms. <i>IScience</i> , 2023, 26, 106483.	4.1	3
4000	De novo transcriptome assemblies of five major European oilseed rape insect pests. <i>BMC Genomic Data</i> , 2023, 24, .	1.7	2
4002	Comprehensive Analysis of the INDETERMINATE DOMAIN (IDD) Gene Family and Their Response to Abiotic Stress in <i>Zea mays</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 6185.	4.1	1
4003	A general mechanism for transcription bubble nucleation in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	2
4004	Transposable elements in the transcriptome of the velvetbean caterpillar <i>Anticarsia gemmatilis</i> H&Aner, 1818 (Lepidoptera: Erebiidae). <i>Genome</i> , 0, , .	2.0	0
4005	Genome-Wide Identification of the Rose SWEET Gene Family and Their Different Expression Profiles in Cold Response between Two Rose Species. <i>Plants</i> , 2023, 12, 1474.	3.5	3
4006	LTR Retroelements and Bird Adaptation to Arid Environments. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6332.	4.1	0
4007	Characterisation and phylogenetic analysis of the complete mitogenome of the edible insect bamboo worm <i>Omphisa fuscidentalis</i> in Yunnan Province, China. <i>Journal of Insects As Food and Feed</i> , 2023, 9, 1075-1087.	3.9	0
4008	The Australasian dingo archetype: <i>de novo</i> chromosome-length genome assembly, DNA methylome, and cranial morphology. <i>GigaScience</i> , 2023, 12, .	6.4	0
4009	The genome of <i>Lactuca saligna</i> , a wild relative of lettuce, provides insight into non-host resistance to the downy mildew <i>Bremia lactucae</i> . <i>Plant Journal</i> , 2023, 115, 108-126.	5.7	2
4011	<i>Streptomonospora mangrovi</i> sp. nov., isolated from mangrove soil showing similar metabolic capabilities, but distinct secondary metabolites profiles. <i>Archives of Microbiology</i> , 2023, 205, .	2.2	0
4012	Comprehensive evolutionary analysis of growth-regulating factor gene family revealing the potential molecular basis under multiple hormonal stress in Gramineae crops. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
4013	Whole-genome sequencing and comparative genomic analysis of potential biotechnological strains of <i>Trichoderma harzianum</i> , <i>Trichoderma atroviride</i> , and <i>Trichoderma reesei</i> . <i>Molecular Genetics and Genomics</i> , 2023, 298, 735-754.	2.1	4

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4014	Maturases and Group II Introns in the Mitochondrial Genomes of the Deepest Jakobid Branch. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	1
4015	Genome-Wide Analysis and Abiotic Stress-Responsive Patterns of COBRA-like Gene Family in <i>Liriodendron chinense</i> . <i>Plants</i> , 2023, 12, 1616.	3.5	3
4018	Bioinformatic identification of ClpI, a distinct class of Clp unfoldases in Actinomycetota. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
4020	Genome-Wide Identification, Characterization, and Expression of TCP Genes Family in Orchardgrass. <i>Genes</i> , 2023, 14, 925.	2.4	2
4021	Dynamic Evolution of Retroviral Envelope Genes in Egg-Laying Mammalian Genomes. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	4
4023	The Complete Chloroplast Genomes of <i>Gynostemma</i> Reveal the Phylogenetic Relationships of Species within the Genus. <i>Genes</i> , 2023, 14, 929.	2.4	2
4024	Tilapia lake virus: A structured phylogenetic approach. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	3
4025	The <i>Dictyostelium discoideum</i> genome lacks significant DNA methylation and uncovers palindromic sequences as a source of false positives in bisulfite sequencing. <i>NAR Genomics and Bioinformatics</i> , 2023, 5, .	3.2	1
4026	Regulation of Cell Proliferation and Nrf2-Mediated Antioxidant Defense: Conservation of Keap1 Cysteines and Nrf2 Binding Site in the Context of the Evolution of KLHL Family. <i>Life</i> , 2023, 13, 1045.	2.4	5
4027	The persistent homology of mitochondrial ATP synthases. <i>IScience</i> , 2023, 26, 106700.	4.1	4
4028	Mirusviruses link herpesviruses to giant viruses. <i>Nature</i> , 2023, 616, 783-789.	27.8	28
4029	Insights into the Molecular Basis of Huanglongbing Tolerance in Persian Lime ( <i>Citrus latifolia</i> Tan.) through a Transcriptomic Approach. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7497.	4.1	2
4030	Genome-wide identification and functional analysis of ICE genes reveal that <i>Gossypium thurberi</i> <i>GthICE2</i> is responsible for cold and drought stress tolerance. <i>Plant Physiology and Biochemistry</i> , 2023, 199, 107708.	5.8	3
4031	Diversity, distribution, and functional potentials of magroviruses from marine and brackish waters. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
4032	Genome-Wide Characterization of the R2R3-MYB Gene Family in <i>Diospyros oleifera</i> . <i>Agriculture (Switzerland)</i> , 2023, 13, 955.	3.1	1
4034	Phylogenetic and Evolutionary Analysis of Plant Small RNA 2'-O-Methyltransferase (HEN1) Protein Family. <i>Journal of Molecular Evolution</i> , 0, , .	1.8	0
4035	An extracellular protease containing a novel C-terminal extension produced by a marine-originated haloarchaeon. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	2
4036	Genome-wide analysis of the CDPK gene family and their important roles response to cold stress in white clover. <i>Plant Signaling and Behavior</i> , 2023, 18, .	2.4	2

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4037	Genome-wide identification and expression analysis of BZR gene family and associated responses to abiotic stresses in cucumber ( <i>Cucumis sativus</i> L.). <i>BMC Plant Biology</i> , 2023, 23, .	3.6	4
4038	A chromosome-scale genome assembly of <i>Castanopsis hystrix</i> provides new insights into the evolution and adaptation of Fagaceae species. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
4039	Identification of the <sc>CRISPR-Cas9</sc> system on a metagenome and its application to genome engineering. <i>Microbial Biotechnology</i> , 2023, 16, 1505-1523.	4.2	1
4040	The construction and analysis of wax gourd pangenome uncover fruit quality-related and resistance genes. <i>Scientia Horticulturae</i> , 2023, 318, 112084.	3.6	1
4042	Four ciliate-specific expansion events occurred during actin gene family evolution of eukaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2023, 184, 107789.	2.7	0
4043	Genome-wide analysis of HSF family and overexpression of <i>PsnHSF21</i> confers salt tolerance in <i>Populus simonii</i> Å— <i>P. nigra</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
4044	Chromosome-level genome assembly of bean flower thrips <i>Megalurothrips usitatus</i> (Thysanoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	5.3	4
4045	Baseline metagenome-assembled genome (MAG) data of Sikkim hot springs from Indian Himalayan geothermal belt (IHGB) showcasing its potential CAZymes, and sulfur-nitrogen metabolic activity. <i>World Journal of Microbiology and Biotechnology</i> , 2023, 39, .	3.6	1
4046	Zona pellucida family genes in Chinese pond turtle: identification, expression profiles, and role in the spermatozoa acrosome reaction. <i>Biology of Reproduction</i> , 0, , .	2.7	0
4048	Comprehensive identification and expression analysis of <i>CAMTA</i> gene family in <i>Phyllostachys edulis</i> under abiotic stress. <i>PeerJ</i> , 0, 11, e15358.	2.0	2
4049	Genomic characterization of the NAC transcription factors, directed at understanding their functions involved in endocarp lignification of iron walnut ( <i>Juglans sigillata</i> Dode). <i>Frontiers in Genetics</i> , 0, 14, .	2.3	2
4050	Evolutionary pathways for deep-sea adaptation in marine planktonic Actinobacteriota. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
4051	Chromosome-scale genome assembly of the freshwater cladoceran crustacean <i>Chydorus sphaericus</i> : A resource for discovery of genes responsive to ecological challenges. <i>Aquatic Toxicology</i> , 2023, 260, 106565.	4.0	0
4052	Genome-wide identification and expression analysis of anthocyanin synthesis-related <i>R2R3-MYB</i> gene family in purple passion fruit (<i>Passiflora edulis</i>). <i>Materials Express</i> , 2023, 13, 467-481.	0.5	0
4053	ResFinderFG v2.0: a database of antibiotic resistance genes obtained by functional metagenomics. <i>Nucleic Acids Research</i> , 2023, 51, W493-W500.	14.5	5
4054	Unsupervised Deep Learning Can Identify Protein Functional Groups from Unaligned Sequences. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	0
4056	Viromics Reveals the High Diversity of Viruses from Fishes of the Tibet Highland. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	3
4057	Variation of Gene Expression in the Endemic Dinaric Karst Cave-Dwelling Bivalve Mollusk <i>Congeria kusceri</i> during the Summer Season. <i>Diversity</i> , 2023, 15, 707.	1.7	0

#	ARTICLE	IF	CITATIONS
4061	Whole-genome and dispersed duplication, including transposed duplication, jointly advance the evolution of TLP genes in seven representative Poaceae lineages. BMC Genomics, 2023, 24, .	2.8	3
4062	Characterization of HSP70 family in watermelon ( <i>Citrullus lanatus</i> ): identification, structure, evolution, and potential function in response to ABA, cold and drought stress. Frontiers in Genetics, 0, 14, .	2.3	0
4063	Physiological and transcriptomic effects of formulated diets including the prebiotics inulin, $\beta$ -glucan, and chitosan on juveniles of <i>Totoaba macdonaldi</i> . Aquaculture International, 2024, 32, 61-85.	2.2	1
4064	Genome-Enabled Insights into Downy Mildew Biology and Evolution. Annual Review of Phytopathology, 2023, 61, .	7.8	0
4065	Genomic survey of MYB gene family in six pearl millet ( <i>Pennisetum glaucum</i> ) varieties and their response to abiotic stresses. Genetica, 2023, 151, 251-265.	1.1	3
4066	Genome-wide identification and analysis of the invertase gene family in tobacco ( <i>Nicotiana tabacum</i> ) reveals NtNIN10 participating the sugar metabolism. Frontiers in Plant Science, 0, 14, .	3.6	5
4067	Genetic portrait of polyamine transporters in barley: insights in the regulation of leaf senescence. Frontiers in Plant Science, 0, 14, .	3.6	1
4068	Gut phageome of the giant panda ( <i>Ailuropoda melanoleuca</i> ) reveals greater diversity than relative species. MSystems, 2023, 8, .	3.8	0
4069	Bacteriophage therapy against pathological <i>Klebsiella pneumoniae</i> ameliorates the course of primary sclerosing cholangitis. Nature Communications, 2023, 14, .	12.8	12
4070	Contrasting outcomes of genome reduction in mikrocytids and microsporidians. BMC Biology, 2023, 21, .	3.8	3
4071	Genome-wide identification and expression analyses of phenylalanine ammonia-lyase gene family members from tomato ( <i>Solanum lycopersicum</i> ) reveal their role in root-knot nematode infection. Frontiers in Plant Science, 0, 14, .	3.6	1
4073	A novel computational pipeline for var gene expression augments the discovery of changes in the <i>Plasmodium falciparum</i> transcriptome during transition from in vivo to short-term in vitro culture. ELife, 0, 12, .	6.0	0
4074	Genome-wide identification of the NRAMP gene family in <i>Populus trichocarpa</i> and their function as heavy metal transporters. Ecotoxicology and Environmental Safety, 2023, 261, 115110.	6.0	5
4075	Community structure and abundance of ACC deaminase containing bacteria in soils with 16S-PICRUSt2 inference or direct <i>acdS</i> gene sequencing. Journal of Microbiological Methods, 2023, 211, 106740.	1.6	6
4076	The hidden diversity of ancient bornaviral sequences from X and P genes in vertebrate genomes. Virus Evolution, 2023, 9, .	4.9	0
4077	Human small-intestinal gluten-degrading bacteria and its potential implication in celiac disease. Journal of Biosciences, 2023, 48, .	1.1	1
4079	Pectin modifications promote haustoria development in the parasitic plant <i>Phtheirospermum japonicum</i> . Plant Physiology, 2023, 194, 229-242.	4.8	5
4081	Comparison of viral communities in the blood, feces and various tissues of wild brown rats ( <i>Rattus</i> ) Tj ETQq1 1 0.784314 rgBJ /Overlock	3.2	0

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4083	Polygalacturonase gene family analysis identifies FcPG12 as a key player in fig ( <i>Ficus carica</i> L.) fruit softening. <i>BMC Plant Biology</i> , 2023, 23, .	3.6	1
4084	Genome-Wide Identification of the RsSWEET Gene Family and Functional Analysis of RsSWEET17 in Root Growth and Development in Radish. <i>Horticulturae</i> , 2023, 9, 698.	2.8	1
4087	Characterization and Coexpression Analysis of the TIFY Family Genes in <i>Euryale ferox</i> Related to Leaf Development. <i>Plants</i> , 2023, 12, 2323.	3.5	1
4089	Genome-Wide Analysis of ZAT Gene Family in <i>Osmanthus fragrans</i> and the Function Exploration of OfZAT35 in Cold Stress. <i>Plants</i> , 2023, 12, 2346.	3.5	1
4091	Local adaptation and demographic history of vulnerable conifer <i>Cephalotaxus oliveri</i> in southern China. <i>Journal of Systematics and Evolution</i> , 0, , .	3.1	1
4092	Harnessing extremophilic carboxylesterases for applications in polyester depolymerisation and plastic waste recycling. <i>Essays in Biochemistry</i> , 0, , .	4.7	1
4093	The genome of <i>Acorus</i> deciphers insights into early monocot evolution. <i>Nature Communications</i> , 2023, 14, .	12.8	1
4094	Carnivorous <i>Nepenthes</i> Pitchers with Less Acidic Fluid House Nitrogen-Fixing Bacteria. <i>Applied and Environmental Microbiology</i> , 0, , .	3.1	1
4095	High-quality chromosome-level scaffolds of the plant bug <i>Pachypeltis micranthus</i> provide insights into the availability of <i>Mikania micrantha</i> control. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
4096	The universal Sua5/TsaC family evolved different mechanisms for the synthesis of a key tRNA modification. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
4097	Genome-wide Identification of the Auxin Transporter Gene Families in Sweet Potato ( <i>Ipomoea batatas</i> ) and their Expression During Tuberization. <i>Tropical Plant Biology</i> , 2023, 16, 75-93.	1.9	0
4098	Chemical profile and analysis of biosynthetic pathways and genes of volatile terpenes in <i>Pityopsis ruthii</i> , a rare and endangered flowering plant. <i>PLoS ONE</i> , 2023, 18, e0287524.	2.5	0
4100	CrusTome: a transcriptome database resource for large-scale analyses across Crustacea. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	4
4101	Identification and transcriptome data analysis of ARF family genes in five Orchidaceae species. <i>Plant Molecular Biology</i> , 2023, 112, 85-98.	3.9	2
4102	Genomic survey of high-throughput RNA-Seq data implicates involvement of long intergenic non-coding RNAs (lincRNAs) in cytoplasmic male-sterility and fertility restoration in pigeon pea. <i>Genes and Genomics</i> , 2023, 45, 783-811.	1.4	0
4103	First report on the regulation and function of carbon metabolism during large sclerotia formation in medicinal fungus <i>Wolfiporia cocos</i> . <i>Fungal Genetics and Biology</i> , 2023, 166, 103793.	2.1	1
4104	Identification of F-box gene family in <i>Brassica oleracea</i> and expression analysis in response to low-temperature stress. <i>Plant Physiology and Biochemistry</i> , 2023, 199, 107717.	5.8	3
4105	Building a genome-based understanding of bacterial pH preferences. <i>Science Advances</i> , 2023, 9, .	10.3	12

#	ARTICLE	IF	CITATIONS
4106	Quantitative model for genome-wide cyclic AMP receptor protein binding site identification and characteristic analysis. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	0
4107	Marine <i>Bacteroidetes</i> enzymatically digest xylans from terrestrial plants. <i>Environmental Microbiology</i> , 2023, 25, 1713-1727.	3.8	3
4108	Protein-Gene Orthology in Baculoviridae: An Exhaustive Analysis to Redefine the Ancestrally Common Coding Sequences. <i>Viruses</i> , 2023, 15, 1091.	3.3	1
4109	Understanding the Molecular Basis for Homodimer Formation of the Pneumococcal Endolysin Cpl-1. <i>ACS Infectious Diseases</i> , 2023, 9, 1092-1104.	3.8	1
4111	Transcriptomic analysis of Chinese yam ( <i>Dioscorea polystachya</i> Turcz.) variants indicates brassinosteroid involvement in tuber development. <i>Frontiers in Nutrition</i> , 0, 10, .	3.7	1
4113	Genome mining for anti-CRISPR operons using machine learning. <i>Bioinformatics</i> , 2023, 39, .	4.1	1
4115	Identification, Culture Characteristics and Whole-Genome Analysis of <i>Pestalotiopsis neglecta</i> Causing Black Spot Blight of <i>Pinus sylvestris</i> var. <i>mongolica</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2023, 9, 564.	3.5	1
4116	Genome-wide Identification of the Upland Cotton ( <i>Gossypium hirsutum</i> L.) B-BOX gene Family and its Expression After Drought Stress. <i>Journal of Plant Growth Regulation</i> , 0, , .	5.1	0
4117	In Vitro Biochemical Characterization of Excised Macrocyclizing Thioesterase Domains from Non-ribosomal Peptide Synthetases. <i>Methods in Molecular Biology</i> , 2023, , 101-125.	0.9	2
4118	The toxins of vertically transmitted <i>Spiroplasma</i> . <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
4119	Flotillin-associated rhodopsin (FARhodopsin), a widespread paralog of proteorhodopsin in aquatic bacteria with streamlined genomes. <i>MSystems</i> , 2023, 8, .	3.8	0
4120	Genome-wide identification of TPS genes in sesame and analysis of their expression in response to abiotic stresses. <i>Oil Crop Science</i> , 2023, 8, 81-88.	2.0	2
4121	Recovery of metagenomic data from the <i>Aedes aegypti</i> microbiome using a reproducible snakemake pipeline: MINUUR. <i>Wellcome Open Research</i> , 0, 8, 131.	1.8	0
4122	Characterization of Malectin/Malectin-like Receptor-like Kinase Family Members in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Life</i> , 2023, 13, 1302.	2.4	0
4123	Molecular Evolution and Genetic Variation of G2-Like Transcription Factor Genes in Wheat ( <i>Triticum</i> ) Tj ETQqO O O rgBT /Overlock 10 Tf 5	2.4	0
4124	Genome-wide identification of the PYL gene family of tea plants ( <i>Camellia sinensis</i> ) revealed its expression profiles under different stress and tissues. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
4125	Discovery of deaminase functions by structure-based protein clustering. <i>Cell</i> , 2023, 186, 3182-3195.e14.	28.9	27
4126	Evolution of antimicrobial cysteine-rich peptides in plants. <i>Plant Cell Reports</i> , 2023, 42, 1517-1527.	5.6	2



#	ARTICLE	IF	CITATIONS
4127	Structure snapshots reveal the mechanism of a bacterial membrane lipoprotein <i>N</i> -acyltransferase. <i>Science Advances</i> , 2023, 9, .	10.3	4
4128	Functional annotation of uncharacterized proteins from <i>Fusobacterium nucleatum</i> : identification of virulence factors. <i>Genomics and Informatics</i> , 2023, 21, e21.	0.8	1
4129	Transcriptomic profile of lettuce seedlings ( <i>Lactuca sativa</i> ) response to microalgae extracts used as biostimulant agents. <i>AoB PLANTS</i> , 2023, 15, .	2.3	1
4130	Evolutionary history of an Alpine Archaeognath ( <i>Machilis pallida</i> ): Insights from different variant. <i>Ecology and Evolution</i> , 2023, 13, .	1.9	0
4131	Generating interacting protein sequences using domain-to-domain translation. <i>Bioinformatics</i> , 2023, 39, .	4.1	1
4132	Genome-Wide Identification of MADS-Box Genes in <i>Taraxacum kok-saghyz</i> and <i>Taraxacum mongolicum</i> : Evolutionary Mechanisms, Conserved Functions and New Functions Related to Natural Rubber Yield Formation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 10997.	4.1	1
4133	The glycoside hydrolase 28 member VdEPG1 is a virulence factor of <i>Verticillium dahliae</i> and interacts with the jasmonic acid pathway-related gene <i>GhOPR9</i> . <i>Molecular Plant Pathology</i> , 2023, 24, 1238-1255.	4.2	2
4134	Whole-genome Duplications and the Long-term Evolution of Gene Regulatory Networks in Angiosperms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	2
4135	bHLH transcription factor family identification, phylogeny, and its response to abiotic stress in <i>Chenopodium quinoa</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	4
4137	Evolution of the triplet BRCT domain. <i>DNA Repair</i> , 2023, 129, 103532.	2.8	0
4138	Genome analysis of Parmales, the sister group of diatoms, reveals the evolutionary specialization of diatoms from phago-mixotrophs to photoautotrophs. <i>Communications Biology</i> , 2023, 6, .	4.4	3
4139	Integrative meta-omics in Galaxy and beyond. <i>Environmental Microbiomes</i> , 2023, 18, .	5.0	1
4140	Expanding Antarctic biogeography: microbial ecology of Antarctic island soils. <i>Ecography</i> , 2023, 2023, .	4.5	1
4141	CsBZIP40 confers resistance against citrus bacterial canker by repressing CsWRKY43-CsPrx53/CsSOD13 cascade mediated ROS scavenging. <i>Horticulture Research</i> , 2023, 10, .	6.3	3
4142	Genome-wide analysis of the WRKY genes and their important roles during cold stress in white clover. <i>PeerJ</i> , 0, 11, e15610.	2.0	3
4143	Comparison of the Strengths and Weaknesses of Machine Learning Algorithms and Feature Selection on KEGG Database Microbial Gene Pathway Annotation and Its Effects on Reconstructed Network Topology. <i>Journal of Computational Biology</i> , 2023, 30, 766-782.	1.6	0
4146	HypoRiPPAtlas as an Atlas of hypothetical natural products for mass spectrometry database search. <i>Nature Communications</i> , 2023, 14, .	12.8	3
4147	Genome-Wide Identification and Expression Analysis of the PLATZ Transcription Factor in Tomato. <i>Plants</i> , 2023, 12, 2632.	3.5	0

#	ARTICLE	IF	CITATIONS
4148	The complete and fully-phased diploid genome of a male Han Chinese. <i>Cell Research</i> , 2023, 33, 745-761.	12.0	8
4149	High-quality RNA extraction and the regulation of genes encoding cellulosomes are correlated with growth stage in anaerobic fungi. <i>Frontiers in Fungal Biology</i> , 0, 4, .	2.0	0
4151	Genome-wide characterization of NmrA-like proteins and the regulatory function of soybean GmNmrA6 in response to salt and oxidative stresses. <i>Environmental and Experimental Botany</i> , 2023, 213, 105447.	4.2	0
4153	Complete chloroplast genomes of three wild perennial <i>Hordeum</i> species from Central Asia: genome structure, mutation hotspot, phylogenetic relationships, and comparative analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
4154	Genome-Wide Identification, Evolution Analysis of PI-PLC Family and Their Expression Patterns in Response to Different Hormones and Growth in Banana ( <i>Musa L.</i> ). <i>Tropical Plant Biology</i> , 2023, 16, 187-198.	1.9	0
4155	Transcriptome profiling reveals the strategy of thermal tolerance enhancement caused by heat-hardening in <i>Mytilus coruscus</i> . <i>Science of the Total Environment</i> , 2023, 903, 165785.	8.0	4
4156	Genome-wide identification of KCS gene family in <i>Carya illinoensis</i> and their roles under abiotic stress conditions. <i>Scientia Horticulturae</i> , 2023, 321, 112343.	3.6	2
4157	Mixed precision support in HPC applications: What about reliability?. <i>Journal of Parallel and Distributed Computing</i> , 2023, 181, 104746.	4.1	0
4158	Small protein modules dictate prophage fates during polylysogeny. <i>Nature</i> , 2023, 620, 625-633.	27.8	4
4159	Understanding the salt overly sensitive pathway in <i>Prunus</i> : Identification and characterization of <i>NHX</i> , <i>CIPK</i> , and <i>CBL</i> genes. <i>Plant Genome</i> , 0, , .	2.8	4
4160	Feature architecture aware phylogenetic profiling indicates a functional diversification of type IVa pili in the nosocomial pathogen <i>Acinetobacter baumannii</i> . <i>PLoS Genetics</i> , 2023, 19, e1010646.	3.5	0
4162	Identification and expression analysis of the SWEET genes in radish reveal their potential functions in reproductive organ development. <i>Molecular Biology Reports</i> , 0, , .	2.3	0
4163	Tissue-specific transcriptomes reveal potential mechanisms of microbiome heterogeneity in an ancient fish. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	3.0	1
4164	New protein families with hendecad coiled coils in the proteome of life. <i>Journal of Structural Biology</i> , 2023, 215, 108007.	2.8	2
4165	A genome catalogue of lake bacterial diversity and its drivers at continental scale. <i>Nature Microbiology</i> , 2023, 8, 1920-1934.	13.3	3
4166	DIPS-Plus: The enhanced database of interacting protein structures for interface prediction. <i>Scientific Data</i> , 2023, 10, .	5.3	0
4167	Identification of novel anelloviruses in the blood of giant panda ( <i>Ailuropoda melanoleuca</i> ). <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2023, 100, 102038.	1.6	0
4168	Functional annotation of proteins for signaling network inference in non-model species. <i>Nature Communications</i> , 2023, 14, .	12.8	0

#	ARTICLE	IF	CITATIONS
4169	Chromosome-scale genomes of commercial timber trees ( <i>Ochroma pyramidale</i> , <i>Mesua ferrea</i> , and) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	5.3	6
4170	RNA-Sequencing Analysis Indicates That N-Cadherin Promotes Prostate Cancer Progression by the Epigenetic Modification of Key Genes. <i>DNA and Cell Biology</i> , 0, , .	1.9	0
4172	Climate has contributed to population diversification of <i>Daphnia galeata</i> across Eurasia. <i>Molecular Ecology</i> , 0, , .	3.9	0
4173	Identification, Evolutionary Relationship Analysis of the Trehalose-6-Phosphate Synthase (TPS) Gene Family in Common Bean ( <i>Phaseolus vulgaris</i> ) and Their Expression in Response to Cold Stress. <i>Journal of Plant Growth Regulation</i> , 2024, 43, 323-340.	5.1	2
4174	Evolution and expression of the duck TRIM gene repertoire. <i>Frontiers in Immunology</i> , 0, 14, .	4.8	1
4176	Expansion of the cytochrome C oxidase subunit I database and description of four new lobose testate amoebae species (Amoebozoa; Arcellinida). <i>European Journal of Protistology</i> , 2023, 91, 126013.	1.5	0
4178	Genome-Wide Identification, Characterization, and Expression Analysis of the Geranylgeranyl Pyrophosphate Synthase (GGPPS) Gene Family Reveals Its Importance in Chloroplasts of Brassica oleracea L.. <i>Agriculture (Switzerland)</i> , 2023, 13, 1615.	3.1	1
4179	HiFun: homology independent protein function prediction by a novel protein-language self-attention model. <i>Briefings in Bioinformatics</i> , 2023, 24, .	6.5	1
4180	Identification of HuSWEET Family in Pitaya ( <i>Hylocereus undatus</i> ) and Key Roles of HuSWEET12a and HuSWEET13d in Sugar Accumulation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 12882.	4.1	0
4181	A moderately thermophilic origin of a novel family of marine group II euryarchaeota from deep ocean. <i>IScience</i> , 2023, 26, 107664.	4.1	0
4182	A systematic analysis of the phloem protein 2 (PP2) proteins in <i>Gossypium hirsutum</i> reveals that GhPP2-33 regulates salt tolerance. <i>BMC Genomics</i> , 2023, 24, .	2.8	0
4183	GsPKS24, a calcineurin B-like protein-interacting protein kinase gene from Glycine soja, positively regulates tolerance to pH stress and ABA signal transduction. <i>Functional and Integrative Genomics</i> , 2023, 23, .	3.5	2
4184	Genome-Wide Identification and Functional Analysis of Nitrate Transporter Genes (NPF, NRT2 and NRT3) in Maize. <i>International Journal of Molecular Sciences</i> , 2023, 24, 12941.	4.1	1
4185	When digestive physiology doesn't match "diet": <i>Lumpenus sagitta</i> (Stichaeidae) is an "omnivore" with a carnivorous gut. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2023, 285, 111508.	1.8	2
4186	Isolation and Characterization of the Acadevirus Members BigMira and MidiMira Infecting a Highly Pathogenic <i>Proteus mirabilis</i> Strain. <i>Microorganisms</i> , 2023, 11, 2141.	3.6	0
4187	The core bacteriobiome of Côte d'Ivoire soils across three vegetation zones. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
4188	Antibiotic Resistance Mediated by <i>Escherichia coli</i> in Kuwait Marine Environment as Revealed through Genomic Analysis. <i>Antibiotics</i> , 2023, 12, 1366.	3.7	1
4189	Environmental stress responses and adaptive evolution in the alpine ground beetle <i>Nebria vandykei</i> . <i>Biological Journal of the Linnean Society</i> , 0, , .	1.6	0

#	ARTICLE	IF	CITATIONS
4191	Genome-Wide Analysis and Expression Profiling of Trehalose-6-Phosphate Phosphatase (TPP) in <i>Punica granatum</i> in Response to Absciscic-Acid-Mediated Drought Stress. <i>Plants</i> , 2023, 12, 3076.	3.5	0
4192	Predicting and Interpreting Protein Developability Via Transfer of Convolutional Sequence Representation. <i>ACS Synthetic Biology</i> , 0, , .	3.8	0
4193	Study on the Interactions of Cyclins with CDKs Involved in Auxin Signal during Leaf Development by WGCNA in <i>Populus alba</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 13445.	4.1	0
4194	Comparative and population genomics of buckwheat species reveal key determinants of flavor and fertility. <i>Molecular Plant</i> , 2023, 16, 1427-1444.	8.3	2
4195	Identification of R2R3-MYB family in blueberry and its potential involvement of anthocyanin biosynthesis in fruits. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
4196	Comprehensive Analysis of the DNA Methyltransferase Genes and Their Association with Salt Response in <i>Pyrus betulaefolia</i> . <i>Forests</i> , 2023, 14, 1751.	2.1	0
4197	Integrations, transposons and <sc>IS</sc> elements promote diversification of multidrug resistance plasmids and adaptation of their hosts to antibiotic pollutants from pharmaceutical companies. <i>Environmental Microbiology</i> , 2023, 25, 3035-3051.	3.8	2
4198	Redox gradient shapes the abundance and diversity of mercury-methylating microorganisms along the water column of the Black Sea. <i>MSystems</i> , 0, , .	3.8	0
4199	Identification and Functional Characterization of the Nonexpressor of Pathogenesis-Related Genes 1 (NPR1) Gene in the Tea Plant ( <i>Camellia sinensis</i> ). <i>Forests</i> , 2023, 14, 1578.	2.1	1
4200	Genome-wide identification and expression analysis of Hsp70 family genes in Cassava ( <i>Manihot</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2.2	2.2	0
4201	Identification, Characterization, and Expression Profiling of Maize GATA Gene Family in Response to Abiotic and Biotic Stresses. <i>Agronomy</i> , 2023, 13, 1921.	3.0	1
4202	Structural and Functional Analysis of the MADS-Box Genes Reveals Their Functions in Cold Stress Responses and Flower Development in Tea Plant ( <i>Camellia sinensis</i> ). <i>Plants</i> , 2023, 12, 2929.	3.5	2
4203	Role of ABC Proteins in Secondary Metabolism and Immune (=Defensive) Response in Seaweeds. <i>Cells</i> , 2023, 12, 2259.	4.1	0
4204	Genome-Wide Identification and Expression Profiling Analysis of SWEET Family Genes Involved in Fruit Development in Plum ( <i>Prunus salicina</i> Lindl). <i>Genes</i> , 2023, 14, 1679.	2.4	2
4205	Genome-Wide Identification of the Phytocyanin Gene Family and Its Potential Function in Salt Stress in Soybean ( <i>Glycine max</i> (L.) Merr.). <i>Agronomy</i> , 2023, 13, 2484.	3.0	1
4206	Adaptive evolution in virulence effectors of the rice blast fungus <i>Piricularia oryzae</i> . <i>PLoS Pathogens</i> , 2023, 19, e1011294.	4.7	4
4207	Long-read assembled metagenomic approaches improve our understanding on metabolic potentials of microbial community in mangrove sediments. <i>Microbiome</i> , 2023, 11, .	11.1	2
4208	<i>In silico</i> analysis of Hsp70 genes in <i>Ctenopharyngodon idella</i> and their expression profiles in response to environmental stresses. <i>Biotechnology and Biotechnological Equipment</i> , 2023, 37, .	1.3	0

#	ARTICLE	IF	CITATIONS
4209	Biochemical and Transcriptome Analysis Reveals Pigment Biosynthesis Influenced Chlorina Leaf Formation in <i>Anoectochilus roxburghii</i> (Wall.) Lindl. <i>Biochemical Genetics</i> , 0, , .	1.7	0
4210	Double-stranded RNA mediated knockdown of sucrase gene induced mortality and reduced offspring production in <i>Aphis gossypii</i> . <i>Functional and Integrative Genomics</i> , 2023, 23, .	3.5	0
4211	Global Gene Expression of Post-Senescent Telomerase-Negative <i>ter1<sup>+</sup></i> Strain of <i>Ustilago maydis</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2023, 9, 896.	3.5	0
4212	Genome and whole-genome resequencing of <i>Cinnamomum camphora</i> elucidate its dominance in subtropical urban landscapes. <i>BMC Biology</i> , 2023, 21, .	3.8	1
4213	Genome-wide identification and characterization of ADH gene family and the expression under different abiotic stresses in tomato ( <i>Solanum lycopersicum</i> L.). <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
4214	Hsp70 Gene Family in <i>Sebastiscus marmoratus</i> : The Genome-Wide Identification and Transcriptome Analysis under Thermal Stress. <i>Genes</i> , 2023, 14, 1779.	2.4	1
4215	BASIDIN as a New Protein Effector of the Phytopathogen Causing Witchéâ€™s Broom Disease in Cocoa. <i>International Journal of Molecular Sciences</i> , 2023, 24, 11714.	4.1	0
4216	Data-driven large-scale genomic analysis reveals an intricate phylogenetic and functional landscape in J-domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	7
4217	Rotational Grazing Strategies Minimally Impact Soil Microbial Communities and Carbon Dynamicsâ€™A Texas Case Study. <i>Land</i> , 2023, 12, 1517.	2.9	0
4218	Efficient plant genome engineering using a probiotic sourced CRISPR-Cas9 system. <i>Nature Communications</i> , 2023, 14, .	12.8	3
4219	Genome-wide analysis and characterization of the LRR-RLK gene family provides insights into anthracnose resistance in common bean. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
4220	Structure reveals why genome folding is necessary for site-specific integration of foreign DNA into CRISPR arrays. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 1675-1685.	8.2	1
4221	Identification and Expression Analysis of the Ethylene Response Factor Gene Family in Tea Plant ( <i>Camellia sinensis</i> ). <i>Agronomy</i> , 2023, 13, 1900.	3.0	0
4222	Whole genome sequence analysis of <i>Aeromonas</i> -infecting bacteriophage AHPMCC7, a new species of genus <i>Alphavirus</i> and its application in <i>Litopenaeus vannamei</i> culture. <i>Virology</i> , 2023, 588, 109887.	2.4	1
4223	Divergence time estimates for the hypoxiaâ€™inducible factorâ€™1 alpha (<sc>HIF1</sc>) reveal an ancient emergence of animals in lowâ€™oxygen environments. <i>Geobiology</i> , 2024, 22, .	2.4	0
4224	Microbial-enrichment method enables high-throughput metagenomic characterization from host-rich samples. <i>Nature Methods</i> , 2023, 20, 1672-1682.	19.0	2
4225	Genome-wide identification of the MADS-box gene family and SEP1 target genes regulating young embryo development in hazel ( <i>Corylus</i> spp.) via ChIP sequencing. <i>Scientia Horticulturae</i> , 2024, 323, 112449.	3.6	0
4226	Streamlining N-terminally anchored yeast surface display via structural insights into <i>S. cerevisiae</i> Pir proteins. <i>Microbial Cell Factories</i> , 2023, 22, .	4.0	1

#	ARTICLE	IF	CITATIONS
4227	Genome assembly and analysis of <i>Lactuca virosa</i> : implications for lettuce breeding. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	0
4228	A chromosome-level assembly supports genome-wide investigation of the DMRT gene family in the golden mussel ( <i>Limnoperna fortunei</i> ). GigaScience, 2022, 12, .	6.4	0
4229	Predicting <i>Blomia tropicalis</i> allergens using a multiomics approach. Clinical and Translational Allergy, 2023, 13, .	3.2	3
4230	Genome-wide identification, evolution and expression pattern analysis of the GATA gene family in <i>Sorghum bicolor</i> . Frontiers in Plant Science, 0, 14, .	3.6	1
4231	Genome sequencing of <i>Syzygium cumini</i> (jamun) reveals adaptive evolution in secondary metabolism pathways associated with its medicinal properties. Frontiers in Plant Science, 0, 14, .	3.6	1
4232	Homologous Pairs of Low and High Temperature Originating Proteins Spanning the Known Prokaryotic Universe. Scientific Data, 2023, 10, .	5.3	1
4233	Design and engineering of artificial biosynthetic pathways—where do we stand and where do we go?. FEBS Letters, 2023, 597, 2897-2907.	2.8	1
4234	Protein remote homology detection and structural alignment using deep learning. Nature Biotechnology, 0, , .	17.5	11
4235	Chromosome-Wide Distribution and Characterization of H3K36me3 and H3K27Ac in the Marine Model Diatom <i>Phaeodactylum tricornutum</i> . Plants, 2023, 12, 2852.	3.5	0
4237	Designing Efficient SIMD Kernels for High Performance Sequence Alignment. , 2023, , .		0
4238	Integrated 3D genome, epigenome and transcriptome analyses reveal transcriptional coordination of circadian rhythm in rice. Nucleic Acids Research, 2023, 51, 9001-9018.	14.5	1
4239	Genome-wide analysis of the R2R3-MYB gene family in <i>Spatholobus suberectus</i> and identification of its function in flavonoid biosynthesis. Frontiers in Plant Science, 0, 14, .	3.6	1
4240	Comparative genome analysis of the freshwater fungus <i>Filosporella fistucella</i> indicates potential for plant-litter degradation at cold temperatures. G3: Genes, Genomes, Genetics, 2023, 13, .	1.8	0
4242	Genome of <i>Phyllanthus emblica</i> : the medicinal plant Amla with super antioxidant properties. Frontiers in Plant Science, 0, 14, .	3.6	2
4243	Transcriptome analysis of tomato plants following salicylic acid-induced immunity against <i>Clavibacter michiganensis</i> ssp. <i>michiganensis</i> . Plant Biotechnology, 2023, 40, 273-282.	1.0	0
4244	The First Genome-Wide Mildew Locus O Genes Characterization in the Lamiaceae Plant Family. International Journal of Molecular Sciences, 2023, 24, 13627.	4.1	1
4245	Phenotypic Analysis and Molecular Characterization of Enlarged Cell Size Mutant in <i>Nannochloropsis oceanica</i> . International Journal of Molecular Sciences, 2023, 24, 13595.	4.1	0
4246	Genome-Wide Identification of Bilberry WRKY Transcription Factors: Go Wild and Duplicate. Plants, 2023, 12, 3176.	3.5	1



#	ARTICLE	IF	CITATIONS
4247	Proline Metabolism Process and Antioxidant Potential of <i>Lycium ruthenicum</i> Murr. in Response to NaCl Treatments. <i>International Journal of Molecular Sciences</i> , 2023, 24, 13794.	4.1	0
4249	<i>Alkalimarinus alittae</i> sp. nov., isolated from gut of marine sandworm ( <i>Alitta virens</i> ) and emended description of the genus <i>Alkalimarinus</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2023, 73, .	1.7	0
4250	Methodology for Constructing a Knowledgebase for Plant Gene Regulation Information. <i>Methods in Molecular Biology</i> , 2023, , 277-300.	0.9	0
4251	One high quality genome and two transcriptome datasets for new species of <i>Mantamonas</i> , a deep-branching eukaryote clade. <i>Scientific Data</i> , 2023, 10, .	5.3	1
4252	Genome-wide identification and evolutionary analysis of the FGF gene family in buffalo. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-12.	3.5	0
4254	Analysis of the transcriptome and heat-shock protein (HSP) family expression in the spikelets of hulless oat ( <i>Avena sativa</i> L.) under heat stress. <i>Plant Growth Regulation</i> , 2024, 102, 395-408.	3.4	0
4255	Identification and adaptive evolution analysis of glutaredoxin genes in <i>Populus</i> spp.. <i>Plant Biology</i> , 2023, 25, 1154-1170.	3.8	0
4256	A transposon-derived gene family regulates heading date in rice. <i>Plant Science</i> , 2023, 337, 111871.	3.6	0
4257	Model of shrimp pond-mediated spatiotemporal dynamic distribution of antibiotic resistance genes in the mangrove habitat of a subtropical gulf. <i>Science of the Total Environment</i> , 2023, 905, 167199.	8.0	1
4258	Genome-wide identification, characterization, and expression analysis of the Ovate family protein in <i>Oryza sativa</i> under biotic and abiotic stresses. <i>Plant Stress</i> , 2023, 10, 100228.	5.5	1
4259	Investigation of the applicability of the zebrafish model for the evaluation of aristolochic acid-related nephrotoxicity. <i>Phytomedicine</i> , 2023, 121, 155092.	5.3	0
4260	Identification of atypical T4SS effector proteins mediating bacterial defense. , 2023, 2, 295-307.		0
4261	Insights into bacterial community metatranscriptome and metabolome in river water influenced by palm oil mill effluent final discharge. <i>Journal of Applied Microbiology</i> , 2023, 134, .	3.1	0
4263	Genome-wide analysis of the <i>Pleurotus eryngii</i> laccase gene (PeLac) family and functional identification of PeLac5. <i>AMB Express</i> , 2023, 13, .	3.0	1
4264	Substrate Specificity of Biofilms Proximate to Historic Shipwrecks. <i>Microorganisms</i> , 2023, 11, 2416.	3.6	0
4265	Genome-wide identification and analysis of <i>Lateral Organ Boundaries Domain</i> ( <i>LBD</i> ) transcription factor gene family in melon ( <i>Cucumis melo</i> L.). <i>PeerJ</i> , 0, 11, e16020.	2.0	1
4266	Biochemical characterization and key catalytic residue identification of a novel alpha-agarase with CBM2 domain. <i>Food Chemistry: X</i> , 2023, 20, 100915.	4.3	0
4267	Understanding the structure and function of GDSL-type esterase/lipase genes in pigeon pea for their role under moisture stress conditions. <i>Plant Stress</i> , 2023, 10, 100246.	5.5	0



#	ARTICLE	IF	CITATIONS
4268	FAM111A regulates replication origin activation and cell fitness. Life Science Alliance, 2023, 6, e202302111.	2.8	2
4270	MetaCC allows scalable and integrative analyses of both long-read and short-read metagenomic Hi-C data. Nature Communications, 2023, 14, .	12.8	0
4271	The mRNA-lncRNA landscape of multiple tissues uncovers key regulators and molecular pathways that underlie heterosis for feed intake and efficiency in laying chickens. Genetics Selection Evolution, 2023, 55, .	3.0	1
4272	The highly improved genome of <i>Ixodes scapularis</i> with X and Y pseudochromosomes. Life Science Alliance, 2023, 6, e202302109.	2.8	2
4273	Genome-Wide Evolutionary Characterization and Expression Analysis of Major Latex Protein (MLP) Family Genes in Tomato. International Journal of Molecular Sciences, 2023, 24, 15005.	4.1	1
4274	Genome-Wide Identification of WRKY Transcription Factor Family and Its Expression Patterns in <i>Dalbergia odorifera</i> T. Chen. Agronomy, 2023, 13, 2591.	3.0	1
4276	Identification and characterization of BES1 genes involved in grain size development of <i>Oryza sativa</i> L.. International Journal of Biological Macromolecules, 2023, 253, 127327.	7.5	3
4277	Comparative analysis of chloroplast genomes of two Chinese local citrus varieties and haplotype analysis with other citrus species. South African Journal of Botany, 2023, 162, 783-793.	2.5	0
4278	Microbiota plasticity in tilapia gut revealed by meta-analysis evaluating the effect of probiotics, prebiotics, and biofloc. PeerJ, 0, 11, e16213.	2.0	2
4279	Genome sequencing and analysis of <i>Bacillus velezensis</i> VJH504 reveal biocontrol mechanism against cucumber <i>Fusarium</i> wilt. Frontiers in Microbiology, 0, 14, .	3.5	2
4280	Accumulated metagenomic studies reveal recent migration, whole genome evolution, and undiscovered diversity of orthomyxoviruses. Journal of Virology, 0, , .	3.4	0
4281	PreHom-PCLM: protein remote homology detection by combing motifs and protein cubic language model. Briefings in Bioinformatics, 2023, 24, .	6.5	0
4282	Identification of SRS transcription factor family in <i>Solanum lycopersicum</i> , and functional characterization of their responses to hormones and abiotic stresses. BMC Plant Biology, 2023, 23, .	3.6	0
4283	Composition and distribution of diazotrophs in the Baltic Sea. Estuarine, Coastal and Shelf Science, 2023, 294, 108527.	2.1	0
4284	Metatranscriptomics reveals diversity of symbiotic interaction and mechanisms of carbon exchange in the marine cyanolichen <i>Lichina pygmaea</i> . New Phytologist, 2024, 241, 2243-2257.	7.3	3
4286	Novel virulent and temperate cyanophages predicted to infect <i>Microcoleus</i> associated with anatoxinâ€producing benthic mats. Environmental Microbiology, 2023, 25, 3319-3332.	3.8	0
4288	Characterization and genomic analysis of a novel bacteriophage BUCT_49532 lysing <i>Klebsiella pneumoniae</i> . Virus Genes, 0, , .	1.6	0
4289	Metabolic modeling predicts unique drug targets in <i>Borrelia burgdorferi</i> . MSystems, 0, , .	3.8	1

#	ARTICLE	IF	CITATIONS
4292	Genetic diversity, population structure and anthracnose resistance response in a novel sweet sorghum diversity panel. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
4293	Genetic mechanisms of petal morphogenesis in <i>Eustoma grandiflorum</i> . <i>Scientia Horticulturae</i> , 2024, 324, 112558.	3.6	0
4294	Exploring new galaxies: Perspectives on the discovery of novel PET-degrading enzymes. <i>Applied Catalysis B: Environmental</i> , 2024, 342, 123404.	20.2	1
4296	Chromosome-scale assembly of the wild wheat relative <i>Aegilops umbellulata</i> . <i>Scientific Data</i> , 2023, 10, .	5.3	2
4297	Evolution of the ability to evade host innate immune defense by <i>Talaromyces marneffe</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 253, 127597.	7.5	1
4298	Genome-Wide Identification and Characterization of CLAVATA3/EMBRYO SURROUNDING REGION (CLE) Gene Family in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Genes</i> , 2023, 14, 2046.	2.4	0
4299	Genome-Wide Identification and Expression Analysis of the Cucumber FKBP Gene Family in Response to Abiotic and Biotic Stresses. <i>Genes</i> , 2023, 14, 2006.	2.4	1
4300	Unzipped chromosome-level genomes reveal allopolyploid nematode origin pattern as unreduced gamete hybridization. <i>Nature Communications</i> , 2023, 14, .	12.8	4
4301	Comparative genomics profiling revealed multi-stress responsive roles of the CC-NBS-LRR genes in three mango cultivars. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
4303	ATP synthase evolution on a cross-braced dated tree of life. <i>Nature Communications</i> , 2023, 14, .	12.8	3
4304	The <i>Rauvolfia tetraphylla</i> genome suggests multiple distinct biosynthetic routes for yohimbane monoterpene indole alkaloids. <i>Communications Biology</i> , 2023, 6, .	4.4	2
4305	Comprehensive Genome-Wide Identification of the RNA-Binding Glycine-Rich Gene Family and Expression Profiling under Abiotic Stress in <i>Brassica oleracea</i> . <i>Plants</i> , 2023, 12, 3706.	3.5	1
4306	Climate-resilient crops: Lessons from xerophytes. <i>Plant Journal</i> , 2024, 117, 1815-1835.	5.7	1
4307	PRACTICAL APPLICATIONS OF MACHINE LEARNING FOR ANTI-INFECTIVE DRUG DISCOVERY. <i>Medicinal Chemistry Reviews</i> , 0, , 345-375.	0.1	0
4308	Identification of Acetylcholinesterase Like Gene Family and Its Expression Under Salinity Stress in <i>Solanum lycopersicum</i> . <i>Journal of Plant Growth Regulation</i> , 0, , .	5.1	0
4309	Interrogating two extensively self-targeting Type I CRISPR-Cas systems in <i>Xanthomonas albilineans</i> reveals distinct anti-CRISPR proteins that block DNA degradation. <i>Nucleic Acids Research</i> , 0, , .	14.5	0
4310	De novo transcriptome assembly of <i>Dalbergia sissoo</i> Roxb. (Fabaceae) under Botryodiplodia theobromae-induced dieback disease. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
4311	Diversity at single nucleotide to pangenome scales among sulfur cycling bacteria in salt marshes. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	0

#	ARTICLE	IF	CITATIONS
4312	CRISPR-Cas systems feature and targeting phages diversity in Lacticaseibacillus rhamnosus strains. Frontiers in Microbiology, 0, 14, .	3.5	0
4313	Biological effects of trans, trans-farnesol in Leishmania amazonensis. Frontiers in Cellular and Infection Microbiology, 0, 13, .	3.9	0
4314	An automated model annotation system (AMAS) for SBML models. Bioinformatics, 2023, 39, .	4.1	0
4315	Genome and transcriptome reveal lithophilic adaptation of <i>Cladophialophora brunneola</i> , a new rock-inhabiting fungus. Mycology, 2023, 14, 326-343.	4.4	0
4316	Natural product biosynthetic potential reflects macroevolutionary diversification within a widely distributed bacterial taxon. MSystems, 2023, 8, .	3.8	1
4317	Genome-wide identification, expression analysis, and functional study of the bZIP transcription factor family and its response to hormone treatments in pea (Pisum sativum L.). BMC Genomics, 2023, 24, .	2.8	2
4318	Collaborative Expression: Transcriptomics of Conus virgo Suggests Contribution of Multiple Secretory Glands to Venom Production. Journal of Molecular Evolution, 0, , .	1.8	0
4319	Genome-wide identification, characterization, and expression analysis of the sweet potato (Ipomoea) Tj ETQq1 1 0.784314 rgBT /Overlo	3.6	1
4320	Revisiting the mercury cycle in marine sediments: A potential multifaceted role for Desulfobacterota. Journal of Hazardous Materials, 2024, 465, 133120.	12.4	1
4321	A genome assembly for Orinus kokonorica provides insights into the origin, adaptive evolution and further diversification of two closely related grass genera. Communications Biology, 2023, 6, .	4.4	0
4322	Genome-wide characterization of the tomato UDP-glycosyltransferase gene family and functional identification of SLUDPGT52 in drought tolerance. , 2023, 1, .		0
4327	VBCG: 20 validated bacterial core genes for phylogenomic analysis with high fidelity and resolution. Microbiome, 2023, 11, .	11.1	1
4328	<scp>SSDraw</scp>: <scp>Software</scp> for generating comparative protein secondary structure diagrams. Protein Science, 2023, 32, .	7.6	1
4329	Role of Relebactam in the Antibiotic Resistance Acquisition in Pseudomonas aeruginosa: In Vitro Study. Antibiotics, 2023, 12, 1619.	3.7	0
4330	VIGA: a one-stop tool for eukaryotic virus identification and genome assembly from next-generation-sequencing data. Briefings in Bioinformatics, 2023, 25, .	6.5	0
4331	A metagenomic view of novel microbial and metabolic diversity found within the deep terrestrial biosphere at <scp>DeMMO: A</scp> microbial observatory in <scp>South Dakota</scp>, <scp>USA</scp>. Environmental Microbiology, 2023, 25, 3719-3737.	3.8	0
4333	Origin and early divergence of tandem duplicated sorbitol transporter genes in Rosaceae: insights from evolutionary analysis of the <scp>SOT</scp> gene family in angiosperms. Plant Journal, 2024, 117, 856-872.	5.7	0
4335	REC protein family expansion by the emergence of a new signaling pathway. MBio, 0, , .	4.1	0

#	ARTICLE	IF	CITATIONS
4337	Genome-Wide and Transcriptome Analysis of Jacalin-Related Lectin Genes in Barley and the Functional Characterization of HvHorch in Low-Nitrogen Tolerance in Arabidopsis. International Journal of Molecular Sciences, 2023, 24, 16641.	4.1	0
4338	PanPA: generation and alignment of panproteome graphs. Bioinformatics Advances, 0, , .	2.4	0
4339	Genome-wide identification of long intergenic non-coding RNAs of responsive to powdery mildew stress in wheat ( <i>Triticum aestivum</i> ). Frontiers in Plant Science, 0, 14, .	3.6	0
4340	Taxonomic Distribution and Molecular Evolution of Mytillectins. Marine Drugs, 2023, 21, 614.	4.6	0
4341	Genome sequences of Mx1, the first <i>Myxococcus</i> phage isolated, and Mx4, a generalized transducing myxophage. Microbiology Resource Announcements, 0, , .	0.6	0
4343	The Plant Parasitic Nematodes Database: A Comprehensive Genomic Data Platform for Plant Parasitic Nematode Research. International Journal of Molecular Sciences, 2023, 24, 16841.	4.1	0
4344	iCAZyGFADB: an insect CAZyme and gene function annotation database. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	0
4345	MVDINET: A Novel Multi-Level Enzyme Function Predictor With Multi-View Deep Interactive Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2024, 21, 84-94.	3.0	0
4346	Comparative Transcriptome Sequencing and Endogenous Phytohormone Content of Annual Grafted Branches of <i>Zelkova schneideriana</i> and Its Dwarf Variety HenTianGao. International Journal of Molecular Sciences, 2023, 24, 16902.	4.1	0
4347	Bioinformatics Methods for Prediction of Gene Families Encoding Extracellular Peptides. Methods in Molecular Biology, 2024, , 3-21.	0.9	0
4348	Characterization of a unique repression system present in arbitrium phages of the SPbeta family. Cell Host and Microbe, 2023, 31, 2023-2037.e8.	11.0	1
4349	Genome-wide identification of bZIP gene family and expression analysis of BhbZIP58 under heat stress in wax gourd. BMC Plant Biology, 2023, 23, .	3.6	0
4350	The crystal structure of insecticidal protein Txp40 from <i>Xenorhabdus nematophila</i> reveals a two-domain unique binary toxin with homology to the toxin-antitoxin (TA) system. Insect Biochemistry and Molecular Biology, 2024, 164, 104045.	2.7	0
4352	Identification of the CNGC Gene Family in Rice and Mining of Alleles for Application in Rice Improvement. Plants, 2023, 12, 4089.	3.5	0
4353	Phosphate-related genomic islands as drivers of environmental adaptation in the streamlined marine alphaproteobacterial HIMB59. MSystems, 0, , .	3.8	0
4354	Genome-wide identification of RNA recognition motif (RRM1) in <i>Brassica rapa</i> and functional analysis of RNA-binding protein (BrRBP) under low-temperature stress. BMC Plant Biology, 2023, 23, .	3.6	1
4355	Full-length transcriptome characterization and comparative analysis of <i>Gleditsia sinensis</i> . BMC Genomics, 2023, 24, .	2.8	2
4357	Chromosome-level genome assembly and annotation of the Antarctica whitefin plunderfish <i>Pogonophryne albipinna</i> . Scientific Data, 2023, 10, .	5.3	0

#	ARTICLE	IF	CITATIONS
4358	From genomics to metabolomics: Deciphering sanguinarine biosynthesis in <i>Dicranostigma leptopodum</i> . <i>International Journal of Biological Macromolecules</i> , 2024, 257, 128727.	7.5	0
4360	Genome-wide analysis of SET domain genes and the function of GhSDG51 during salt stress in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>BMC Plant Biology</i> , 2023, 23, .	3.6	1
4361	A conserved ribosomal protein has entirely dissimilar structures in different organisms. <i>Molecular Biology and Evolution</i> , 0, , .	8.9	0
4362	Low H3K27me3 deposition at CYP82E4 determines the nicotinic conversion rate in <i>Nicotiana tabacum</i> . <i>Plant Physiology and Biochemistry</i> , 2024, 206, 108234.	5.8	0
4363	A <i>ScWIP5</i> gene confers fall armyworm resistance by reducing digestive enzyme activities in sugarcane. <i>Pest Management Science</i> , 0, , .	3.4	0
4364	The intrinsically disordered transcriptional activation domain of <i>ClITA</i> is functionally tuneable by single substitutions: <i>An</i> exception or a new paradigm?. <i>Protein Science</i> , 2024, 33, .	7.6	1
4365	SSR Marker Acquisition and Application from Transcriptome of Captive Chinese Forest Musk Deer ( <i>Moschus berezovskii</i> ). <i>Biochemical Genetics</i> , 0, , .	1.7	0
4366	High-quality haplotype-resolved genome assembly for ringcup oak ( <i>Quercus glauca</i> ) provides insight into oaks demographic dynamics. <i>Molecular Ecology Resources</i> , 2024, 24, .	4.8	0
4367	The Viromes of Six Ecosystem Service Provider Parasitoid Wasps. <i>Viruses</i> , 2023, 15, 2448.	3.3	1
4368	Adaptation of an arthropod predator to a challenging environment is associated with a loss of a genome-wide plastic transcriptional response. <i>Pest Management Science</i> , 0, , .	3.4	0
4369	Full-Length Transcriptome and Gene Expression Analysis of Different Ovis aries Adipose Tissues Reveals Transcript Variants Involved in Lipid Biosynthesis. <i>Animals</i> , 2024, 14, 7.	2.3	0
4372	<i>Termitidicoccus mucosus</i> gen. nov. sp. nov. a novel Verrucomicrobiota species isolated from <i>Reticulitermes chinensis</i> gives insights of high adaptability of symbiotic bacteria to termite gut ecosystem. <i>Research in Microbiology</i> , 2023, , 104173.	2.1	0
4373	The evolution history of an allotetraploid mangrove tree analysed with a new tool Allo4D. <i>Plant Biotechnology Journal</i> , 0, , .	8.3	0
4374	Phylogenetic and Structure-Function Analyses of ENA ATPases: A Case Study of the ENA1 Protein from the Fungus <i>Neurospora crassa</i> . <i>International Journal of Molecular Sciences</i> , 2024, 25, 514.	4.1	0
4375	Interactive dynamics between rhizosphere bacterial and viral communities facilitate soybean fitness to cadmium stress revealed by time-series metagenomics. <i>Soil Biology and Biochemistry</i> , 2024, 190, 109313.	8.8	0
4377	Genome-wide characterization and expression analysis of MADS-box transcription factor gene family in <i>Perilla frutescens</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
4378	Comprehensive Identification of the $\alpha$ -Amylase (BAM) Gene Family in Response to Cold Stress in White Clover. <i>Plants</i> , 2024, 13, 154.	3.5	0
4379	Two novel phages, Klebsiella phage GADU21 and Escherichia phage GADU22, from the urine samples of patients with urinary tract infection. <i>Virus Genes</i> , 2024, 60, 208-221.	1.6	0

#	ARTICLE	IF	CITATIONS
4380	Reciprocal expression of MADS-box genes and DNA methylation reconfiguration initiate bisexual cones in spruce. Communications Biology, 2024, 7, .	4.4	1
4381	Thaumatococcal protein family genes VfTLP4-3 and VfTLP5 are critical for faba bean's response to drought stress at the seedling stage. Plant Physiology and Biochemistry, 2024, 206, 108243.	5.8	0
4382	The Identification, Characterization, and Functional Analysis of the Sugar Transporter Gene Family of the Rice False Smut Pathogen, Villosiclava virens. International Journal of Molecular Sciences, 2024, 25, 600.	4.1	0
4383	Differential expression and gene correlation analyses reveal core <scp>CAZymes</scp> in <i>Fusarium oxysporum</i> f.sp.&#x2013;<i>lycopersici</i> exposed to mutagen and heat stress. Journal of Phytopathology, 2024, 172, .	1.0	0
4386	A novel starch-active lytic polysaccharide monooxygenase discovered with bioinformatics screening and its application in textile desizing. BMC Biotechnology, 2024, 24, .	3.3	0
4388	<scp>TbsP</scp> and <scp>TrmB</scp> jointly regulate <i>gapI</i> to influence cell development phenotypes in the archaeon <i>Haloferax volcanii</i>. Molecular Microbiology, 2024, 121, 742-766.	2.5	0
4389	Transcriptome profiling and RXR gene family identification reveals the molecular mechanism of rapid aging after spawning of cuttlefish Sepiella japonica. Journal of Oceanology and Limnology, 0, , .	1.3	0
4390	A whole-body transcriptome assembly of the annelid worm Hediste diversicolor. Marine Genomics, 2024, 74, 101084.	1.1	0
4391	GRAS gene family in rye (Secale cereale L.): genome-wide identification, phylogeny, evolutionary expansion and expression analyses. BMC Plant Biology, 2024, 24, .	3.6	0
4393	Mixta mediterraneensis as a novel and abundant gut symbiont of the allergen-producing domestic mite Blomia tropicalis. Experimental and Applied Acarology, 2024, 92, 161-181.	1.6	0
4394	Aquilaria sinensis: An Upstart Resource for Cucurbitacin Production Offers Insights into the Origin of Plant Bitter (Bi) Gene Clusters. Plants, 2024, 13, 260.	3.5	0
4395	Basic helix-loop-helix (bHLH) gene family in rye (Secale cereale L.): genome-wide identification, phylogeny, evolutionary expansion and expression analyses. BMC Genomics, 2024, 25, .	2.8	0
4398	The histone chaperone SPT2 regulates chromatin structure and function in Metazoa. Nature Structural and Molecular Biology, 2024, 31, 523-535.	8.2	0
4399	Genome-Wide Identification and Characterization of CHROMO Domain Family Genes Reveal Roles of the Maize Genes in Heat Stress Response. Biology Bulletin, 2023, 50, S289-S297.	0.5	0
4400	Characterization and gene expression analysis reveal universal stress proteins respond to abiotic stress in Gossypium hirsutum. BMC Genomics, 2024, 25, .	2.8	0
4401	<scp>AlphaFold2</scp>-guided description of <scp>CoBaHMA</scp>, a novel family of bacterial domains within the heavy&#x2013;metal&#x2013;associated superfamily. Proteins: Structure, Function and Bioinformatics, 2024, 92, 776-794.	2.6	0
4402	Exploring Nocardia&#x2013;s ecological spectrum and novel therapeutic frontiers through whole-genome sequencing: unraveling drug resistance and virulence factors. Archives of Microbiology, 2024, 206, .	2.2	0
4403	Amplification of Immune Genes in Ancient Stony Corals for Adapting to Unstable Marine Environments. , 2024, 3, .		0



#	ARTICLE	IF	CITATIONS
4404	Transcriptome Analysis and Genome-Wide Gene Family Identification Enhance Insights into Bacterial Wilt Resistance in Tobacco. <i>Agronomy</i> , 2024, 14, 250.	3.0	0
4406	A novel computational pipeline for var gene expression augments the discovery of changes in the <i>Plasmodium falciparum</i> transcriptome during transition from in vivo to short-term in vitro culture. <i>ELife</i> , 0, 12, .	6.0	0
4407	Characterization and analysis of multi-organ full-length transcriptomes in <i>Sphaeropteris brunoniana</i> and <i>Alsophila latebrosa</i> highlight secondary metabolism and chloroplast RNA editing pattern of tree ferns. <i>BMC Plant Biology</i> , 2024, 24, .	3.6	0
4408	Iron coatings on carbonate rocks shape the attached bacterial aquifer community. <i>Science of the Total Environment</i> , 2024, 917, 170384.	8.0	0
4409	Knockdown of the atypical protein kinase genes GhABC1K2-A05 and GhABC1K12-A07 make cotton more sensitive to salt and PEG stress. <i>Journal of Integrative Agriculture</i> , 2024, , .	3.5	0
4411	Functional similarity, despite taxonomical divergence in the millipede gut microbiota, points to a common trophic strategy. <i>Microbiome</i> , 2024, 12, .	11.1	1
4412	Genome-Wide Bioinformatics Analysis of SWEET Gene Family and Expression Verification of Candidate PaSWEET Genes in <i>Potentilla anserina</i> . <i>Plants</i> , 2024, 13, 406.	3.5	0
4414	Hydrolytic endonucleolytic ribozyme (HYER) is programmable for sequence-specific DNA cleavage. <i>Science</i> , 2024, 383, .	12.6	0
4415	Mechanism of 2- $\alpha$ -fucosyllactose degradation by human-associated <i>Akkermansia</i> . <i>Journal of Bacteriology</i> , 2024, 206, .	2.2	0
4416	A structural vista of phosducin-like PhLP2A-chaperonin TRiC cooperation during the ATP-driven folding cycle. <i>Nature Communications</i> , 2024, 15, .	12.8	1
4417	Genome sequencing and functional analysis of a multipurpose medicinal herb <i>Tinospora cordifolia</i> (Giloy). <i>Scientific Reports</i> , 2024, 14, .	3.3	0
4418	A comprehensive evaluation of the potential of plant growth-promoting rhizobacteria for applications in agriculture in stressed environments. <i>Pedosphere</i> , 2024, , .	4.0	0
4419	Genome-Wide Identification of B-Box Gene Family and Candidate Light-Related Member Analysis of Tung Tree ( <i>Vernicia fordii</i> ). <i>International Journal of Molecular Sciences</i> , 2024, 25, 1977.	4.1	0
4420	Distinct structural variants and repeat landscape shape the genomes of the ancient grapes <i>Aglianico</i> and <i>Falanghina</i> . <i>BMC Plant Biology</i> , 2024, 24, .	3.6	0
4422	Gene inversion led to the emergence of brackish archaeal heterotrophs in the aftermath of the Cryogenian Snowball Earth. , 2024, 3, .		0
4423	Biogenic manganese oxides promote metal(loid) remediation by shaping microbial communities in biological aqua crust. <i>Water Research</i> , 2024, 253, 121287.	11.3	1
4425	Characterization of soybean chitinase genes induced by rhizobacteria involved in the defense against <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
4427	Comprehensive analysis of sesame LRR-RLKs: structure, evolution and dynamic expression profiles under <i>Macrophomina phaseolina</i> stress. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0



#	ARTICLE	IF	CITATIONS
4428	In silico molecular characterization of TGF- $\beta^2$ gene family in <i>Bufo bufo</i> : genome-wide analysis. Journal of Biomolecular Structure and Dynamics, 0, , 1-15.	3.5	0
4430	Folded Alpha Helical Putative New Proteins from <i>Apilactobacillus kunkeei</i> . Journal of Molecular Biology, 2024, 436, 168490.	4.2	0
4431	Characterisation of IS1311 in <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> genomes: Typing, continental clustering, microbial evolution and host adaptation. PLoS ONE, 2024, 19, e0294570.	2.5	0
4432	Evolution of parasitism genes in the plant parasitic nematodes. Scientific Reports, 2024, 14, .	3.3	0
4433	Exploring the role of <i>FBXL</i> gene family in Soybean: Implications for plant height and seed size regulation. Physiologia Plantarum, 2024, 176, .	5.2	0
4434	DNA-(cytosine-C5) methyltransferases and demethylases in <i>Theobroma cacao</i> : insights into genomic features, phylogenetic relationships, and protein-protein interactions. Tree Genetics and Genomes, 2024, 20, .	1.6	0
4435	Angiosperm-wide analysis of fruit and ovary evolution aided by a new nuclear phylogeny supports association of the same ovary type with both dry and fleshy fruits. Journal of Integrative Plant Biology, 2024, 66, 228-251.	8.5	0
4436	Ranking the risk of antibiotic resistance genes by metagenomic and multifactorial analysis in hospital wastewater systems. Journal of Hazardous Materials, 2024, 468, 133790.	12.4	0
4438	Genome-wide identification, expression profiling, and network analysis of calcium and cadmium transporters in rice ( <i>Oryza sativa</i> L.). Cereal Research Communications, 0, , .	1.6	0
4439	KINtaro: protein kinase-like database. BMC Research Notes, 2024, 17, .	1.4	0
4441	Protein homeostasis imprinting across evolution. NAR Genomics and Bioinformatics, 2024, 6, .	3.2	0
4442	Machine Learning and Deep Learning in Synthetic Biology: Key Architectures, Applications, and Challenges. ACS Omega, 2024, 9, 9921-9945.	3.5	0
4443	Serpentoviruses Exhibit Diverse Organization and ORF Composition with Evidence of Recombination. Viruses, 2024, 16, 310.	3.3	0
4444	A novel <i>Bartonella</i> -like bacterium forms an interdependent mutualistic symbiosis with its host, the stored-product mite <i>Tyrophagus putrescentiae</i> . MSystems, 2024, 9, .	3.8	0
4445	Biogeographic patterns and drivers of soil viromes. Nature Ecology and Evolution, 2024, 8, 717-728.	7.8	0
4446	Dipterocarpaceae genomics reveal their demography and adaptations to Asian rainforests. Nature Communications, 2024, 15, .	12.8	0
4447	Accumulation of defense systems in phage-resistant strains of <i>Pseudomonas aeruginosa</i> . Science Advances, 2024, 10, .	10.3	0
4448	Genomic and metabolomic diversity within a familial population of <i>Aspergillus flavus</i> . Molecular Microbiology, 0, , .	2.5	0

#	ARTICLE	IF	CITATIONS
4449	Genome-wide identification of bZIP gene family in Pearl millet and transcriptional profiling under abiotic stress, phytohormonal treatments; and functional characterization of PgbZIP9. <i>Frontiers in Plant Science</i> , 0, 15, .	3.6	0
4450	Genome-Wide Identification and Transcriptome Analysis of the Hsp70 Gene Family in <i>Monodonta labio</i> Reveals Its Role in Response to Nanoplastics Stress. <i>Genes</i> , 2024, 15, 291.	2.4	0
4452	Pan-chloroplast genomes for accession-specific marker development in <i>Hibiscus syriacus</i> . <i>Scientific Data</i> , 2024, 11, .	5.3	0
4453	An historical "wreck": A transcriptome assembly of the naval shipworm, <i>Teredo navalis</i> Linnaeus, 1978. <i>Marine Genomics</i> , 2024, 74, 101097.	1.1	0
4454	Genome-Wide Characterization and Expression Analyses of Major Latex Protein Gene Family in <i>Populus simonii</i> – <i>P. nigra</i> . <i>International Journal of Molecular Sciences</i> , 2024, 25, 2748.	4.1	0
4457	Genome-wide analysis of the cytochrome P450 superfamily suggests its roles in coumarin biosynthesis and salt stress response in <i>Melilotus albus</i> . <i>Environmental and Experimental Botany</i> , 2024, 220, 105718.	4.2	0
4458	Suppressing a mitochondrial calcium uniporter activates the calcium signaling pathway and promotes cell elongation in cotton. <i>Crop Journal</i> , 2024, 12, 411-421.	5.2	0
4459	Genome-wide identification and expression analysis of NF-Y gene family in tobacco ( <i>Nicotiana tabacum</i> ) Tj ETQq1 1.0,784314rgBT /Ove	3.3	0
4460	Analysis of the UDP-Glucosyltransferase (UGT) Gene Family and Its Functional Involvement in Drought and Salt Stress Tolerance in <i>Phoebe bournei</i> . <i>Plants</i> , 2024, 13, 722.	3.5	0
4461	Characterization of <i>PYL</i> gene family and identification of <i>HaPYL</i> genes response to drought and salt stress in sunflower. <i>PeerJ</i> , 0, 12, e16831.	2.0	0
4462	Role for gene conversion in the evolution of cell-surface antigens of the malaria parasite <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2024, 22, e3002507.	5.6	0
4463	Diversity of sugar-diphospholipid-utilizing glycosyltransferase families. <i>Communications Biology</i> , 2024, 7, .	4.4	0
4464	Field application of de novo transcriptomic analysis to evaluate the effects of sublethal freshwater salinization on <i>Gasterosteus aculeatus</i> in urban streams. <i>PLoS ONE</i> , 2024, 19, e0298213.	2.5	0
4465	The first A-to-I RNA editome of hemipteran species <i>Coridius chinensis</i> reveals overrepresented recoding and prevalent intron editing in early-diverging insects. <i>Cellular and Molecular Life Sciences</i> , 2024, 81, .	5.4	0
4466	Determining the genetic basis of ginsenosides variation during ginseng domestication by evolutionary transcriptomics. <i>Industrial Crops and Products</i> , 2024, 212, 118369.	5.2	0
4467	Spatial ecology of <i>Haemophilus</i> and <i>Aggregatibacter</i> in the human oral cavity. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
4468	Genome-Wide Prediction and Expression Characterization of the GATA Gene Family under Nitrogen and Phosphate Deficiency in <i>Panax ginseng</i> . <i>Horticulturae</i> , 2024, 10, 282.	2.8	0
4469	Sequence-structure-function characterization of the emerging tetracycline destructase family of antibiotic resistance enzymes. <i>Communications Biology</i> , 2024, 7, .	4.4	0

#	ARTICLE	IF	CITATIONS
4472	Role of Distributed Computing in Biology Research Field and Its Challenges. Series in Bioengineering, 2024, , 147-162.	0.6	0
4473	Genome-wide analysis of the KNOX gene family in Moso bamboo: insights into their role in promoting the rapid shoot growth. BMC Plant Biology, 2024, 24, .	3.6	0
4474	Genome-Wide Identification of Osmanthus fragrans Histone Modification Genes and Analysis of Their Expression during the Flowering Process and under Azacytidine and Ethylene Treatments. Plants, 2024, 13, 777.	3.5	0
4475	Identification of the NCED gene family in tomato (Solanum lycopersicum) and functional analysis of SINCED2 in response to drought stress. Scientia Horticulturae, 2024, 330, 113087.	3.6	0
4476	Characterization and expression of heat shock protein 70s in Liposcelis bostrychophila: Insights into their roles in insecticidal stress response. Journal of Stored Products Research, 2024, 106, 102289.	2.6	0
4479	Multi-omics provides insights into genome evolution and betacyanin biosynthesis in halophyte of Suaeda salsa. Journal of Systematics and Evolution, 0, , .	3.1	0
4480	The Madagascar palm genome provides new insights on the evolution of Apocynaceae specialized metabolism. Heliyon, 2024, 10, e28078.	3.2	0
4481	Legionella metaeffector MavL reverses ubiquitin ADP-ribosylation via a conserved arginine-specific macrodomain. Nature Communications, 2024, 15, .	12.8	0
4482	Identification and Functional Analysis of 1-Deoxy-D-xylulose-5-phosphate Synthase Gene in Tomatoes (Solanum lycopersicum). Horticulturae, 2024, 10, 304.	2.8	0
4483	A systematic analysis of ARM genes revealed that GhARM144 regulates the resistance against Verticillium dahliae via interaction with GhOSM34. Physiologia Plantarum, 2024, 176, .	5.2	0
4484	Comprehensive identification and analysis of DUF640 genes associated with rice growth. Gene, 2024, 914, 148404.	2.2	0
4485	Genome-wide identification of GATA transcription factors in tetraploid potato and expression analysis in differently colored potato flesh. Frontiers in Plant Science, 0, 15, .	3.6	0
4486	Co-inoculation of the endophytes Bacillus thuringiensis CAPE95 and Paenibacillus polymyxa CAPE238 promotes Tropaeolum majus L. growth and enhances its root bacterial diversity. Frontiers in Microbiology, 0, 15, .	3.5	0
4487	Genomic and phenotypic analyses reveal Paenibacillus polymyxa PJH16 is a potential biocontrol agent against cucumber fusarium wilt. Frontiers in Microbiology, 0, 15, .	3.5	0
4488	Bioinformatic analysis of microbial type terpene synthase genes in plants. Methods in Enzymology, 2024, , .	1.0	0
4489	Identification of the lateral organ boundary domain gene family and its preservation by exogenous salicylic acid in Cerasus humilis. Physiology and Molecular Biology of Plants, 2024, 30, 401-415.	3.1	0
4490	Genome-wide characterization of the bHLH gene family in Gynostemma pentaphyllum reveals its potential role in the regulation of gypenoside biosynthesis. BMC Plant Biology, 2024, 24, .	3.6	0
4491	Towards the Exploration and Evolution of Insulin-like Venoms in Actiniaria (Sea anemones). Marine Drugs, 2024, 22, 136.	4.6	0

#	ARTICLE	IF	CITATIONS
4492	The evolutionary origin of naturally occurring intermolecular Diels-Alderase from <i>Morus alba</i> . Nature Communications, 2024, 15, .	12.8	0