

# InterProScan: protein domains identifier

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Citation Report

#	ARTICLE	IF	CITATIONS
1	InterPro. , 2005, , .		9
2	Genome-wide review of transcriptional complexity in mouse protein kinases and phosphatases. <i>Genome Biology</i> , 2006, 7, R5.	13.9	48
3	Proteomic and Computational Analysis of Secreted Proteins with Type I Signal Peptides from the Antarctic Archaeon <i>Methanococcus burtonii</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2457-2464.	1.8	33
4	Bioinformatics database infrastructure for biotechnology research. <i>Journal of Biotechnology</i> , 2006, 124, 629-639.	1.9	15
5	Reconstruction and in silico analysis of the MAPK signaling pathways in the human blood fluke, <i>Schistosoma japonicum</i> . <i>FEBS Letters</i> , 2006, 580, 3677-3686.	1.3	24
6	Common genomic structure for the Lepidoptera cadherin-like genes. <i>Gene</i> , 2006, 381, 71-80.	1.0	24
7	Proteomic characterization of acid stress response in <i>Synechocystis</i> sp. PCC 6803. <i>Proteomics</i> , 2006, 6, 3614-3624.	1.3	71
8	Integrating forward and reverse proteomics to unravel protein function. <i>Proteomics</i> , 2006, 6, 5467-5480.	1.3	18
9	Structural characterization of <i>Salmonella typhimurium</i> YeaZ, an M22 O $\alpha$ -sialoglycoprotein endopeptidase homolog. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 111-123.	1.5	36
10	MOLECULAR CHARACTERIZATION OF A PHOSPHATE-REGULATED CELL-SURFACE PROTEIN FROM THE COCCOLITHOPHORID, <i>EMILIANA HUXLEYI</i> (PRYMNESIOPHYCEAE). <i>Journal of Phycology</i> , 2006, 42, 814-821.	1.0	14
11	Identification of genes from the obligate intracellular plant pathogen, <i>Plasmodiophora brassicae</i> . <i>FEMS Microbiology Letters</i> , 2006, 264, 198-204.	0.7	57
12	Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006, 8, 1183-1189.	4.6	33
13	From The Origin of Species to the origin of bacterial flagella. <i>Nature Reviews Microbiology</i> , 2006, 4, 784-790.	13.6	143
14	Human chromosome 11 DNA sequence and analysis including novel gene identification. <i>Nature</i> , 2006, 440, 497-500.	13.7	74
15	DRTF: a database of rice transcription factors. <i>Bioinformatics</i> , 2006, 22, 1286-1287.	1.8	141
16	Identification and analysis of genes expressed in the adult filarial parasitic nematode <i>Dirofilaria immitis</i> . <i>International Journal for Parasitology</i> , 2006, 36, 829-839.	1.3	15
17	Identification and evolutionary analysis of novel exons and alternative splicing events using cross-species EST-to-genome comparisons in human, mouse and rat. <i>BMC Bioinformatics</i> , 2006, 7, 136.	1.2	30
18	The effects of multiple features of alternatively spliced exons on the K A /K S ratio test. <i>BMC Bioinformatics</i> , 2006, 7, 259.	1.2	8

#	ARTICLE	IF	CITATIONS
19	Java GUI for InterProScan (JIPS): A tool to help process multiple InterProScans and perform ortholog analysis. <i>BMC Bioinformatics</i> , 2006, 7, 462.	1.2	7
20	GO-Diff: mining functional differentiation between EST-based transcriptomes. <i>BMC Bioinformatics</i> , 2006, 7, 72.	1.2	16
21	PhosphoregDB: the tissue and sub-cellular distribution of mammalian protein kinases and phosphatases. <i>BMC Bioinformatics</i> , 2006, 7, 82.	1.2	18
22	Analysis of the prostate cancer cell line LNCaP transcriptome using a sequencing-by-synthesis approach. <i>BMC Genomics</i> , 2006, 7, 246.	1.2	173
23	Huntingtin gene evolution in Chordata and its peculiar features in the ascidian <i>Ciona</i> genus. <i>BMC Genomics</i> , 2006, 7, 288.	1.2	24
24	Jupiter, a new <i>Drosophila</i> protein associated with microtubules. <i>Cytoskeleton</i> , 2006, 63, 301-312.	4.4	110
25	A RecA-mediated exon profiling method. <i>Nucleic Acids Research</i> , 2006, 34, e97-e97.	6.5	5
26	Phytome: a platform for plant comparative genomics. <i>Nucleic Acids Research</i> , 2006, 34, D724-D730.	6.5	35
27	ASAP: a resource for annotating, curating, comparing, and disseminating genomic data. <i>Nucleic Acids Research</i> , 2006, 34, D41-D45.	6.5	56
28	CryptoDB: a <i>Cryptosporidium</i> bioinformatics resource update. <i>Nucleic Acids Research</i> , 2006, 34, D419-D422.	6.5	141
29	Comparative Genomic and Phylogenetic Analyses of Calcium ATPases and Calcium-Regulated Proteins in the Apicomplexa. <i>Molecular Biology and Evolution</i> , 2006, 23, 1613-1627.	3.5	138
30	The Evolution of Two-Component Systems in Bacteria Reveals Different Strategies for Niche Adaptation. <i>PLoS Computational Biology</i> , 2006, 2, e143.	1.5	181
31	Alternatively and Constitutively Spliced Exons Are Subject to Different Evolutionary Forces. <i>Molecular Biology and Evolution</i> , 2006, 23, 675-682.	3.5	55
32	Human-specific insertions and deletions inferred from mammalian genome sequences. <i>Genome Research</i> , 2006, 17, 16-22.	2.4	58
33	Integrating biological data through the genome. <i>Human Molecular Genetics</i> , 2006, 15, R81-R87.	1.4	16
34	Thirteen nodule-specific or nodule-enhanced genes encoding products homologous to cysteine cluster proteins or plant lipid transfer proteins are identified in <i>Astragalus sinicus</i> L. by suppressive subtractive hybridization. <i>Journal of Experimental Botany</i> , 2006, 57, 2673-2685.	2.4	33
35	ProtoBee: Hierarchical classification and annotation of the honey bee proteome. <i>Genome Research</i> , 2006, 16, 1431-1438.	2.4	17
36	PlanTAPDB, a Phylogeny-Based Resource of Plant Transcription-Associated Proteins. <i>Plant Physiology</i> , 2007, 143, 1452-1466.	2.3	79

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37	A sub-proteome of <i>Arabidopsis thaliana</i> mature stems trapped on Concanavalin A is enriched in cell wall glycoside hydrolases. <i>Journal of Experimental Botany</i> , 2007, 58, 2503-2512.	2.4	111
38	Genome Sequence of <i>Babesia bovis</i> and Comparative Analysis of Apicomplexan Hemoprotezoa. <i>PLoS Pathogens</i> , 2007, 3, e148.	2.1	335
39	Web Services at the European Bioinformatics Institute. <i>Nucleic Acids Research</i> , 2007, 35, W6-W11.	6.5	166
40	Sequencing and analysis of chromosome 1 of <i>Eimeria tenella</i> reveals a unique segmental organization. <i>Genome Research</i> , 2007, 17, 311-319.	2.4	49
41	A Comparative and Phylogenetic Analysis of the $\hat{\text{A}}$ -Actinin Rod Domain. <i>Molecular Biology and Evolution</i> , 2007, 24, 2254-2265.	3.5	27
42	Identification of Functional Subclasses in the DJ-1 Superfamily Proteins. <i>PLoS Computational Biology</i> , 2007, 3, e15.	1.5	64
43	POGs/PlantRBP: a resource for comparative genomics in plants. <i>Nucleic Acids Research</i> , 2007, 35, D852-D856.	6.5	31
44	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444
45	Expanded protein information at SGD: new pages and proteome browser. <i>Nucleic Acids Research</i> , 2007, 35, D468-D471.	6.5	69
46	Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. <i>Plant Physiology</i> , 2007, 144, 1642-1653.	2.3	17
47	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. <i>Nucleic Acids Research</i> , 2007, 35, D247-D252.	6.5	333
48	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
49	Predicting and Annotating Catalytic Residues: An Information Theoretic Approach. <i>Journal of Computational Biology</i> , 2007, 14, 1058-1073.	0.8	24
50	A Chemogenomic Screening of Sulfanilamide-Hypersensitive <i>Saccharomyces cerevisiae</i> Mutants Uncovers <i>ABZ2</i> , the Gene Encoding a Fungal Aminodeoxychorismate Lyase. <i>Eukaryotic Cell</i> , 2007, 6, 2102-2111.	3.4	28
51	Shotgun Identification of the Structural Proteome of Shrimp White Spot Syndrome Virus and iTRAQ Differentiation of Envelope and Nucleocapsid Subproteomes. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1609-1620.	2.5	83
52	Alpha-Agarases Define a New Family of Glycoside Hydrolases, Distinct from Beta-Agarase Families. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4691-4694.	1.4	57
53	ESTpass: a web-based server for processing and annotating expressed sequence tag (EST) sequences. <i>Nucleic Acids Research</i> , 2007, 35, W159-W162.	6.5	30
54	<i>Sinorhizobium meliloti</i> pSymB carries genes necessary for arabinose transport and catabolism. <i>Microbiology (United Kingdom)</i> , 2007, 153, 727-736.	0.7	37

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55	AutoSCOP: automated prediction of SCOP classifications using unique pattern-class mappings. <i>Bioinformatics</i> , 2007, 23, 1203-1210.	1.8	23
56	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, W143-W147.	6.5	60
57	Gene Ontology annotations at SGD: new data sources and annotation methods. <i>Nucleic Acids Research</i> , 2007, 36, D577-D581.	6.5	218
58	DPTF: a database of poplar transcription factors. <i>Bioinformatics</i> , 2007, 23, 1307-1308.	1.8	94
59	A Ribonuclease III Domain Protein Functions in Group II Intron Splicing in Maize Chloroplasts. <i>Plant Cell</i> , 2007, 19, 2606-2623.	3.1	100
60	AutoPSI: a database for automatic structural classification of protein sequences and structures. <i>Nucleic Acids Research</i> , 2007, 36, D398-D401.	6.5	3
61	Comparison of Envelope-Related Genes in Unicellular and Filamentous Cyanobacteria. <i>Comparative and Functional Genomics</i> , 2007, 2007, 1-10.	2.0	15
62	Telomeric co-localization of the modified base J and contingency genes in the protozoan parasite <i>Trypanosoma cruzi</i> . <i>Nucleic Acids Research</i> , 2007, 35, 6367-6377.	6.5	20
63	Comparative Genomics of Viruses Using Bioinformatics Tools. , 2007, , 49-72.		0
64	Two metalloproteases from the protozoan <i>Trypanosoma cruzi</i> belong to the M32 family, found so far only in prokaryotes. <i>Biochemical Journal</i> , 2007, 401, 399-410.	1.7	44
65	Degradation of Î»-carrageenan by <i>Pseudoalteromonas carrageenovora</i> Î»-carrageenase: a new family of glycoside hydrolases unrelated to Î²- and Î¹-carrageenases. <i>Biochemical Journal</i> , 2007, 404, 105.	1.7	38
66	REP27, a Tetratricopeptide Repeat Nuclear-Encoded and Chloroplast-Localized Protein, Functions in D1/32-kD Reaction Center Protein Turnover and Photosystem II Repair from Photodamage. <i>Plant Physiology</i> , 2007, 143, 1547-1560.	2.3	40
67	Degradation of Î»-carrageenan by <i>Pseudoalteromonas carrageenovora</i> Î»-carrageenase: a new family of glycoside hydrolases unrelated to Î²- and Î¹-carrageenases. <i>Biochemical Journal</i> , 2007, 404, 105-114.	1.7	83
68	Genomic differences of Vaccinia virus clones from Dryvax smallpox vaccine: The Dryvax-like ACAM2000 and the mouse neurovirulent Clone-3. <i>Vaccine</i> , 2007, 25, 8807-8832.	1.7	40
69	Sequence Polymorphism of 2 Pioneer Genes Expressed in Phytoparasitic Nematodes Showing Different Host Ranges. <i>Journal of Heredity</i> , 2007, 98, 611-619.	1.0	5
70	Phylogenomics of caspase-activated DNA fragmentation factor. <i>Biochemical and Biophysical Research Communications</i> , 2007, 356, 293-299.	1.0	15
71	IDC1, a Pezizomycotina-specific gene that belongs to the PaMpk1 MAP kinase transduction cascade of the filamentous fungus <i>Podospora anserina</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 1219-1230.	0.9	53
72	Novel Families of Toxin-like Peptides in Insects and Mammals: A Computational Approach. <i>Journal of Molecular Biology</i> , 2007, 369, 553-566.	2.0	41

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73	Differences in collagen prolyl 4-hydroxylase assembly between two <i>Caenorhabditis</i> nematode species despite high amino acid sequence identity of the enzyme subunits. <i>Matrix Biology</i> , 2007, 26, 382-395.	1.5	7
74	Cloning and functional characterization of the <i>Anopheles albimanus</i> DMT1/NRAMP homolog: Implications in iron metabolism in mosquitoes. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 532-539.	1.2	25
75	Rice Genome Annotation: Beginnings of Functional Genomics. , 2007, , 21-30.		3
76	Computational prediction of host-pathogen protein-protein interactions. <i>Bioinformatics</i> , 2007, 23, i159-i166.	1.8	164
77	A Tool for Creating and Parallelizing Bioinformatics Pipelines. , 2007, , .		2
78	Plant Gene and Alternatively Spliced Variant Annotator. A Plant Genome Annotation Pipeline for Rice Gene and Alternatively Spliced Variant Identification with Cross-Species Expressed Sequence Tag Conservation from Seven Plant Species. <i>Plant Physiology</i> , 2007, 143, 1086-1095.	2.3	24
79	Generalized Sequence Signatures through Symbolic Clustering. , 2007, , .		0
80	Identification of Human Olfactory Cleft Mucus Proteins Using Proteomic Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 1985-1996.	1.8	73
81	InterPro and InterProScan. <i>Methods in Molecular Biology</i> , 2007, 396, 59-70.	0.4	339
82	SitCon: Binding site residue conservation visualization and protein sequence-to-function tool. <i>International Journal of Quantum Chemistry</i> , 2007, 107, 2100-2110.	1.0	0
83	Characterization of <i>Salmonella typhimurium</i> YegS, a putative lipid kinase homologous to eukaryotic sphingosine and diacylglycerol kinases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 13-25.	1.5	20
84	Crystal structure of an acetyltransferase protein from <i>Vibrio cholerae</i> strain N16961. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 422-427.	1.5	4
85	Functional proteomic view of metabolic regulation in <i>Aromatoleum aromaticum</i> strain EbN1. <i>Proteomics</i> , 2007, 7, 2222-2239.	1.3	90
86	Expressed sequence tags from the midgut of <i>Epiphyas postvittana</i> (Walker) (Lepidoptera): Tj ETQq1 1 0.784314 rgBT /Overl	1.0	42
87	Genome-wide identification and analyses of the rice calmodulin and related potential calcium sensor proteins. <i>BMC Plant Biology</i> , 2007, 7, 4.	1.6	166
88	ConiferEST: an integrated bioinformatics system for data reprocessing and mining of conifer expressed sequence tags (ESTs). <i>BMC Genomics</i> , 2007, 8, 134.	1.2	14
89	The complement of protein kinases of the microsporidium <i>Encephalitozoon cuniculi</i> in relation to those of <i>Saccharomyces cerevisiae</i> and <i>Schizosaccharomyces pombe</i> . <i>BMC Genomics</i> , 2007, 8, 309.	1.2	68
90	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. <i>BMC Genomics</i> , 2007, 8, 31.	1.2	64

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91	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007, 8, 325.	1.2	44
92	Analysis of <i>Schistosoma mansoni</i> genes shared with <i>Deuterostomia</i> and with possible roles in host interactions. <i>BMC Genomics</i> , 2007, 8, 407.	1.2	11
93	The <i>Schistosoma mansoni</i> transcriptome: An update. <i>Experimental Parasitology</i> , 2007, 117, 229-235.	0.5	23
94	Intron-rich Gene Structure in the Intracellular Plant Parasite <i>Plasmodiophora brassicae</i> . <i>Protist</i> , 2007, 158, 423-433.	0.6	44
95	The surface protein Pvs25 of <i>Plasmodium vivax</i> ookinetes interacts with calreticulin on the midgut apical surface of the malaria vector <i>Anopheles albimanus</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 153, 167-177.	0.5	26
96	Characterization of <i>Entamoeba histolytica</i> $\alpha$ -actinin2. <i>Molecular and Biochemical Parasitology</i> , 2007, 154, 82-89.	0.5	14
97	Genome-wide identification of C2H2 zinc-finger gene family in rice and their phylogeny and expression analysis. <i>Plant Molecular Biology</i> , 2007, 65, 467-485.	2.0	227
98	The <i>Taenia saginata</i> homologue of the major surface antigen of <i>Echinococcus</i> spp. is immunogenic and 97% identical to its <i>Taenia solium</i> homologue. <i>Parasitology Research</i> , 2007, 101, 1541-1549.	0.6	9
99	Structure of two melon regions reveals high microsynteny with sequenced plant species. <i>Molecular Genetics and Genomics</i> , 2007, 278, 611-622.	1.0	28
100	Overexpression of OsSAP8, a member of stress associated protein (SAP) gene family of rice confers tolerance to salt, drought and cold stress in transgenic tobacco and rice. <i>Plant Molecular Biology</i> , 2008, 66, 445-462.	2.0	217
101	Plant mitochondrial rhomboid, AtRBL12, has different substrate specificity from its yeast counterpart. <i>Plant Molecular Biology</i> , 2008, 68, 159-171.	2.0	43
102	Caterpillar-Specific Gene Expression in the Legume, <i>Medicago truncatula</i> . <i>Plant Molecular Biology Reporter</i> , 2008, 26, 12-31.	1.0	12
103	Evolution of Exceptionally Large Genes in Prokaryotes. <i>Journal of Molecular Evolution</i> , 2008, 66, 333-349.	0.8	2
104	In Silico Characterization of Proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , 2008, 38, 165-177.	1.3	53
105	AutoMotif Server for prediction of phosphorylation sites in proteins using support vector machine: 2007 update. <i>Journal of Molecular Modeling</i> , 2008, 14, 69-76.	0.8	32
106	<i>Ku70</i> or <i>Ku80</i> deficiencies in the fungus <i>Botrytis cinerea</i> facilitate targeting of genes that are hard to knock out in a wild-type context. <i>FEMS Microbiology Letters</i> , 2008, 289, 225-232.	0.7	64
107	Identification of rice TUBBY-like genes and their evolution. <i>FEBS Journal</i> , 2008, 275, 163-171.	2.2	30
108	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964

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109	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
110	Mining an <i>Ostrinia nubilalis</i> midgut expressed sequence tag (EST) library for candidate genes and single nucleotide polymorphisms (SNPs). <i>Insect Molecular Biology</i> , 2008, 17, 607-620.	1.0	38
111	Identification of a novel protein promoting the colonization and survival of <i>Fingoldia magna</i> , a bacterial commensal and opportunistic pathogen. <i>Molecular Microbiology</i> , 2008, 70, 695-708.	1.2	32
112	Sequence analysis of a non-classified, non-occluded DNA virus that causes salivary gland hypertrophy of <i>Musca domestica</i> , MdSGHV. <i>Virology</i> , 2008, 377, 184-196.	1.1	41
113	NestedMICA as an ab initio protein motif discovery tool. <i>BMC Bioinformatics</i> , 2008, 9, 19.	1.2	32
114	Transcriptome profiling of developmental and xenobiotic responses in a keystone soil animal, the oligochaete annelid <i>Lumbricus rubellus</i> . <i>BMC Genomics</i> , 2008, 9, 266.	1.2	93
115	SjTPdb: integrated transcriptome and proteome database and analysis platform for <i>Schistosoma japonicum</i> . <i>BMC Genomics</i> , 2008, 9, 304.	1.2	21
116	Interspecies data mining to predict novel ING-protein interactions in human. <i>BMC Genomics</i> , 2008, 9, 426.	1.2	12
117	Splice-mediated Variants of Proteins (SpliVaP) data and characterization of changes in signatures among protein isoforms due to alternative splicing. <i>BMC Genomics</i> , 2008, 9, 453.	1.2	8
118	The FEATURE framework for protein function annotation: modeling new functions, improving performance, and extending to novel applications. <i>BMC Genomics</i> , 2008, 9, S2.	1.2	47
119	<i>Eimeria tenella</i> : Genomic organization and expression of an 89kDa cyclophilin. <i>Experimental Parasitology</i> , 2008, 118, 275-279.	0.5	5
120	Protozoan protein tyrosine phosphatases. <i>International Journal for Parasitology</i> , 2008, 38, 1279-1295.	1.3	47
121	A genetic similarity algorithm for searching the Gene Ontology terms and annotating anonymous protein sequences. <i>Journal of Biomedical Informatics</i> , 2008, 41, 65-81.	2.5	43
122	How can ontologies help vector biology?. <i>Trends in Parasitology</i> , 2008, 24, 249-252.	1.5	9
123	Protein Domain Prediction. <i>Methods in Molecular Biology</i> , 2008, 426, 117-143.	0.4	11
124	A genomic search approach to identify esterases in <i>Propionibacterium freudenreichii</i> involved in the formation of flavour in Emmental cheese. <i>Microbial Cell Factories</i> , 2008, 7, 16.	1.9	28
125	Chromatin Central: towards the comparative proteome by accurate mapping of the yeast proteomic environment. <i>Genome Biology</i> , 2008, 9, R167.	13.9	106
126	The SeqFEATURE library of 3D functional site models: comparison to existing methods and applications to protein function annotation. <i>Genome Biology</i> , 2008, 9, R8.	13.9	20



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127	The Classification of Protein Domains. <i>Methods in Molecular Biology</i> , 2008, 453, 123-146.	0.4	5
128	High-throughput functional annotation and data mining with the Blast2GO suite. <i>Nucleic Acids Research</i> , 2008, 36, 3420-3435.	6.5	3,905
129	Insight into DNA and Protein Transport in Double-Stranded DNA Viruses: The Structure of Bacteriophage N4. <i>Journal of Molecular Biology</i> , 2008, 378, 726-736.	2.0	100
130	<i>Staphylococcus aureus</i> giant protein Ehb is involved in tolerance to transient hyperosmotic pressure. <i>Biochemical and Biophysical Research Communications</i> , 2008, 374, 237-241.	1.0	24
131	<i>Staphylococcus aureus</i> surface protein SasG contributes to intercellular autoaggregation of <i>Staphylococcus aureus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 1102-1106.	1.0	27
132	Molecular evolution of the MLO gene family in <i>Oryza sativa</i> and their functional divergence. <i>Gene</i> , 2008, 409, 1-10.	1.0	62
133	Evolution and functional divergence of monocarboxylate transporter genes in vertebrates. <i>Gene</i> , 2008, 423, 14-22.	1.0	11
134	Bioinformatics and Database of the Rice Genome. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 13-21.	0.2	0
135	ESTplus: An Integrative System for Comprehensive and Customized EST Analysis and Proteomic Data Matching. , 2008, , .		2
136	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2008, 21, Unit 2.7.	25.8	69
137	Selecting Folded Proteins from a Library of Secondary Structural Elements. <i>Journal of the American Chemical Society</i> , 2008, 130, 176-185.	6.6	17
138	High Sensitivity Proteomics Assisted Discovery of a Novel Operon Involved in the Assembly of Photosystem II, a Membrane Protein Complex. <i>Journal of Biological Chemistry</i> , 2008, 283, 27829-27837.	1.6	39
139	Genome-Scale Genotype-Phenotype Matching of Two <i>Lactococcus lactis</i> Isolates from Plants Identifies Mechanisms of Adaptation to the Plant Niche. <i>Applied and Environmental Microbiology</i> , 2008, 74, 424-436.	1.4	112
140	Whole-genome expression profiling of the marine diatom <i>Thalassiosira pseudonana</i> identifies genes involved in silicon bioprocesses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1579-1584.	3.3	247
141	Identification of woolliness response genes in peach fruit after post-harvest treatments. <i>Journal of Experimental Botany</i> , 2008, 59, 1973-1986.	2.4	78
142	<i>Campylobacter jejuni</i> : A Human Pathogen Feeding at the Surface of Epithelial Cells and Phagocytes. <i>PLoS Pathogens</i> , 2008, 4, e1000164.	2.1	58
143	Data curation + process curation=data integration + science. <i>Briefings in Bioinformatics</i> , 2008, 9, 506-517.	3.2	53
144	Whole-Genome Transcriptional Profiling of <i>Bradyrhizobium japonicum</i> during Chemoautotrophic Growth. <i>Journal of Bacteriology</i> , 2008, 190, 6697-6705.	1.0	47

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145	Ribonomic Analysis of Human Pum1 Reveals <i>cis-trans</i> Conservation across Species despite Evolution of Diverse mRNA Target Sets. <i>Molecular and Cellular Biology</i> , 2008, 28, 4093-4103.	1.1	142
146	Expression and immunogenicity of six putative variable surface proteins in <i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC. <i>Microbiology (United Kingdom)</i> , 2008, 154, 539-549.	0.7	13
147	Semidominant Mutations in <i>Reduced Epidermal Fluorescence 4</i> Reduce Phenylpropanoid Content in <i>Arabidopsis</i> . <i>Genetics</i> , 2008, 178, 2237-2251.	1.2	36
148	Gene function prediction using protein domain probability and hierarchical Gene Ontology information. , 2008, , .		3
149	Insight into DNA and Protein Transport in Double-stranded DNA Viruses: The Structure of Bacteriophage N4. <i>Microscopy and Microanalysis</i> , 2008, 14, 1574-1575.	0.2	4
150	Niche-Specificity and the Variable Fraction of the <i>Pectobacterium</i> Pan-Genome. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1549-1560.	1.4	93
151	Genome Organization and Evolution of the <i>AVR-Pita</i> Avirulence Gene Family in the <i>Magnaporthe grisea</i> Species Complex. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 658-670.	1.4	127
152	Computational Analyses of TBC Protein Family in Eukaryotes. <i>Protein and Peptide Letters</i> , 2008, 15, 505-509.	0.4	8
153	GOlet: Annotation of anonymous sequence data with Gene Ontology and Pathway terms. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	3
154	Intestinal Transcriptomes of Nematodes: Comparison of the Parasites <i>Ascaris suum</i> and <i>Haemonchus contortus</i> with the Free-living <i>Caenorhabditis elegans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e269.	1.3	42
155	Target Identification in Ory S1 Pollen Protein Allergen from <i>Oryza sativa</i> in the Course of Construction of Hypoallergenic Vaccines. <i>American Journal of Infectious Diseases</i> , 2009, 5, 142-147.	0.1	2
156	Run-Off Replication of Host-Adaptability Genes Is Associated with Gene Transfer Agents in the Genome of Mouse-Infecting <i>Bartonella grahamii</i> . <i>PLoS Genetics</i> , 2009, 5, e1000546.	1.5	87
157	Speckled-like Pattern in the Germinal Center (SLIP-GC), a Nuclear GTPase Expressed in Activation-induced Deaminase-expressing Lymphomas and Germinal Center B Cells. <i>Journal of Biological Chemistry</i> , 2009, 284, 30652-30661.	1.6	20
158	Metabolite Profiling Reveals YihU as a Novel Hydroxybutyrate Dehydrogenase for Alternative Succinic Semialdehyde Metabolism in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 16442-16451.	1.6	58
159	Functional Analysis of Transcription Factors in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2009, 50, 1232-1248.	1.5	256
160	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	6.5	97
161	d-Omix: a mixer of generic protein domain analysis tools. <i>Nucleic Acids Research</i> , 2009, 37, W417-W421.	6.5	4
162	Significant speedup of database searches with HMMs by search space reduction with PSSM family models. <i>Bioinformatics</i> , 2009, 25, 3251-3258.	1.8	8

#	ARTICLE	IF	CITATIONS
163	PIG—the pathogen interaction gateway. <i>Nucleic Acids Research</i> , 2009, 37, D647-D650.	6.5	57
164	Cloning of feather-degrading minor extracellular protease from <i>Bacillus cereus</i> DCUW: dissection of the structural domains. <i>Microbiology (United Kingdom)</i> , 2009, 155, 2049-2057.	0.7	18
165	QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap010.	1.4	42
166	<i>Blufensin1</i> Negatively Impacts Basal Defense in Response to Barley Powdery Mildew. <i>Plant Physiology</i> , 2009, 149, 271-285.	2.3	66
167	Integrated analyses of the rice secretome. <i>Plant Signaling and Behavior</i> , 2009, 4, 345-347.	1.2	3
168	Mechanism of REP27 Protein Action in the D1 Protein Turnover and Photosystem II Repair from Photodamage. <i>Plant Physiology</i> , 2009, 151, 88-99.	2.3	24
169	The family 6 carbohydrate-binding modules have coevolved with their appended catalytic modules toward similar substrate specificity. <i>Glycobiology</i> , 2009, 19, 615-623.	1.3	36
170	The Complete Genome and Proteome of <i>Laribacter hongkongensis</i> Reveal Potential Mechanisms for Adaptations to Different Temperatures and Habitats. <i>PLoS Genetics</i> , 2009, 5, e1000416.	1.5	52
171	Web services at the European Bioinformatics Institute-2009. <i>Nucleic Acids Research</i> , 2009, 37, W6-W10.	6.5	65
172	Novel Multiprotein Complexes Identified in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> by Non-denaturing Fractionation of the Native Proteome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 735-751.	2.5	39
173	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
174	A unique virulence factor for proliferation and dwarfism in plants identified from a phytopathogenic bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6416-6421.	3.3	277
175	Analysis of early hepatic stage schistosomula gene expression by subtractive expressed sequence tags library. <i>Molecular and Biochemical Parasitology</i> , 2009, 166, 62-69.	0.5	13
176	Complete sequence of three plasmids from <i>Bacillus thuringiensis</i> INTA-FR7-4 environmental isolate and comparison with related plasmids from the <i>Bacillus cereus</i> group. <i>Plasmid</i> , 2009, 62, 172-182.	0.4	16
177	Origin and evolution of the Notch signalling pathway: an overview from eukaryotic genomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 249.	3.2	191
178	Molecular determinants archetypical to the phylum Nematoda. <i>BMC Genomics</i> , 2009, 10, 114.	1.2	11
179	Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. <i>BMC Genomics</i> , 2009, 10, 117.	1.2	23
180	ChlamyCyc: an integrative systems biology database and web-portal for <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2009, 10, 209.	1.2	73

#	ARTICLE	IF	CITATIONS
181	plantsUPS: a database of plants' Ubiquitin Proteasome System. BMC Genomics, 2009, 10, 227.	1.2	66
182	Transcriptomes and pathways associated with infectivity, survival and immunogenicity in <i>Brugia malayi</i> L3. BMC Genomics, 2009, 10, 267.	1.2	35
183	Inconsistencies of genome annotations in apicomplexan parasites revealed by 5'-end-one-pass and full-length sequences of oligo-capped cDNAs. BMC Genomics, 2009, 10, 312.	1.2	31
184	Divergence in function and expression of the NOD26-like intrinsic proteins in plants. BMC Genomics, 2009, 10, 313.	1.2	76
185	Comprehensive EST analysis of the symbiotic sea anemone, <i>Anemonia viridis</i> . BMC Genomics, 2009, 10, 333.	1.2	43
186	UFO: a web server for ultra-fast functional profiling of whole genome protein sequences. BMC Genomics, 2009, 10, 409.	1.2	15
187	Cell wall biogenesis of <i>Arabidopsis thaliana</i> elongating cells: transcriptomics complements proteomics. BMC Genomics, 2009, 10, 505.	1.2	39
188	MytiBase: a knowledgebase of mussel ( <i>M. galloprovincialis</i> ) transcribed sequences. BMC Genomics, 2009, 10, 72.	1.2	102
189	Phylogenetic analysis, subcellular localization, and expression patterns of RPD3/HDA1 family histone deacetylases in plants. BMC Plant Biology, 2009, 9, 37.	1.6	117
190	A membrane-bound matrix metalloproteinase from <i>Nicotiana tabacum</i> cv. BY-2 is induced by bacterial pathogens. BMC Plant Biology, 2009, 9, 83.	1.6	31
191	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance – Fundamental insights toward biotechnological outcomes. Biotechnology Advances, 2009, 27, 439-448.	6.0	29
192	Genome-wide validation of <i>Magnaporthe grisea</i> gene structures based on transcription evidence. FEBS Letters, 2009, 583, 797-800.	1.3	3
193	Characterisation of novel protein families secreted by muscle stage larvae of <i>Trichinella spiralis</i> . International Journal for Parasitology, 2009, 39, 515-524.	1.3	15
194	Biosynthesis of 2-Hydroxy and Iso-Even Fatty Acids is Connected to Sphingolipid Formation in <i>Myxobacteria</i> . ChemBioChem, 2009, 10, 2003-2010.	1.3	19
195	Screening of chondrogenic factors with a real-time fluorescence monitoring cell line ATDC5-C2ER: Identification of sorting nexin 19 as a novel factor. Arthritis and Rheumatism, 2009, 60, 3314-3323.	6.7	26
196	Membrane transporters and carbon metabolism implicated in chloride homeostasis differentiate salt stress responses in tolerant and sensitive Citrus rootstocks. Functional and Integrative Genomics, 2009, 9, 293-309.	1.4	80
197	Dicer-like (DCL) proteins in plants. Functional and Integrative Genomics, 2009, 9, 277-286.	1.4	136
198	HRGD: a database for mining potential heterosis-related genes in plants. Plant Molecular Biology, 2009, 69, 255-260.	2.0	6

#	ARTICLE	IF	CITATIONS
199	The first genome-level transcriptome of the wood-degrading fungus <i>Phanerochaete chrysosporium</i> grown on red oak. <i>Current Genetics</i> , 2009, 55, 273-286.	0.8	53
200	Proteomic comparison of four <i>Eimeria tenella</i> life cycle stages: Unsporulated oocyst, sporulated oocyst, sporozoite and second generation merozoite. <i>Proteomics</i> , 2009, 9, 4566-4576.	1.3	91
201	Candidate effector gene identification in the ascomycete fungal phytopathogen <i>Venturia inaequalis</i> by expressed sequence tag analysis. <i>Molecular Plant Pathology</i> , 2009, 10, 431-448.	2.0	33
202	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. <i>ISME Journal</i> , 2009, 3, 1335-1348.	4.4	80
203	AmbR1 is a key transcriptional regulator for production of antifungal activity of <i>Burkholderia contaminans</i> strain MS14. <i>FEMS Microbiology Letters</i> , 2009, 297, 54-60.	0.7	23
204	Proteomics-inferred genome typing (PIGT) demonstrates interpopulation recombination as a strategy for environmental adaptation. <i>Environmental Microbiology</i> , 2009, 11, 313-325.	1.8	59
205	MOLECULAR CHARACTERIZATION AND ANTIBODY DETECTION OF A NITROGEN-REGULATED CELL SURFACE PROTEIN OF THE COCCOLITHOPHORE <i>EMILIANA HUXLEYI</i> (PRYMNESIOPHYCEAE). <i>Journal of Phycology</i> , 2009, 45, 650-659.	1.0	1
206	Soybean Proteome Database: A Data Resource for Plant Differential Omics. <i>Journal of Proteome Research</i> , 2009, 8, 3539-3548.	1.8	63
207	The diversity of C-type lectins in the genome of a basal metazoan, <i>Nematostella vectensis</i> . <i>Developmental and Comparative Immunology</i> , 2009, 33, 881-889.	1.0	54
208	Biosynthesis of an antifungal oligopeptide in <i>Burkholderia contaminans</i> strain MS14. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 328-332.	1.0	41
209	Functional annotations for the <i>Saccharomyces cerevisiae</i> genome: the knowns and the known unknowns. <i>Trends in Microbiology</i> , 2009, 17, 286-294.	3.5	49
210	Variability in the cadherin gene in an <i>Ostrinia nubilalis</i> strain selected for Cry1Ab resistance. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 218-223.	1.2	24
211	Online Tools for Predicting Integral Membrane Proteins. <i>Methods in Molecular Biology</i> , 2009, 528, 3-23.	0.4	8
212	Proteins recruited by SH3 domains of Ruk/CIN85 adaptor identified by LC-MS/MS. <i>Proteome Science</i> , 2009, 7, 21.	0.7	41
213	Identification and bioinformatic characterization of a multidrug resistance associated protein (ABCC) gene in <i>Plasmodium berghei</i> . <i>Malaria Journal</i> , 2009, 8, 1.	0.8	183
214	Tandem and cryptic amino acid repeats accumulate in disordered regions of proteins. <i>Genome Biology</i> , 2009, 10, R59.	13.9	104
215	Transcriptome Analysis and Identification of Genes Related to Immune Function in Skin of the Chinese Brown Frog. <i>Zoological Science</i> , 2009, 26, 80.	0.3	25
216	Chapter 11 Unexpected Turns and Twists in Structure/Function of PR-Proteins that Connect Energy Metabolism and Immunity. <i>Advances in Botanical Research</i> , 2009, 51, 439-489.	0.5	18

#	ARTICLE	IF	CITATIONS
217	Plant Genome Annotation Methods. <i>Methods in Molecular Biology</i> , 2009, 513, 263-282.	0.4	7
218	The Signal Peptide of the <i>Medicago truncatula</i> Modular Nodulin MtNOD25 Operates as an Address Label for the Specific Targeting of Proteins to Nitrogen-Fixing Symbiosomes. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 63-72.	1.4	22
219	A Draft Genome Sequence of <i>Pseudomonas syringae</i> pv. <i>tomato</i> T1 Reveals a Type III Effector Repertoire Significantly Divergent from That of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 52-62.	1.4	134
220	Bioinformatics as a Tool for Assessing the Quality of Sub-Cellular Proteomic Strategies and Inferring Functions of Proteins: Plant Cell Wall Proteomics as a Test Case. <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S2065.	1.0	32
221	Structure-Based Drug Discovery for Tropical Diseases. <i>Current Topics in Medicinal Chemistry</i> , 2009, 9, 824-843.	1.0	24
222	Inferring Protein-Protein Interactions Using a Hybrid Genetic Algorithm/Support Vector Machine Method. <i>Protein and Peptide Letters</i> , 2010, 17, 1079-1084.	0.4	9
223	Generalised Sequence Signatures through symbolic clustering. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 656.	0.1	2
224	Host Range and Complete Genome Sequence of <i>Cucurbit chlorotic yellows virus</i> , a New Member of the Genus <i>Crinivirus</i> . <i>Phytopathology</i> , 2010, 100, 560-566.	1.1	76
225	Gene ontology study of methyl jasmonate-treated and non-treated hairy roots of <i>Panax ginseng</i> to identify genes involved in secondary metabolic pathway. <i>Russian Journal of Genetics</i> , 2010, 46, 828-835.	0.2	9
226	Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2010, 609, 83-95.	0.4	2
227	MACC1 "more than metastasis? Facts and predictions about a novel gene. <i>Journal of Molecular Medicine</i> , 2010, 88, 11-18.	1.7	63
228	Structure, allelic diversity and selection of <i>Asr</i> genes, candidate for drought tolerance, in <i>Oryza sativa</i> L. and wild relatives. <i>Theoretical and Applied Genetics</i> , 2010, 121, 769-787.	1.8	68
229	Discovery of a new tyrosinase-like enzyme family lacking a C-terminally processed domain: production and characterization of an <i>Aspergillus oryzae</i> catechol oxidase. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 213-226.	1.7	41
230	EST analysis and annotation of transcripts derived from a trichome-specific cDNA library from <i>Salvia fruticosa</i> . <i>Plant Cell Reports</i> , 2010, 29, 523-534.	2.8	33
231	Functional Impact of Transposable Elements Using Bioinformatic Analysis and a Comparative Genomic Approach. <i>Molecules and Cells</i> , 2010, 30, 77-88.	1.0	2
232	A knowledge-based method to predict the cooperative relationship between transcription factors. <i>Molecular Diversity</i> , 2010, 14, 815-819.	2.1	5
233	Partial resistance to leaf rust ( <i>Hemileia vastatrix</i> ) in coffee ( <i>Coffea arabica</i> L.): genetic analysis and molecular characterization of putative candidate genes. <i>Molecular Breeding</i> , 2010, 25, 685-697.	1.0	13
234	A gene family encoding RING finger proteins in rice: their expansion, expression diversity, and co-expressed genes. <i>Plant Molecular Biology</i> , 2010, 72, 369-380.	2.0	70

#	ARTICLE	IF	CITATIONS
235	Functional Domain Marker (FDM): an In Silico Demonstration in Solanaceae Using Simple Sequence Repeats (SSRs). <i>Plant Molecular Biology Reporter</i> , 2010, 28, 352-356.	1.0	22
236	Investigation of highly unsaturated fatty acid metabolism in the Asian sea bass, <i>Lates calcarifer</i> . <i>Fish Physiology and Biochemistry</i> , 2010, 36, 827-843.	0.9	103
237	PoGO: Prediction of Gene Ontology terms for fungal proteins. <i>BMC Bioinformatics</i> , 2010, 11, 215.	1.2	14
238	Massive gene losses in Asian cultivated rice unveiled by comparative genome analysis. <i>BMC Genomics</i> , 2010, 11, 121.	1.2	36
239	Large-scale analysis of full-length cDNAs from the tomato ( <i>Solanum lycopersicum</i> ) cultivar Micro-Tom, a reference system for the Solanaceae genomics. <i>BMC Genomics</i> , 2010, 11, 210.	1.2	179
240	Computational prediction of the osmoregulation network in <i>Synechococcus</i> sp. WH8102. <i>BMC Genomics</i> , 2010, 11, 291.	1.2	14
241	The <i>Pinus taeda</i> genome is characterized by diverse and highly diverged repetitive sequences. <i>BMC Genomics</i> , 2010, 11, 420.	1.2	144
242	Comprehensive Analysis of NAC Domain Transcription Factor Gene Family in <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2010, 10, 145.	1.6	386
243	Mechanisms of haplotype divergence at the RGA08 nucleotide-binding leucine-rich repeat gene locus in wild banana ( <i>Musa balbisiana</i> ). <i>BMC Plant Biology</i> , 2010, 10, 149.	1.6	17
244	Functional divergence of the NIP III subgroup proteins involved altered selective constraints and positive selection. <i>BMC Plant Biology</i> , 2010, 10, 256.	1.6	23
245	A var2 leaf variegation suppressor locus, SUPPRESSOR OF VARIATION3, encodes a putative chloroplast translation elongation factor that is important for chloroplast development in the cold. <i>BMC Plant Biology</i> , 2010, 10, 287.	1.6	83
246	A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.	1.6	16
247	Wheat beta-expansin (EXPB11) genes: Identification of the expressed gene on chromosome 3BS carrying a pollen allergen domain. <i>BMC Plant Biology</i> , 2010, 10, 99.	1.6	17
248	Secreted fungal sulfhydryl oxidases: sequence analysis and characterisation of a representative flavin-dependent enzyme from <i>Aspergillus oryzae</i> . <i>BMC Biochemistry</i> , 2010, 11, 31.	4.4	12
249	MARINE-EXPRESS: taking advantage of high throughput cloning and expression strategies for the post-genomic analysis of marine organisms. <i>Microbial Cell Factories</i> , 2010, 9, 45.	1.9	55
250	A proteomic approach towards the identification of the matrix protein content of the two types of microbodies in <i>Neurospora crassa</i> . <i>Proteomics</i> , 2010, 10, 3222-3234.	1.3	25
251	Relationships between functional subclasses and information contained in active-site and ligand-binding residues in diverse superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2369-2384.	1.5	6
252	The draft genome sequence of <i>Arsenophonus nasoniae</i> , sonâ€killer bacterium of <i>Nasonia vitripennis</i> , reveals genes associated with virulence and symbiosis. <i>Insect Molecular Biology</i> , 2010, 19, 59-73.	1.0	46

#	ARTICLE	IF	CITATIONS
253	Microbial metalloproteomes are largely uncharacterized. <i>Nature</i> , 2010, 466, 779-782.	13.7	330
254	GO-Atâ€š:in silicoprediction of gene function in <i>Arabidopsis thaliana</i> by combining heterogeneous data. <i>Plant Journal</i> , 2010, 61, 713-721.	2.8	17
255	Molecular characterization and heterologous expression of quinate dehydrogenase gene from <i>Gluconobacter oxydans</i> IFO3244. <i>Biochemistry (Moscow)</i> , 2010, 75, 452-459.	0.7	10
256	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439
257	Homologues of nitrite reductases in ammoniaâ€šoxidizing archaea: diversity and genomic context. <i>Environmental Microbiology</i> , 2010, 12, 1075-1088.	1.8	137
258	The metavirome of a hypersaline environment. <i>Environmental Microbiology</i> , 2010, 12, 2965-2976.	1.8	78
259	Alternative Splice Variants, a New Class of Protein Cancer Biomarker Candidates: Findings in Pancreatic Cancer and Breast Cancer with Systems Biology Implications. <i>Disease Markers</i> , 2010, 28, 241-251.	0.6	51
260	The Enzyme and the cDNA Sequence of a Thermolabile and Double-Strand Specific DNase from Northern Shrimps ( <i>Pandalus borealis</i> ). <i>PLoS ONE</i> , 2010, 5, e10295.	1.1	25
261	Re-Annotation Is an Essential Step in Systems Biology Modeling of Functional Genomics Data. <i>PLoS ONE</i> , 2010, 5, e10642.	1.1	21
262	Design, Validation and Annotation of Transcriptome-Wide Oligonucleotide Probes for the Oligochaete Annelid <i>Eisenia fetida</i> . <i>PLoS ONE</i> , 2010, 5, e14266.	1.1	22
263	AlexSys: a knowledge-based expert system for multiple sequence alignment construction and analysis. <i>Nucleic Acids Research</i> , 2010, 38, 6338-6349.	6.5	12
264	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> KF147, a Plant-Associated Lactic Acid Bacterium. <i>Journal of Bacteriology</i> , 2010, 192, 2649-2650.	1.0	105
265	Gene function prediction using semantic similarity clustering and enrichment analysis in the malaria parasite <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2010, 26, 2431-2437.	1.8	17
266	A predictor for toxin-like proteins exposes cell modulator candidates within viral genomes. <i>Bioinformatics</i> , 2010, 26, i482-i488.	1.8	8
267	A new bioinformatics analysis tools framework at EMBL-EBI. <i>Nucleic Acids Research</i> , 2010, 38, W695-W699.	6.5	1,553
268	Genetic characterization of slow bee paralysis virus of the honeybee ( <i>Apis mellifera</i> L.). <i>Journal of General Virology</i> , 2010, 91, 2524-2530.	1.3	76
269	Identification of Lipoprotein MslA as a Neoteric Virulence Factor of <i>Mycoplasma gallisepticum</i> . <i>Infection and Immunity</i> , 2010, 78, 3475-3483.	1.0	54
270	Functional and phenotypic characterization of a protein from <i>Lactobacillus acidophilus</i> involved in cell morphology, stress tolerance and adherence to intestinal cells. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3360-3367.	0.7	54



#	ARTICLE	IF	CITATIONS
271	Coexpression Analysis of Tomato Genes and Experimental Verification of Coordinated Expression of Genes Found in a Functionally Enriched Coexpression Module. <i>DNA Research</i> , 2010, 17, 105-116.	1.5	45
272	Transcriptional Responses of <i>Leptospira interrogans</i> to Host Innate Immunity: Significant Changes in Metabolism, Oxygen Tolerance, and Outer Membrane. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e857.	1.3	78
273	Purification and Functional Characterisation of Rhiminopeptidase A, a Novel Aminopeptidase from the Venom of <i>Bitis gabonica</i> rhinoceros. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e796.	1.3	33
274	Practical Applications of the Gene Ontology Resource. , 2010, , 319-339.		0
275	Transcription Factor MtATB2: About Nodulation, Sucrose and Senescence. <i>Plant and Cell Physiology</i> , 2010, 51, 1416-1424.	1.5	24
276	An Arabidopsis Pentatricopeptide Repeat Protein, SUPPRESSOR OF VARIATION7, Is Required for FtsH-Mediated Chloroplast Biogenesis. <i>Plant Physiology</i> , 2010, 154, 1588-1601.	2.3	86
277	The ANISEED database: Digital representation, formalization, and elucidation of a chordate developmental program. <i>Genome Research</i> , 2010, 20, 1459-1468.	2.4	105
278	Complete Genomic Structure of the Cultivated Rice Endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , 2010, 17, 37-50.	1.5	148
279	From raw materials to validated system: the construction of a genomic library and microarray to interpret systemic perturbations in Northern bobwhite. <i>Physiological Genomics</i> , 2010, 42, 219-235.	1.0	55
280	Phosphatidylinositol 4,5-bisphosphate regulates plant K <sup>+</sup> channels. <i>Biochemical Society Transactions</i> , 2010, 38, 705-709.	1.6	9
282	Identification and characterisation of <i>eroA</i> and <i>ervA</i> , encoding two putative thiol oxidases from <i>Aspergillus niger</i> . <i>Gene</i> , 2010, 461, 32-41.	1.0	3
283	Detecting novel genes with sparse arrays. <i>Gene</i> , 2010, 467, 41-51.	1.0	12
284	The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.	13.5	399
285	Feline programmed death and its ligand: Characterization and changes with feline immunodeficiency virus infection. <i>Veterinary Immunology and Immunopathology</i> , 2010, 134, 107-114.	0.5	24
286	agriGO: a GO analysis toolkit for the agricultural community. <i>Nucleic Acids Research</i> , 2010, 38, W64-W70.	6.5	2,289
287	A planarian p53 homolog regulates proliferation and self-renewal in adult stem cell lineages. <i>Development (Cambridge)</i> , 2010, 137, 213-221.	1.2	157
288	Novel venom gene discovery in the platypus. <i>Genome Biology</i> , 2010, 11, R95.	13.9	72
289	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391

#	ARTICLE	IF	CITATIONS
290	Comparative Gene Expression Analysis of Susceptible and Resistant Near-Isogenic Lines in Common Wheat Infected by <i>Puccinia triticina</i> . <i>DNA Research</i> , 2010, 17, 211-222.	1.5	59
291	Bioinformatics and Systems Biology of Cancers. <i>Progress in Molecular Biology and Translational Science</i> , 2010, 95, 159-191.	0.9	5
292	Genetic and Biochemical Map for the Biosynthesis of Occidiofungin, an Antifungal Produced by <i>Burkholderia contaminans</i> Strain MS14. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6189-6198.	1.4	49
293	Image-Based Surface Matching Algorithm Oriented to Structural Biology. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1004-1016.	1.9	22
294	New Family of Biuret Hydrolases Involved in <i>s</i> -Triazine Ring Metabolism. <i>ACS Catalysis</i> , 2011, 1, 1075-1082.	5.5	24
295	Construction and characterization of Japanese medaka ( <i>Oryzias latipes</i> ) hepatic cDNA library and its implementation to biomarker screening in aquatic toxicology. <i>Aquatic Toxicology</i> , 2011, 105, 569-575.	1.9	8
296	Bioinformatics analysis on ORF1 protein of Torque teno virus (SANBAN isolate). <i>Asian Pacific Journal of Tropical Medicine</i> , 2011, 4, 850-856.	0.4	7
299	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
300	Construction and analysis of full-length cDNA library of <i>Cryptosporidium parvum</i> . <i>Parasitology International</i> , 2011, 60, 199-202.	0.6	18
301	The draft genome of the carcinogenic human liver fluke <i>Clonorchis sinensis</i> . <i>Genome Biology</i> , 2011, 12, R107.	13.9	183
302	Expressed sequence tags reveal genetic diversity and putative virulence factors of the pathogenic oomycete <i>Pythium insidiosum</i> . <i>Fungal Biology</i> , 2011, 115, 683-696.	1.1	53
303	Identification of the <i>Plasmodium falciparum</i> rhopty neck protein 5 (PFRON5). <i>Gene</i> , 2011, 474, 22-28.	1.0	19
304	Efficient markerless gene replacement in <i>Corynebacterium glutamicum</i> using a new temperature-sensitive plasmid. <i>Journal of Microbiological Methods</i> , 2011, 85, 155-163.	0.7	50
305	Data-mining of the <i>Meloidogyne incognita</i> degradome and comparative analysis of proteases in nematodes. <i>Genomics</i> , 2011, 97, 29-36.	1.3	23
306	Identification of Alternatively Spliced Transcripts Using a Proteomic Informatics Approach. <i>Methods in Molecular Biology</i> , 2011, 696, 319-326.	0.4	14
307	InterPro Protein Classification. <i>Methods in Molecular Biology</i> , 2011, 694, 37-47.	0.4	63
308	Proteomics Analysis of the Effects of Cyanate on <i>Chromobacterium violaceum</i> Metabolism. <i>Genes</i> , 2011, 2, 736-747.	1.0	5
309	Genome Characterization of the Oleaginous Fungus <i>Mortierella alpina</i> . <i>PLoS ONE</i> , 2011, 6, e28319.	1.1	133

#	ARTICLE	IF	CITATIONS
310	Plasmodium vivax Tryptophan-Rich Antigen PvTRAg33.5 Contains Alpha Helical Structure and Multidomain Architecture. PLoS ONE, 2011, 6, e16294.	1.1	12
311	Transcriptome Analysis of the Desert Locust Central Nervous System: Production and Annotation of a Schistocerca gregaria EST Database. PLoS ONE, 2011, 6, e17274.	1.1	90
312	HMMerThread: Detecting Remote, Functional Conserved Domains in Entire Genomes by Combining Relaxed Sequence-Database Searches with Fold Recognition. PLoS ONE, 2011, 6, e17568.	1.1	2
313	Transcriptome Sequencing, and Rapid Development and Application of SNP Markers for the Legume Pod Borer Maruca vitrata (Lepidoptera: Crambidae). PLoS ONE, 2011, 6, e21388.	1.1	30
314	Discovery and Genomic Characterization of a Novel Ovine Partetravirus and a New Genotype of Bovine Partetravirus. PLoS ONE, 2011, 6, e25619.	1.1	35
315	Computational Analysis of the ESX-1 Region of Mycobacterium tuberculosis: Insights into the Mechanism of Type VII Secretion System. PLoS ONE, 2011, 6, e27980.	1.1	33
316	Cloning and sequencing of PR5-like gene from high altitude adapted ecotype of <i>Lepidium latifolium</i> . Archives of Phytopathology and Plant Protection, 2011, 44, 1025-1032.	0.6	2
317	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing <i>Deltaproteobacterium</i> N47. Environmental Microbiology, 2011, 13, 1125-1137.	1.8	66
318	Distinct evolutionary patterns of <i>Oryza glaberrima</i> deciphered by genome sequencing and comparative analysis. Plant Journal, 2011, 66, 796-805.	2.8	28
319	Genomics of Biotrophic, Plant-infecting Plasmodiophorids Using In Vitro Dual Cultures. Protist, 2011, 162, 449-461.	0.6	28
320	MAKER2: an annotation pipeline and genome-database management tool for second-generation genome projects. BMC Bioinformatics, 2011, 12, 491.	1.2	1,654
321	The neurexin superfamily of <i>Caenorhabditis elegans</i> . Gene Expression Patterns, 2011, 11, 144-150.	0.3	46
322	Rice G-protein coupled receptor (GPCR). Plant Signaling and Behavior, 2011, 6, 1079-1086.	1.2	18
323	<i>Ascaris suum</i> draft genome. Nature, 2011, 479, 529-533.	13.7	246
324	Structural Bioinformatics of <i>Neisseria meningitidis</i> LD-Carboxypeptidase: Implications for Substrate Binding and Specificity. Protein Journal, 2011, 30, 558-565.	0.7	4
325	Expression of <i>lorelei</i> -like genes in aposporous and sexual <i>Paspalum notatum</i> plants. Plant Molecular Biology, 2011, 77, 337-354.	2.0	34
326	Genome wide identification of Dof transcription factor gene family in sorghum and its comparative phylogenetic analysis with rice and Arabidopsis. Molecular Biology Reports, 2011, 38, 5037-5053.	1.0	92
327	An RNA-dependent RNA polymerase gene of a distinct Brazilian tospovirus. Virus Genes, 2011, 43, 385-389.	0.7	17

#	ARTICLE	IF	CITATIONS
328	Evolution of nematode-resistant Mi-1 gene homologs in three species of Solanum. <i>Molecular Genetics and Genomics</i> , 2011, 285, 207-218.	1.0	15
329	Molecular characterization of the RNA-dependent RNA polymerase from groundnut ringspot virus (genus <i>Tospovirus</i> , family <i>Bunyaviridae</i> ). <i>Archives of Virology</i> , 2011, 156, 1425-1429.	0.9	4
330	Metallothionein-like gene from <i>Cicer microphyllum</i> is regulated by multiple abiotic stresses. <i>Protoplasma</i> , 2011, 248, 839-847.	1.0	52
331	TI2BioP: Topological Indices to BioPolymers. Its practical use to unravel cryptic bacteriocin-like domains. <i>Amino Acids</i> , 2011, 40, 431-442.	1.2	14
332	Transcriptome profiling and insilico analysis of <i>Gynostemma pentaphyllum</i> using a next generation sequencer. <i>Plant Cell Reports</i> , 2011, 30, 2075-2083.	2.8	21
333	Positive Darwinian Selection Drives the Evolution of the Morphology-Related Gene, <i>EPCAM</i> , in Particularly Species-Rich Lineages of African Cichlid Fishes. <i>Journal of Molecular Evolution</i> , 2011, 73, 1-9.	0.8	9
334	A Closer Look at <i>Bacteroides</i> : Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. <i>Microbial Ecology</i> , 2011, 61, 473-485.	1.4	135
335	Bioinformatic analysis of fruit-specific expressed sequence tag libraries of <i>Diospyros kaki</i> Thunb.: view at the transcriptome at different developmental stages. <i>3 Biotech</i> , 2011, 1, 35-45.	1.1	8
336	Genome sequences and comparative genomics of two <i>Lactobacillus ruminis</i> strains from the bovine and human intestinal tracts. <i>Microbial Cell Factories</i> , 2011, 10, S13.	1.9	65
337	Modularity analysis based on predicted protein-protein interactions provides new insights into pathogenicity and cellular process of <i>Escherichia coli</i> O157:H7. <i>Theoretical Biology and Medical Modelling</i> , 2011, 8, 47.	2.1	8
338	Expressed sequence tags from <i>Atta laevigata</i> and identification of candidate genes for the control of pest leaf-cutting ants. <i>BMC Research Notes</i> , 2011, 4, 203.	0.6	3
339	Prediction of a novel RNA binding domain in crocodilepox Zimbabwe Gene 157. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 12.	7.6	1
340	Taxonomically restricted genes are associated with the evolution of sociality in the honey bee. <i>BMC Genomics</i> , 2011, 12, 164.	1.2	131
341	Interactions of a pesticide/heavy metal mixture in marine bivalves: a transcriptomic assessment. <i>BMC Genomics</i> , 2011, 12, 195.	1.2	83
342	Correlation of gene expression and protein production rate - a system wide study. <i>BMC Genomics</i> , 2011, 12, 616.	1.2	67
343	Insights into the innate immunity of the Mediterranean mussel <i>Mytilus galloprovincialis</i> . <i>BMC Genomics</i> , 2011, 12, 69.	1.2	159
344	An Expressed Sequence Tag collection from the male antennae of the Noctuid moth <i>Spodoptera littoralis</i> : a resource for olfactory and pheromone detection research. <i>BMC Genomics</i> , 2011, 12, 86.	1.2	145
345	Comparative metabolic capabilities for <i>Micrococcus luteus</i> NCTC 2665, the "Fleming" strain, and actinobacteria. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2770-2775.	1.7	6

#	ARTICLE	IF	CITATIONS
346	Supervised learning and prediction of physical interactions between human and HIV proteins. <i>Infection, Genetics and Evolution</i> , 2011, 11, 917-923.	1.0	83
347	Deep sequencing of <i>Ptilidium</i> (Ptilidiaceae) suggests evolutionary stasis in liverwort plastid genome structure. <i>Plant Ecology and Evolution</i> , 2011, 144, 29-43.	0.3	37
348	Nucleocytoplasmic Distribution Is Required for Activation of Resistance by the Potato NB-LRR Receptor Rx1 and Is Balanced by Its Functional Domains. <i>Plant Cell</i> , 2011, 22, 4195-4215.	3.1	140
349	The Mediator Complex in Plants: Structure, Phylogeny, and Expression Profiling of Representative Genes in a Dicot ( <i>Arabidopsis</i> ) and a Monocot (Rice) during Reproduction and Abiotic Stress. <i>Plant Physiology</i> , 2011, 157, 1609-1627.	2.3	158
350	Transcription Analysis of a Lantibiotic Gene Cluster from <i>Bifidobacterium longum</i> DJO10A. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5879-5887.	1.4	41
351	Classical Swine Fever Virus Nucleoprotein Limits Type I Interferon Induction in Plasmacytoid Dendritic Cells by Interacting with Interferon Regulatory Factor 7. <i>Journal of Virology</i> , 2011, 85, 8002-8011.	1.5	85
352	Membrane Topological Structure of Neutral System N/A Amino Acid Transporter 4 (SNAT4) Protein. <i>Journal of Biological Chemistry</i> , 2011, 286, 38086-38094.	1.6	11
353	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	1.8	137
354	Draft genome of the globally widespread and invasive Argentine ant ( <i>Linepithema humile</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5673-5678.	3.3	257
355	Complete Genome Sequence of the Commensal <i>Enterococcus faecalis</i> 62, Isolated from a Healthy Norwegian Infant. <i>Journal of Bacteriology</i> , 2011, 193, 2377-2378.	1.0	46
356	Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. <i>Nature Communications</i> , 2011, 2, 202.	5.8	481
357	Biochemical characterization of the tetrahydrobiopterin synthesis pathway in the oleaginous fungus <i>Mortierella alpina</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 3059-3070.	0.7	28
358	Analysis of Leaf and Root Transcriptomes of Soil-Grown <i>Avena barbata</i> Plants. <i>Plant and Cell Physiology</i> , 2011, 52, 317-332.	1.5	34
359	The Psb32 Protein Aids in Repairing Photodamaged Photosystem II in the Cyanobacterium <i>Synechocystis</i> 6803. <i>Molecular Plant</i> , 2011, 4, 1052-1061.	3.9	23
360	An Infant-associated Bacterial Commensal Utilizes Breast Milk Sialyloligosaccharides. <i>Journal of Biological Chemistry</i> , 2011, 286, 11909-11918.	1.6	164
361	A bacterial process for selenium nanosphere assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13480-13485.	3.3	165
362	Long-Chain N-Acyl Amino Acid Synthases Are Linked to the Putative PEP-CTERM/Exosortase Protein-Sorting System in Gram-Negative Bacteria. <i>Journal of Bacteriology</i> , 2011, 193, 5707-5715.	1.0	29
363	Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5667-5672.	3.3	222

#	ARTICLE	IF	CITATIONS
364	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2011, 39, D402-D410.	6.5	64
365	A novel hybrid gene prediction method employing protein multiple sequence alignments. <i>Bioinformatics</i> , 2011, 27, 757-763.	1.8	468
366	Generation of expressed sequence tags, development of microsatellite and single nucleotide polymorphism markers in <i>Primula sieboldii</i> E. Morren (Primulaceae) for analysis of genetic diversity in natural and horticultural populations. <i>Breeding Science</i> , 2011, 61, 234-243.	0.9	4
367	Gender-Associated Genes in Filarial Nematodes Are Important for Reproduction and Potential Intervention Targets. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e947.	1.3	26
368	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen <i>Bursaphelenchus xylophilus</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002219.	2.1	351
369	Proteomic Analysis of Excretory-Secretory Products of <i>Heligmosomoides polygyrus</i> Assessed with Next-Generation Sequencing Transcriptomic Information. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1370.	1.3	80
370	Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga <i>Nannochloropsis oceanica</i> CCMP1779. <i>PLoS Genetics</i> , 2012, 8, e1003064.	1.5	376
371	Novel <i>scpA</i> -Cysteine-Dependent Maleylpyruvate Isomerase in the Gentisate Pathway of <i>Paenibacillus</i> sp. Strain NyZ101. <i>Journal of Bacteriology</i> , 2012, 194, 3987-3994.	1.0	22
372	The Non-Flagellar Type III Secretion System Evolved from the Bacterial Flagellum and Diversified into Host-Cell Adapted Systems. <i>PLoS Genetics</i> , 2012, 8, e1002983.	1.5	254
373	Origin and Evolution of Laminin Gene Family Diversity. <i>Molecular Biology and Evolution</i> , 2012, 29, 1823-1836.	3.5	45
374	LegumelP: an integrative database for comparative genomics and transcriptomics of model legumes. <i>Nucleic Acids Research</i> , 2012, 40, D1221-D1229.	6.5	91
375	The Plant Growth Promoting Substance, Lumichrome, Mimics Starch, and Ethylene-Associated Symbiotic Responses in Lotus and Tomato Roots. <i>Frontiers in Plant Science</i> , 2012, 3, 120.	1.7	20
376	Genome Sequence of the Naturally Plasmid-Free <i>Lactobacillus plantarum</i> Strain NC8 (CCUG 61730). <i>Journal of Bacteriology</i> , 2012, 194, 2391-2392.	1.0	61
377	Complete Resequencing and Reannotation of the <i>Lactobacillus plantarum</i> WCFS1 Genome. <i>Journal of Bacteriology</i> , 2012, 194, 195-196.	1.0	109
378	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6309-6320.	1.4	83
379	GenColors-based comparative genome databases for small eukaryotic genomes. <i>Nucleic Acids Research</i> , 2012, 41, D692-D699.	6.5	7
380	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	6.5	217
381	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar068-bar068.	1.4	108

#	ARTICLE	IF	CITATIONS
382	FungiDB: an integrated functional genomics database for fungi. <i>Nucleic Acids Research</i> , 2012, 40, D675-D681.	6.5	321
383	SANS: high-throughput retrieval of protein sequences allowing 50% mismatches. <i>Bioinformatics</i> , 2012, 28, i438-i443.	1.8	22
384	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. <i>Nucleic Acids Research</i> , 2012, 41, D483-D489.	6.5	238
385	Article Withdrawn: GNARE: A Grid-based Server for the Analysis of User Submitted Genomes. <i>Nucleic Acids Research</i> , 2012, 40, e177-e177.	6.5	4
386	Sequence and comparative analysis of the MIP gene in Chinese straw mushroom, <i>Volvariella volvacea</i> . <i>Genome</i> , 2012, 55, 667-672.	0.9	2
387	Phylogenomic Study of Lipid Genes Involved in Microalgal Biofuel Production—Candidate Gene Mining and Metabolic Pathway Analyses. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S10159.	0.6	26
388	Acinetobacter Insertion Sequence IS <i>Aba11</i> Belongs to a Novel Family That Encodes Transposases with a Signature HHEK Motif. <i>Applied and Environmental Microbiology</i> , 2012, 78, 471-480.	1.4	7
389	Novel Roles of SoxR, a Transcriptional Regulator from <i>Xanthomonas campestris</i> , in Sensing Redox-Cycling Drugs and Regulating a Protective Gene That Have Overall Implications for Bacterial Stress Physiology and Virulence on a Host Plant. <i>Journal of Bacteriology</i> , 2012, 194, 209-217.	1.0	14
390	Widespread Polymorphism in the Positions of Stop Codons in <i>Drosophila melanogaster</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 533-549.	1.1	25
391	Phylogenetic Analysis of Mitochondrial Outer Membrane $\beta$ -Barrel Channels. <i>Genome Biology and Evolution</i> , 2012, 4, 110-125.	1.1	14
392	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012, 40, D91-D97.	6.5	179
393	Genetic Analysis of the Upper Phenylacetate Catabolic Pathway in the Production of Tropodithietic Acid by <i>Phaeobacter gallaeciensis</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 3539-3551.	1.4	48
394	Comprehensive Functional Analyses of Expressed Sequence Tags in Common Wheat ( <i>Triticum turgidum</i> ) Using a High-Throughput Approach. <i>PLoS ONE</i> , 2012, 7, e35393.	1.5	46
395	Members of <i>Ectocarpus siliculosus</i> F-box Family Are Subjected to Differential Selective Forces. <i>Interdisciplinary Bio Central</i> , 2012, 4, 1.1-1.7.	0.1	2
396	Complete Genome Sequence of <i>Geobacillus thermoglucosidans</i> TNO-09.020, a Thermophilic Sporeformer Associated with a Dairy-Processing Environment. <i>Journal of Bacteriology</i> , 2012, 194, 4118-4118.	1.0	31
397	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
399	Amylases without known homologues discovered in an acid mine drainage: significance and impact. <i>Scientific Reports</i> , 2012, 2, 354.	1.6	21
400	<i>Sugarwin</i> : A Sugarcane Insect-Induced Gene with Antipathogenic Activity. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 613-624.	1.4	31

#	ARTICLE	IF	CITATIONS
401	Gene expression associated with apogamy commitment in <i>Ceratopteris richardii</i> . <i>Sexual Plant Reproduction</i> , 2012, 25, 293-304.	2.2	17
402	Characterization of the <i>Salmonella</i> bacteriophage vB_SenS-Ent1. <i>Journal of General Virology</i> , 2012, 93, 2046-2056.	1.3	30
403	Genome sequences of wild and domestic bactrian camels. <i>Nature Communications</i> , 2012, 3, 1202.	5.8	176
404	Molecular characterization of an $\hat{\text{I}}\pm$ -N-acetylgalactosaminidase from <i>Clonorchis sinensis</i> . <i>Parasitology Research</i> , 2012, 111, 2149-2156.	0.6	2
405	Functional analysis of glycoside hydrolase family 18 and 20 genes in <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 717-730.	0.9	73
406	Cloning and transcript analysis of type 2 metallothionein gene (SbMT-2) from extreme halophyte <i>Salicornia brachiata</i> and its heterologous expression in <i>E. coli</i> . <i>Gene</i> , 2012, 499, 280-287.	1.0	93
407	Proteomic profiles of soluble proteins from the esophageal gland in female <i>Meloidogyne incognita</i> . <i>International Journal for Parasitology</i> , 2012, 42, 1177-1183.	1.3	15
408	Protective immunity against tick infestation in cattle vaccinated with recombinant trypsin inhibitor of <i>Rhipicephalus microplus</i> . <i>Vaccine</i> , 2012, 30, 6678-6685.	1.7	36
409	Selection and characterisation of guanidine-resistant mutants of human enterovirus 71. <i>Virus Research</i> , 2012, 169, 72-79.	1.1	22
410	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. <i>Methods</i> , 2012, 57, 508-518.	1.9	49
411	Contrasting patterns of evolution following whole genome versus tandem duplication events in <i>Populus</i> . <i>Genome Research</i> , 2012, 22, 95-105.	2.4	126
412	MonarchBase: the monarch butterfly genome database. <i>Nucleic Acids Research</i> , 2012, 41, D758-D763.	6.5	91
413	Caspar-like Gene Depletion Reduces <i>Leishmania</i> Infection in Sand Fly Host <i>Lutzomyia longipalpis</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 12985-12993.	1.6	55
414	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. <i>Science</i> , 2012, 337, 1661-1665.	6.0	637
415	A root-knot nematode-secreted protein is injected into giant cells and targeted to the nuclei. <i>New Phytologist</i> , 2012, 194, 924-931.	3.5	85
416	GFam: a platform for automatic annotation of gene families. <i>Nucleic Acids Research</i> , 2012, 40, e152-e152.	6.5	3
417	Insect transferrins: Multifunctional proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2012, 1820, 437-451.	1.1	97
418	Accurate discrimination of bHLH domains in plants, animals, and fungi using biologically meaningful sites. <i>BMC Evolutionary Biology</i> , 2012, 12, 154.	3.2	30



#	ARTICLE	IF	CITATIONS
419	Comprehensive analysis of CCCH zinc finger family in poplar ( <i>Populus trichocarpa</i> ). BMC Genomics, 2012, 13, 253.	1.2	96
420	Developing the anemone <i>Aiptasia</i> as a tractable model for cnidarian-dinoflagellate symbiosis: the transcriptome of aposymbiotic <i>A. pallida</i> . BMC Genomics, 2012, 13, 271.	1.2	99
421	Identification of essential genes of the periodontal pathogen <i>Porphyromonas gingivalis</i> . BMC Genomics, 2012, 13, 578.	1.2	123
422	Transcriptome database resource and gene expression atlas for the rose. BMC Genomics, 2012, 13, 638.	1.2	76
423	Next generation sequencing and de novo transcriptome analysis of <i>Costus pictus</i> D. Don, a non-model plant with potent anti-diabetic properties. BMC Genomics, 2012, 13, 663.	1.2	66
424	Transcriptional profile analysis of E3 ligase and hormone-related genes expressed during wheat grain development. BMC Plant Biology, 2012, 12, 35.	1.6	29
425	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.	1.9	173
426	Genome and proteome analysis of 7-7-1, a flagellotropic phage infecting <i>Agrobacterium</i> sp H13-3. Virology Journal, 2012, 9, 102.	1.4	23
427	A novel virus genome discovered in an extreme environment suggests recombination between unrelated groups of RNA and DNA viruses. Biology Direct, 2012, 7, 13.	1.9	141
428	A comprehensive cDNA library of light- and temperature-stressed <i>Saccharina latissima</i> (Phaeophyceae). European Journal of Phycology, 2012, 47, 83-94.	0.9	22
429	Sequence of <i>Leptospira santarosai</i> serovar Shermani genome and prediction of virulence-associated genes. Gene, 2012, 511, 364-370.	1.0	43
430	In silico identification of novel hevein-like peptide precursors. Peptides, 2012, 38, 127-136.	1.2	48
431	SchistoDB: an updated genome resource for the three key schistosomes of humans. Nucleic Acids Research, 2012, 41, D728-D731.	6.5	45
432	The cloning, expression, purification, characterization and modeled structure of <i>Caulobacter crescentus</i> $\beta$ -Xylosidase I. World Journal of Microbiology and Biotechnology, 2012, 28, 2879-2888.	1.7	22
433	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. BMC Genomics, 2012, 13, S10.	1.2	18
434	Genome-wide identification, classification and expression analysis of genes encoding putative fasciclin-like arabinogalactan proteins in Chinese cabbage ( <i>Brassica rapa</i> L.). Molecular Biology Reports, 2012, 39, 10541-10555.	1.0	34
435	The Biochemical Adaptations of Mitochondrion-Related Organelles of Parasitic and Free-Living Microbial Eukaryotes to Low Oxygen Environments. Cellular Origin and Life in Extreme Habitats, 2012, , 51-81.	0.3	5
436	Nitrile Hydratase Genes Are Present in Multiple Eukaryotic Supergroups. PLoS ONE, 2012, 7, e32867.	1.1	20

#	ARTICLE	IF	CITATIONS
437	Disruption of the Eng18B ENGase Gene in the Fungal Biocontrol Agent <i>Trichoderma atroviride</i> Affects Growth, Conidiation and Antagonistic Ability. <i>PLoS ONE</i> , 2012, 7, e36152.	1.1	52
438	Comparative Analysis of the 5S rRNA and Its Associated Proteins Reveals Unique Primitive Rather Than Parasitic Features in <i>Giardia lamblia</i> . <i>PLoS ONE</i> , 2012, 7, e36878.	1.1	6
439	Gene Isoform Specificity through Enhancer-Associated Antisense Transcription. <i>PLoS ONE</i> , 2012, 7, e43511.	1.1	27
440	Pan-Genomic Analysis Provides Insights into the Genomic Variation and Evolution of <i>Salmonella Paratyphi A</i> . <i>PLoS ONE</i> , 2012, 7, e45346.	1.1	26
441	Comparative functional genomics approach for the annotation of proteins in Unclassified Halophilic archaeon DL31. <i>Nature Precedings</i> , 2012, , .	0.1	1
442	Identification and annotation of abiotic stress responsive candidate genes in peanut ESTs. <i>Bioinformatics</i> , 2012, 8, 1211-1219.	0.2	10
443	Use of Enterobacterial Repetitive Intergenic Consensus PCR in Detecting Target(s) of Hapalindole-T, From a Cyanobacterium, in <i>Escherichia Coli</i> : <i>In Silico</i> Validation. <i>Current Research in Bioinformatics</i> , 2012, 1, 30-40.	0.1	0
444	A Novel Type III Endosome Transmembrane Protein, TEMP. <i>Cells</i> , 2012, 1, 1029-1044.	1.8	1
445	Candidate chemosensory Genes in Female Antennae of the Noctuid Moth <i>Spodoptera littoralis</i> . <i>International Journal of Biological Sciences</i> , 2012, 8, 1036-1050.	2.6	83
446	Untangling Genomes from Metagenomes: Revealing an Uncultured Class of Marine Euryarchaeota. <i>Science</i> , 2012, 335, 587-590.	6.0	427
447	A <i>Lissencephaly-1</i> homologue is essential for mitotic progression in the planarian <i>Schmidtea mediterranea</i> . <i>Developmental Dynamics</i> , 2012, 241, 901-910.	0.8	20
448	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1798-1807.	1.7	19
449	Novel Molluskan Biomineralization Proteins Retrieved from Proteomics: A Case Study with Upsalin. <i>ChemBioChem</i> , 2012, 13, 1067-1078.	1.3	17
450	Genome sequence of foxtail millet ( <i>Setaria italica</i> ) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012, 30, 549-554.	9.4	636
451	Isolation and characterization of cold responsive NAC gene from <i>Lepidium latifolium</i> . <i>Molecular Biology Reports</i> , 2012, 39, 9629-9638.	1.0	28
452	Characterization of Tannase Protein Sequences of Bacteria and Fungi: An <i>In Silico</i> Study. <i>Protein Journal</i> , 2012, 31, 306-327.	0.7	28
453	Exploiting BAC-end sequences for the mining, characterization and utility of new short sequences repeat (SSR) markers in Citrus. <i>Molecular Biology Reports</i> , 2012, 39, 5373-5386.	1.0	41
454	Generation, functional analysis and utility of <i>Citrus grandis</i> EST from a flower-derived cDNA library. <i>Molecular Biology Reports</i> , 2012, 39, 7221-7235.	1.0	14

#	ARTICLE	IF	CITATIONS
455	Genetic basis of destruxin production in the entomopathogen <i>Metarhizium robertsii</i> . <i>Current Genetics</i> , 2012, 58, 105-116.	0.8	43
456	Identification and characterization of a novel 21.6-kDa tegumental protein from <i>Clonorchis sinensis</i> . <i>Parasitology Research</i> , 2012, 110, 2061-2066.	0.6	26
457	LOX genes in blast fungus ( <i>Magnaporthe grisea</i> ) resistance in rice. <i>Functional and Integrative Genomics</i> , 2012, 12, 265-275.	1.4	34
458	A novel xylanase with tolerance to ethanol, salt, protease, SDS, heat, and alkali from actinomycete <i>Lechevalieria</i> sp. HJ3. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 965-975.	1.4	25
459	Annotation and analysis of malic enzyme genes encoding for multiple isoforms in the fungus <i>Mucor circinelloides</i> CBS 277.49. <i>Biotechnology Letters</i> , 2012, 34, 941-947.	1.1	23
460	Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. <i>Influenza and Other Respiratory Viruses</i> , 2012, 6, 404-416.	1.5	270
461	The effects of gamma irradiation on growth and expression of genes encoding DNA repair-related proteins in Lombardy poplar ( <i>Populus nigra</i> var. <i>italica</i> ). <i>Journal of Environmental Radioactivity</i> , 2012, 109, 19-28.	0.9	31
462	Ancient diversity of splicing motifs and protein surfaces in the wild emmer wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Pathology, 2012, 13, 276-287.	2.0	45
463	Generation and analysis of expressed sequence tags from the bone marrow of Chinese Sika deer. <i>Molecular Biology Reports</i> , 2012, 39, 2981-2990.	1.0	4
464	Identification and characterization of a LEA family gene CarLEA4 from chickpea ( <i>Cicer arietinum</i> L.). <i>Molecular Biology Reports</i> , 2012, 39, 3565-3572.	1.0	17
465	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. <i>Genome Biology</i> , 2013, 14, R58.	3.8	125
466	A human skeletal muscle interactome centered on proteins involved in muscular dystrophies: LGMD interactome. <i>Skeletal Muscle</i> , 2013, 3, 3.	1.9	36
467	Viral categorization and discovery in human circulation by transcriptome sequencing. <i>Biochemical and Biophysical Research Communications</i> , 2013, 436, 525-529.	1.0	4
468	Genome sequence of a novel deep-sea vent epsilonproteobacterial phage provides new insight into the co-evolution of Epsilonproteobacteria and their phages. <i>Extremophiles</i> , 2013, 17, 405-419.	0.9	22
469	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from <i>Salmonella Typhimurium</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 1-10.	1.2	4
470	Generation and analysis of expressed sequence tags for microsatellite marker development in <i>Calamus simplicifolius</i> C. F. Wei. <i>Molecular Breeding</i> , 2013, 31, 867-877.	1.0	1
471	Sequence and expression analyses of KIX domain proteins suggest their importance in seed development and determination of seed size in rice, and genome stability in <i>Arabidopsis</i> . <i>Molecular Genetics and Genomics</i> , 2013, 288, 329-346.	1.0	32
472	Reactivating head regrowth in a regeneration-deficient planarian species. <i>Nature</i> , 2013, 500, 81-84.	13.7	149

#	ARTICLE	IF	CITATIONS
473	Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods – Unprecedented Prospects for Fundamental and Applied Research. , 2013, , 287-314.		1
474	The glyoxylate cycle is involved in pleiotropic phenotypes, antagonism and induction of plant defence responses in the fungal biocontrol agent <i>Trichoderma atroviride</i> . <i>Fungal Genetics and Biology</i> , 2013, 58-59, 33-41.	0.9	36
475	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013, 31, 759-765.	9.4	340
476	The attack of the phytopathogens and the trumpet solo: Identification of a novel plant antifungal peptide with distinct fold and disulfide bond pattern. <i>Biochimie</i> , 2013, 95, 1939-1948.	1.3	34
477	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	1.2	170
478	De-novo assembly and characterization of the transcriptome of <i>Metschnikowia fructicola</i> reveals differences in gene expression following interaction with <i>Penicillium digitatum</i> and grapefruit peel. <i>BMC Genomics</i> , 2013, 14, 168.	1.2	79
479	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, <i>Ostertagia ostertagi</i> and <i>Cooperia oncophora</i> . <i>BMC Genomics</i> , 2013, 14, 118.	1.2	31
480	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	5.8	201
481	The <i>Capsaspora</i> genome reveals a complex unicellular prehistory of animals. <i>Nature Communications</i> , 2013, 4, 2325.	5.8	244
482	De novo sequencing and assembly of <i>Centella asiatica</i> leaf transcriptome for mapping of structural, functional and regulatory genes with special reference to secondary metabolism. <i>Gene</i> , 2013, 525, 58-76.	1.0	96
483	Antisense expression of peach mildew resistance locus O ( <i>PpMlo1</i> ) gene confers cross-species resistance to powdery mildew in <i>Fragaria x ananassa</i> . <i>Transgenic Research</i> , 2013, 22, 1119-1131.	1.3	51
484	Mitochondrial genome sequences of <i>Artemia tibetiana</i> and <i>Artemia urmiana</i> : assessing molecular changes for high plateau adaptation. <i>Science China Life Sciences</i> , 2013, 56, 440-452.	2.3	37
485	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomics – Prospects for new interventions. <i>Biotechnology Advances</i> , 2013, 31, 1486-1500.	6.0	18
486	Characterization and genomic analysis of two <i>Staphylococcus aureus</i> bacteriophages isolated from poultry/livestock farms. <i>Journal of General Virology</i> , 2013, 94, 2569-2576.	1.3	13
487	Comparative genomics and evolutionary analysis of hydrophobins from three species of wood-degrading fungi. <i>Mycologia</i> , 2013, 105, 1471-1478.	0.8	14
488	Polygalacturonases from <i>Moniliophthora perniciosa</i> are regulated by fermentable carbon sources and possible post-translational modifications. <i>Fungal Genetics and Biology</i> , 2013, 60, 110-121.	0.9	7
489	Structural, Expression and Interaction Analysis of Rice SKP1-Like Genes. <i>DNA Research</i> , 2013, 20, 67-78.	1.5	24
490	The genome sequence of the hydrocarbon-degrading <i>Acinetobacter venetianus</i> VE-C3. <i>Research in Microbiology</i> , 2013, 164, 439-449.	1.0	30

#	ARTICLE	IF	CITATIONS
491	Cloning and characterization of NBS-LRR encoding resistance gene candidates from Tomato Leaf Curl New Delhi Virus resistant genotype of <i>Luffa cylindrica</i> Roem. <i>Physiological and Molecular Plant Pathology</i> , 2013, 81, 107-117.	1.3	16
492	Model animals for the study of oxidative stress from complex II. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2013, 1827, 588-597.	0.5	43
493	Analysis of the canine brain transcriptome with an emphasis on the hypothalamus and cerebral cortex. <i>Mammalian Genome</i> , 2013, 24, 484-499.	1.0	26
494	Diverse Broad-Host-Range Plasmids from Freshwater Carry Few Accessory Genes. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7684-7695.	1.4	64
495	A heterozygous moth genome provides insights into herbivory and detoxification. <i>Nature Genetics</i> , 2013, 45, 220-225.	9.4	472
496	The genome of the hydatid tapeworm <i>Echinococcus granulosus</i> . <i>Nature Genetics</i> , 2013, 45, 1168-1175.	9.4	260
497	Analysis Tool Web Services from the EMBL-EBI. <i>Nucleic Acids Research</i> , 2013, 41, W597-W600.	6.5	1,483
498	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2013, 14, 689.	1.2	172
499	Integrating microRNA and mRNA expression profiling in <i>Symbiodinium microadriaticum</i> , a dinoflagellate symbiont of reef-building corals. <i>BMC Genomics</i> , 2013, 14, 704.	1.2	109
500	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2013, 14, 664.	1.2	99
501	Comparative analysis of two members of the metal ion-containing group III-alcohol dehydrogenases from <i>Dickeya zeae</i> . <i>Biotechnology Letters</i> , 2013, 35, 725-733.	1.1	7
502	PROGRESS IN COMPUTATIONAL STUDIES OF HOST-PATHOGEN INTERACTIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1230001.	0.3	54
503	The genome of <i>Romanomermis culicivorax</i> : revealing fundamental changes in the core developmental genetic toolkit in Nematoda. <i>BMC Genomics</i> , 2013, 14, 923.	1.2	43
504	Stringent DDI-based Prediction of <i>H. sapiens</i> - <i>M. tuberculosis</i> H37Rv Protein-Protein Interactions. <i>BMC Systems Biology</i> , 2013, 7, S6.	3.0	34
505	A detailed gene expression study of the <i>Miscanthus</i> genus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. <i>BMC Genomics</i> , 2013, 14, 864.	1.2	27
506	Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. <i>BMC Microbiology</i> , 2013, 13, 259.	1.3	9
507	Tetraploid Rangpur lime rootstock increases drought tolerance via enhanced constitutive root abscisic acid production. <i>Plant, Cell and Environment</i> , 2013, 36, 856-868.	2.8	167
508	Application of <i>Cydia pomonella</i> expressed sequence tags: Identification and expression of three general odorant binding proteins in codling moth. <i>Insect Science</i> , 2013, 20, 559-574.	1.5	16

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509	Novel cassette array in a class 1 integron in clinical isolates of <i>Acinetobacter baumannii</i> from central Iran. <i>International Journal of Medical Microbiology</i> , 2013, 303, 645-650.	1.5	27
510	Microbial Eukaryote Globins. <i>Advances in Microbial Physiology</i> , 2013, 63, 391-446.	1.0	36
511	Tips and tricks for the assembly of a <i>Corynebacterium pseudotuberculosis</i> genome using a semiconductor sequencer. <i>Microbial Biotechnology</i> , 2013, 6, 150-156.	2.0	14
512	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein-protein interaction network. <i>Molecular BioSystems</i> , 2013, 9, 2720.	2.9	47
513	Expression of hsp70, hsp100 and ubiquitin in <i>Aloe barbadensis</i> Miller under direct heat stress and under temperature acclimation conditions. <i>Plant Cell Reports</i> , 2013, 32, 293-307.	2.8	19
514	R4 regulators of G protein signaling (RGS) identify an ancient MHC-linked synteny group. <i>Immunogenetics</i> , 2013, 65, 145-156.	1.2	8
515	Characterization of human NLZ1/ZNF703 identifies conserved domains essential for proper subcellular localization and transcriptional repression. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 120-133.	1.2	18
516	Structural Characterization of the RLCK Family Member BSK8: A Pseudokinase with an Unprecedented Architecture. <i>Journal of Molecular Biology</i> , 2013, 425, 4455-4467.	2.0	30
517	A comprehensive analysis of the <i>Manduca sexta</i> immunotranscriptome. <i>Developmental and Comparative Immunology</i> , 2013, 39, 388-398.	1.0	52
518	Genome-scale analysis of the metabolic networks of oleaginous Zygomycete fungi. <i>Gene</i> , 2013, 521, 180-190.	1.0	41
519	Maturin is a novel protein required for differentiation during primary neurogenesis. <i>Developmental Biology</i> , 2013, 384, 26-40.	0.9	21
520	Interaction of dihydrofolate reductase and aminoglycoside adenylyltransferase enzyme from <i>Klebsiella pneumoniae</i> multidrug resistant strain DF12SA with clindamycin: a molecular modelling and docking study. <i>Journal of Molecular Modeling</i> , 2013, 19, 973-983.	0.8	15
521	Overview of tomato ( <i>Solanum lycopersicum</i> ) candidate pathogen recognition genes reveals important <i>Solanum</i> R locus dynamics. <i>New Phytologist</i> , 2013, 197, 223-237.	3.5	90
522	CartograTree: connecting tree genomes, phenotypes and environment. <i>Molecular Ecology Resources</i> , 2013, 13, 528-537.	2.2	9
523	Novel receptor-like kinases in cacao contain PR1 extracellular domains. <i>Molecular Plant Pathology</i> , 2013, 14, 602-609.	2.0	12
524	In Search of Actionable Targets for Agrigenomics and Microalgal Biofuel Production: Sequence-Structural Diversity Studies on Algal and Higher Plants with a Focus on GPAT Protein. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 173-186.	1.0	20
525	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 633-642.	1.4	190
526	Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and development. <i>Toxicology and Applied Pharmacology</i> , 2013, 270, 149-157.	1.3	61

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527	Cloning, In Silico Characterization and Prediction of Three Dimensional Structure of SbDof1, SbDof19, SbDof23 and SbDof24 Proteins from Sorghum [ <i>Sorghum bicolor</i> (L.) Moench]. <i>Molecular Biotechnology</i> , 2013, 54, 1-12.	1.3	11
528	Nitrate signals determine the sensing of nitrogen through differential expression of genes involved in nitrogen uptake and assimilation in finger millet. <i>Functional and Integrative Genomics</i> , 2013, 13, 179-190.	1.4	39
529	Recombinant Î <sup>2</sup> -1,3-1,4-glucanase from <i>Theobroma cacao</i> impairs <i>Moniliophthora perniciosa</i> mycelial growth. <i>Molecular Biology Reports</i> , 2013, 40, 5417-5427.	1.0	10
530	Functional Annotation of the Human Chromosome 7 "Missing" Proteins: A Bioinformatics Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2504-2510.	1.8	17
531	Transcriptomic analysis of four developmental stages of <i>Strongyloides venezuelensis</i> . <i>Parasitology International</i> , 2013, 62, 57-65.	0.6	15
532	Development and Characterization of cDNA Resources for the Common Marmoset: One of the Experimental Primate Models. <i>DNA Research</i> , 2013, 20, 255-262.	1.5	12
533	Unlocking the Puzzling Biology of the Black Périgord Truffle <i>Tuber melanosporum</i> . <i>Journal of Proteome Research</i> , 2013, 12, 5349-5356.	1.8	24
534	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013, 9, 352-367.	0.5	34
535	Interplay of the fungal sumoylation network for control of multicellular development. <i>Molecular Microbiology</i> , 2013, 90, 1125-1145.	1.2	40
536	Role of the methylcitrate cycle in growth, antagonism and induction of systemic defence responses in the fungal biocontrol agent <i>Trichoderma atroviride</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 2492-2500.	0.7	37
537	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. <i>Genome Research</i> , 2013, 23, 111-120.	2.4	409
538	Complete Genome Sequence of <i>Anoxybacillus flavithermus</i> TNO-09.006, a Thermophilic Sporeformer Associated with a Dairy-Processing Environment. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
539	Complete Genome Sequence of <i>Marinobacter</i> sp. BSs20148. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
540	A thrombospondin in the anthozoan <i>Nematostella vectensis</i> is associated with the nervous system and upregulated during regeneration. <i>Biology Open</i> , 2013, 2, 217-226.	0.6	11
541	Draft Genome Sequence of <i>Pseudomonas</i> Strain P818, Isolated from Glyphosate-Polluted Soil. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
542	A Sensitive and Accurate protein domain Classification Tool (SALT) for short reads. <i>Bioinformatics</i> , 2013, 29, 2103-2111.	1.8	10
543	Complete Genome Sequence of <i>Glaciecola psychrophila</i> Strain 170 T. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
544	The Transition from a Phytopathogenic Smut Ancestor to an Anamorphic Biocontrol Agent Deciphered by Comparative Whole-Genome Analysis. <i>Plant Cell</i> , 2013, 25, 1946-1959.	3.1	59

#	ARTICLE	IF	CITATIONS
545	Three Infectious Viral Species Lying in Wait in the Banana Genome. <i>Journal of Virology</i> , 2013, 87, 8624-8637.	1.5	80
546	Badgerâ€™an accessible genome exploration environment. <i>Bioinformatics</i> , 2013, 29, 2788-2789.	1.8	8
547	Identification of R2TP complex of <i>Leishmania donovani</i> and <i>Plasmodium falciparum</i> using genome wide in-silico analysis. <i>Communicative and Integrative Biology</i> , 2013, 6, e26005.	0.6	14
548	eFG: an electronic resource for <i>Fusarium graminearum</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat042-bat042.	1.4	5
549	<i>In Silico</i> Expressed Sequence Tag Analysis in Identification of Probable Diabetic Genes as Virtual Therapeutic Targets. <i>BioMed Research International</i> , 2013, 2013, 1-9.	0.9	5
550	Deletion and Gene Expression Analyses Define the Paxilline Biosynthetic Gene Cluster in <i>Penicillium paxilli</i> . <i>Toxins</i> , 2013, 5, 1422-1446.	1.5	29
551	Functional Diversity of Genes for the Biosynthesis of Paeoniflorin and Its Derivatives in <i>Paeonia</i> . <i>International Journal of Molecular Sciences</i> , 2013, 14, 18502-18519.	1.8	19
552	A Compendium of <i>Caenorhabditis elegans</i> RNA Binding Proteins Predicts Extensive Regulation at Multiple Levels. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 297-304.	0.8	31
553	GOLink: Finding Cooccurring Terms across Gene Ontology Namespaces. <i>International Journal of Genomics</i> , 2013, 2013, 1-10.	0.8	3
554	FLYING SAUCER1 Is a Transmembrane RING E3 Ubiquitin Ligase That Regulates the Degree of Pectin Methylesterification in <i>Arabidopsis</i> Seed Mucilage. <i>Plant Cell</i> , 2013, 25, 944-959.	3.1	76
555	Role of the Phenylalanine-Hydroxylating System in Aromatic Substance Degradation and Lipid Metabolism in the Oleaginous Fungus <i>Mortierella alpina</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 3225-3233.	1.4	31
556	Diversity of Virophages in Metagenomic Data Sets. <i>Journal of Virology</i> , 2013, 87, 4225-4236.	1.5	93
557	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6755-6764.	1.4	37
558	Molecular Cloning and Characterization of Novel Glutamate-Gated Chloride Channel Subunits from <i>Schistosoma mansoni</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003586.	2.1	32
559	Systems biology methods and developments of filamentous fungi in relation to the production of food ingredients. , 2013, , 19-41.		0
560	Identification of Genes Involved in the Biosynthesis of the Third and Fourth Sugars of the Methanococcus maripaludis Archaeal N-Linked Tetrasaccharide. <i>Journal of Bacteriology</i> , 2013, 195, 4094-4104.	1.0	19
561	The genome and developmental transcriptome of the strongylid nematode <i>Haemonchus contortus</i> . <i>Genome Biology</i> , 2013, 14, R89.	13.9	192
562	Annotated genes and nonannotated genomes: cross-species use of Gene Ontology in ecology and evolution research. <i>Molecular Ecology</i> , 2013, 22, 3216-3241.	2.0	77



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563	Sequencing and de novo transcriptome assembly of <i>Brachypodium sylvaticum</i> (Poaceae). <i>Applications in Plant Sciences</i> , 2013, 1, 1200011.	0.8	31
564	Novel <i>OTOA</i> mutations cause autosomal recessive non-syndromic hearing impairment in Pakistani families. <i>Clinical Genetics</i> , 2013, 84, 294-296.	1.0	14
565	Management and dissemination of MS proteomic data with PROTEOMICS: Example of a quantitative comparison between methods of protein extraction. <i>Proteomics</i> , 2013, 13, 1457-1466.	1.3	25
566	<i>HvLUX1</i> is a candidate gene underlying the early maturity 10 locus in barley: phylogeny, diversity, and interactions with the circadian clock and photoperiodic pathways. <i>New Phytologist</i> , 2013, 199, 1045-1059.	3.5	110
567	Fungus-Specific Sirtuin HstD Coordinates Secondary Metabolism and Development through Control of <i>LaeA</i> . <i>Eukaryotic Cell</i> , 2013, 12, 1087-1096.	3.4	68
568	Genome-Wide Patterns of Genetic Variation in Two Domestic Chickens. <i>Genome Biology and Evolution</i> , 2013, 5, 1376-1392.	1.1	65
569	PPR-SMRs. <i>RNA Biology</i> , 2013, 10, 1501-1510.	1.5	57
570	Re-annotation of the <i>Saccharopolyspora erythraea</i> genome using a systems biology approach. <i>BMC Genomics</i> , 2013, 14, 699.	1.2	21
572	Analysis of castor bean ribosome-inactivating proteins and their gene expression during seed development. <i>Genetics and Molecular Biology</i> , 2013, 36, 74-86.	0.6	18
573	Abiotic and Biotic Stress Responses in <i>Solanum tuberosum</i> Group Phureja DM1-516 R44 as Measured through Whole Transcriptome Sequencing. <i>Plant Genome</i> , 2013, 6, plantgenome2013.05.0014.	1.6	40
574	De Novo Transcriptome Sequencing and Analysis for <i>Venturia inaequalis</i> , the Devastating Apple Scab Pathogen. <i>PLoS ONE</i> , 2013, 8, e53937.	1.1	32
575	De Novo Transcriptome Assembly (NGS) of <i>Curcuma longa</i> L. Rhizome Reveals Novel Transcripts Related to Anticancer and Antimalarial Terpenoids. <i>PLoS ONE</i> , 2013, 8, e56217.	1.1	82
576	Profiling of Differentially Expressed Genes in Roots of <i>Robinia pseudoacacia</i> during Nodule Development Using Suppressive Subtractive Hybridization. <i>PLoS ONE</i> , 2013, 8, e63930.	1.1	13
577	Comprehensive Genome-Wide Survey, Genomic Constitution and Expression Profiling of the NAC Transcription Factor Family in Foxtail Millet ( <i>Setaria italica</i> L.). <i>PLoS ONE</i> , 2013, 8, e64594.	1.1	148
578	Carbohydrate-Active Enzymes in <i>Pythium</i> and Their Role in Plant Cell Wall and Storage Polysaccharide Degradation. <i>PLoS ONE</i> , 2013, 8, e72572.	1.1	106
579	Genome-Wide Analysis of the Dof Transcription Factor Gene Family Reveals Soybean-Specific Duplicable and Functional Characteristics. <i>PLoS ONE</i> , 2013, 8, e76809.	1.1	59
580	A Distinct and Divergent Lineage of Genomic Island-Associated Type IV Secretion Systems in <i>Legionella</i> . <i>PLoS ONE</i> , 2013, 8, e82221.	1.1	19
581	TFpredict and SABINE: Sequence-Based Prediction of Structural and Functional Characteristics of Transcription Factors. <i>PLoS ONE</i> , 2013, 8, e82238.	1.1	17

#	ARTICLE	IF	CITATIONS
582	Characterization and Phylogenetic Analysis of the Mitochondrial Genome of <i>Glarea lozoyensis</i> Indicates High Diversity within the Order Helotiales. PLoS ONE, 2013, 8, e74792.	1.1	9
583	Biotechnology of polyketides: new breath of life for the novel antibiotic genetic pathways discovery through metagenomics. Brazilian Journal of Microbiology, 2013, 44, 1007-1034.	0.8	67
584	Comprehensive Analysis of Alternative Splicing in <i>Digitalis purpurea</i> by Strand-Specific RNA-Seq. PLoS ONE, 2014, 9, e106001.	1.1	12
585	Identification and Differential Expression of microRNAs in Ovaries of Laying and Broody Geese ( <i>Anser</i> ) Tj ETQq1 1 0,784314 rgBT /Ov... PLOS ONE, 2014, 9, e106001.	1.1	24
586	New Hydrocarbon Degradation Pathways in the Microbial Metagenome from Brazilian Petroleum Reservoirs. PLoS ONE, 2014, 9, e90087.	1.1	83
587	Shedding Some Light over the Floral Metabolism by Arum Lily ( <i>Zantedeschia aethiopica</i> ) Spathe De Novo Transcriptome Assembly. PLoS ONE, 2014, 9, e90487.	1.1	16
588	Identification and Analysis of Differential miRNAs in PK-15 Cells after Foot-and-Mouth Disease Virus Infection. PLoS ONE, 2014, 9, e90865.	1.1	8
589	De Novo Assembly of <i>Auricularia polytricha</i> Transcriptome Using Illumina Sequencing for Gene Discovery and SSR Marker Identification. PLoS ONE, 2014, 9, e91740.	1.1	45
590	New Insights into <i>Dehalococcoides mccartyi</i> Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of <i>D. mccartyi</i> Transcriptomes. PLoS ONE, 2014, 9, e94808.	1.1	14
591	Evolution of the F-Box Gene Family in Euarchontoglires: Gene Number Variation and Selection Patterns. PLoS ONE, 2014, 9, e94899.	1.1	6
592	Zamilon, a Novel Virophage with Mimiviridae Host Specificity. PLoS ONE, 2014, 9, e94923.	1.1	101
593	Genome-Wide Analysis of the bZIP Transcription Factors in Cucumber. PLoS ONE, 2014, 9, e96014.	1.1	191
594	De Novo Transcriptome Assembly and Analyses of Gene Expression during Photomorphogenesis in Diploid Wheat <i>Triticum monococcum</i> . PLoS ONE, 2014, 9, e96855.	1.1	55
595	Analysis of Genome Sequences from Plant Pathogenic <i>Rhodococcus</i> Reveals Genetic Novelities in Virulence Loci. PLoS ONE, 2014, 9, e101996.	1.1	54
596	A Novel Method for Functional Annotation Prediction Based on Combination of Classification Methods. Scientific World Journal, The, 2014, 2014, 1-9.	0.8	0
597	SDS, a structural disruption score for assessment of missense variant deleteriousness. Frontiers in Genetics, 2014, 5, 82.	1.1	13
598	Mining a database of single amplified genomes from Red Sea brine pool extremophiles - improving reliability of gene function prediction using a profile and pattern matching algorithm (PPMA). Frontiers in Microbiology, 2014, 5, 134.	1.5	15
599	Forest Carbon Stocks and Variations along Altitudinal Gradients in Egdu Forest: Implications of Managing Forests for Climate Change Mitigation. Science, Technology and Arts Research, 2014, 2, 40.	0.1	37

#	ARTICLE	IF	CITATIONS
600	Use of Bioinformatics Tools in Different Spheres of Life Sciences. Journal of Data Mining in Genomics & Proteomics, 2014, 05, .	0.5	16
601	Bioinformatics based structural characterization of glucose dehydrogenase (gdh) gene and growth promoting activity of <i>Leclercia</i> sp. QAU-66. Brazilian Journal of Microbiology, 2014, 45, 603-611.	0.8	20
602	Identification of <i>Influenza A</i> /H7N9 Virus Infection-Related Human Genes Based on Shortest Paths in a Virus-Human Protein Interaction Network. BioMed Research International, 2014, 2014, 1-11.	0.9	14
603	Conservation and Diversification of Floral Homeotic MADS-box Genes in <i>Eustoma grandiflorum</i> . Japanese Society for Horticultural Science, 2014, 83, 172-180.	0.8	6
604	Synteny Approach of Drug Target Prediction among Unique Hypothetical Proteins of <i>Streptococcus Gordonii</i> ; Causing Infective Endocarditis. Science, Technology and Arts Research, 2014, 2, 34.	0.1	1
605	Molecular cloning and characterization of coumarin glucosyltransferase in hairy roots of <i>Pharbitis nil</i> ( <i>Ipomoea nil</i> ). Plant Biotechnology, 2014, 31, 21-28.	0.5	6
606	Cyanobacteriochrome SesA Is a Diguanylate Cyclase That Induces Cell Aggregation in <i>Thermosynechococcus</i> . Journal of Biological Chemistry, 2014, 289, 24801-24809.	1.6	103
607	Draft Genome Sequence of <i>Streptomyces iranensis</i> . Genome Announcements, 2014, 2, .	0.8	8
608	Concurrent transcriptional profiling of <i>Dirofilaria immitis</i> and its <i>Wolbachia</i> endosymbiont throughout the nematode life cycle reveals coordinated gene expression. BMC Genomics, 2014, 15, 1041.	1.2	33
609	Preliminary Investigation of Bottlenose Dolphins ( <i>Tursiops truncatus</i> ) for <i>hfe</i> -related Hemochromatosis. Journal of Wildlife Diseases, 2014, 50, 891-895.	0.3	5
610	Transposable element-assisted evolution and adaptation to host plant within the <i>Leptosphaeria maculans</i> - <i>Leptosphaeria biglobosa</i> species complex of fungal pathogens. BMC Genomics, 2014, 15, 891.	1.2	189
611	Structural and sequence diversity of the transposon Galileo in the <i>Drosophila willistoni</i> genome. BMC Genomics, 2014, 15, 792.	1.2	1
612	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . Genome Biology, 2014, 15, 459.	3.8	119
613	Genomic Organization, Transcriptomic Analysis, and Functional Characterization of Avian $\beta$ - and $\beta$ 2-Keratins in Diverse Feather Forms. Genome Biology and Evolution, 2014, 6, 2258-2273.	1.1	67
614	Genome Annotation and Curation Using MAKER and MAKER. Current Protocols in Bioinformatics, 2014, 48, 4.11.1-39.	25.8	543
615	Additional Bioinformatic Analyses Involving Protein Sequences. , 2014, , 183-207.		6
616	Mining Novel Effector Proteins from the Esophageal Gland Cells of <i>Meloidogyne incognita</i> . Molecular Plant-Microbe Interactions, 2014, 27, 965-974.	1.4	45
617	Sequencing and de novo assembly of a Dahlia hybrid cultivar transcriptome. Frontiers in Plant Science, 2014, 5, 340.	1.7	8

#	ARTICLE	IF	CITATIONS
618	A Lack of Parasitic Reduction in the Obligate Parasitic Green Alga <i>Helicosporidium</i> . <i>PLoS Genetics</i> , 2014, 10, e1004355.	1.5	57
619	CZT-1 Is a Novel Transcription Factor Controlling Cell Death and Natural Drug Resistance in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1091-1102.	0.8	16
620	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014, 5, 5443.	5.8	453
621	Draft Genome Sequences of Two Clinical Isolates of <i>Streptococcus mutans</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	1
622	AtTRB1 Mediates Structural Changes in AtPOT1b to Hold ssDNA. <i>ISRN Structural Biology</i> , 2014, 2014, 1-16.	1.3	2
623	Evolution and Comparative Genomics of <i>Campylobacter jejuni</i> ST-677 Clonal Complex. <i>Genome Biology and Evolution</i> , 2014, 6, 2424-2438.	1.1	21
624	Single Nucleus Genome Sequencing Reveals High Similarity among Nuclei of an Endomycorrhizal Fungus. <i>PLoS Genetics</i> , 2014, 10, e1004078.	1.5	238
625	Genome-Wide Tissue-Specific Gene Expression, Co-expression and Regulation of Co-expressed Genes in Adult Nematode <i>Ascaris suum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2678.	1.3	50
626	A Scalable and Accurate Targeted Gene Assembly Tool (SAT-Assembler) for Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003737.	1.5	31
627	Systems Biology Studies of Adult <i>Paragonimus</i> Lung Flukes Facilitate the Identification of Immunodominant Parasite Antigens. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e3242.	1.3	24
628	The Structure and Dynamics of BmR1 Protein from <i>Brugia malayi</i> : In Silico Approaches. <i>International Journal of Molecular Sciences</i> , 2014, 15, 11082-11099.	1.8	16
629	Genome of brown tide virus (AaV), the little giant of the Megaviridae, elucidates NCLDV genome expansion and host-virus coevolution. <i>Virology</i> , 2014, 466-467, 60-70.	1.1	86
630	SeqDepot: streamlined database of biological sequences and precomputed features. <i>Bioinformatics</i> , 2014, 30, 295-297.	1.8	10
631	Potential Conservation of Circadian Clock Proteins in the phylum Nematoda as Revealed by Bioinformatic Searches. <i>PLoS ONE</i> , 2014, 9, e112871.	1.1	13
632	Extracellular calcium triggers unique transcriptional programs and modulates staurosporine-induced cell death in <i>Neurospora crassa</i> . <i>Microbial Cell</i> , 2014, 1, 289-302.	1.4	8
633	Structural Comparison, Substrate Specificity, and Inhibitor Binding of AGPase Small Subunit from Monocot and Dicot: Present Insight and Future Potential. <i>BioMed Research International</i> , 2014, 2014, 1-20.	0.9	9
634	Draft Genome Sequence of the Toxic Bloom-Forming Cyanobacterium <i>Aphanizomenon flos-aquae</i> NIES-81. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
635	Draft Genome Sequences of Two Cellulolytic <i>Paenibacillus</i> sp. Strains, MAEPY1 and MAEPY2, from Malaysian Landfill Leachate. <i>Genome Announcements</i> , 2014, 2, .	0.8	6

#	ARTICLE	IF	CITATIONS
636	Draft Genome Sequence of <i>Bacillus thuringiensis</i> Strain LM1212, Isolated from the Cadaver of an <i>Oryctes gigas</i> Larva in Madagascar. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
637	<i>Saccharomyces</i> genome database provides new regulation data. <i>Nucleic Acids Research</i> , 2014, 42, D717-D725.	6.5	59
638	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
639	De Novo Whole-Genome Sequence and Genome Annotation of <i>Lichtheimia ramosa</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	27
640	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 1-10.	1.9	43
641	Draft Genome Sequence of Eggplant ( <i>Solanum melongena</i> L.): the Representative <i>Solanum</i> Species Indigenous to the Old World. <i>DNA Research</i> , 2014, 21, 649-660.	1.5	254
642	Transcriptomic response to estrogen exposure in the male Zhikong scallop, <i>Chlamys farreri</i> . <i>Marine Pollution Bulletin</i> , 2014, 89, 59-66.	2.3	7
643	<i>In silico</i> Characterization of an Atypical MAPK Phosphatase of <i>Plasmodium falciparum</i> as a Suitable Target for Drug Discovery. <i>Chemical Biology and Drug Design</i> , 2014, 84, 158-168.	1.5	6
644	Chorismate Pyruvate-Lyase and 4-Hydroxy-3-solaneylbenzoate Decarboxylase Are Required for Plastoquinone Biosynthesis in the Cyanobacterium <i>Synechocystis</i> sp. PCC6803. <i>Journal of Biological Chemistry</i> , 2014, 289, 2675-2686.	1.6	20
645	Molecular Mechanism of Nematophagous Fungi Infection of Nematodes. <i>Fungal Diversity Research Series</i> , 2014, , 263-311.	0.6	1
646	Draft Sequences of the Radish ( <i>Raphanus sativus</i> L.) Genome. <i>DNA Research</i> , 2014, 21, 481-490.	1.5	165
647	Proteomic Analysis of Solid Pseudopapillary Tumor of the Pancreas Reveals Dysfunction of the Endoplasmic Reticulum Protein Processing Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2593-2603.	2.5	87
648	BuT2 Is a Member of the Third Major Group of hAT Transposons and Is Involved in Horizontal Transfer Events in the Genus <i>Drosophila</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 352-365.	1.1	12
649	Comparison of environmental and isolate <i>Sulfobacillus</i> genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. <i>BMC Genomics</i> , 2014, 15, 1107.	1.2	65
650	Genomic characterisation of the effector complement of the potato cyst nematode <i>Globodera pallida</i> . <i>BMC Genomics</i> , 2014, 15, 923.	1.2	81
651	Complete genome determination and analysis of <i>Acholeplasma oculi</i> strain 19L, highlighting the loss of basic genetic features in the <i>Acholeplasmataceae</i> . <i>BMC Genomics</i> , 2014, 15, 931.	1.2	9
652	Comparative genomics for mycobacterial peptidoglycan remodelling enzymes reveals extensive genetic multiplicity. <i>BMC Microbiology</i> , 2014, 14, 75.	1.3	42
653	History of a prolific family: the Hes/Hey-related genes of the annelid <i>Platynereis</i> . <i>EvoDevo</i> , 2014, 5, 29.	1.3	21

#	ARTICLE	IF	CITATIONS
654	Leishmania braziliensis replication protein A subunit 1: molecular modelling, protein expression and analysis of its affinity for both DNA and RNA. Parasites and Vectors, 2014, 7, 573.	1.0	7
655	The Draft Assembly of the Radically Organized Stylonychia lemnae Macronuclear Genome. Genome Biology and Evolution, 2014, 6, 1707-1723.	1.1	58
656	Divergent and Conserved Elements Comprise the Chemoreceptive Repertoire of the Nonblood-Feeding Mosquito Toxorhynchites amboinensis. Genome Biology and Evolution, 2014, 6, 2883-2896.	1.1	31
657	Insights into organohalide respiration and the versatile catabolism of <i>ScpS</i> gained from comparative genomics and physiological studies. Environmental Microbiology, 2014, 16, 3562-3580.	1.8	76
658	Molecular Characterization of a Heterothallic Mating System in <i>Pseudogymnoascus destructans</i> , the Fungus Causing White-Nose Syndrome of Bats. G3: Genes, Genomes, Genetics, 2014, 4, 1755-1763.	0.8	41
659	Genome Sequence of Lactobacillus plantarum 19L3, a Strain Proposed as a Starter Culture for Slovensk Bryndza Ovine Cheese. Genome Announcements, 2014, 2, .	0.8	1
660	Analysis of Expressed Genes of the Bacterium â€Candidatus Phytoplasma Maliâ€™ Highlights Key Features of Virulence and Metabolism. PLoS ONE, 2014, 9, e94391.	1.1	29
661	Chromosomal Distribution of Cytonuclear Genes in a Dioecious Plant with Sex Chromosomes. Genome Biology and Evolution, 2014, 6, 2439-2443.	1.1	9
662	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau006-bau006.	1.4	64
663	Genome Sequencing of a Mung Bean Plant Growth Promoting Strain of <i>P. aeruginosa</i> with Biocontrol Ability. International Journal of Genomics, 2014, 2014, 1-10.	0.8	12
664	Small but Powerful, the Primary Endosymbiont of Moss Bugs, <i>Candidatus Evansia muelleri</i> , Holds a Reduced Genome with Large Biosynthetic Capabilities. Genome Biology and Evolution, 2014, 6, 1875-1893.	1.1	42
665	Mapping-by-Sequencing Identifies <i>HvPHYTOCHROME C</i> as a Candidate Gene for the <i>early maturity 5</i> Locus Modulating the Circadian Clock and Photoperiodic Flowering in Barley. Genetics, 2014, 198, 383-396.	1.2	102
666	Fighting a Losing Battle: Vigorous Immune Response Countered by Pathogen Suppression of Host Defenses in the Chytridiomycosis-Susceptible Frog <i>Atelopus zeteki</i> . G3: Genes, Genomes, Genetics, 2014, 4, 1275-1289.	0.8	95
667	Lynx: a database and knowledge extraction engine for integrative medicine. Nucleic Acids Research, 2014, 42, D1007-D1012.	6.5	40
668	Genome Comparison of <i>Candida orthopsilosis</i> Clinical Strains Reveals the Existence of Hybrids between Two Distinct Subspecies. Genome Biology and Evolution, 2014, 6, 1069-1078.	1.1	138
669	BBProF: An Asynchronous Application Server for Rapid Identification of Proteins Associated with Bacterial Bioleaching. Geomicrobiology Journal, 2014, 31, 299-314.	1.0	8
670	Whole genome comparison between table and wine grapes reveals a comprehensive catalog of structural variants. BMC Plant Biology, 2014, 14, 7.	1.6	115
671	Functional annotation of putative hypothetical proteins from <i>Candida dubliniensis</i> . Gene, 2014, 543, 93-100.	1.0	51

#	ARTICLE	IF	CITATIONS
672	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	9.4	166
673	Conservation and divergence in the frog immunome: pyrosequencing and de novo assembly of immune tissue transcriptomes. <i>Gene</i> , 2014, 542, 98-108.	1.0	26
674	High expression of MACC1 predicts poor prognosis in patients with osteosarcoma. <i>Tumor Biology</i> , 2014, 35, 1343-1350.	0.8	21
675	Genetic analysis of a type IV pili-like locus in the archaeon <i>Methanococcus maripaludis</i> . <i>Archives of Microbiology</i> , 2014, 196, 179-191.	1.0	11
676	In silico identification of transcription factors in <i>Medicago sativa</i> using available transcriptomic resources. <i>Molecular Genetics and Genomics</i> , 2014, 289, 457-468.	1.0	9
677	Comparative genomics of <i>Cylindrospermopsis raciborskii</i> strains with differential toxicities. <i>BMC Genomics</i> , 2014, 15, 83.	1.2	64
678	Hydrophobins are required for conidial hydrophobicity and plant root colonization in the fungal biocontrol agent <i>Clonostachys rosea</i> . <i>BMC Microbiology</i> , 2014, 14, 18.	1.3	66
679	Rapid identification of novel antigens of <i>Salmonella Enteritidis</i> by microarray-based immunoscreening. <i>Mikrochimica Acta</i> , 2014, 181, 1707-1714.	2.5	7
680	Two promising alkaline $\beta$ -glucosidases isolated by functional metagenomics from agricultural soil, including one showing high tolerance towards harsh detergents, oxidants and glucose. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 479-488.	1.4	34
681	Genome sequencing of high-penicillin producing industrial strain of <i>Penicillium chrysogenum</i> . <i>BMC Genomics</i> , 2014, 15, S11.	1.2	41
682	Comparative phylogenetic analysis of genome-wide Mlo gene family members from <i>Glycine max</i> and <i>Arabidopsis thaliana</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 345-359.	1.0	38
683	The transcriptome of the NZ endemic sea urchin <i>Kina</i> ( <i>Evechinus chloroticus</i> ). <i>BMC Genomics</i> , 2014, 15, 45.	1.2	22
684	Genome-wide single nucleotide polymorphism discovery and validation in adzuki bean. <i>Molecular Breeding</i> , 2014, 33, 497-501.	1.0	22
685	Identification of putative insulin-like peptides and components of insulin signaling pathways in parasitic platyhelminths by the use of genome-wide screening. <i>FEBS Journal</i> , 2014, 281, 877-893.	2.2	23
686	Structural insights into the MDP binding and CARD-CARD interaction in zebrafish ( <i>Danio rerio</i> ) NOD2: a molecular dynamics approach. <i>Journal of Molecular Recognition</i> , 2014, 27, 260-275.	1.1	38
687	Sulfur Oxidation Genes in Diverse Deep-Sea Viruses. <i>Science</i> , 2014, 344, 757-760.	6.0	223
688	Exploiting genes and functional diversity of chlorogenic acid and luteolin biosyntheses in <i>Lonicera japonica</i> and their substitutes. <i>Gene</i> , 2014, 534, 408-416.	1.0	53
689	Proteomic evaluation of citrate-coated silver nanoparticles toxicity in <i>Daphnia magna</i> . <i>Analyst</i> , The, 2014, 139, 1678-1686.	1.7	51

#	ARTICLE	IF	CITATIONS
690	Genetic variation of the whole <i>ICAM4</i> gene in Caucasians and African Americans. <i>Transfusion</i> , 2014, 54, 2315-2324.	0.8	6
691	Cloning and enzymatic characterization of four thermostable fungal endo-1,4- $\beta$ -xylanases. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3613-3628.	1.7	14
692	Stick Insect Genomes Reveal Natural Selection's Role in Parallel Speciation. <i>Science</i> , 2014, 344, 738-742.	6.0	386
693	The pea seedling mitochondrial $\beta$ -lysine acetylome. <i>Mitochondrion</i> , 2014, 19, 154-165.	1.6	47
694	Comprehensive analysis of CCCH-type zinc finger gene family in citrus (Clementine mandarin) by genome-wide characterization. <i>Molecular Genetics and Genomics</i> , 2014, 289, 855-872.	1.0	26
695	Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the Human Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 76-83.	1.8	13
696	Towards revealing the functions of all genes in plants. <i>Trends in Plant Science</i> , 2014, 19, 212-221.	4.3	221
697	MAKER-P: A Tool Kit for the Rapid Creation, Management, and Quality Control of Plant Genome Annotations. <i>Plant Physiology</i> , 2014, 164, 513-524.	2.3	412
698	MEGANTE: A Web-Based System for Integrated Plant Genome Annotation. <i>Plant and Cell Physiology</i> , 2014, 55, e2-e2.	1.5	27
699	InterProScan 5: genome-scale protein function classification. <i>Bioinformatics</i> , 2014, 30, 1236-1240.	1.8	6,553
700	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. <i>Journal of Molecular Evolution</i> , 2014, 79, 117-129.	0.8	23
701	Comparative Transcriptomic Analysis of Two Closely Related Ground Beetle Species with Marked Genital Divergence Using Pyrosequencing. <i>Zoological Science</i> , 2014, 31, 587.	0.3	5
702	Identification of Nucleotide-Level Changes Impacting Gene Content and Genome Evolution in Orthopoxviruses. <i>Journal of Virology</i> , 2014, 88, 13651-13668.	1.5	22
703	The AtCathB3 gene, encoding a cathepsin B-like protease, is expressed during germination of <i>Arabidopsis thaliana</i> and transcriptionally repressed by the basic leucine zipper protein GBF1. <i>Journal of Experimental Botany</i> , 2014, 65, 2009-2021.	2.4	25
704	A Root-Expressed <i>Phenylalanine:4-Hydroxyphenylpyruvate</i> Aminotransferase Is Required for Tropane Alkaloid Biosynthesis in <i>Atropa belladonna</i> . <i>Plant Cell</i> , 2014, 26, 3745-3762.	3.1	69
705	Comparative Analysis of the Secretome from a Model Filarial Nematode ( <i>Litomosoides sigmodontis</i> ) Reveals Maximal Diversity in Gravid Female Parasites. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2527-2544.	2.5	32
706	(Post-)Genomics approaches in fungal research. <i>Briefings in Functional Genomics</i> , 2014, 13, 424-439.	1.3	16
707	Structural and functional investigation of zebrafish ( <i>Danio rerio</i> ) NOD1 leucine rich repeat domain and its interaction with iE-DAP. <i>Molecular BioSystems</i> , 2014, 10, 2942-2953.	2.9	23



#	ARTICLE	IF	CITATIONS
708	Proteomic and genomic analysis reveals novel <i>Campylobacter jejuni</i> outer membrane proteins and potential heterogeneity. <i>EuPA Open Proteomics</i> , 2014, 4, 184-194.	2.5	11
709	EnsembleGASVR: a novel ensemble method for classifying missense single nucleotide polymorphisms. <i>Bioinformatics</i> , 2014, 30, 2324-2333.	1.8	17
710	Genome and transcriptome of the porcine whipworm <i>Trichuris suis</i> . <i>Nature Genetics</i> , 2014, 46, 701-706.	9.4	93
711	Comparative Genomic and Morphological Analyses of <i>Listeria</i> Phages Isolated from Farm Environments. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4616-4625.	1.4	72
712	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. <i>Nature Biotechnology</i> , 2014, 32, 1045-1052.	9.4	535
713	Nodes occupying central positions in human tissue specific PPI networks are enriched with many splice variants. <i>Proteomics</i> , 2014, 14, 2242-2248.	1.3	9
714	SP10 Infectivity Is Aborted after Bacteriophage SP10 Infection Induces <i>nonA</i> Transcription on the Prophage SP12 Region of the <i>Bacillus subtilis</i> Genome. <i>Journal of Bacteriology</i> , 2014, 196, 693-706.	1.0	12
715	Comparative Genomics of Flatworms (Platyhelminthes) Reveals Shared Genomic Features of Ecto- and Endoparasitic Neodermata. <i>Genome Biology and Evolution</i> , 2014, 6, 1105-1117.	1.1	73
716	Expansion of banana ( <i>Musa acuminata</i> ) gene families involved in ethylene biosynthesis and signalling after lineage-specific whole-genome duplications. <i>New Phytologist</i> , 2014, 202, 986-1000.	3.5	47
717	An integrative computational model for large-scale identification of metalloproteins in microbial genomes: a focus on iron-sulfur cluster proteins. <i>Metallomics</i> , 2014, 6, 1913-1930.	1.0	20
718	The diversity of rice phytocystatins. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1321-1330.	1.0	12
719	Infection routes matter in population-specific responses of the red flour beetle to the entomopathogen <i>Bacillus thuringiensis</i> . <i>BMC Genomics</i> , 2014, 15, 445.	1.2	60
720	Quantitative proteomics and transcriptomics of potato in response to <i>Phytophthora infestans</i> in compatible and incompatible interactions. <i>BMC Genomics</i> , 2014, 15, 497.	1.2	77
721	Compositions of fungal secretomes indicate a greater impact of phylogenetic history than lifestyle adaptation. <i>BMC Genomics</i> , 2014, 15, 722.	1.2	70
722	The pathogenesis-related protein PR-4b from <i>Theobroma cacao</i> presents RNase activity, Ca <sup>2+</sup> and Mg <sup>2+</sup> dependent-DNase activity and antifungal action on <i>Monilophthora perniciosa</i> . <i>BMC Plant Biology</i> , 2014, 14, 161.	1.6	36
723	Proteomic Identification of a Candidate Sequence of Wheat Cytokinin-Binding Protein 1. <i>Journal of Plant Growth Regulation</i> , 2014, 33, 896-902.	2.8	8
724	Molecular characterization of the hippeastrum chlorotic ringspot virus L segment and its protein. <i>Archives of Virology</i> , 2014, 159, 2805-2807.	0.9	8
725	Molecular cloning and characterization of cDNA encoding a Translocon-Associated Protein (TRAP1) from the root-lesion nematode <i>Pratylenchus goodeyi</i> . <i>European Journal of Plant Pathology</i> , 2014, 139, 289.	0.8	1

#	ARTICLE	IF	CITATIONS
726	Genome-Wide Analysis and Expression Patterns of NAC Transcription Factor Family Under Different Developmental Stages and Abiotic Stresses in Chinese Cabbage. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 1041-1056.	1.0	55
727	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
728	Identification and characterization of alternative splicing in parasitic nematode transcriptomes. <i>Parasites and Vectors</i> , 2014, 7, 151.	1.0	10
729	Rediscovering Medicinal Plants' Potential with OMICS: Microsatellite Survey in Expressed Sequence Tags of Eleven Traditional Plants with Potent Antidiabetic Properties. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 298-309.	1.0	20
730	Isolation, Characterization and Immunolocalization of a Seed Dominant CaM from Finger Millet ( <i>Eleusine coracana</i> L. Gartn.) for Studying Its Functional Role in Differential Accumulation of Calcium in Developing Grains. <i>Applied Biochemistry and Biotechnology</i> , 2014, 172, 2955-2973.	1.4	36
731	Characteristics of the new plasmid, pMTB1, from the metagenome of the microbial community of underground thermal waters of Western Siberia. <i>Biology Bulletin</i> , 2014, 41, 223-227.	0.1	0
732	Dramatic expansion of the black widow toxin arsenal uncovered by multi-tissue transcriptomics and venom proteomics. <i>BMC Genomics</i> , 2014, 15, 366.	1.2	93
733	RNA sequencing on <i>Solanum lycopersicum</i> trichomes identifies transcription factors that activate terpene synthase promoters. <i>BMC Genomics</i> , 2014, 15, 402.	1.2	123
734	Insights into naturally minimised <i>Streptomyces albus</i> J1074 genome. <i>BMC Genomics</i> , 2014, 15, 97.	1.2	137
735	Genetic architecture of rind penetrometer resistance in two maize recombinant inbred line populations. <i>BMC Plant Biology</i> , 2014, 14, 152.	1.6	41
736	A Sco protein among the hypothetical proteins of <i>Bacillus lehensis</i> G1: Its 3D macromolecular structure and association with Cytochrome C Oxidase. <i>BMC Structural Biology</i> , 2014, 14, 11.	2.3	3
737	In silico identification, structural characterization, and phylogenetic analysis of MdesDEF-2: a novel defensin from the Hessian fly, <i>Mayetiola destructor</i> . <i>Journal of Molecular Modeling</i> , 2014, 20, 2339.	0.8	15
738	Prohibitin 2 Regulates Cell Proliferation and Mitochondrial Cristae Morphogenesis in Planarian Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2014, 10, 871-887.	5.6	32
739	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. <i>DNA Research</i> , 2014, 21, 169-181.	1.5	201
740	Anthocyanins from buds of <i>Lonicera japonica</i> Thunb. var. <i>chinensis</i> (Wats.) Bak.. <i>Food Research International</i> , 2014, 62, 812-818.	2.9	13
741	A comparative genomic analysis of the alkali-tolerant soil bacterium <i>Bacillus lehensis</i> G1. <i>Gene</i> , 2014, 545, 253-261.	1.0	10
742	Comparative genomics of oral isolates of <i>Streptococcus mutans</i> by in silico genome subtraction does not reveal accessory DNA associated with severe early childhood caries. <i>Infection, Genetics and Evolution</i> , 2014, 21, 269-278.	1.0	18
743	The predicted secretomes of <i>Monosiga brevicollis</i> and <i>Capsaspora owczarzaki</i> , close unicellular relatives of metazoans, reveal new insights into the evolution of the metazoan extracellular matrix. <i>Matrix Biology</i> , 2014, 37, 60-68.	1.5	27

#	ARTICLE	IF	CITATIONS
744	Unique Features of the Loblolly Pine ( <i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
745	Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in <i>Emiliana huxleyi</i> . <i>BMC Genomics</i> , 2014, 15, 148.	1.2	31
746	Whipworm genome and dual-species transcriptome analyses provide molecular insights into an intimate host-parasite interaction. <i>Nature Genetics</i> , 2014, 46, 693-700.	9.4	139
747	The first set of expressed sequence tags (EST) from the medicinal mushroom <i>Agaricus subrufescens</i> delivers resource for gene discovery and marker development. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7879-7892.	1.7	13
748	Omics and the Future of Sustainable Biomaterials. <i>ACS Symposium Series</i> , 2014, , 59-79.	0.5	3
749	Genome-wide identification and expression pattern of drought-responsive members of the NAC family in maize. <i>Meta Gene</i> , 2014, 2, 407-417.	0.3	109
750	Transcriptomic responses to heat stress and nickel in the mussel <i>Mytilus galloprovincialis</i> . <i>Aquatic Toxicology</i> , 2014, 148, 104-112.	1.9	31
751	Functional analysis of the C-II subgroup killer toxin-like chitinases in the filamentous ascomycete <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2014, 64, 58-66.	0.9	18
752	Predicting genome-scale <i>Arabidopsis-Pseudomonas syringae</i> interactome using domain and interolog-based approaches. <i>BMC Bioinformatics</i> , 2014, 15, S13.	1.2	41
753	Draft Genome Sequence of <i>Vibrio fortis</i> Dalian14 Isolated from Diseased Sea Urchin ( <i>Tytocheilus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 382 0,8	0,8	7
754	Genomic and expression analysis of transition proteins in <i>Drosophila</i> . <i>Spermatogenesis</i> , 2015, 5, e1178518.	0.8	5
755	Identification, molecular characterization and expression analysis of <i>RPL24</i> genes in three Cucurbitaceae family members: cucumber, melon and watermelon. <i>Biotechnology and Biotechnological Equipment</i> , 2015, 29, 1024-1034.	0.5	12
756	The first whole genome and transcriptome of the cinereous vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution between the Old and New World vultures. <i>Genome Biology</i> , 2015, 16, 215.	3.8	41
757	Biocuration: A New Challenge for the Tunicate Community. <i>Genesis</i> , 2015, 53, 132-142.	0.8	10
758	Pyrosequencing and de novo assembly of Antarctic krill ( <i>Euphausia superba</i> ) transcriptome to study the adaptability of krill to climate-induced environmental changes. <i>Molecular Ecology Resources</i> , 2015, 15, 1460-1471.	2.2	30
759	Genome analysis of Excretory/Secretory proteins in <i>Taenia solium</i> reveals their Abundance of Antigenic Regions (AAR). <i>Scientific Reports</i> , 2015, 5, 9683.	1.6	54
760	Computational discovery of small open reading frames in <i>Bacillus lehensis</i> . <i>AIP Conference Proceedings</i> , 2015, , .	0.3	0
761	Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. <i>Royal Society Open Science</i> , 2015, 2, 150377.	1.1	21

#	ARTICLE	IF	CITATIONS
762	The fate of recent duplicated genes following a fourth-round whole genome duplication in a tetraploid fish, common carp ( <i>Cyprinus carpio</i> ). <i>Scientific Reports</i> , 2015, 5, 8199.	1.6	60
763	Transcriptional profiling of predator-induced phenotypic plasticity in <i>Daphnia pulex</i> . <i>Frontiers in Zoology</i> , 2015, 12, 18.	0.9	32
764	Genome analysis of <i>Daldinia eschscholtzii</i> strains UM 1400 and UM 1020, wood-decaying fungi isolated from human hosts. <i>BMC Genomics</i> , 2015, 16, 966.	1.2	16
765	Draft Genome Sequence and Gene Annotation of <i>Stemphylium lycopersici</i> Strain CIDEFI-216. <i>Genome Announcements</i> , 2015, 3, .	0.8	18
766	Transcription analysis of neonicotinoid resistance in Mediterranean (MED) populations of <i>B. tabaci</i> reveal novel cytochrome P450s, but no nAChR mutations associated with the phenotype. <i>BMC Genomics</i> , 2015, 16, 939.	1.2	59
767	De novo transcriptome assembly and analysis of Sf21 cells using illumina paired end sequencing. <i>Biology Direct</i> , 2015, 10, 44.	1.9	15
768	An Integrated Multiomics Approach to Identify Candidate Antigens for Serodiagnosis of Human Onchocerciasis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3224-3233.	2.5	12
769	Enzymatic Transformations Involved in the Biosynthesis of Microbial Exopolysaccharides Based on the Assembly of Repeat Units. <i>ChemBioChem</i> , 2015, 16, 1141-1147.	1.3	38
770	Selection of recombinant anti- <i>SH3</i> domain antibodies by high-throughput phage display. <i>Protein Science</i> , 2015, 24, 1890-1900.	3.1	15
771	A population genomic scan in <i>Chorthippus</i> grasshoppers unveils previously unknown phenotypic divergence. <i>Molecular Ecology</i> , 2015, 24, 3918-3930.	2.0	25
772	SBMDb: first whole genome putative microsatellite DNA marker database of sugarbeet for bioenergy and industrial applications. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav111.	1.4	7
773	Temperature- and sex-related effects of serine protease alleles on larval development in the Glanville fritillary butterfly. <i>Journal of Evolutionary Biology</i> , 2015, 28, 2224-2235.	0.8	14
774	PTGBase: an integrated database to study tandem duplicated genes in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	46
775	Full-length <i>de novo</i> assembly of RNA-seq data in pea ( <i>Pisum sativum</i> L.) provides a gene expression atlas and gives insights into root nodulation in this species. <i>Plant Journal</i> , 2015, 84, 1-19.	2.8	173
776	Draft Genome Sequence of the Fungus <i>Penicillium brasilianum</i> MG11. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
777	Cloning and Expression Analysis of <i>Vlcc3</i> , a Novel and Functional Laccase Gene Possibly Involved in Stipe Elongation. <i>International Journal of Molecular Sciences</i> , 2015, 16, 28498-28509.	1.8	11
778	Transcriptome Characterization for Non-Model Endangered Lycaenids, <i>Protantigius superans</i> and <i>Spindasis takanosis</i> , Using Illumina HiSeq 2500 Sequencing. <i>International Journal of Molecular Sciences</i> , 2015, 16, 29948-29970.	1.8	13
779	Accumulation of Phosphorus-Containing Compounds in Developing Seeds of Low-Phytate Pea ( <i>Pisum</i> ) Tj ETQq1 1 Q.784314 rgBT /Over	1.6	22

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780	Genome-wide DNA methylation analysis of <i>Haloferax volcanii</i> H26 and identification of DNA methyltransferase related PD-(D/E)XK nuclease family protein HVO_A0006. <i>Frontiers in Microbiology</i> , 2015, 6, 251.	1.5	28
781	Comparative genomics reveals diversified CRISPR-Cas systems of globally distributed <i>Microcystis aeruginosa</i> , a freshwater bloom-forming cyanobacterium. <i>Frontiers in Microbiology</i> , 2015, 6, 394.	1.5	58
782	Direct sequencing of human gut virome fractions obtained by flow cytometry. <i>Frontiers in Microbiology</i> , 2015, 6, 955.	1.5	18
783	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015, 6, 978.	1.5	83
784	Nmf9 Encodes a Highly Conserved Protein Important to Neurological Function in Mice and Flies. <i>PLoS Genetics</i> , 2015, 11, e1005344.	1.5	11
785	In Silico/In Vivo Insights into the Functional and Evolutionary Pathway of <i>Pseudomonas aeruginosa</i> Oleate-Diol Synthase. Discovery of a New Bacterial Di-Heme Cytochrome C Peroxidase Subfamily. <i>PLoS ONE</i> , 2015, 10, e0131462.	1.1	11
786	A cupin domain-containing protein with a quercetinase activity (VdQase) regulates <i>Verticillium dahliae</i> 's pathogenicity and contributes to counteracting host defenses. <i>Frontiers in Plant Science</i> , 2015, 6, 440.	1.7	23
787	Foxtail Millet NF-Y Families: Genome-Wide Survey and Evolution Analyses Identified Two Functional Genes Important in Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2015, 6, 1142.	1.7	73
788	Developing of the Computer Method for Annotation of Bacterial Genes. <i>Advances in Bioinformatics</i> , 2015, 2015, 1-9.	5.7	15
789	Inside the Pan-genome - Methods and Software Overview. <i>Current Genomics</i> , 2015, 16, 245-252.	0.7	79
790	High quality reference genome of drumstick tree ( <i>Moringa oleifera</i> Lam.), a potential perennial crop. <i>Science China Life Sciences</i> , 2015, 58, 627-638.	2.3	53
791	Analysis of protein expression changes of the Vero E6 cells infected with classic PEDV strain CV777 by using quantitative proteomic technique. <i>Journal of Virological Methods</i> , 2015, 218, 27-39.	1.0	44
792	Inferring bona fide transfrags in RNA-Seq derived-transcriptome assemblies of non-model organisms. <i>BMC Bioinformatics</i> , 2015, 16, 58.	1.2	7
793	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. <i>New Phytologist</i> , 2015, 208, 1227-1240.	3.5	165
794	OsTCTP, encoding a translationally controlled tumor protein, plays an important role in mercury tolerance in rice. <i>BMC Plant Biology</i> , 2015, 15, 123.	1.6	34
795	NCBI-compliant genome submissions: tips and tricks to save time and money: Table 1. <i>Briefings in Bioinformatics</i> , 2015, 18, bbv104.	3.2	14
796	Draft Genome Sequences of Five Spore-Forming Food Isolates of <i>Bacillus pumilus</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	3
797	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <i>Nature</i> , 2015, 527, 508-511.	13.7	291

#	ARTICLE	IF	CITATIONS
798	Identification of novel and differentially expressed microRNAs in ovine ovary and testis tissues using Solexa sequencing and bioinformatics. <i>Journal of Integrative Agriculture</i> , 2015, 14, 1604-1616.	1.7	2
799	Deciphering Genome Content and Evolutionary Relationships of Isolates from the Fungus <i>Magnaporthe oryzae</i> Attacking Different Host Plants. <i>Genome Biology and Evolution</i> , 2015, 7, 2896-2912.	1.1	96
800	Molecular inhibition of telomerase recruitment using designer peptides: an in silico approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 1442-1459.	2.0	1
801	RNA-Seq analysis of rye-grass transcriptomic response to an herbicide inhibiting acetolactate-synthase identifies transcripts linked to non-target-site-based resistance. <i>Plant Molecular Biology</i> , 2015, 87, 473-487.	2.0	115
802	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	0.9	141
803	Genome-wide identification and expression analysis of TCP transcription factors in <i>Gossypium raimondii</i> . <i>Scientific Reports</i> , 2014, 4, 6645.	1.6	90
804	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015, 5, 8069.	1.6	144
805	Draft Genome Sequence and Gene Annotation of the Entomopathogenic Fungus <i>Verticillium hemipterigenum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	1
806	PLAZA 3.0: an access point for plant comparative genomics. <i>Nucleic Acids Research</i> , 2015, 43, D974-D981.	6.5	329
807	The phage growth limitation system in <i>Streptomyces coelicolor</i> A(3)2 is a toxin/antitoxin system, comprising enzymes with DNA methyltransferase, protein kinase and ATPase activity. <i>Virology</i> , 2015, 477, 100-109.	1.1	47
808	Defining the transcriptomic landscape of <i>Candida glabrata</i> by RNA-Seq. <i>Nucleic Acids Research</i> , 2015, 43, 1392-1406.	6.5	74
809	Structure-based functional annotation of hypothetical proteins from <i>Candida dubliniensis</i> : a quest for potential drug targets. <i>3 Biotech</i> , 2015, 5, 561-576.	1.1	27
810	Homocitrate Synthase Expression and Lysine Content in Fruiting Body of Different Developmental Stages in <i>Flammulina velutipes</i> . <i>Current Microbiology</i> , 2015, 70, 821-828.	1.0	15
811	Presence of a plant-like proton-translocating pyrophosphatase in a scuticociliate parasite and its role as a possible drug target. <i>Parasitology</i> , 2015, 142, 449-462.	0.7	15
812	Genomic characterization of a temperate phage of the psychrotolerant deep-sea bacterium <i>Aurantimonas</i> sp.. <i>Extremophiles</i> , 2015, 19, 49-58.	0.9	15
813	The Lipoxygenase Gene Family in Poplar: Identification, Classification, and Expression in Response to MeJA Treatment. <i>PLoS ONE</i> , 2015, 10, e0125526.	1.1	57
814	Eighteen New Candidate Effectors of the Phytonematode <i>Heterodera glycines</i> Produced Specifically in the Secretory Esophageal Gland Cells During Parasitism. <i>Phytopathology</i> , 2015, 105, 1362-1372.	1.1	57
815	The barber's pole worm CAP protein superfamily – A basis for fundamental discovery and biotechnology advances. <i>Biotechnology Advances</i> , 2015, 33, 1744-1754.	6.0	16

#	ARTICLE	IF	CITATIONS
816	Functional Operons in Secondary Metabolic Gene Clusters in <i>Glarea lozoyensis</i> (Fungi). <i>Trends in Microbiology</i> , 2015, 23, 107-115.	1.8	15
817	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015, 33, 980-991.	6.0	21
818	Pan-Nematoda Transcriptomic Elucidation of Essential Intestinal Functions and Therapeutic Targets With Broad Potential. <i>EBioMedicine</i> , 2015, 2, 1079-1089.	2.7	20
819	Identification and genomic analysis of temperate <i>Pseudomonas</i> bacteriophage PstS-1 from the Japan trench at a depth of 7000 m. <i>Research in Microbiology</i> , 2015, 166, 668-676.	1.0	12
820	New Insight into Microbial Iron Oxidation as Revealed by the Proteomic Profile of an Obligate Iron-Oxidizing Chemolithoautotroph. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5927-5937.	1.4	134
821	Towards New Drug Targets? Function Prediction of Putative Proteins of <i>Neisseria meningitidis</i> MC58 and Their Virulence Characterization. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 416-434.	1.0	18
822	Identification of functional candidates amongst hypothetical proteins of <i>Mycobacterium leprae</i> Br4923, a causative agent of leprosy. <i>Genome</i> , 2015, 58, 25-42.	0.9	16
823	A transcriptomic analysis of the response of the arctic pteropod <i>Limacina helicina</i> to carbon dioxide-driven seawater acidification. <i>Polar Biology</i> , 2015, 38, 1727-1740.	0.5	33
824	Purification and characterization of CHpro1, a thermotolerant, alkali-stable and oxidation-resisting protease of Chumathang hot spring. <i>Science Bulletin</i> , 2015, 60, 1252-1260.	4.3	18
825	An expressed sequence tags analysis for leaves of Chinese milk vetch ( <i>Astragalus sinicus</i> ). <i>Legume Research</i> , 2015, 38, 1.	0.0	4
826	Genome-wide analysis of phylogeny, expression profile and sub-cellular localization of SKP1-Like genes in wild tomato. <i>Plant Science</i> , 2015, 238, 105-114.	1.7	33
827	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
828	Evolutionary analysis of the global landscape of protein domain types and domain architectures associated with family 14 carbohydrate-binding modules. <i>FEBS Letters</i> , 2015, 589, 1813-1818.	1.3	5
829	A novel salt-tolerant chitinase discovered by genetic screening of a metagenomic library derived from chitin-amended agricultural soil. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8199-8215.	1.7	20
830	The WRKY Transcription Factor Genes in Eggplant ( <i>Solanum melongena</i> L.) and Turkey Berry ( <i>Solanum</i> ). <i>Trends in Microbiology</i> , 2015, 23, 107-115.	1.8	23
831	Computational approaches for prediction of pathogen-host protein-protein interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 94.	1.5	96
832	The EMBL-EBI bioinformatics web and programmatic tools framework. <i>Nucleic Acids Research</i> , 2015, 43, W580-W584.	6.5	934
833	Molecular and functional characterization of porcine Siglec-3/CD33 and analysis of its expression in blood and tissues. <i>Developmental and Comparative Immunology</i> , 2015, 51, 238-250.	1.0	12

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834	Allele Mining in Solanum Germplasm: Cloning and Characterization of RB-Homologous Gene Fragments from Late Blight Resistant Wild Potato Species. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1584-1598.	1.0	27
835	Small-Scale duplication as a genomic signature for crop improvement. <i>Journal of Crop Science and Biotechnology</i> , 2015, 18, 45-51.	0.7	2
836	Structure-based function analysis of putative conserved proteins with isomerase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 741-763.	1.1	14
837	More than Skin Deep: Functional Genomic Basis for Resistance to Amphibian Chytridiomycosis. <i>Genome Biology and Evolution</i> , 2015, 7, 286-298.	1.1	110
838	Defining the gene repertoire and spatiotemporal expression profiles of adhesion G protein-coupled receptors in zebrafish. <i>BMC Genomics</i> , 2015, 16, 62.	1.2	31
839	Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes. <i>BMC Genomics</i> , 2015, 16, 141.	1.2	105
840	The genome of the basal agaricomycete <i>Xanthophyllomyces dendrorhous</i> provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. <i>BMC Genomics</i> , 2015, 16, 233.	1.2	47
841	Transcriptome responses to <i>Ralstonia solanacearum</i> infection in the roots of the wild potato <i>Solanum commersonii</i> . <i>BMC Genomics</i> , 2015, 16, 246.	1.2	85
842	Chemosensory genes identified in the antennal transcriptome of the blowfly <i>Calliphora stygia</i> . <i>BMC Genomics</i> , 2015, 16, 255.	1.2	58
843	AtEAF1 is a potential platform protein for Arabidopsis NuA4 acetyltransferase complex. <i>BMC Plant Biology</i> , 2015, 15, 75.	1.6	59
844	WallProtDB, a database resource for plant cell wall proteomics. <i>Plant Methods</i> , 2015, 11, 2.	1.9	70
845	The draft genome of <i>Primula veris</i> yields insights into the molecular basis of heterostyly. <i>Genome Biology</i> , 2015, 16, 12.	3.8	96
846	Transcriptome of an entomophthoralean fungus ( <i>Pandora formicae</i> ) shows molecular machinery adjusted for successful host exploitation and transmission. <i>Journal of Invertebrate Pathology</i> , 2015, 128, 47-56.	1.5	42
847	The floral transcriptome of ylang ylang ( <i>Cananga odorata</i> var. <i>fruticosa</i> ) uncovers biosynthetic pathways for volatile organic compounds and a multifunctional and novel sesquiterpene synthase. <i>Journal of Experimental Botany</i> , 2015, 66, 3959-3975.	2.4	50
848	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
849	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.	1.1	39
850	The multigene family of fungal laccases and their expression in the white rot basidiomycete <i>Flammulina velutipes</i> . <i>Gene</i> , 2015, 563, 142-149.	1.0	60
851	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	4.4	35



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852	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	13.7	995
853	Identification of the transcriptionally active cytochrome P450 repertoire in <i>Coffea arabica</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 2399-2412.	0.3	4
854	The goose genome sequence leads to insights into the evolution of waterfowl and susceptibility to fatty liver. <i>Genome Biology</i> , 2015, 16, 89.	3.8	98
855	Patterns of Evolutionary Conservation of Ascorbic Acid-Related Genes Following Whole-Genome Triplication in <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 299-313.	1.1	18
856	Functional Exposed Amino Acids of BauA as Potential Immunogen Against <i>Acinetobacter baumannii</i> . <i>Acta Biotheoretica</i> , 2015, 63, 129-149.	0.7	30
857	The Accordant Trend of Both Parameters (rgs Expression and cAMP Content) Follows the Pattern of Development of Fruiting Body in <i>Volvariella volvacea</i> . <i>Current Microbiology</i> , 2015, 71, 579-584.	1.0	8
858	RNA-seq-Based Gene Annotation and Comparative Genomics of Four Fungal Grass Pathogens in the Genus <i>Zymoseptoria</i> Identify Novel Orphan Genes and Species-Specific Invasions of Transposable Elements. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1323-1333.	0.8	122
859	Characterization of fossilized relatives of the White Spot Syndrome Virus in genomes of decapod crustaceans. <i>BMC Evolutionary Biology</i> , 2015, 15, 142.	3.2	14
860	The venomous cocktail of the vampire snail <i>Colubraria reticulata</i> (Mollusca, Gastropoda). <i>BMC Genomics</i> , 2015, 16, 441.	1.2	41
861	Genomic Foundation of Starch-to-Lipid Switch in Oleaginous <i>Chlorella</i> spp.. <i>Plant Physiology</i> , 2015, 169, 2444-2461.	2.3	111
862	Survey of genome sequences in a wild sweet potato, <i>Ipomoea trifida</i> (H. B. K.) G. Don. <i>DNA Research</i> , 2015, 22, 171-179.	1.5	107
863	ALOMYbase, a resource to investigate non-target-site-based resistance to herbicides inhibiting acetolactate-synthase (ALS) in the major grass weed <i>Alopecurus myosuroides</i> (black-grass). <i>BMC Genomics</i> , 2015, 16, 590.	1.2	66
864	The Genome of Winter Moth ( <i>Operophtera brumata</i> ) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. <i>Genome Biology and Evolution</i> , 2015, 7, 2321-2332.	1.1	70
865	Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. <i>Nature Communications</i> , 2015, 6, 8322.	5.8	488
866	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12628-12640.	4.6	72
867	Chitinase from <i>Thermomyces lanuginosus</i> SSBP and its biotechnological applications. <i>Extremophiles</i> , 2015, 19, 1055-1066.	0.9	42
868	Caste biases in gene expression are specific to developmental stage in the ant <i>Formica exsecta</i> . <i>Journal of Evolutionary Biology</i> , 2015, 28, 1705-1718.	0.8	28
869	Comparative transcriptomics unravel biochemical specialization of leaf tissues of <i>Stevia</i> ( <i>Stevia</i> ) Tj ETQq1 1 0.784314 rgBT /Qyerlock 10	2.3	17

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870	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. <i>Genome Biology and Evolution</i> , 2015, 7, 2781-2798.	1.1	16
871	Dissecting the fungal biology of <i>Bipolaris papendorffii</i> : from phylogenetic to comparative genomic analysis. <i>DNA Research</i> , 2015, 22, 219-232.	1.5	29
872	Differential expression of the chemosensory transcriptome in two populations of the stemborer <i>Sesamia nonagrioides</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2015, 65, 28-34.	1.2	16
873	Comparative Genomics of Environmental and Clinical <i>Stenotrophomonas maltophilia</i> Strains with Different Antibiotic Resistance Profiles. <i>Genome Biology and Evolution</i> , 2015, 7, 2484-2505.	1.1	90
874	Genome-wide identification, expression profiling, and SSR marker development of the bZIP transcription factor family in <i>Medicago truncatula</i> . <i>Biochemical Systematics and Ecology</i> , 2015, 61, 218-228.	0.6	30
875	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
876	<i>Gekko japonicus</i> genome reveals evolution of adhesive toe pads and tail regeneration. <i>Nature Communications</i> , 2015, 6, 10033.	5.8	142
877	â€Candidatus <i>Phytoplasma phoenicium</i> â€™ associated with almond witchesâ€™-broom disease: from draft genome to genetic diversity among strain populations. <i>BMC Microbiology</i> , 2015, 15, 148.	1.3	38
878	Origin and Diversification of a Salamander Sex Pheromone System. <i>Molecular Biology and Evolution</i> , 2015, 32, 472-480.	3.5	34
879	Overexpression of two ATNAC3-related genes improves drought and salt tolerance in tomato ( <i>Solanum lycopersicum</i> L.). <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 120, 989-1001.	1.2	24
880	Sinbase: An Integrated Database to Study Genomics, Genetics and Comparative Genomics in <i>Sesamum indicum</i> . <i>Plant and Cell Physiology</i> , 2015, 56, e2-e2.	1.5	46
881	Molecular principles of human virus proteinâ€“protein interactions. <i>Bioinformatics</i> , 2015, 31, 1025-1033.	1.8	41
882	Genomic and transcriptome analyses reveal that MAPK- and phosphatidylinositol-signaling pathways mediate tolerance to 5-hydroxymethyl-2-furaldehyde for industrial yeast <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2014, 4, 6556.	1.6	45
883	Genome wide in silico characterization of Dof gene families of pigeonpea ( <i>Cajanus cajan</i> (L) Millsp.). <i>Molecular Biology Reports</i> , 2015, 42, 535-552.	1.0	31
884	Outer membrane vesicles are vehicles for the delivery of <i>Vibrio tasmaniensis</i> virulence factors to oyster immune cells. <i>Environmental Microbiology</i> , 2015, 17, 1152-1165.	1.8	75
885	Structure-based functional annotation of putative conserved proteins having lyase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 317-336.	1.1	15
886	A near complete snapshot of the <i>Zea mays</i> seedling transcriptome revealed from ultra-deep sequencing. <i>Scientific Reports</i> , 2015, 4, 4519.	1.6	28
887	RGAugury: a pipeline for genome-wide prediction of resistance gene analogs (RGAs) in plants. <i>BMC Genomics</i> , 2016, 17, 852.	1.2	162

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888	RNA-Seq analysis reveals new evidence for inflammation-related changes in aged kidney. <i>Oncotarget</i> , 2016, 7, 30037-30048.	0.8	14
889	De novo Transcriptome Generation and Annotation for Two Korean Endemic Land Snails, <i>Aegista chejuensis</i> and <i>Aegista quepartensis</i> , Using Illumina Paired-End Sequencing Technology. <i>International Journal of Molecular Sciences</i> , 2016, 17, 379.	1.8	7
890	Identification and characterisation of Mlo genes in pea ( <i>Pisum sativum</i> L.)vis-À-vis validation of Mlo gene-specific markers. <i>Turkish Journal of Biology</i> , 2016, 40, 184-195.	2.1	10
891	Analyses of <i>Physcomitrella patens</i> Ankyrin Repeat Proteins by Computational Approach. <i>Molecular Biology International</i> , 2016, 2016, 1-8.	1.7	1
892	A Survey of the Gene Repertoire of <i>Gigaspora rosea</i> Unravels Conserved Features among Glomeromycota for Obligate Biotrophy. <i>Frontiers in Microbiology</i> , 2016, 7, 233.	1.5	113
893	Characterization and Comparative Overview of Complete Sequences of the First Plasmids of <i>Pandoraea</i> across Clinical and Non-clinical Strains. <i>Frontiers in Microbiology</i> , 2016, 7, 1606.	1.5	4
894	Diversity of the Germination Apparatus in <i>Clostridium botulinum</i> Groups I, II, III, and IV. <i>Frontiers in Microbiology</i> , 2016, 7, 1702.	1.5	25
895	Cytosolic Proteome Profiling of Aminoglycosides Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolates Using MALDI-TOF/MS. <i>Frontiers in Microbiology</i> , 2016, 7, 1816.	1.5	35
896	Aerobic Lineage of the Oxidative Stress Response Protein Rubrerythrin Emerged in an Ancient Microaerobic, (Hyper)Thermophilic Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1822.	1.5	38
897	A Jacalin-Related Lectin Regulated the Formation of Aerial Mycelium and Fruiting Body in <i>Flammulina velutipes</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1884.	1.8	17
898	De Novo Sequencing and Transcriptome Analysis of <i>Pleurotus eryngii</i> subsp. <i>tuoliensis</i> (Bailinggu) Mycelia in Response to Cold Stimulation. <i>Molecules</i> , 2016, 21, 560.	1.7	48
899	Conservation and diversification of the transcriptomes of adult <i>Paragonimus westermani</i> and <i>P. skrjabini</i> . <i>Parasites and Vectors</i> , 2016, 9, 497.	1.0	10
900	Genome Anatomy of <i>Pyrenochaeta unguis-hominis</i> UM 256, a Multidrug Resistant Strain Isolated from Skin Scraping. <i>PLoS ONE</i> , 2016, 11, e0162095.	1.1	9
901	Characterization and Genomic Study of the Novel Bacteriophage HY01 Infecting Both <i>Escherichia coli</i> O157:H7 and <i>Shigella flexneri</i> : Potential as a Biocontrol Agent in Food. <i>PLoS ONE</i> , 2016, 11, e0168985.	1.1	59
902	De Novo Transcriptome Analysis of the Common New Zealand Stick Insect <i>Clitarchus hookeri</i> (Phasmatodea) Reveals Genes Involved in Olfaction, Digestion and Sexual Reproduction. <i>PLoS ONE</i> , 2016, 11, e0157783.	1.1	18
903	Genomic Analyses of <i>Cladophialophora bantiana</i> , a Major Cause of Cerebral Phaeohyphomycosis Provides Insight into Its Lifestyle, Virulence and Adaption in Host. <i>PLoS ONE</i> , 2016, 11, e0161008.	1.1	17
904	Transcriptome Characterization of <i>Dendrolimus punctatus</i> and Expression Profiles at Different Developmental Stages. <i>PLoS ONE</i> , 2016, 11, e0161667.	1.1	29
905	Insecticidal Activity of <i>Melaleuca alternifolia</i> Essential Oil and RNA-Seq Analysis of <i>Sitophilus zeamais</i> Transcriptome in Response to Oil Fumigation. <i>PLoS ONE</i> , 2016, 11, e0167748.	1.1	85

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906	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 139.	1.7	81
907	Learning from Co-expression Networks: Possibilities and Challenges. <i>Frontiers in Plant Science</i> , 2016, 7, 444.	1.7	268
908	PlantFuncSSR: Integrating First and Next Generation Transcriptomics for Mining of SSR-Functional Domains Markers. <i>Frontiers in Plant Science</i> , 2016, 7, 878.	1.7	5
909	SPRYSEC Effectors: A Versatile Protein-Binding Platform to Disrupt Plant Innate Immunity. <i>Frontiers in Plant Science</i> , 2016, 7, 1575.	1.7	37
910	Lineage-Specific Evolutionary Histories and Regulation of Major Starch Metabolism Genes during Banana Ripening. <i>Frontiers in Plant Science</i> , 2016, 7, 1778.	1.7	19
911	DemaDb: an integrated dematiaceous fungal genomes database. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw008.	1.4	4
912	Functional, structural and epitopic prediction of hypothetical proteins of <i>Mycobacterium tuberculosis</i> H37Rv: An in silico approach for prioritizing the targets. <i>Gene</i> , 2016, 591, 442-455.	1.0	18
913	Draft Genome Sequences of Fungus <i>Aspergillus calidoustus</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	13
914	A genes eye view of ontogeny: <i>de novo</i> assembly and profiling of the <i>Gryllus rubens</i> transcriptome. <i>Molecular Ecology Resources</i> , 2016, 16, 1478-1490.	2.2	37
915	Comprehensive analysis of TCP transcription factors and their expression during cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.6	35
916	Gibberellin deficiency is responsible for shy-flowering nature of <i>Epipremnum aureum</i> . <i>Scientific Reports</i> , 2016, 6, 28598.	1.6	16
917	Fruiting Body Formation in <i>Volvariella volvacea</i> Can Occur Independently of Its <i>MAT-A</i> -Controlled Bipolar Mating System, Enabling Homothallic and Heterothallic Life Cycles. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2135-2146.	0.8	13
918	Evolutionary Histories of Gene Families in Angiosperm Trees. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 121-137.	0.3	0
919	Expression and biochemical characterization and substrate specificity of the fucoidanase from <i>Formosa algae</i> . <i>Glycobiology</i> , 2017, 27, 254-263.	1.3	39
920	Identification of protein secretion systems in bacterial genomes. <i>Scientific Reports</i> , 2016, 6, 23080.	1.6	315
921	Characterization of mycobacteria and mycobacteriophages isolated from compost at the São Paulo Zoo Park Foundation in Brazil and creation of the new mycobacteriophage Cluster U. <i>BMC Microbiology</i> , 2016, 16, 111.	1.3	12
922	The genome of the Gulf pipefish enables understanding of evolutionary innovations. <i>Genome Biology</i> , 2016, 17, 258.	3.8	76
923	Draft genome sequence of subterranean clover, a reference for genus <i>Trifolium</i> . <i>Scientific Reports</i> , 2016, 6, 30358.	1.6	33

#	ARTICLE	IF	CITATIONS
924	The Spermatophore in <i>Glossina morsitans morsitans</i> : Insights into Male Contributions to Reproduction. <i>Scientific Reports</i> , 2016, 6, 20334.	1.6	40
925	Exploring genomic databases for in silico discovery of Pht1 genes in high syntenic close related grass species with focus in sugarcane ( <i>Saccharum</i> spp.). <i>Current Plant Biology</i> , 2016, 6, 11-18.	2.3	1
926	The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. <i>Scientific Reports</i> , 2016, 6, 28594.	1.6	118
927	Gene Family Evolution Reflects Adaptation to Soil Environmental Stressors in the Genome of the Collembolan <i>Orchesella cincta</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2106-2117.	1.1	56
928	Genome-wide analysis and expression profiling of the phospholipase D gene family in <i>Gossypium arboreum</i> . <i>Science China Life Sciences</i> , 2016, 59, 130-141.	2.3	22
929	Lipolytic enzymes involving lipolysis in Teleost: Synteny, structure, tissue distribution, and expression in grass carp ( <i>Ctenopharyngodon idella</i> ). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2016, 198, 110-118.	0.7	33
930	Thermotolerance and molecular chaperone function of an SGT1-like protein from the psychrophilic yeast, <i>Glaciozyma antarctica</i> . <i>Cell Stress and Chaperones</i> , 2016, 21, 707-715.	1.2	10
931	Experimental validation of in silico model-predicted isocitrate dehydrogenase and phosphomannose isomerase from <i>D. ehalococcoides mccartyi</i> . <i>Microbial Biotechnology</i> , 2016, 9, 47-60.	2.0	1
932	Functional Analysis of an S-Layer-Associated Fibronectin-Binding Protein in <i>Lactobacillus acidophilus</i> NCFM. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2676-2685.	1.4	71
933	Genome-wide characterization of Nuclear Factor Y (NF-Y) gene family of sorghum [ <i>Sorghum bicolor</i> (L.) Moench]: a bioinformatics approach. <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 33-49.	1.4	22
934	Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. <i>BMC Genomics</i> , 2016, 17, 245.	1.2	69
935	Genome-wide analysis of superoxide dismutase gene family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . <i>Plant Gene</i> , 2016, 6, 18-29.	1.4	43
936	Sequencing and comparative analyses of the genomes of zoysiagrasses. <i>DNA Research</i> , 2016, 23, 171-180.	1.5	68
937	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. <i>Genome Research</i> , 2016, 26, 812-825.	2.4	88
938	Production of GDP-l-fucose from exogenous fucose through the salvage pathway in <i>Mortierella alpina</i> . <i>RSC Advances</i> , 2016, 6, 46308-46316.	1.7	0
939	Identification and expression analysis of DXS1 gene isolated from <i>Aconitum balfourii</i> Stapf.. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	6
940	Data set for phylogenetic tree and RAMPAGE Ramachandran plot analysis of SODs in <i>Gossypium raimondii</i> and <i>G. arboreum</i> . <i>Data in Brief</i> , 2016, 9, 345-348.	0.5	49
941	Transcriptome sequencing of <i>Mycosphaerella fijiensis</i> during association with <i>Musa acuminata</i> reveals candidate pathogenicity genes. <i>BMC Genomics</i> , 2016, 17, 690.	1.2	20

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942	Draft genome sequence of an inbred line of <i>Chenopodium quinoa</i> , an allotetraploid crop with great environmental adaptability and outstanding nutritional properties. <i>DNA Research</i> , 2016, 23, 535-546.	1.5	84
943	Genome Sequences of 11 Human Vaginal Actinobacteria Strains. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
944	Dry and wet approaches for genome-wide functional annotation of conventional and unconventional transcriptional activators. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 262-270.	1.9	6
945	Evolution and expression patterns of cytokinin oxidase genes in <i>Fragaria vesca</i> . <i>Scientia Horticulturae</i> , 2016, 212, 115-125.	1.7	12
946	RNA Sequencing-Based Genome Reannotation of the Dermatophyte <i>Arthroderma benhamiae</i> and Characterization of Its Secretome and Whole Gene Expression Profile during Infection. <i>MSystems</i> , 2016, 1, .	1.7	31
947	Sequence comparison, molecular modeling, and network analysis predict structural diversity in cysteine proteases from the Cape sundew, <i>Drosera capensis</i> . <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 271-282.	1.9	19
948	A novel sweet potato potyvirus open reading frame (ORF) is expressed via polymerase slippage and suppresses RNA silencing. <i>Molecular Plant Pathology</i> , 2016, 17, 1111-1123.	2.0	61
949	Reannotation of <i>Yersinia pestis</i> Strain 91001 Based on Omics Data. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 562-570.	0.6	11
950	Genome-wide identification of salinity responsive HSP70s in common bean. <i>Molecular Biology Reports</i> , 2016, 43, 1251-1266.	1.0	31
951	Genome Sequence of Jumbo Phage vB_AbaM_ME3 of <i>Acinetobacter baumannii</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	10
952	Genome-wide identification and characterization of <i>TCP</i> genes involved in ovule development of <i>Phalaenopsis equestris</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 5051-5066.	2.4	55
953	Comparative analysis of transcriptomes in aerial stems and roots of <i>Ephedra sinica</i> based on high-throughput mRNA sequencing. <i>Genomics Data</i> , 2016, 10, 4-11.	1.3	6
954	The Diversification of Plant <i>NBS-LRR</i> Defense Genes Directs the Evolution of MicroRNAs That Target Them. <i>Molecular Biology and Evolution</i> , 2016, 33, 2692-2705.	3.5	200
955	Transcriptome signatures in common carp spleen in response to <i>Aeromonas hydrophila</i> infection. <i>Fish and Shellfish Immunology</i> , 2016, 57, 41-48.	1.6	57
956	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. <i>BMC Genomics</i> , 2016, 17, 623.	1.2	35
957	Identification of a gene involved in the regulation of hyphal growth of <i>Epichloa festucae</i> during symbiosis. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw214.	0.7	9
958	Metagenomics as a preliminary screen for antimicrobial bioprospecting. <i>Gene</i> , 2016, 594, 248-258.	1.0	26
959	Microarray-based annotation of the gut transcriptome of the migratory locust, <i>Locusta migratoria</i> . <i>Insect Molecular Biology</i> , 2016, 25, 745-756.	1.0	8

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960	Novel proteases from the genome of the carnivorous plant <i>Drosera capensis</i> : Structural prediction and comparative analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1517-1533.	1.5	29
961	Genome Sequences of Nine Gram-Negative Vaginal Bacterial Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
962	Genome-wide identification and expression analysis of the IQD gene family in moso bamboo ( <i>Phyllostachys edulis</i> ). <i>Scientific Reports</i> , 2016, 6, 24520.	1.6	64
963	De novo transcriptome sequencing and gene expression profiling of <i>Elymus nutans</i> under cold stress. <i>BMC Genomics</i> , 2016, 17, 870.	1.2	49
964	Evolutionary and Expression Analysis Provides Evidence for the Plant Glutamate-like Receptors Family is Involved in Woody Growth-related Function. <i>Scientific Reports</i> , 2016, 6, 32013.	1.6	16
965	Whole-genome de novo sequencing, combined with RNA-Seq analysis, reveals unique genome and physiological features of the amylolytic yeast <i>Saccharomycopsis fibuligera</i> and its interspecies hybrid. <i>Biotechnology for Biofuels</i> , 2016, 9, 246.	6.2	43
966	Identification and characterization of AP2/ERF transcription factors in moso bamboo ( <i>Phyllostachys</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	8.4	6
967	In silico identification of outer membrane protein (Omp) and subunit vaccine design against pathogenic <i>Vibrio cholerae</i> . <i>Computational Biology and Chemistry</i> , 2016, 65, 61-68.	1.1	16
968	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016, 1, 16146.	5.9	207
969	Danger lurking in the "unknowns" structure-to-function studies of hypothetical protein Bleg1_2437 from <i>Bacillus lehensisG1</i> alkaliphile revealed an evolutionary divergent B3 metallo-beta-lactamase. <i>Journal of Biochemistry</i> , 2016, 161, mvw058.	0.9	4
970	Genome Sequences of 15 <i>Gardnerella vaginalis</i> Strains Isolated from the Vaginas of Women with and without Bacterial Vaginosis. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
971	Genome Sequences of 14 <i>Firmicutes</i> Strains Isolated from the Human Vagina. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
972	Occurrence, structure, and evolution of nitric oxide synthase-like proteins in the plant kingdom. <i>Science Signaling</i> , 2016, 9, re2.	1.6	213
973	Proteome-wide analysis of lysine acetylation in the plant pathogen <i>Botrytis cinerea</i> . <i>Scientific Reports</i> , 2016, 6, 29313.	1.6	77
974	Transcriptional Analysis of The Adaptive Digestive System of The Migratory Locust in Response to Plant Defensive Protease Inhibitors. <i>Scientific Reports</i> , 2016, 6, 32460.	1.6	19
975	Genome and transcriptome sequencing characterises the gene space of <i>Macadamia integrifolia</i> (Proteaceae). <i>BMC Genomics</i> , 2016, 17, 937.	1.2	45
976	Gene set of chemosensory receptors in the polyembryonic endoparasitoid <i>Macrocentrus cingulum</i> . <i>Scientific Reports</i> , 2016, 6, 24078.	1.6	20
977	Resequencing of <i>Capsicum annuum</i> parental lines (YCM334 and Taaan) for the genetic analysis of bacterial wilt resistance. <i>BMC Plant Biology</i> , 2016, 16, 235.	1.6	25

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978	Complete genome sequence of new bacteriophage phiE142, which causes simultaneously lysis of multidrug-resistant <i>Escherichia coli</i> O157:H7 and <i>Salmonella enterica</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 89.	1.5	17
979	The walnut ( <i>Juglans regia</i> ) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	2.8	233
980	The plasma membrane proton pump gene family in cucumber. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	16
981	Assembly of the draft genome of buckwheat and its applications in identifying agronomically useful genes. <i>DNA Research</i> , 2016, 23, 215-224.	1.5	122
982	Identification of Lysine Acetylation in <i>Mycobacterium abscessus</i> Using LC-MS/MS after Immunoprecipitation. <i>Journal of Proteome Research</i> , 2016, 15, 2567-2578.	1.8	22
983	An acyltransferase gene that putatively functions in anthocyanin modification was horizontally transferred from Fabaceae into the genus <i>Cuscuta</i> . <i>Plant Diversity</i> , 2016, 38, 149-155.	1.8	9
984	In silico characterization and differential expression pattern analysis of conserved HMG CoA reductase domain isolated from <i>Aconitum balfourii</i> Stapf. <i>3 Biotech</i> , 2016, 6, 89.	1.1	2
985	The genome of newly classified <i>Ochroconis mirabilis</i> : Insights into fungal adaptation to different living conditions. <i>BMC Genomics</i> , 2016, 17, 91.	1.2	26
986	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.	1.2	109
987	Transcriptome dynamics in the asexual cycle of the chordate <i>Botryllus schlosseri</i> . <i>BMC Genomics</i> , 2016, 17, 275.	1.2	20
988	Selection pressure on human STR loci and its relevance in repeat expansion disease. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1851-1869.	1.0	15
989	Identification and expression analysis of LEA gene family members in cucumber genome. <i>Plant Growth Regulation</i> , 2016, 80, 225-241.	1.8	41
990	Transcriptome and metabolome of synthetic <i>Solanum</i> autotetraploids reveal key genomic stress events following polyploidization. <i>New Phytologist</i> , 2016, 210, 1382-1394.	3.5	67
991	Isolation of a gene encoding a novel atypical LEA protein from the halophyte <i>Prosopis strombulifera</i> with a sodium salt-specific expression. <i>Plant Growth Regulation</i> , 2016, 78, 93-103.	1.8	4
992	Identification and profiling of microRNAs in the ovaries of polytocous and monotocous goats during estrus. <i>Theriogenology</i> , 2016, 85, 769-780.	0.9	21
993	Draft genome sequence of the silver pomfret fish, <i>Pampus argenteus</i> . <i>Genome</i> , 2016, 59, 51-58.	0.9	14
994	Regulation of cell wall remodeling in grapevine ( <i>Vitis vinifera</i> L.) callus under individual mineral stress deficiency. <i>Journal of Plant Physiology</i> , 2016, 190, 95-105.	1.6	16
995	Pleurochrysome: A Web Database of Pleurochrysis Transcripts and Orthologs Among Heterogeneous Algae. <i>Plant and Cell Physiology</i> , 2016, 57, e6-e6.	1.5	4



#	ARTICLE	IF	CITATIONS
996	Recombinant pediocin in <i>Lactococcus lactis</i> : increased production by propeptide fusion and improved potency by co-production with PedC. <i>Microbial Biotechnology</i> , 2016, 9, 466-477.	2.0	12
997	Fast forward genetics by radiation hybrids to saturate the locus regulating nuclear-cytoplasmic compatibility in <i>Triticum</i> . <i>Plant Biotechnology Journal</i> , 2016, 14, 1716-1726.	4.1	9
998	Genome-scale metabolic modeling of <i>Mucor circinelloides</i> and comparative analysis with other oleaginous species. <i>Gene</i> , 2016, 583, 121-129.	1.0	28
999	The plant natriuretic peptide receptor is a guanylyl cyclase and enables cGMP-dependent signaling. <i>Plant Molecular Biology</i> , 2016, 91, 275-286.	2.0	40
1000	Characterization of a fungal l-fucokinase involved in <i>Mortierella alpina</i> GDP-l-fucose salvage pathway. <i>Glycobiology</i> , 2016, 26, 880-887.	1.3	9
1001	Complete genome sequence of a deeply branched marine Bacteroidia bacterium <i>Draconibacterium orientale</i> type strain FH5T. <i>Marine Genomics</i> , 2016, 26, 13-16.	0.4	6
1002	Complete genome of <i>Marinobacter psychrophilus</i> strain 20041T isolated from sea-ice of the Canadian Basin. <i>Marine Genomics</i> , 2016, 28, 1-3.	0.4	0
1003	Comparative analysis of genome-wide Mlo gene family in <i>Cajanus cajan</i> and <i>Phaseolus vulgaris</i> . <i>Genetica</i> , 2016, 144, 229-241.	0.5	3
1004	Databases for Solanaceae and Cucurbitaceae Research. <i>Biotechnology in Agriculture and Forestry</i> , 2016, , 31-42.	0.2	1
1005	Mycelial development preceding basidioma formation in <i>Moniliophthora perniciosa</i> is associated to chitin, sugar and nutrient metabolism alterations involving autophagy. <i>Fungal Genetics and Biology</i> , 2016, 86, 33-46.	0.9	11
1006	Drought-Responsive Hsp70 Gene Analysis in <i>Populus</i> at Genome-Wide Level. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 483-500.	1.0	24
1007	ABC Transporter from Sugarcane Grassy Shoot Phytoplasma: Gene Sequencing and Sequence Characterization. <i>Sugar Tech</i> , 2016, 18, 407-413.	0.9	4
1008	Transcriptome analysis in <i>Coffea eugenioides</i> , an Arabica coffee ancestor, reveals differentially expressed genes in leaves and fruits. <i>Molecular Genetics and Genomics</i> , 2016, 291, 323-336.	1.0	26
1009	Genome-wide identification of SF1 and SF2 helicases from archaea. <i>Gene</i> , 2016, 576, 214-228.	1.0	18
1010	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	2.2	108
1011	Compartmentalization of functions and predicted miRNA regulation among contiguous regions of the nematode intestine. <i>RNA Biology</i> , 2017, 14, 1335-1352.	1.5	11
1012	Large-scale gene expression reveals different adaptations of <i>Hyalopterus persikonus</i> to winter and summer host plants. <i>Insect Science</i> , 2017, 24, 431-442.	1.5	12
1013	Soybean NAC gene family: sequence analysis and expression under low nitrogen supply. <i>Biologia Plantarum</i> , 2017, 61, 473-482.	1.9	8

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1014	Genome-wide identification and comparative expression analysis of LEA genes in watermelon and melon genomes. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 5-21.	1.4	30
1015	Co-option and <i>de novo</i> gene evolution underlie molluscan shell diversity. <i>Molecular Biology and Evolution</i> , 2017, 34, msw294.	3.5	67
1016	Structure prediction and network analysis of chitinases from the Cape sundew, <i>Drosera capensis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 636-643.	1.1	13
1017	Range expansion underlies historical introgressive hybridization in the Iberian hare. <i>Scientific Reports</i> , 2017, 7, 40788.	1.6	35
1018	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.	2.8	97
1019	Genome Sequence of <i>Christensenella minuta</i> DSM 22607 <sup>T</sup> . <i>Genome Announcements</i> , 2017, 5, .	0.8	19
1020	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
1021	Comparative metabolite and genome analysis of tuber-bearing potato species. <i>Phytochemistry</i> , 2017, 137, 42-51.	1.4	41
1022	Genome Sequence of Type Strain <i>Fonsecaea multimorphosa</i> CBS 980.96 <sup>T</sup> , a Causal Agent of Feline Cerebral Phaeocephalomycosis. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
1023	Diversity in sequences, post-translational modifications and expected pharmacological activities of toxins from four <i>Conus</i> species revealed by the combination of cutting-edge proteomics, transcriptomics and bioinformatics. <i>Toxicon</i> , 2017, 130, 116-125.	0.8	14
1024	The Notch pathway in the annelid <i>Platynereis</i> : insights into chaetogenesis and neurogenesis processes. <i>Open Biology</i> , 2017, 7, 160242.	1.5	28
1025	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
1026	The <i>Echinococcus canadensis</i> (G7) genome: a key knowledge of parasitic plathyhelminth human diseases. <i>BMC Genomics</i> , 2017, 18, 204.	1.2	42
1027	Molecular adaptation in the world's deepest-living animal: Insights from transcriptome sequencing of the hadal amphipod <i>Hirondellea gigas</i> . <i>Molecular Ecology</i> , 2017, 26, 3732-3743.	2.0	69
1028	Probing the Complex Architecture of Multimodular Carbohydrate-Active Enzymes Using a Combination of Small Angle X-Ray Scattering and X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2017, 1588, 239-253.	0.4	3
1029	Genome-scale metabolic network of <i>Cordyceps militaris</i> useful for comparative analysis of entomopathogenic fungi. <i>Gene</i> , 2017, 626, 132-139.	1.0	35
1030	The Whole-Genome and Transcriptome of the Manila Clam ( <i>Ruditapes philippinarum</i> ). <i>Genome Biology and Evolution</i> , 2017, 9, 1487-1498.	1.1	75
1031	<i>Sporobolus stapfianus</i> : Insights into desiccation tolerance in the resurrection grasses from linking transcriptomics to metabolomics. <i>BMC Plant Biology</i> , 2017, 17, 67.	1.6	61

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1032	Mining the <i>Cicer arietinum</i> genome for the mildew locus O (Mlo) gene family and comparative evolutionary analysis of the Mlo genes from <i>Medicago truncatula</i> and some other plant species. <i>Journal of Plant Research</i> , 2017, 130, 239-253.	1.2	10
1033	Forkhead box O1 in grass carp <i>Ctenopharyngodon idella</i> : Molecular characterization, gene structure, tissue distribution and mRNA expression in insulin-inhibited adipocyte lipolysis. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2017, 204, 76-84.	0.8	14
1034	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2017, 215, 1009-1025.	3.5	108
1035	Differential effects of a post-anthesis heat stress on wheat ( <i>Triticum aestivum</i> L.) grain proteome determined by iTRAQ. <i>Scientific Reports</i> , 2017, 7, 3468.	1.6	44
1036	TmCactin plays an important role in Gram-negative and -positive bacterial infection by regulating expression of 7 AMP genes in <i>Tenebrio molitor</i> . <i>Scientific Reports</i> , 2017, 7, 46459.	1.6	34
1037	Integrated metabolome and transcriptome analysis of <i>Magnolia champaca</i> identifies biosynthetic pathways for floral volatile organic compounds. <i>BMC Genomics</i> , 2017, 18, 463.	1.2	32
1038	Antennal and abdominal transcriptomes reveal chemosensory gene families in the coconut hispine beetle, <i>Brontispa longissima</i> . <i>Scientific Reports</i> , 2017, 7, 2809.	1.6	24
1039	Identification and comparative analysis of the ovarian microRNAs of prolific and non-prolific goats during the follicular phase using high-throughput sequencing. <i>Scientific Reports</i> , 2017, 7, 1921.	1.6	25
1040	The genome sequence of sweet cherry ( <i>Prunus avium</i> ) for use in genomics-assisted breeding. <i>DNA Research</i> , 2017, 24, 499-508.	1.5	212
1041	A misannotated locus positively influencing <i>Arabidopsis</i> seed germination is deconvoluted using multiple methods, including surrogate splicing. <i>Plant Gene</i> , 2017, 10, 74-85.	1.4	2
1042	In silico functional elucidation of uncharacterized proteins of <i>Chlamydia abortus</i> strain LLG. <i>Future Science OA</i> , 2017, 3, FSO169.	0.9	10
1043	RNA-seq reveals mechanisms of SIMX1 for enhanced carotenoids and terpenoids accumulation along with stress resistance in tomato. <i>Science Bulletin</i> , 2017, 62, 476-485.	4.3	20
1044	PhaR, a Negative Regulator of PhaP, Modulates the Colonization of a <i>Burkholderia</i> Gut Symbiont in the Midgut of the Host Insect, <i>Riptortus pedestris</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	13
1045	Identification of conserved proteins from diverse shell matrix proteome in <i>Crassostrea gigas</i> : characterization of genetic bases regulating shell formation. <i>Scientific Reports</i> , 2017, 7, 45754.	1.6	58
1046	TOMATOMICS: A Web Database for Integrated Omics Information in Tomato. <i>Plant and Cell Physiology</i> , 2017, 58, pcw207.	1.5	29
1047	Comparative transcriptome analyses of flower development in four species of <i>Achimenes</i> ( <i>Gesneriaceae</i> ). <i>BMC Genomics</i> , 2017, 18, 240.	1.2	41
1048	In silico analysis of cacao ( <i>Theobroma cacao</i> L.) genes that involved in pathogen and disease responses. <i>AIP Conference Proceedings</i> , 2017, , .	0.3	0
1049	Development of Dof (DNA binding with one finger) transcription factor gene-specific primers through data mining as a functional marker and their use for genetic diversity study in barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784304rgBT / Overlock 10		

#	ARTICLE	IF	CITATIONS
1050	Secretory Proteome Analysis of Streptomycin-Resistant Mycobacterium tuberculosis Clinical Isolates. SLAS Discovery, 2017, 22, 1229-1238.	1.4	40
1051	Purification, biochemical characterization and Insilico modeling of Î±-amylase from Vicia faba. Journal of Molecular Liquids, 2017, 234, 133-141.	2.3	10
1052	Characterization and genome analysis of novel bacteriophages infecting the opportunistic human pathogens Klebsiella oxytoca and K. pneumoniae. Archives of Virology, 2017, 162, 1129-1139.	0.9	18
1053	Transcriptomic analysis of Casuarina equisetifolia L. in responses to cold stress. Tree Genetics and Genomes, 2017, 13, 1.	0.6	15
1054	De Novo Peptide Sequencing: Deep Mining of High-Resolution Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1549, 119-134.	0.4	10
1055	Construction of the Leaf Senescence Database and Functional Assessment of Senescence-Associated Genes. Methods in Molecular Biology, 2017, 1533, 315-333.	0.4	18
1056	Proteome Bioinformatics. Methods in Molecular Biology, 2017, , .	0.4	5
1057	A Systematic Bioinformatics Approach to Identify High Quality Mass Spectrometry Data and Functionally Annotate Proteins and Proteomes. Methods in Molecular Biology, 2017, 1549, 163-176.	0.4	3
1058	Transcriptome analysis of immune response against Vibrio harveyi infection in orange-spotted grouper (Epinephelus coioides). Fish and Shellfish Immunology, 2017, 70, 628-637.	1.6	41
1059	Long-read transcriptome data for improved gene prediction in Lentinula edodes. Data in Brief, 2017, 15, 454-458.	0.5	13
1061	Antennal transcriptome and expression analyses of olfactory genes in the sweetpotato weevil Cylas formicarius. Scientific Reports, 2017, 7, 11073.	1.6	40
1062	Mechanistic insights in X-chromosome inactivation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160356.	1.8	59
1063	Draft Genome Sequence of Grammothele lineata SDL-CO-2015-1, a Jute Endophyte with a Potential for Paclitaxel Biosynthesis. Genome Announcements, 2017, 5, .	0.8	5
1064	ALGLY I gene implicated in salt stress response from halophyte Aeluropus litoralis. Russian Journal of Plant Physiology, 2017, 64, 850-860.	0.5	1
1065	Transcriptomic responses of the endangered freshwater mussel Margaritifera margaritifera to trace metal contamination in the Dronne River, France. Environmental Science and Pollution Research, 2017, 24, 27145-27159.	2.7	26
1066	Chemosensing of honeybee parasite, Varroa destructor: Transcriptomic analysis. Scientific Reports, 2017, 7, 13091.	1.6	38
1067	CRIMeToYHU: a new web tool to develop yeast-based functional assays for characterizing cancer-associated missense variants. FEMS Yeast Research, 2017, 17, .	1.1	4
1068	The genomic basis of cichlid fish adaptation within the deepwater "twilight zone" of Lake Malawi. Evolution Letters, 2017, 1, 184-198.	1.6	21

#	ARTICLE	IF	CITATIONS
1069	A moso bamboo WRKY gene PeWRKY83 confers salinity tolerance in transgenic Arabidopsis plants. <i>Scientific Reports</i> , 2017, 7, 11721.	1.6	67
1070	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	9.4	356
1071	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. <i>Structure</i> , 2017, 25, 1598-1610.e3.	1.6	105
1072	Screening of miRNA profiles and construction of regulation networks in early and late lactation of dairy goat mammary glands. <i>Scientific Reports</i> , 2017, 7, 11933.	1.6	26
1073	Chickpea-Fusarium oxysporum interaction transcriptome reveals differential modulation of plant defense strategies. <i>Scientific Reports</i> , 2017, 7, 7746.	1.6	31
1074	Tm SR-C, scavenger receptor class C, plays a pivotal role in antifungal and antibacterial immunity in the coleopteran insect <i>Tenebrio molitor</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2017, 89, 31-42.	1.2	16
1075	Transcriptome sequencing of <i>Tessarotoma papillosa</i> antennae to identify and analyze expression patterns of putative olfaction genes. <i>Scientific Reports</i> , 2017, 7, 3070.	1.6	38
1076	The xenobiotic sensor PXR in a marine flatfish species ( <i>Solea senegalensis</i> ): Gene expression patterns and its regulation under different physiological conditions. <i>Marine Environmental Research</i> , 2017, 130, 187-199.	1.1	13
1077	Structure, enzymatic transformation, anticancer activity of fucoidan and sulphated fucooligosaccharides from <i>Sargassum horneri</i> . <i>Carbohydrate Polymers</i> , 2017, 175, 654-660.	5.1	68
1078	Complete Genome Sequence of <i>Achromobacter denitrificans</i> PR1. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
1079	Transcription factor repertoire in Ashwagandha ( <i>Withania somnifera</i> ) through analytics of transcriptomic resources: Insights into regulation of development and withanolide metabolism. <i>Scientific Reports</i> , 2017, 7, 16649.	1.6	17
1081	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. <i>Nature Communications</i> , 2017, 8, 1843.	5.8	85
1082	Methanogenesis in oxygenated soils is a substantial fraction of wetland methane emissions. <i>Nature Communications</i> , 2017, 8, 1567.	5.8	195
1083	Transcriptome sequencing and differential gene expression analysis of the schistosome-transmitting snail <i>Oncomelania hupensis</i> inhabiting hilly and marshland regions. <i>Scientific Reports</i> , 2017, 7, 15809.	1.6	7
1084	An Insight Into Structure, Function, and Expression Analysis of 3-Hydroxy-3-Methylglutaryl-CoA Reductase of <i>Cymbopogon winterianus</i> . <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221770173.	1.0	6
1085	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
1086	Genomic Analysis of <i>Clavibacter michiganensis</i> Reveals Insight Into Virulence Strategies and Genetic Diversity of a Gram-Positive Bacterial Pathogen. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 786-802.	1.4	56
1087	Coping with living in the soil: the genome of the parthenogenetic springtail <i>Folsomia candida</i> . <i>BMC Genomics</i> , 2017, 18, 493.	1.2	103

#	ARTICLE	IF	CITATIONS
1088	Genome-wide identification and expression analysis of SBP-like transcription factor genes in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>BMC Genomics</i> , 2017, 18, 486.	1.2	64
1089	House spider genome uncovers evolutionary shifts in the diversity and expression of black widow venom proteins associated with extreme toxicity. <i>BMC Genomics</i> , 2017, 18, 178.	1.2	57
1090	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	1.2	17
1091	Genome-wide characterization and expression analyses of superoxide dismutase (SOD) genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2017, 18, 376.	1.2	101
1092	Transcriptome analysis explores genes related to shikonin biosynthesis in Lithospermeae plants and provides insights into Boraginales™ evolutionary history. <i>Scientific Reports</i> , 2017, 7, 4477.	1.6	26
1093	Identification of Protein Secretion Systems in Bacterial Genomes Using MacSyFinder. <i>Methods in Molecular Biology</i> , 2017, 1615, 1-21.	0.4	92
1094	Sequencing and de novo assembly of visceral mass transcriptome of the critically endangered land snail <i>Satsuma myomphala</i> : Annotation and SSR discovery. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 21, 77-89.	0.4	10
1095	Post-translational regulation by structural changes of 4-dihydromethyltrisporate dehydrogenase, a key enzyme in sexual and parasitic communication mediated by the trisporic acid pheromone system, of the fungal fusion parasite <i>Parasitella parasitica</i> . <i>Journal of Theoretical Biology</i> , 2017, 413, 50-57.	0.8	2
1096	Structural and functional characterisation of a class I endochitinase of the carnivorous sundew ( <i>Drosera rotundifolia</i> L.). <i>Planta</i> , 2017, 245, 313-327.	1.6	14
1097	Structural and functional annotation of human FAM26F: A multifaceted protein having a critical role in the immune system. <i>Gene</i> , 2017, 597, 66-75.	1.0	20
1098	Genomic Basis of Adaptive Evolution: The Survival of Amur Ide ( <i>Leuciscus waleckii</i> ) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	3.5	66
1099	A comprehensive draft genome sequence for lupin ( <i>Lupinus angustifolius</i> ), an emerging health food: insights into plant-microbe interactions and legume evolution. <i>Plant Biotechnology Journal</i> , 2017, 15, 318-330.	4.1	153
1100	Restriction site associated DNA (RAD) for de novo sequencing and marker discovery in sugarcane borer, <i>Diatraea saccharalis</i> Fab. (Lepidoptera: Crambidae). <i>Molecular Ecology Resources</i> , 2017, 17, 454-465.	2.2	5
1101	Draft genome sequence of pectic polysaccharide-degrading moderate thermophilic bacterium <i>Geobacillus thermodenitrificans</i> DSM 101594. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 7-8.	0.8	6
1102	SymB and SymC, two membrane associated proteins, are required for <i>E. coli</i> hyphal cell-cell fusion and maintenance of a mutualistic interaction with <i>Lotus perenne</i> . <i>Molecular Microbiology</i> , 2017, 103, 657-677.	1.2	23
1103	Estimation of long terminal repeat element content in the <i>Helicoverpa zea</i> genome from high-throughput sequencing of bacterial artificial chromosome pools. <i>Genome</i> , 2017, 60, 310-324.	0.9	7
1104	Comparative whole-genome analysis reveals artificial selection effects on <i>Ustilago esculenta</i> genome. <i>DNA Research</i> , 2017, 24, 635-648.	1.5	58
1105	Differences in the genetic control of early egg development and reproduction between <i>C. elegans</i> and its parthenogenetic relative <i>D. coronatus</i> . <i>EvoDevo</i> , 2017, 8, 16.	1.3	4

#	ARTICLE	IF	CITATIONS
1106	Evidence-based gene models for structural and functional annotations of the oil palm genome. <i>Biology Direct</i> , 2017, 12, 21.	1.9	24
1107	Programmatic access to bioinformatics tools from EMBL-EBI update: 2017. <i>Nucleic Acids Research</i> , 2017, 45, W550-W553.	6.5	285
1108	An Annotated Draft Genome for <i>Radix auricularia</i> (Gastropoda, Mollusca). <i>Genome Biology and Evolution</i> , 2017, 9, 585-592.	1.1	57
1109	Evolution and expression analysis reveal the potential role of the HD-Zip gene family in regulation of embryo abortion in grapes ( <i>Vitis vinifera</i> L.). <i>BMC Genomics</i> , 2017, 18, 744.	1.2	51
1110	Genome-Wide Identification of the MIKC-Type MADS-Box Gene Family in <i>Gossypium hirsutum</i> L. Unravels Their Roles in Flowering. <i>Frontiers in Plant Science</i> , 2017, 8, 384.	1.7	54
1111	Genome-Wide Identification and Expression Analysis of the Biotin Carboxyl Carrier Subunits of Heteromeric Acetyl-CoA Carboxylase in <i>Gossypium</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 624.	1.7	33
1112	Comparative Transcriptome Analysis Reveal Candidate Genes Potentially Involved in Regulation of Primocane Apex Rooting in Raspberry ( <i>Rubus</i> spp.). <i>Frontiers in Plant Science</i> , 2017, 8, 1036.	1.7	14
1113	Transcriptome Profiling Using Single-Molecule Direct RNA Sequencing Approach for In-depth Understanding of Genes in Secondary Metabolism Pathways of <i>Camellia sinensis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1205.	1.7	74
1114	Isoform Sequencing Provides a More Comprehensive View of the <i>Panax ginseng</i> Transcriptome. <i>Genes</i> , 2017, 8, 228.	1.0	42
1115	Comparative Study of Lectin Domains in Model Species: New Insights into Evolutionary Dynamics. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1136.	1.8	40
1116	Draft sequencing and assembly of the genome of the world's largest fish, the whale shark: <i>Rhincodon typus</i> Smith 1828. <i>BMC Genomics</i> , 2017, 18, 532.	1.2	91
1117	Expression Profiling in <i>Pinus pinaster</i> in Response to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2017, 8, 279.	0.9	22
1118	Molecular and Structural Characterization of the Tegumental 20.6-kDa Protein in <i>Clonorchis sinensis</i> as a Potential Druggable Target. <i>International Journal of Molecular Sciences</i> , 2017, 18, 557.	1.8	13
1119	Single-Molecule Long-Read Transcriptome Dataset of Halophyte <i>Halogeton glomeratus</i> . <i>Frontiers in Genetics</i> , 2017, 8, 197.	1.1	6
1120	Genome Wide In silico Analysis of the Mismatch Repair Components of <i>Plasmodium falciparum</i> and Their Comparison with Human Host. <i>Frontiers in Microbiology</i> , 2017, 08, 130.	1.5	16
1121	The Histidine Decarboxylase Gene Cluster of <i>Lactobacillus parabuchneri</i> Was Gained by Horizontal Gene Transfer and Is Mobile within the Species. <i>Frontiers in Microbiology</i> , 2017, 8, 218.	1.5	40
1122	InlL from <i>Listeria monocytogenes</i> Is Involved in Biofilm Formation and Adhesion to Mucin. <i>Frontiers in Microbiology</i> , 2017, 8, 660.	1.5	59
1123	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. <i>Frontiers in Microbiology</i> , 2017, 8, 1772.	1.5	31

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1124	Comparative Genomics of Sibling Species of <i>Fonsecaea</i> Associated with Human Chromoblastomycosis. <i>Frontiers in Microbiology</i> , 2017, 8, 1924.	1.5	31
1125	Distinct herpesvirus resistances and immune responses of three gynogenetic clones of gibel carp revealed by comprehensive transcriptomes. <i>BMC Genomics</i> , 2017, 18, 561.	1.2	56
1126	Characterisation and genome sequence of the lytic <i>Acinetobacter baumannii</i> bacteriophage vB_AbaS_Loki. <i>PLoS ONE</i> , 2017, 12, e0172303.	1.1	26
1127	Comparative transcriptomics of <i>Entelegyne</i> spiders (Araneae, Entelegynae), with emphasis on molecular evolution of orphan genes. <i>PLoS ONE</i> , 2017, 12, e0174102.	1.1	8
1128	Alternative oxidase (AOX) constitutes a small family of proteins in <i>Citrus clementina</i> and <i>Citrus sinensis</i> L. Osb. <i>PLoS ONE</i> , 2017, 12, e0176878.	1.1	11
1129	Transcriptome profiling of ontogeny in the acridid grasshopper <i>Chorthippus biguttulus</i> . <i>PLoS ONE</i> , 2017, 12, e0177367.	1.1	4
1130	<i>Bacillus</i> sp. JR3 esterase LipJ: A new mesophilic enzyme showing traces of a thermophilic past. <i>PLoS ONE</i> , 2017, 12, e0181029.	1.1	6
1131	Positive selection and comparative molecular evolution of reproductive proteins from New Zealand tree weta ( <i>Orthoptera</i> , <i>Hemideina</i> ). <i>PLoS ONE</i> , 2017, 12, e0188147.	1.1	4
1132	A novel <i>Meloidogyne graminicola</i> effector, MgGPP, is secreted into host cells and undergoes glycosylation in concert with proteolysis to suppress plant defenses and promote parasitism. <i>PLoS Pathogens</i> , 2017, 13, e1006301.	2.1	90
1133	Tyrosine kinase 4 is involved in the reproduction of the platyhelminth parasite <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2017, 10, 498.	1.0	9
1134	<i>Leishmania braziliensis</i> SCD6 and RBP42 proteins, two factors with RNA binding capacity. <i>Parasites and Vectors</i> , 2017, 10, 610.	1.0	5
1135	Members of the Candidate Phyla Radiation are functionally differentiated by carbon- and nitrogen-cycling capabilities. <i>Microbiome</i> , 2017, 5, 112.	4.9	118
1136	The genome of the cotton bacterial blight pathogen <i>Xanthomonas citri</i> pv. <i>malvacearum</i> strain MSCT1. <i>Standards in Genomic Sciences</i> , 2017, 12, 42.	1.5	7
1137	Putrescine independent wound response phenotype is produced by ODC-like RNAi in planarians. <i>Scientific Reports</i> , 2017, 7, 9736.	1.6	15
1138	A modified GC-specific MAKER gene annotation method reveals improved and novel gene predictions of high and low GC content in <i>Oryza sativa</i> . <i>BMC Bioinformatics</i> , 2017, 18, 522.	1.2	17
1139	The genomic sequence of <i>Exiguobacterium chiriqhucha</i> str. N139 reveals a species that thrives in cold waters and extreme environmental conditions. <i>PeerJ</i> , 2017, 5, e3162.	0.9	27
1140	Molecular Cloning, Characterization, and Functional Analysis of Acetyl-CoA C-Acetyltransferase and Mevalonate Kinase Genes Involved in Terpene Trilactone Biosynthesis from <i>Ginkgo biloba</i> . <i>Molecules</i> , 2017, 22, 74.	1.7	26
1141	De Novo Assembly and Analysis of the Testes Transcriptome from the Menhaden, <i>Bervoortia tyrannus</i> . <i>Fisheries and Aquaculture Journal</i> , 2017, 08, .	0.2	0



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1142	Improved genomic resources and new bioinformatic workflow for the carcinogenic parasite <i>Clonorchis sinensis</i> : Biotechnological implications. <i>Biotechnology Advances</i> , 2018, 36, 894-904.	6.0	20
1143	Secretome Analysis Identifies Potential Pathogenicity/Virulence Factors of <i>Tilletia indica</i> , a Quarantined Fungal Pathogen Inciting Karnal Bunt Disease in Wheat. <i>Proteomics</i> , 2018, 18, e1700473.	1.3	15
1144	The transcriptomic signature of different sexes in two protogynous hermaphrodites: Insights into the molecular network underlying sex phenotype in fish. <i>Scientific Reports</i> , 2018, 8, 3564.	1.6	32
1145	Comparative proteomic analysis of ovaries from Huoyan geese between pre-laying and laying periods using an iTRAQ-based approach. <i>Poultry Science</i> , 2018, 97, 2170-2182.	1.5	8
1146	Characterisation of novel biomass degradation enzymes from the genome of <i>Cellulomonas fimi</i> . <i>Enzyme and Microbial Technology</i> , 2018, 113, 9-17.	1.6	35
1147	De novo assembly and analysis of the <i>Artemisia argyi</i> transcriptome and identification of genes involved in terpenoid biosynthesis. <i>Scientific Reports</i> , 2018, 8, 5824.	1.6	30
1148	Genomic and transcriptomic alterations following intergeneric hybridization and polyploidization in the <i>Chrysanthemum nankingense</i> – <i>Tanacetum vulgare</i> hybrid and allopolyploid (Asteraceae). <i>Horticulture Research</i> , 2018, 5, 5.	2.9	17
1149	Phosphoproteomics unveils stable energy supply as key to flooding tolerance in <i>Kandelia candel</i> . <i>Journal of Proteomics</i> , 2018, 176, 1-12.	1.2	15
1150	MicroRNA profile of silk gland reveals different silk yields of three silkworm strains. <i>Gene</i> , 2018, 653, 1-9.	1.0	10
1151	New insight into ovary abortion during ovary development of hazelnut through a combined proteomic and transcriptomic analysis. <i>Scientia Horticulturae</i> , 2018, 234, 36-48.	1.7	8
1152	<i>ELIGULUM-A</i> Regulates Lateral Branch and Leaf Development in Barley. <i>Plant Physiology</i> , 2018, 176, 2750-2760.	2.3	22
1153	The systematic analysis of ultraconserved genomic regions in the budding yeast. <i>Bioinformatics</i> , 2018, 34, 361-366.	1.8	1
1155	The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. <i>Nucleic Acids Research</i> , 2018, 46, D1168-D1180.	6.5	133
1156	<i>In silico</i> identification, characterization and expression analysis of <i>attacin</i> gene family in response to bacterial and fungal pathogens in <i>Tenebrio molitor</i> . <i>Entomological Research</i> , 2018, 48, 45-54.	0.6	19
1157	Conserved noncoding sequences conserve biological networks and influence genome evolution. <i>Heredity</i> , 2018, 120, 437-451.	1.2	13
1158	Blood transcriptomics of captive forest musk deer ( <i>Moschus berezovskii</i> ) and possible associations with the immune response to abscesses. <i>Scientific Reports</i> , 2018, 8, 599.	1.6	17
1159	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. <i>Mycology</i> , 2018, 9, 59-69.	2.0	12
1160	The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution. <i>Nature Genetics</i> , 2018, 50, 270-277.	9.4	262

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1161	Mechanistic and structural insight into promiscuity based metabolism of cardiac drug digoxin by gut microbial enzyme. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 5287-5296.	1.2	20
1162	Transcriptome analysis provides insights into the mechanism of albinism during different pigmentation stages of the albino sea cucumber <i>Apostichopus japonicus</i> . <i>Aquaculture</i> , 2018, 486, 148-160.	1.7	13
1163	Comparative genomic analyses reveal the features for adaptation to nematodes in fungi. <i>DNA Research</i> , 2018, 25, 245-256.	1.5	28
1164	Whole transcriptome analysis reveals potential novel mechanisms of low-level linezolid resistance in <i>Enterococcus faecalis</i> . <i>Gene</i> , 2018, 647, 143-149.	1.0	22
1165	Protein acetylation as a mechanism for <i>Kandelia candel</i> 's adaption to daily flooding. <i>Tree Physiology</i> , 2018, 38, 895-910.	1.4	7
1166	The 4-Celled <i>Tetrabaena socialis</i> Nuclear Genome Reveals the Essential Components for Genetic Control of Cell Number at the Origin of Multicellularity in the Volvocine Lineage. <i>Molecular Biology and Evolution</i> , 2018, 35, 855-870.	3.5	43
1167	Comparative genomics of the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> reveals chromosomal variations and genome plasticity. <i>BMC Genomics</i> , 2018, 19, 279.	1.2	56
1168	Comparative genomic analysis of <i>Geosporobacter ferrireducens</i> and its versatility of anaerobic energy metabolism. <i>Journal of Microbiology</i> , 2018, 56, 365-371.	1.3	8
1169	CoNekT: an open-source framework for comparative genomic and transcriptomic network analyses. <i>Nucleic Acids Research</i> , 2018, 46, W133-W140.	6.5	81
1170	De novo transcriptome analysis of immune response on cobia ( <i>Rachycentron canadum</i> ) infected with <i>Photobacterium damsela</i> subsp. <i>piscicida</i> revealed inhibition of complement components and involvement of MyD88-independent pathway. <i>Fish and Shellfish Immunology</i> , 2018, 77, 120-130.	1.6	16
1171	Uncovering tea-specific secondary metabolism using transcriptomic and metabolomic analyses in grafts of <i>Camellia sinensis</i> and <i>C. oleifera</i> . <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	17
1172	GOS2a1 (GO/G1 switch gene 2a1) is downregulated by TNF- $\alpha$ in grass carp ( <i>Ctenopharyngodon idellus</i> ) hepatocytes through PPAR $\alpha$ inhibition. <i>Gene</i> , 2018, 641, 1-7.	1.0	11
1173	Proteomics in plasma of ovariectomized rats and those exposed to estradiol valerate. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2018, 178, 1-12.	1.2	10
1174	Genome structure of <i>Rosa multiflora</i> , a wild ancestor of cultivated roses. <i>DNA Research</i> , 2018, 25, 113-121.	1.5	70
1175	Diversity and distribution of CYP gene family in Bactrian camel. <i>Functional and Integrative Genomics</i> , 2018, 18, 23-29.	1.4	5
1176	The repeat structure of two paralogous genes, <i>Yersinia ruckeri</i> invasin ( <i>yrInV</i> ) and a $\alpha$ -Y. <i>ruckeri</i> invasin-like molecule ( <i>yrIIm</i> ) sheds light on the evolution of adhesive capacities of a fish pathogen. <i>Journal of Structural Biology</i> , 2018, 201, 171-183.	1.3	22
1177	Cell-Type Transcriptomes of the Multicellular Green Alga <i>Volvox carteri</i> Yield Insights into the Evolutionary Origins of Germ and Somatic Differentiation Programs. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 531-550.	0.8	29
1178	Phylogenetic characterization of transporter proteins in the cnidarian-dinoflagellate symbiosis. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 307-320.	1.2	30

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1179	Ensemble gene function prediction database reveals genes important for complex I formation in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2018, 217, 1521-1534.	3.5	27
1180	Transcriptome “Scale characterization of salt responsive bean TCP transcription factors. <i>Gene</i> , 2018, 642, 64-73.	1.0	24
1181	OsZIP48, a HY5 Transcription Factor Ortholog, Exerts Pleiotropic Effects in Light-Regulated Development. <i>Plant Physiology</i> , 2018, 176, 1262-1285.	2.3	56
1182	Secreted Cysteine-Rich Repeat Proteins “SCREPs”: A Novel Multi-Domain Architecture. <i>Frontiers in Pharmacology</i> , 2018, 9, 1333.	1.6	15
1183	Draft Genome Sequences of Sporulating (CIDEFI-213) and Nonsporulating (CIDEFI-212) Strains of <i>Stemphylium lycopersici</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
1184	Protein structure networks provide insight into active site flexibility in esterase/lipases from the carnivorous plant <i>Drosera capensis</i> . <i>Integrative Biology (United Kingdom)</i> , 2018, 10, 768-779.	0.6	10
1185	The gold-standard genome of <i>Aspergillus niger</i> NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. <i>Studies in Mycology</i> , 2018, 91, 61-78.	4.5	62
1186	The chromosome-level quality genome provides insights into the evolution of the biosynthesis genes for aroma compounds of <i>Osmanthus fragrans</i> . <i>Horticulture Research</i> , 2018, 5, 72.	2.9	77
1187	Genome-wide identification and characterization of long non-coding RNAs involved in the early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2018, 19, 805.	1.2	45
1188	Comparative genomics and physiology of the genus <i>Methanohalophilus</i> , a prevalent methanogen in hydraulically fractured shale. <i>Environmental Microbiology</i> , 2018, 20, 4596-4611.	1.8	28
1189	Functional and taxonomic classification of a greenhouse water drain metagenome. <i>Standards in Genomic Sciences</i> , 2018, 13, 20.	1.5	2
1190	Draft Macronuclear Genome Sequence of the Ruminal Ciliate <i>Entodinium caudatum</i> . <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	18
1191	Genome Sequence of the Soybean Cyst Nematode ( <i>Heterodera glycines</i> ) Endosymbiont “Candidatus <i>Cardinium hertigi</i> ” Strain cHgTN10. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
1192	Genome of <i>Tenualosa ilisha</i> from the river Padma, Bangladesh. <i>BMC Research Notes</i> , 2018, 11, 921.	0.6	7
1193	Finer-Scale Phylosymbiosis: Insights from Insect Viromes. <i>MSystems</i> , 2018, 3, .	1.7	27
1194	Genome-wide Analysis and Expression Profiling Suggest Diverse Roles of TCP Genes During Development and Stress Responses in Grapevine ( <i>Vitis vinifera</i> L). <i>South African Journal of Enology and Viticulture</i> , 2018, 39, .	0.8	1
1195	Label-Free Quantitative Proteomics of Lysine Acetylome Identifies Substrates of Gcn5 in <i>Magnaporthe oryzae</i> Autophagy and Epigenetic Regulation. <i>MSystems</i> , 2018, 3, .	1.7	23
1196	Members of <i>Marinobacter</i> and <i>Arcobacter</i> Influence System Biogeochemistry During Early Production of Hydraulically Fractured Natural Gas Wells in the Appalachian Basin. <i>Frontiers in Microbiology</i> , 2018, 9, 2646.	1.5	33

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1197	RNA-seq data from mature male gonads of marine mussels <i>Mytilus edulis</i> and <i>M. galloprovincialis</i> . Data in Brief, 2018, 21, 167-175.	0.5	7
1198	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. Genome Biology and Evolution, 2018, 10, 2785-2800.	1.1	42
1199	Genome-wide identification and expression analyses of TCP transcription factor genes in <i>Gossypium barbadense</i> . Scientific Reports, 2018, 8, 14526.	1.6	37
1200	Genotypic response of pollen germination in Dura, Pisifera and Tenera oil palm ( <i>Elaeis guineensis</i> ) Tj ETQq1 1 0.784314 rgBT 1/Overloc	0.6	1
1201	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. MSystems, 2018, 3, .	1.7	189
1202	Fucoidan Sulfatases from Marine Bacterium <i>Wenyngzhuangia fucanilytica</i> CZ1127T. Biomolecules, 2018, 8, 98.	1.8	29
1203	Comprehensive Transcriptome Profiling and Identification of Potential Genes Responsible for Salt Tolerance in Tall Fescue Leaves under Salinity Stress. Genes, 2018, 9, 466.	1.0	5
1204	MmpL8 <sub>MAB</sub> controls <i>Mycobacterium abscessus</i> virulence and production of a previously unknown glycolipid family. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10147-E10156.	3.3	42
1205	De Novo assembly and comparative transcriptome analyses of purple and green morphs of <i>Apostichopus japonicus</i> during body wall pigmentation process. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 28, 151-161.	0.4	11
1206	Transcriptome Dynamics During Turbot Spermatogenesis Predicting the Potential Key Genes Regulating Male Germ Cell Proliferation and Maturation. Scientific Reports, 2018, 8, 15825.	1.6	17
1207	Proteome and Transcriptome Reveal Involvement of Heat Shock Proteins and Indoleacetic Acid Metabolism Process in <i>Lentinula Edodes</i> Thermotolerance. Cellular Physiology and Biochemistry, 2018, 50, 1617-1637.	1.1	46
1208	Proteomic analysis of human prostate cancer PC-3M-1E8 cells and PC-3M-2B4 cells of same origin but with different metastatic potential. PLoS ONE, 2018, 13, e0206139.	1.1	5
1209	Genomic distribution of a novel <i>Pyrenophora tritici-repentis</i> ToxA insertion element. PLoS ONE, 2018, 13, e0206586.	1.1	16
1210	Tripal Developer Toolkit. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	3
1211	Genome sequencing of <i>Prototheca zopfii</i> genotypes 1 and 2 provides evidence of a severe reduction in organellar genomes. Scientific Reports, 2018, 8, 14637.	1.6	34
1212	âœœOut of the Canâœ A Draft Genome Assembly, Liver Transcriptome, and Nutrigenomics of the European Sardine, <i>Sardina pilchardus</i> . Genes, 2018, 9, 485.	1.0	30
1213	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. Journal of Plant Physiology, 2018, 231, 318-328.	1.6	47
1214	Analysis of the <i>Trichuris suis</i> excretory/secretory proteins as a function of life cycle stage and their immunomodulatory properties. Scientific Reports, 2018, 8, 15921.	1.6	37

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1215	Shared Transcriptional Control and Disparate Gain and Loss of Aphid Parasitism Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 2716-2733.	1.1	53
1216	Analysis of the hybrid genomes of two field isolates of the soil-borne fungal species <i>Verticillium longisporum</i> . <i>BMC Genomics</i> , 2018, 19, 14.	1.2	23
1217	Whole-transcriptome response to wastewater treatment plant and stormwater effluents in the Asian clam, <i>Corbicula fluminea</i> . <i>Ecotoxicology and Environmental Safety</i> , 2018, 165, 96-106.	2.9	20
1218	Characterizing the DNA Methyltransferases of <i>Haloferax volcanii</i> via Bioinformatics, Gene Deletion, and SMRT Sequencing. <i>Genes</i> , 2018, 9, 129.	1.0	18
1219	A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. <i>Microbiome</i> , 2018, 6, 149.	4.9	41
1220	Genome Wide Identification of Mutational Hotspots in the Apicomplexan Parasite <i>Neospora caninum</i> and the Implications for Virulence. <i>Genome Biology and Evolution</i> , 2018, 10, 2417-2431.	1.1	17
1221	Genome Sequences of <i>Listeria</i> Phages Induced from Lysogenic Isolates of <i>Listeria monocytogenes</i> from Seafood and a Seafood Processing Environment in Thailand. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
1222	A comprehensive annotation for the root-knot nematode <i>Meloidogyne incognita</i> proteome data. <i>Data in Brief</i> , 2018, 19, 1073-1079.	0.5	6
1223	Transcriptome profiling reveals differential gene expression of detoxification enzymes in <i>Sitophilus zeamais</i> responding to terpinen-4-ol fumigation. <i>Pesticide Biochemistry and Physiology</i> , 2018, 149, 44-53.	1.6	36
1224	Integrated proteomics, genomics, metabolomics approaches reveal oxalic acid as pathogenicity factor in <i>Tilletia indica</i> inciting Karnal bunt disease of wheat. <i>Scientific Reports</i> , 2018, 8, 7826.	1.6	21
1225	Cellulases. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	1
1226	Discovery of Novel Cellulases Using Proteomic Strategies. <i>Methods in Molecular Biology</i> , 2018, 1796, 103-113.	0.4	1
1227	De novo genome assembly of the red silk cotton tree ( <i>Bombax ceiba</i> ). <i>GigaScience</i> , 2018, 7, .	3.3	27
1228	The genome of tapeworm <i>Taenia multiceps</i> sheds light on understanding parasitic mechanism and control of coenurosis disease. <i>DNA Research</i> , 2018, 25, 499-510.	1.5	36
1229	De novo genome assembly of <i>Oryza granulata</i> reveals rapid genome expansion and adaptive evolution. <i>Communications Biology</i> , 2018, 1, 84.	2.0	24
1230	Valorisation of deinking sludge as a substrate for lignocellulolytic enzymes production by <i>Pleurotus ostreatus</i> . <i>Journal of Cleaner Production</i> , 2018, 197, 253-263.	4.6	5
1231	Identification and characterization of candidates involved in production of OMEGAs in microalgae: a gene mining and phylogenomic approach. <i>Preparative Biochemistry and Biotechnology</i> , 2018, 48, 619-628.	1.0	3
1232	High-quality assembly of the reference genome for scarlet sage, <i>Salvia splendens</i> , an economically important ornamental plant. <i>GigaScience</i> , 2018, 7, .	3.3	49

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1233	A Suppressor/Avirulence Gene Combination in <i>Hyaloperonospora arabidopsidis</i> Determines Race Specificity in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 265.	1.7	14
1234	Antennal transcriptome analysis of the chemosensory gene families in <i>Carposina sasakii</i> (Lepidoptera: Tj ETQq1 1 0.784314 <sub>28</sub> /Over	1.2	28
1235	Comparative Transcriptome Profiling of Virulent and Attenuated <i>Ehrlichia ruminantium</i> Strains Highlighted Strong Regulation of map1- and Metabolism Related Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 153.	1.8	9
1236	Two New Lytic Bacteriophages of the Myoviridae Family Against Carbapenem-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 850.	1.5	47
1237	Trehalose Contributes to Gamma-Linolenic Acid Accumulation in <i>Cunninghamella echinulata</i> Based on de Novo Transcriptomic and Lipidomic Analyses. <i>Frontiers in Microbiology</i> , 2018, 9, 1296.	1.5	12
1238	Genome-Wide Identification and Expression Profiling of Cytokinin Oxidase/Dehydrogenase (CKX) Genes Reveal Likely Roles in Pod Development and Stress Responses in Oilseed Rape ( <i>Brassica napus</i> L.). <i>Genes</i> , 2018, 9, 168.	1.0	41
1239	In silico Phylogenetic Analysis of hAT Transposable Elements in Plants. <i>Genes</i> , 2018, 9, 284.	1.0	6
1240	Genomic signatures of mitonuclear coevolution across populations of <i>Tigriopus californicus</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1250-1257.	3.4	154
1241	De Novo Assembly and Characterization of the <i>Xenocatantops brachycerus</i> Transcriptome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 520.	1.8	17
1242	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	1.5	37
1243	Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018, 3, 870-880.	5.9	372
1244	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6585-E6594.	3.3	69
1245	In vitro genomic and proteomic evidence of a type IV pili-like structure in the fish pathogen <i>Piscirickettsia salmonis</i> . <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	9
1246	Response analysis of host <i>Spodoptera exigua</i> larvae to infection by <i>Heliothis virescens</i> ascovirus 3h (HvAV-3h) via transcriptome. <i>Scientific Reports</i> , 2018, 8, 5367.	1.6	26
1247	Identification of genes regulating ovary differentiation after pollination in hazel by comparative transcriptome analysis. <i>BMC Plant Biology</i> , 2018, 18, 84.	1.6	14
1248	Comparative genomics of <i>Pseudomonas syringae</i> reveals convergent gene gain and loss associated with specialization onto cherry ( <i>Prunus avium</i> ). <i>New Phytologist</i> , 2018, 219, 672-696.	3.5	52
1249	Genome-wide identification and characterization of cysteine-rich polycomb-like protein (CPP) family genes in cucumber ( <i>Cucumis sativus</i> ) and their roles in stress responses. <i>Biologia (Poland)</i> , 2018, 73, 425-435.	0.8	16
1250	MicroRNA Expression Analysis of Naked Silkworms. <i>Journal of Economic Entomology</i> , 2018, 111, 2876-2883.	0.8	4

#	ARTICLE	IF	CITATIONS
1251	Genome-wide identification of lipoxygenase gene family in cotton and functional characterization in response to abiotic stresses. <i>BMC Genomics</i> , 2018, 19, 599.	1.2	47
1252	The genome of a prasinoviruses-related freshwater virus reveals unusual diversity of phycodnaviruses. <i>BMC Genomics</i> , 2018, 19, 49.	1.2	10
1253	Genome Plasticity in Cultured <i>Leishmania donovani</i> : Comparison of Early and Late Passages. <i>Frontiers in Microbiology</i> , 2018, 9, 1279.	1.5	43
1254	The genome of the golden apple snail <i>Pomacea canaliculata</i> provides insight into stress tolerance and invasive adaptation. <i>GigaScience</i> , 2018, 7, .	3.3	68
1255	De novo transcriptomic analysis of the alimentary tract of the tephritid gall fly, <i>Procecidochares utilis</i> . <i>PLoS ONE</i> , 2018, 13, e0201679.	1.1	6
1256	Horizontal gene transfer plays a major role in the pathological convergence of <i>Xanthomonas</i> lineages on common bean. <i>BMC Genomics</i> , 2018, 19, 606.	1.2	38
1257	De novo transcriptomic assembly and mRNA expression patterns of <i>Botryosphaeria dothidea</i> infection with mycoviruses chrysovirus 1 (BdCV1) and partitivirus 1 (BdPV1). <i>Virology Journal</i> , 2018, 15, 126.	1.4	14
1258	Biology and genome of a newly discovered sibling species of <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2018, 9, 3216.	5.8	102
1259	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. <i>Scientific Reports</i> , 2018, 8, 12106.	1.6	2
1260	Tung Tree ( <i>Vernicia fordii</i> , Hemsl.) Genome and Transcriptome Sequencing Reveals Co-Ordinate Up-Regulation of Fatty Acid $\beta$ -Oxidation and Triacylglycerol Biosynthesis Pathways During Eleostearic Acid Accumulation in Seeds. <i>Plant and Cell Physiology</i> , 2018, 59, 1990-2003.	1.5	45
1261	Mammalian CYP2E1 gene triggered changes of relative ions fluxes, CaM content and genes expression profiles in <i>Petunia hybrida</i> cells to enhance resistance to formaldehyde. <i>Plant Cell, Tissue and Organ Culture</i> , 2018, 135, 433-444.	1.2	3
1262	Fungal Genomics. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
1263	Transcriptomic analysis of embryo development in the invasive snail <i>Pomacea canaliculata</i> . <i>Journal of Molluscan Studies</i> , 2018, 84, 233-239.	0.4	3
1264	Improved de novo genome assembly and analysis of the Chinese cucurbit <i>Siraitia grosvenorii</i> , also known as monk fruit or luo-han-guo. <i>GigaScience</i> , 2018, 7, .	3.3	32
1265	Novel RNA viruses within plant parasitic cyst nematodes. <i>PLoS ONE</i> , 2018, 13, e0193881.	1.1	15
1266	Comprehensive transcriptome analysis and flavonoid profiling of <i>Ginkgo</i> leaves reveals flavonoid content alterations in day-night cycles. <i>PLoS ONE</i> , 2018, 13, e0193897.	1.1	31
1267	Fungal Genome Annotation. <i>Methods in Molecular Biology</i> , 2018, 1775, 171-184.	0.4	14
1268	Comparative identification and evolutionary relationship of fatty acid desaturase ( <i>FAD</i> ) genes in some oil crops: the sunflower model for evaluation of gene expression pattern under drought stress. <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 846-857.	0.5	12

#	ARTICLE	IF	CITATIONS
1269	Identifying changes in the wheat kernel proteome under heat stress using iTRAQ. <i>Crop Journal</i> , 2018, 6, 600-610.	2.3	23
1270	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	4.7	303
1271	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019, 17, 517-530.	4.1	56
1272	Evolutionary and structure-function analysis elucidates diversification of prokaryotic and eukaryotic trehalases. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 2926-2937.	2.0	5
1273	Sequence Analysis. , 2019, , 292-322.		8
1274	GhKLCR1, a kinesin light chain-related gene, induces drought-stress sensitivity in <i>Arabidopsis</i> . <i>Science China Life Sciences</i> , 2019, 62, 63-75.	2.3	26
1275	Functional genetic discovery of enzymes using full-scan mass spectrometry metabolomics. <i>Biochemistry and Cell Biology</i> , 2019, 97, 73-84.	0.9	5
1276	Lysozyme-Assisted Photothermal Eradication of Methicillin-Resistant <i>Staphylococcus aureus</i> Infection and Accelerated Tissue Repair with Natural Melanosome Nanostructures. <i>ACS Nano</i> , 2019, 13, 11153-11167.	7.3	74
1277	A unique life cycle transition in the red seaweed <i>Pyropia yezoensis</i> depends on apospory. <i>Communications Biology</i> , 2019, 2, 299.	2.0	27
1278	HVA22 from citrus: A small gene family whose some members are involved in plant response to abiotic stress. <i>Plant Physiology and Biochemistry</i> , 2019, 142, 395-404.	2.8	16
1279	Integrated metabolomic and transcriptomic analyses suggest that high dietary lipid levels facilitate ovary development through the enhanced arachidonic acid metabolism, cholesterol biosynthesis and steroid hormone synthesis in Chinese sturgeon ( <i>Acipenser sinensis</i> ). <i>British Journal of Nutrition</i> , 2019, 122, 1230-1241.	1.2	27
1280	Comparative Transcriptome Analysis of Unusual Localized Skin Laxity in Sika Deer ( <i>Cervus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.9	0
1281	A chromosomal-level genome assembly for the insect vector for Chagas disease, <i>Triatoma rubrofasciata</i> . <i>GigaScience</i> , 2019, 8, .	3.3	21
1282	Candidate chemosensory genes identified from the greater wax moth, <i>Galleria mellonella</i> , through a transcriptomic analysis. <i>Scientific Reports</i> , 2019, 9, 10032.	1.6	26
1283	Risk alleles for tuberculosis infection associate with reduced immune reactivity in a wild mammalian host. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190914.	1.2	4
1284	Identifying <i>Verticillium dahliae</i> Resistance in Strawberry Through Disease Screening of Multiple Populations and Image Based Phenotyping. <i>Frontiers in Plant Science</i> , 2019, 10, 924.	1.7	18
1285	Transcriptome analysis of <i>Polygonatum cyrtoneura</i> Hua: identification of genes involved in polysaccharide biosynthesis. <i>Plant Methods</i> , 2019, 15, 65.	1.9	23
1286	Revisiting the Phylogenetic History of Helminths Through Genomics, the Case of the New <i>Echinococcus oligarthrus</i> Genome. <i>Frontiers in Genetics</i> , 2019, 10, 708.	1.1	12



#	ARTICLE	IF	CITATIONS
1287	Comprehensive analysis of WOX genes uncovers that WOX13 is involved in phytohormone-mediated fiber development in cotton. <i>BMC Plant Biology</i> , 2019, 19, 312.	1.6	28
1288	Widespread selection and gene flow shape the genomic landscape during a radiation of monkeyflowers. <i>PLoS Biology</i> , 2019, 17, e3000391.	2.6	111
1289	Label-Free Proteomic Analysis of Molecular Effects of 2-Methoxy-1,4-naphthoquinone on <i>Penicillium italicum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3459.	1.8	21
1290	Diversity of tryptophan halogenases in sponges of the genus <i>Aplysina</i> . <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	11
1291	The genome of the Black Bengal goat ( <i>Capra hircus</i> ). <i>BMC Research Notes</i> , 2019, 12, 362.	0.6	9
1292	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.	2.9	53
1293	Reference gene and small RNA data from multiple tissues of <i>Davidia involucreta</i> Baill. <i>Scientific Data</i> , 2019, 6, 181.	2.4	4
1294	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.	1.5	11
1295	Identification and Expression Analyses of Olfactory Gene Families in the Rice Grasshopper, <i>Oxya chinensis</i> , From Antennal Transcriptomes. <i>Frontiers in Physiology</i> , 2019, 10, 1223.	1.3	19
1296	Fine mapping of <i>Brassica napus</i> blackleg resistance gene <i>Rlm1</i> through bulked segregant RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 14600.	1.6	22
1297	Multi-Tissue Transcriptomes Yield Information on High-Altitude Adaptation and Sex-Determination in <i>Scutiger cf. sikimensis</i> . <i>Genes</i> , 2019, 10, 873.	1.0	1
1298	Effector mining from the <i>Erysiphe pisi</i> haustorial transcriptome identifies novel candidates involved in pea powdery mildew pathogenesis. <i>Molecular Plant Pathology</i> , 2019, 20, 1506-1522.	2.0	21
1299	A Chemosensory GPCR as a Potential Target to Control the Root-Knot Nematode <i>Meloidogyne incognita</i> Parasitism in Plants. <i>Molecules</i> , 2019, 24, 3798.	1.7	11
1300	A deep learning ensemble for function prediction of hypothetical proteins from pathogenic bacterial species. <i>Computational Biology and Chemistry</i> , 2019, 83, 107147.	1.1	15
1301	Small RNA inhibits infection by downy mildew pathogen <i>Hyaloperonospora arabidopsidis</i> . <i>Molecular Plant Pathology</i> , 2019, 20, 1523-1534.	2.0	28
1302	Genome-Wide Characterization and Expression Profiling of Squamosa Promoter Binding Protein-like (SBP) Transcription Factors in <i>Wheat</i> ( <i>Triticum aestivum</i> L.). <i>Agronomy</i> , 2019, 9, 527.	1.3	26
1303	A Transcriptomics Approach Reveals Putative Interaction of <i>Candidatus Liberibacter Solanacearum</i> with the Endoplasmic Reticulum of Its Psyllid Vector. <i>Insects</i> , 2019, 10, 279.	1.0	18
1304	Allorecognition upon Fungal Cell-Cell Contact Determines Social Cooperation and Impacts the Acquisition of Multicellularity. <i>Current Biology</i> , 2019, 29, 3006-3017.e3.	1.8	47

#	ARTICLE	IF	CITATIONS
1305	Capability for arsenic mobilization in groundwater is distributed across broad phylogenetic lineages. PLoS ONE, 2019, 14, e0221694.	1.1	15
1306	Immediate Effects of Ammonia Shock on Transcription and Composition of a Biogas Reactor Microbiome. Frontiers in Microbiology, 2019, 10, 2064.	1.5	18
1307	Comparative Genome Analyses Reveal the Genomic Traits and Host Plant Adaptations of <i>Flavobacterium akiainvivens</i> IK-1T. International Journal of Molecular Sciences, 2019, 20, 4910.	1.8	1
1308	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in <i>Streptomyces</i> . Applied and Environmental Microbiology, 2019, 85, .	1.4	16
1309	Structural and functional insights into TRiC chaperonin from a psychrophilic yeast, <i>Glaciozyma antarctica</i> . Cell Stress and Chaperones, 2019, 24, 351-368.	1.2	6
1310	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. GigaScience, 2019, 8, .	3.3	36
1311	In-depth analysis of the genome of <i>Trypanosoma evansi</i> , an etiologic agent of surra. Science China Life Sciences, 2019, 62, 406-419.	2.3	9
1312	Genome structure and evolution of <i>Antirrhinum majus</i> L. Nature Plants, 2019, 5, 174-183.	4.7	85
1313	Mechanistic elucidation of amphetamine metabolism by tyramine oxidase from human gut microbiota using molecular dynamics simulations. Journal of Cellular Biochemistry, 2019, 120, 11206-11215.	1.2	4
1314	The Genome of <i>Armadillidium vulgare</i> (Crustacea, Isopoda) Provides Insights into Sex Chromosome Evolution in the Context of Cytoplasmic Sex Determination. Molecular Biology and Evolution, 2019, 36, 727-741.	3.5	43
1315	Complementary Proteomics, Genomics approaches identifies potential pathogenicity/virulence factors in <i>Tilletia indica</i> induced under the influence of host factor. Scientific Reports, 2019, 9, 553.	1.6	16
1316	Secretome analysis of <i>Strongyloides venezuelensis</i> parasitic stages reveals that soluble and insoluble proteins are involved in its parasitism. Parasites and Vectors, 2019, 12, 21.	1.0	23
1317	Functional Annotation of Hypothetical Proteins Derived from Suppressive Subtraction Hybridization (SSH) Analysis Shows NPR1 (Non-Pathogenesis Related)-Like Activity. Agronomy, 2019, 9, 57.	1.3	2
1318	The Gene Toolkit Implicated in Functional Sex in Sparidae Hermaphrodites: Inferences From Comparative Transcriptomics. Frontiers in Genetics, 2018, 9, 749.	1.1	20
1319	Histopathological and proteomic analyses identify integrin- $\beta$ 1 as a potential mediator of phlebosclerosis in uremic patients. Clinical and Experimental Nephrology, 2019, 23, 1100-1108.	0.7	1
1320	Two-step non-nitro epimerization pathway in <i>Medicago truncatula</i> . Plant Journal, 2019, 100, 237-250.	2.8	5
1321	Rice susceptibility to root-knot nematodes is enhanced by the <i>Meloidogyne incognita</i> MSP18 effector gene. Planta, 2019, 250, 1215-1227.	1.6	23
1322	Metaproteomics: Sample Preparation and Methodological Considerations. Advances in Experimental Medicine and Biology, 2019, 1073, 187-215.	0.8	26

#	ARTICLE	IF	CITATIONS
1323	Survey of the <i>Bradysia odoriphaga</i> Transcriptome Using PacBio Single-Molecule Long-Read Sequencing. <i>Genes</i> , 2019, 10, 481.	1.0	8
1324	Proteomic Response of Three Marine Ammonia-Oxidizing Archaea to Hydrogen Peroxide and Their Metabolic Interactions with a Heterotrophic Alphaproteobacterium. <i>MSystems</i> , 2019, 4, .	1.7	57
1325	Emerging Sample Treatments in Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2019, , .	0.8	6
1326	A Method for Comprehensive Proteomic Analysis of Human Faecal Samples to Investigate Gut Dysbiosis in Patients with Cystic Fibrosis. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1073, 137-160.	0.8	5
1327	Candidate genes involved in spiroacetal biosynthesis in the oriental fruit fly, <i>Bactrocera dorsalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100601.	0.4	0
1328	Differential expression of innate and adaptive immune genes in the survivors of three gibel carp gynogenetic clones after herpesvirus challenge. <i>BMC Genomics</i> , 2019, 20, 432.	1.2	27
1329	Genome-wide analysis of magnesium transporter genes in <i>Solanum lycopersicum</i> . <i>Computational Biology and Chemistry</i> , 2019, 80, 498-511.	1.1	18
1330	The Draft Genome of Eggplant. <i>Compendium of Plant Genomes</i> , 2019, , 55-63.	0.3	0
1331	Systemic identification and analyses of genes potentially involved in chemosensory in the devastating tea pest <i>Basilepta melanopus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100586.	0.4	4
1332	Genome-Wide Identification and Expression Analyses of the bZIP Transcription Factor Genes in moso bamboo ( <i>Phyllostachys edulis</i> ). <i>International Journal of Molecular Sciences</i> , 2019, 20, 2203.	1.8	26
1333	Superantigen SpeA attenuates the biofilm forming capacity of <i>Streptococcus pyogenes</i> . <i>Journal of Microbiology</i> , 2019, 57, 626-636.	1.3	10
1334	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.	1.2	11
1335	Antimicrobial activity and carbohydrate metabolism in the bacterial metagenome of the soil-living invertebrate <i>Folsomia candida</i> . <i>Scientific Reports</i> , 2019, 9, 7308.	1.6	13
1336	Prediction and characterisation of lantibiotic structures with molecular modelling and molecular dynamics simulations. <i>Scientific Reports</i> , 2019, 9, 7169.	1.6	10
1337	Long-lived <i>Temnothorax</i> ant queens switch from investment in immunity to antioxidant production with age. <i>Scientific Reports</i> , 2019, 9, 7270.	1.6	39
1338	Candidate genes coding for odorant binding proteins and chemosensory proteins identified from dissected antennae and mouthparts of the southern green stink bug <i>Nezara viridula</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100594.	0.4	5
1339	Genome-Wide Identification and Comparative Expression Profile Analysis of the Long-Chain Acyl-CoA synthetase (LACS) Gene Family in Two Different Oil Content Cultivars of <i>Brassica napus</i> . <i>Biochemical Genetics</i> , 2019, 57, 781-800.	0.8	11
1340	The genomes of pecan and Chinese hickory provide insights into <i>Carya</i> evolution and nut nutrition. <i>GigaScience</i> , 2019, 8, .	3.3	88

#	ARTICLE	IF	CITATIONS
1341	Impact of Combined Acidic and Hyperosmotic Shock Conditions on the Proteome of <i>Listeria monocytogenes</i> ATCC 19115 in a Time-Course Study. <i>Journal of Food Quality</i> , 2019, 2019, 1-12.	1.4	2
1342	CIDEA and CIDEC are regulated by CREB and are not induced during fasting in grass carp <i>Ctenopharyngodon idella</i> adipocytes. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2019, 234, 50-57.	0.7	1
1343	Saprotrophic yeasts formerly classified as <i>Pseudozyma</i> have retained a large effector arsenal, including functional Pep1 orthologs. <i>Mycological Progress</i> , 2019, 18, 763-768.	0.5	19
1344	Machine-Learning-Based Predictor of Human Bacteria Protein-Protein Interactions by Incorporating Comprehensive Host-Network Properties. <i>Journal of Proteome Research</i> , 2019, 18, 2195-2205.	1.8	39
1345	Genome sequence analysis of the fairy ring-forming fungus <i>Lepista sordida</i> and gene candidates for interaction with plants. <i>Scientific Reports</i> , 2019, 9, 5888.	1.6	15
1346	Chromosome-Level Assembly of the Chinese Seabass ( <i>Lateolabrax maculatus</i> ) Genome. <i>Frontiers in Genetics</i> , 2019, 10, 275.	1.1	33
1347	A homologue of the fungal tetraspanin Pls1 is required for <i>Epichloa festucae</i> expression formation and establishment of a mutualistic interaction with <i>Lolium perenne</i> . <i>Molecular Plant Pathology</i> , 2019, 20, 961-975.	2.0	10
1348	Differential gene expression in response to eCry3.1Ab ingestion in an unselected and eCry3.1Ab-selected western corn rootworm ( <i>Diabrotica virgifera virgifera</i> LeConte) population. <i>Scientific Reports</i> , 2019, 9, 4896.	1.6	12
1349	MapMan4: A Refined Protein Classification and Annotation Framework Applicable to Multi-Omics Data Analysis. <i>Molecular Plant</i> , 2019, 12, 879-892.	3.9	353
1350	Caffeine Content and Related Gene Expression: Novel Insight into Caffeine Metabolism in <i>Camellia</i> Plants Containing Low, Normal, and High Caffeine Concentrations. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 3400-3411.	2.4	61
1351	Genome-Wide Identification, Sequence Variation, and Expression of the Glycerol-3-Phosphate Acyltransferase (GPAT) Gene Family in <i>Gossypium</i> . <i>Frontiers in Genetics</i> , 2019, 10, 116.	1.1	22
1352	Structural bioinformatics insights into the CARD-CARD interaction mediated by the mitochondrial antiviral signaling protein of black carp. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12534-12543.	1.2	8
1353	TmToll-7 Plays a Crucial Role in Innate Immune Responses Against Gram-Negative Bacteria by Regulating 5 AMP Genes in <i>Tenebrio molitor</i> . <i>Frontiers in Immunology</i> , 2019, 10, 310.	2.2	26
1354	Acquisition and Loss of Secondary Metabolites Shaped the Evolutionary Path of Three Emerging Phytopathogens of Wheat. <i>Genome Biology and Evolution</i> , 2019, 11, 890-905.	1.1	22
1355	Alternative Transcription at Venom Genes and Its Role as a Complementary Mechanism for the Generation of Venom Complexity in the Common House Spider. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	17
1356	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in <i>Taxodium Zhongshanshan</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1225.	1.8	32
1357	Transcriptome profiling of faba bean ( <i>Vicia faba</i> L.) drought-tolerant variety hassawi-2 under drought stress using RNA sequencing. <i>Electronic Journal of Biotechnology</i> , 2019, 39, 15-29.	1.2	19
1358	Cardiac proteomics reveals the potential mechanism of microtubule associated protein 4 phosphorylation-induced mitochondrial dysfunction. <i>Burns and Trauma</i> , 2019, 7, 8.	2.3	5

#	ARTICLE	IF	CITATIONS
1359	<i>De novo</i> genome assembly of the white-spotted flower chafer (<i>Protaetia brevitarsis</i>). GigaScience, 2019, 8, .	3.3	28
1360	Comparative Study of Immune Reaction Against Bacterial Infection From Transcriptome Analysis. Frontiers in Immunology, 2019, 10, 153.	2.2	40
1361	Transcriptional differences provide insight into environmental acclimatization in wild amur ide (<i>Leuciscus waleckii</i>) during spawning migration from alkalized lake to freshwater river. Genomics, 2019, 111, 267-276.	1.3	15
1362	Shift in <i>Bacillus</i> sp. JR3 esterase LipJ activity profile after addition of essential residues from family I.5 thermophilic lipases. Biochemical Engineering Journal, 2019, 144, 166-176.	1.8	2
1363	Optimisation of protein extraction for in-depth profiling of the cereal grain proteome. Journal of Proteomics, 2019, 197, 23-33.	1.2	44
1364	Draft genome of the river water buffalo. Ecology and Evolution, 2019, 9, 3378-3388.	0.8	32
1365	Transcriptome Atlas by Long-Read RNA Sequencing: Contribution to a Reference Transcriptome. , 2019, , .		0
1366	Prediction of Protein Interactions in Rice and Blast Fungus Using Machine Learning. , 2019, , .		3
1367	Parallel selection on ecologically relevant gene functions in the transcriptomes of highly diversifying salmonids. BMC Genomics, 2019, 20, 1010.	1.2	8
1368	SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest. , 2019, , .		7
1369	Identification of watermelon heat shock protein members and tissue-specific gene expression analysis under combined drought and heat stresses. Turkish Journal of Biology, 2019, 43, 404-419.	2.1	11
1370	Genome-Resolved Metagenomics Extends the Environmental Distribution of the <i>Verrucomicrobia</i> Phylum to the Deep Terrestrial Subsurface. MSphere, 2019, 4, .	1.3	38
1371	Phenotypic analysis combined with tandem mass tags (TMT) labeling reveal the heterogeneity of strawberry stolon buds. BMC Plant Biology, 2019, 19, 505.	1.6	8
1372	Non-Specific Lipid Transfer Proteins in <i>Triticum kiharae</i> Dorof. et Migush.: Identification, Characterization and Expression Profiling in Response to Pathogens and Resistance Inducers. Pathogens, 2019, 8, 221.	1.2	15
1373	Comparative Genome-wide Analysis and Expression Profiling of Histone Acetyltransferase (HAT) Gene Family in Response to Hormonal Applications, Metal and Abiotic Stresses in Cotton. International Journal of Molecular Sciences, 2019, 20, 5311.	1.8	26
1374	Genome-wide characterization of the UDP-glycosyltransferase gene family in upland cotton. 3 Biotech, 2019, 9, 453.	1.1	17
1375	De novo transcriptome analysis and identification of genes associated with immunity, detoxification and energy metabolism from the fat body of the tephritid gall fly, <i>Procecidochares utilis</i> . PLoS ONE, 2019, 14, e0226039.	1.1	5
1376	Annotated Draft Genomes of Two Caddisfly Species <i>Plectrocnemia conspersa</i> CURTIS and <i>Hydropsyche tenuis</i> NAVAS (Insecta: Trichoptera). Genome Biology and Evolution, 2019, 11, 3445-3451.	1.1	21

#	ARTICLE	IF	CITATIONS
1377	Evolution of <i>Aspergillus oryzae</i> before and after domestication inferred by large-scale comparative genomic analysis. <i>DNA Research</i> , 2019, 26, 465-472.	1.5	26
1378	Genome-Based Metabolic Reconstruction of a Novel Uncultivated Freshwater Magnetotactic coccus <i>Ca. Magnetaquicoccus inordinatus</i> -UR-1, and Proposal of a Candidate Family <i>Ca. Magnetaquicoccaceae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2290.	1.5	33
1379	Transcriptome Profiling Unravels a Vital Role of Pectin and Pectinase in Anther Dehiscence in <i>Chrysanthemum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5865.	1.8	6
1380	<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, .	3.3	20
1381	Comparative Proteomic Analysis Reveals Immune Competence in Hemolymph of <i>Bombyx mori</i> Pupa Parasitized by Silkworm Maggot <i>Exorista sorbillans</i> . <i>Insects</i> , 2019, 10, 413.	1.0	8
1382	Massive expansion and diversity of nicotinic acetylcholine receptors in lophotrochozoans. <i>BMC Genomics</i> , 2019, 20, 937.	1.2	32
1383	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. <i>BMC Genomics</i> , 2019, 20, 976.	1.2	96
1384	iTRAQ-Based Quantitative Proteomic Analysis of Digestive Juice across the First 48 Hours of the Fifth Instar in Silkworm Larvae. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6113.	1.8	5
1385	Transcriptomic Evidence of Adaptive Evolution of the Epiphytic Fern <i>Asplenium nidus</i> . <i>International Journal of Genomics</i> , 2019, 2019, 1-9.	0.8	15
1386	Characterization and proteomic profiling of pancreatic cancer-derived serum exosomes. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 988-999.	1.2	36
1387	Predicting and visualizing features of CRISPR-Cas systems. <i>Methods in Enzymology</i> , 2019, 616, 1-25.	0.4	13
1388	Population Genetics and Characterization of <i>Campylobacter jejuni</i> Isolates from Western Jackdaws and Game Birds in Finland. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
1389	Annotating the "hypothetical" in hypothetical proteins: In-silico analysis of uncharacterised proteins for the Apicomplexan parasite, <i>Neospora caninum</i> . <i>Veterinary Parasitology</i> , 2019, 265, 29-37.	0.7	4
1390	Hypoxic and Cold Adaptation Insights from the Himalayan Marmot Genome. <i>IScience</i> , 2019, 11, 519-530.	1.9	34
1391	Candidate olfactory genes identified in <i>Heortia vitessoides</i> (Lepidoptera: Crambidae) by antennal transcriptome analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 117-130.	0.4	7
1392	Novel Endotype Xanthanase from Xanthan-Degrading <i>Microbacterium</i> sp. Strain XT11. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
1393	Functional annotation of operome from <i>Methanothermobacter thermautotrophicus</i> H: An insight to metabolic gap filling. <i>International Journal of Biological Macromolecules</i> , 2019, 123, 350-362.	3.6	14
1394	Comparative transcriptome analysis highlights the hormone effects on somatic embryogenesis in <i>Catalpa bungei</i> . <i>Plant Reproduction</i> , 2019, 32, 141-151.	1.3	22

#	ARTICLE	IF	CITATIONS
1395	<i>Rh6</i> gene modulates the visual mechanism of host utilization in fruit fly <i>Bactrocera minax</i> . <i>Pest Management Science</i> , 2019, 75, 1621-1629.	1.7	37
1396	CYC27 Synthetic Derivative of Bromophenol from Red Alga <i>Rhodomela confervoides</i> : Anti-Diabetic Effects of Sensitizing Insulin Signaling Pathways and Modulating RNA Splicing-Associated RBPs. <i>Marine Drugs</i> , 2019, 17, 49.	2.2	9
1397	Transcript profiling reveals an important role of cell wall remodeling and hormone signaling under salt stress in garlic. <i>Plant Physiology and Biochemistry</i> , 2019, 135, 87-98.	2.8	32
1398	Integrative Transcriptome and Proteome Analysis Identifies Major Metabolic Pathways Involved in Pepper Fruit Development. <i>Journal of Proteome Research</i> , 2019, 18, 982-994.	1.8	40
1399	Quantitative Proteomics of Potato Leaves Infected with <i>Phytophthora infestans</i> Provides Insights into Coordinated and Altered Protein Expression during Early and Late Disease Stages. <i>International Journal of Molecular Sciences</i> , 2019, 20, 136.	1.8	20
1400	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee ( <i>Halictidae: Nomia melanderi</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 625-634.	0.8	19
1401	Defensin-like peptides in wheat analyzed by whole-transcriptome sequencing: a focus on structural diversity and role in induced resistance. <i>PeerJ</i> , 2019, 7, e6125.	0.9	17
1402	A unique life-strategy of an endophytic yeast <i>Rhodotorula mucilaginosa</i> JTA-S1—a comparative genomics viewpoint. <i>DNA Research</i> , 2019, 26, 131-146.	1.5	25
1403	Transcriptome-wide identification and characterization of resistant gene analogs (RGAs) of ginger ( <i>Zingiber officinale</i> Rosc.) and mango ginger ( <i>Curcuma amada</i> Roxb.) under stress induced by pathogen. <i>Scientia Horticulturae</i> , 2019, 248, 81-88.	1.7	5
1404	De novo assembly and transcriptome of <i>Pfaffia glomerata</i> uncovers the role of photoautotrophy and the P450 family genes in 20-hydroxyecdysone production. <i>Protoplasma</i> , 2019, 256, 601-614.	1.0	10
1405	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.	2.0	25
1406	Molecular evolution and functional characterisation of insulin related peptides in molluscs: Contributions of <i>Crassostrea gigas</i> genomic and transcriptomic-wide screening. <i>General and Comparative Endocrinology</i> , 2019, 271, 15-29.	0.8	24
1407	RNA-seq coupled to proteomic analysis reveals high sperm proteome variation between two closely related marine mussel species. <i>Journal of Proteomics</i> , 2019, 192, 169-187.	1.2	14
1408	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019, 17, 881-892.	4.1	79
1409	Draft genome analysis of lignocellulolytic enzymes producing <i>Aspergillus terreus</i> with structural insight of Î <sup>2</sup> -glucosidases through molecular docking approach. <i>International Journal of Biological Macromolecules</i> , 2019, 125, 181-190.	3.6	28
1410	Genomic and transcriptomic insights into the ecology and metabolism of benthic archaeal cosmopolitan, Thermopfundales (MBC-D archaea). <i>ISME Journal</i> , 2019, 13, 885-901.	4.4	92
1411	A full-length transcriptome of <i>Sepia esculenta</i> using a combination of single-molecule long-read (SMRT) and Illumina sequencing. <i>Marine Genomics</i> , 2019, 43, 54-57.	0.4	20
1412	Sexual dimorphism and rapid turnover in gene expression in pre-reproductive seedlings of a dioecious herb. <i>Annals of Botany</i> , 2019, 123, 1119-1131.	1.4	23

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1413	Functional characterisation of cellobiohydrolase I (Cbh1) from <i>Trichoderma virens</i> UKM1 expressed in <i>Aspergillus niger</i> . <i>Protein Expression and Purification</i> , 2019, 154, 52-61.	0.6	14
1414	<i>De novo</i> transcriptome combined with spectrophotometry and gas chromatography-mass spectrometer (GC-MS) reveals differentially expressed genes during accumulation of secondary metabolites in purple-leaf tea ( <i>Camellia sinensis</i> cv Hongyafoshou). <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 349-367.	0.9	36
1415	Genome-wide identification and characterization of <i>HSP</i> gene superfamily in whitefly ( <i>Bemisia tabaci</i> ) and expression profiling analysis under temperature stress. <i>Insect Science</i> , 2019, 26, 44-57.	1.5	64
1416	Bioinformatical analysis and prediction of <i>Nicotiana benthamiana</i> bHLH transcription factors in <i>Phytophthora parasitica</i> resistance. <i>Genomics</i> , 2019, 111, 473-482.	1.3	14
1417	Transcriptome analysis of <i>Oncidium</i> petals provides new insights into the initiation of petal senescence. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 12-23.	0.9	5
1418	The genome-wide transcription response underlying the dorsal processes and dorsal setae of the body in <i>Dasyaphis mirabilis</i> (Aphididae: Calaphidinae). <i>Oriental Insects</i> , 2019, 53, 1-18.	0.1	1
1419	Transcriptome wide characterization of water deficit responsive grape mTERF transcription. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 102-113.	0.9	3
1420	Transcriptome analysis of Snow Mountain Garlic for unraveling the organosulfur metabolic pathway. <i>Genomics</i> , 2020, 112, 99-107.	1.3	15
1421	Whole-genome sequencing and analysis of the Chinese herbal plant <i>Gelsemium elegans</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 374-382.	5.7	29
1422	Identification and expression analysis of odorant binding proteins and chemosensory proteins from dissected antennae and mouthparts of the rice bug <i>Leptocorisa acuta</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100631.	0.4	6
1423	NBS-LRR genes—Plant health sentinels: Structure, roles, evolution and biotechnological applications. , 2020, , 63-120.		9
1424	The transcription factor Zt107320 affects the dimorphic switch, growth and virulence of the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , 2020, 21, 124-138.	2.0	22
1425	Insights into the strategy of micro-environmental adaptation: Transcriptomic analysis of two alvinocaridid shrimps at a hydrothermal vent. <i>PLoS ONE</i> , 2020, 15, e0227587.	1.1	8
1426	Domestication and breeding changed tomato fruit transcriptome. <i>Journal of Integrative Agriculture</i> , 2020, 19, 120-132.	1.7	18
1427	Bioinformatics of excretory/secretory proteins of <i>Toxoplasma gondii</i> strain ME49. <i>Microbial Pathogenesis</i> , 2020, 140, 103951.	1.3	3
1428	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.	2.8	6
1429	Study of structural and molecular interaction for the catalytic activity of cellulases: An insight in cellulose hydrolysis for higher bioethanol yield. <i>Journal of Molecular Structure</i> , 2020, 1204, 127547.	1.8	23
1430	Promotion of the Rapid Growth in <i>Haematococcus pluvialis</i> Under 0.16% CO <sub>2</sub> Condition Revealed by Transcriptome and Metabolomic Analysis. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1177-1190.	2.8	2



#	ARTICLE	IF	CITATIONS
1431	Molecular characterization and expression analysis reveal the roles of Cys2/His2 zinc-finger transcription factors during flower development of <i>Brassica rapa</i> subsp. <i>chinensis</i> . <i>Plant Molecular Biology</i> , 2020, 102, 123-141.	2.0	12
1432	Transcriptomic Changes of <i>Piscirickettsia salmonis</i> During Intracellular Growth in a Salmon Macrophage-Like Cell Line. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 426.	1.8	27
1433	Graph Theory-Based Sequence Descriptors as Remote Homology Predictors. <i>Biomolecules</i> , 2020, 10, 26.	1.8	13
1434	Photosynthetic characterization and expression profiles of sugarcane infected by Sugarcane mosaic virus (SCMV). <i>Photosynthesis Research</i> , 2021, 150, 279-294.	1.6	11
1435	A Cu <sup>2+</sup> -only superoxide dismutase from stripe rust fungi functions as a virulence factor deployed for counter defense against host <sup>+</sup> -derived oxidative stress. <i>Environmental Microbiology</i> , 2020, 22, 5309-5326.	1.8	11
1436	Blue genome: chromosome <sup>+</sup> -scale genome reveals the evolutionary and molecular basis of indigo biosynthesis in <i>Strobilanthes cusia</i> . <i>Plant Journal</i> , 2020, 104, 864-879.	2.8	15
1437	Genome Sequence of the Human Opportunistic Fungus <i>Arthrocladium fulminans</i> (CBS 136243). G3: Genes, Genomes, Genetics, 2020, 10, 1817-1821.	0.8	3
1438	Expression and biochemical characterization of two recombinant fucoidanases from the marine bacterium <i>Wenyngzhuangia fucanilytica</i> CZ1127T. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 3025-3037.	3.6	20
1439	Over-expression of rice R1-type MYB transcription factor confers different abiotic stress tolerance in transgenic <i>Arabidopsis</i> . <i>Ecotoxicology and Environmental Safety</i> , 2020, 206, 111361.	2.9	18
1440	The glutathione peroxidase family of <i>Theobroma cacao</i> : Involvement in the oxidative stress during witches' broom disease. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 3698-3708.	3.6	12
1441	Structural and functional annotation of PR/SET Domain (PRDM) protein family: In-silico study elaborating role of PRDM12 mutation in congenital insensitivity to pain. <i>Computational Biology and Chemistry</i> , 2020, 89, 107382.	1.1	2
1442	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	1.1	29
1443	The high <sup>+</sup> -quality genome of diploid strawberry ( <i>Fragaria nilgerrensis</i> ) provides new insights into anthocyanin accumulation. <i>Plant Biotechnology Journal</i> , 2020, 18, 1908-1924.	4.1	51
1444	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020, 50, 101990.	2.4	18
1445	Transcriptome studies of the floodwater mosquito, <i>Aedes vexans</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18 Research, 2020, 50, 563-574.	0.6	5
1446	Transcriptomic analysis of flower opening response to relatively low temperatures in <i>Osmanthus fragrans</i> . <i>BMC Plant Biology</i> , 2020, 20, 337.	1.6	8
1447	First Genome Sequences of Two Multidrug-Resistant <i>Candida haemulonii</i> var. <i>vulnera</i> Isolates From Pediatric Patients With Candidemia. <i>Frontiers in Microbiology</i> , 2020, 11, 1535.	1.5	8
1448	Identification and Expression Profiling of Chemosensory Genes in <i>Hermetia illucens</i> via a Transcriptomic Analysis. <i>Frontiers in Physiology</i> , 2020, 11, 720.	1.3	10

#	ARTICLE	IF	CITATIONS
1449	Comparative Genomics Reveals Novel Target Genes towards Specific Control of Plant-Parasitic Nematodes. <i>Genes</i> , 2020, 11, 1347.	1.0	29
1450	Proteomics and Lipidomics Investigations to Decipher the Behavior of <i>Willaertia magna</i> C2c Maky According to Different Culture Modes. <i>Microorganisms</i> , 2020, 8, 1791.	1.6	1
1451	A chimeric gene paternally instructs female sex determination in the haplodiploid wasp <i>Nasonia</i> . <i>Science</i> , 2020, 370, 1115-1118.	6.0	35
1452	Genome plasticity in <i>Paramecium bursaria</i> revealed by population genomics. <i>BMC Biology</i> , 2020, 18, 180.	1.7	16
1453	Phylogenetic analysis of cell-cycle regulatory proteins within the Symbiodiniaceae. <i>Scientific Reports</i> , 2020, 10, 20473.	1.6	1
1454	In silico studies on structural, functional, and evolutionary analysis of bacterial chromate reductase family responsible for high chromate bioremediation efficiency. <i>SN Applied Sciences</i> , 2020, 2, 1.	1.5	5
1455	CitrusKB: a comprehensive knowledge base for transcriptome and interactome of <i>Citrus</i> spp. infected by <i>Xanthomonas citri</i> subsp. <i>citri</i> at different infection stages. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	2
1456	Synthetic DNA and biosecurity: Nuances of predicting pathogenicity and the impetus for novel computational approaches for screening oligonucleotides. <i>PLoS Pathogens</i> , 2020, 16, e1008649.	2.1	8
1457	Proteomic analysis of extracellular vesicles released from heat-stroked hepatocytes reveals promotion of programmed cell death pathway. <i>Biomedicine and Pharmacotherapy</i> , 2020, 129, 110489.	2.5	12
1458	Genomics and Virulence of <i>Fonsecaea pugnacius</i> , Agent of Disseminated Chromoblastomycosis. <i>Frontiers in Genetics</i> , 2020, 11, 822.	1.1	5
1459	Integrated single-molecule long-read sequencing and Illumina sequencing reveal the resistance mechanism of <i>Psathyrostachys huashanica</i> in response to barley yellow dwarf virus-GAV. <i>Phytopathology Research</i> , 2020, 2, .	0.9	9
1460	Chromosome-level genome assembly of the coastal horseshoe crab ( <i>Tachypleus gigas</i> ). <i>Molecular Ecology Resources</i> , 2020, 20, 1748-1760.	2.2	20
1461	Genome-wide identification and comparative analysis of resistance genes in <i>Brassica juncea</i> . <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	17
1462	The Droserin 1 PSI: A Membrane-Interacting Antimicrobial Peptide from the Carnivorous Plant <i>Drosera capensis</i> . <i>Biomolecules</i> , 2020, 10, 1069.	1.8	7
1463	cAMP-dependent protein kinase A in grass carp <i>Ctenopharyngodon idella</i> : Molecular characterization, gene structure, tissue distribution and mRNA expression in endoplasmic reticulum stress-induced adipocyte lipolysis. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2020, 250, 110479.	0.7	5
1464	Evolution and Expression of the Membrane Attack Complex and Perforin Gene Family in the Poaceae. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5736.	1.8	14
1465	<i>Aedes aegypti</i> from Amazon Basin Harbor High Diversity of Novel Viral Species. <i>Viruses</i> , 2020, 12, 866.	1.5	12
1466	&lt;p>&gt;Analysis of Differential Expression Proteins of Paclitaxel-Treated Lung Adenocarcinoma Cell A549 Using Tandem Mass Tag-Based Quantitative Proteomics&lt;p>&gt;. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 10297-10313.	1.0	7

#	ARTICLE	IF	CITATIONS
1467	Tissue-Specific Transcriptome Analysis Reveals Candidate Transcripts Associated with the Process of Programmed B Chromosome Elimination in <i>Aegilops speltoides</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7596.	1.8	5
1468	Identification and Expression of the Multidrug and Toxic Compound Extrusion (MATE) Gene Family in <i>Capsicum annuum</i> and <i>Solanum tuberosum</i> . <i>Plants</i> , 2020, 9, 1448.	1.6	12
1469	Genome assembly and annotation of <i>Meloidogyne enterolobii</i> , an emerging parthenogenetic root-knot nematode. <i>Scientific Data</i> , 2020, 7, 324.	2.4	33
1470	LSTrAP-Crowd: prediction of novel components of bacterial ribosomes with crowd-sourced analysis of RNA sequencing data. <i>BMC Biology</i> , 2020, 18, 114.	1.7	8
1471	Draft Genome Sequences of <i>Bacillus</i> and <i>Paenibacillus</i> Species Isolated from Seeds of <i>Citrullus lanata</i> (Watermelon), <i>Cucurbita moschata</i> (Butternut Squash), and <i>Cucurbita pepo</i> L. var. <i>pepo</i> L. (Pumpkin). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
1472	Metabolic diversification of anaerobic methanotrophic archaea in a deep-sea cold seep. <i>Marine Life Science and Technology</i> , 2020, 2, 431-441.	1.8	17
1473	PacBio Long-Read Sequencing Transcriptome Dataset of Adult <i>Harmonia axyridis</i> Under Diapause Inducing and Reproductive Inducing Photoperiod. <i>Frontiers in Genetics</i> , 2020, 11, 1010.	1.1	3
1474	Toxicological and molecular profiling of insecticide resistance in a Brazilian strain of fall armyworm resistant to Bt Cry1 proteins. <i>Pest Management Science</i> , 2021, 77, 3713-3726.	1.7	29
1475	The Regulatory Network of CMPG1-V in Wheat- <i>Blumeria graminis</i> f. sp. <i>tritici</i> Interaction Revealed by Temporal Profiling Using RNA-Seq. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5967.	1.8	6
1476	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. <i>Communications Biology</i> , 2020, 3, 502.	2.0	36
1477	De Novo Transcriptomic and Metabolomic Analyses Reveal the Ecological Adaptation of High-Altitude <i>Bombus pyrosoma</i> . <i>Insects</i> , 2020, 11, 631.	1.0	11
1478	Comparative iTRAQ proteomic profiling of proteins associated with the adaptation of brown planthopper to moderately resistant vs. susceptible rice varieties. <i>PLoS ONE</i> , 2020, 15, e0238549.	1.1	6
1479	De novo sequencing, assembly and functional annotation of <i>Armillaria borealis</i> genome. <i>BMC Genomics</i> , 2020, 21, 534.	1.2	7
1480	Hybrid genome assembly and functional annotation reveals insights on lipid biosynthesis of oleaginous native isolate <i>Parachlorella kessleri</i> , a potential industrial strain for production of biofuel precursors. <i>Algal Research</i> , 2020, 52, 102118.	2.4	8
1481	Comparative transcriptomics indicates endogenous differences in detoxification capacity after formic acid treatment between honey bees and varroa mites. <i>Scientific Reports</i> , 2020, 10, 21943.	1.6	9
1482	Identification, Phylogeny, and Comparative Expression of the Lipoxygenase 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.	1.8	13
1483	High-Resolution Linkage Map and QTL Analyses of Fruit Firmness in Autotetraploid Blueberry. <i>Frontiers in Plant Science</i> , 2020, 11, 562171.	1.7	19
1484	Melon short internode (CmSi) encodes an ERECTA-like receptor kinase regulating stem elongation through auxin signaling. <i>Horticulture Research</i> , 2020, 7, 202.	2.9	14

#	ARTICLE	IF	CITATIONS
1485	Whole genome analysis of the koa wilt pathogen ( <i>Fusarium oxysporum</i> f. sp. <i>koae</i> ) and the development of molecular tools for early detection and monitoring. <i>BMC Genomics</i> , 2020, 21, 764.	1.2	11
1486	The <i>Staphylococcus aureus</i> Cystine Transporters TcyABC and TcyP Facilitate Nutrient Sulfur Acquisition during Infection. <i>Infection and Immunity</i> , 2020, 88, .	1.0	16
1487	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. <i>Genome Biology</i> , 2020, 21, 119.	3.8	40
1488	Comparative transcriptome analysis reveals the responses of winter rye to cold stress. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	5
1489	Chromosome-level assembly of the horseshoe crab genome provides insights into its genome evolution. <i>Nature Communications</i> , 2020, 11, 2322.	5.8	57
1490	iMarmot: an integrative platform for comparative and functional genomics of marmots. <i>BMC Genomics</i> , 2020, 21, 266.	1.2	3
1491	Analyses of chemosensory genes provide insight into the evolution of behavioral differences to phytochemicals in <i>Bactrocera</i> species. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106858.	1.2	12
1492	In Silico Identification of Gene Families Encoding Cysteine-Rich Peptides in <i>Solanum lycopersicum</i> L.. <i>Russian Journal of Genetics</i> , 2020, 56, 572-579.	0.2	1
1493	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.	1.1	0
1494	Functional characterization and reclassification of an enzyme previously proposed to be a limonoid UDP-glucosyltransferase. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 4870-4878.	1.7	3
1495	Small RNA and Transcriptome Sequencing Reveals miRNA Regulation of Floral Thermogenesis in <i>Nelumbo nucifera</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 3324.	1.8	9
1496	Draft genome of the famous ornamental plant <i>Paeonia suffruticosa</i> . <i>Ecology and Evolution</i> , 2020, 10, 4518-4530.	0.8	34
1497	EnzymeMiner: automated mining of soluble enzymes with diverse structures, catalytic properties and stabilities. <i>Nucleic Acids Research</i> , 2020, 48, W104-W109.	6.5	51
1498	Draft Genome Sequence of <i>Bacillus</i> sp. Strain EKM601B (Phylum Firmicutes ), Living inside the Seeds of <i>Luffa acutangula</i> (Chinese Okra). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1499	High-quality chromosome-scale assembly of the walnut ( <i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	3.3	83
1500	Higher-order Markov models for metagenomic sequence classification. <i>Bioinformatics</i> , 2020, 36, 4130-4136.	1.8	6
1501	Dissecting the genome of star fruit ( <i>Averrhoa carambola</i> L.). <i>Horticulture Research</i> , 2020, 7, 94.	2.9	16
1502	Non-homology-based prediction of gene functions in maize ( <i>Zea mays</i> ssp. <i>mays</i> ). <i>Plant Genome</i> , 2020, 13, e20015.	1.6	7

#	ARTICLE	IF	CITATIONS
1503	Nuclear factor- $\kappa$ B subunit p65 is involved in lipopolysaccharide-induced lipid accumulation via regulating DGAT1b in <i>Ctenopharyngodon idellus</i> kidney cells. <i>Fish and Shellfish Immunology</i> , 2020, 105, 71-77.	1.6	4
1504	Novel partiti-like viruses are conditional mutualistic symbionts in their normal lepidopteran host, African armyworm, but parasitic in a novel host, Fall armyworm. <i>PLoS Pathogens</i> , 2020, 16, e1008467.	2.1	34
1505	Comparative analyses of caste, sex, and developmental stage-specific transcriptomes in two <i>Temnothorax</i> ants. <i>Ecology and Evolution</i> , 2020, 10, 4193-4203.	0.8	6
1506	Identification and qualitative characterization of new therapeutic targets in <i>Stenotrophomonas maltophilia</i> through in silico proteome exploration. <i>Microbial Pathogenesis</i> , 2020, 149, 104293.	1.3	11
1507	Comprehensive Phosphoproteomic Analysis of Pepper Fruit Development Provides Insight into Plant Signaling Transduction. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1962.	1.8	11
1508	Genome Sequence Analysis of <i>Auricularia heimuer</i> Combined with Genetic Linkage Map. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 37.	1.5	14
1509	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	2.4	8
1510	Chromosome-level analysis of the <i>Crassostrea hongkongensis</i> genome reveals extensive duplication of immune-related genes in bivalves. <i>Molecular Ecology Resources</i> , 2020, 20, 980-994.	2.2	45
1511	Novel Cell-Virus-Virophage Tripartite Infection Systems Discovered in the Freshwater Lake Dishui Lake in Shanghai, China. <i>Journal of Virology</i> , 2020, 94, .	1.5	17
1512	Polyhydroxyalkanoate (PHA) synthase genes and PHA-associated gene clusters in <i>Pseudomonas</i> spp. and <i>Janthinobacterium</i> spp. isolated from Antarctica. <i>Journal of Biotechnology</i> , 2020, 313, 18-28.	1.9	31
1513	Comparative Transcriptomic Response of Two <i>Pinus</i> Species to Infection with the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> . <i>Forests</i> , 2020, 11, 204.	0.9	19
1514	Transcriptomic analysis of hookworm <i>Ancylostoma ceylanicum</i> life cycle stages reveals changes in G-protein coupled receptor diversity associated with the onset of parasitism. <i>International Journal for Parasitology</i> , 2020, 50, 603-610.	1.3	9
1515	Quantitative proteomic analysis of human plasma using tandem mass tags to identify novel biomarkers for herpes zoster. <i>Journal of Proteomics</i> , 2020, 225, 103879.	1.2	11
1516	Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. <i>MSystems</i> , 2020, 5, .	1.7	23
1517	Identification and characterization of two isoforms of acyl-coenzyme A oxidase 1 gene and their expression in fasting-induced grass carp <i>Ctenopharyngodon idella</i> adipocyte lipolysis. <i>Fish Physiology and Biochemistry</i> , 2020, 46, 1645-1652.	0.9	3
1518	Adaptive Molecular Evolution of <i>AKT3</i> Gene for Positive Diversifying Selection in Mammals. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3
1519	A structural UGDH variant associated with standard Munchkin cats. <i>BMC Genetics</i> , 2020, 21, 67.	2.7	6
1520	Genome-Wide Characterization and Analysis of CIPK Gene Family in Two Cultivated Allopolyploid Cotton Species: Sequence Variation, Association with Seed Oil Content, and the Role of GhCIPK6. <i>International Journal of Molecular Sciences</i> , 2020, 21, 863.	1.8	21

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1521	Chromosomal-level assembly of <i>Juglans sigillata</i> genome using Nanopore, BioNano, and Hi-C analysis. <i>GigaScience</i> , 2020, 9, .	3.3	33
1522	Genome Sequence of <i>Micromonospora terminaliae</i> TMS7 <sup>T</sup> , a New Endophytic Actinobacterium Isolated from the Medicinal Plant <i>Terminalia mucronata</i> . <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 721-723.	1.4	5
1523	Major Changes in Plastid Protein Import and the Origin of the Chloroplastida. <i>IScience</i> , 2020, 23, 100896.	1.9	21
1524	Genome-Wide Analysis of Cyclophilin Proteins in 21 Oomycetes. <i>Pathogens</i> , 2020, 9, 24.	1.2	3
1525	FeGenie: A Comprehensive Tool for the Identification of Iron Genes and Iron Gene Neighborhoods in Genome and Metagenome Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 37.	1.5	195
1526	Odorant-binding proteins and chemosensory proteins potentially involved in host plant recognition in the Asian citrus psyllid, <i>Diaphorina citri</i> . <i>Pest Management Science</i> , 2020, 76, 2609-2618.	1.7	27
1527	Serum proteomics analysis reveals the thermal fitness of crossbred dairy buffalo to chronic heat stress. <i>Journal of Thermal Biology</i> , 2020, 89, 102547.	1.1	7
1528	The genome of Shaw's sea snake ( <i>Hydrophis curtus</i> ) reveals secondary adaptation to its marine environment. <i>Molecular Biology and Evolution</i> , 2020, 37, 1744-1760.	3.5	28
1529	<i>Mikania micrantha</i> genome provides insights into the molecular mechanism of rapid growth. <i>Nature Communications</i> , 2020, 11, 340.	5.8	73
1530	Translocation of Drought-Responsive Proteins from the Chloroplasts. <i>Cells</i> , 2020, 9, 259.	1.8	12
1531	Histone Deacetylase (HDAC) Gene Family in Allotetraploid Cotton and Its Diploid Progenitors: In Silico Identification, Molecular Characterization, and Gene Expression Analysis under Multiple Abiotic Stresses, DNA Damage and Phytohormone Treatments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 321.	1.8	26
1532	Whole genome sequence of an edible and medicinal mushroom, <i>Hericium erinaceus</i> (Basidiomycota), Tj ETQq1 1 0.784314 rgBT /Ove	1.3	41
1533	Genome Sequences of vB_RleM_RL38JI and vB_RleM_RL2RES, Two Virulent <i>Rhizobium leguminosarum</i> Transducing Phages. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1
1534	Comparative Genomic Analysis of Capsule-Producing Black Yeasts <i>Exophiala dermatitidis</i> and <i>Exophiala spinifera</i> , Potential Agents of Disseminated Mycoses. <i>Frontiers in Microbiology</i> , 2020, 11, 586.	1.5	22
1535	GrAPFI: predicting enzymatic function of proteins from domain similarity graphs. <i>BMC Bioinformatics</i> , 2020, 21, 168.	1.2	8
1536	Intervention of triethylamine on <i>Dunaliella tertiolecta</i> reveals metabolic insights into triacylglycerol accumulation. <i>Algal Research</i> , 2020, 47, 101876.	2.4	2
1537	Gene expression profiling identifies pathways involved in seed maturation of <i>Jatropha curcas</i> . <i>BMC Genomics</i> , 2020, 21, 290.	1.2	2
1538	Integrated Transcriptional and Proteomic Profiling Reveals Potential Amino Acid Transporters Targeted by Nitrogen Limitation Adaptation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2171.	1.8	4

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1539	Genome and secretome analysis of jute endophyte <i>Grammothele lineata</i> strain SDL-CO-2015-1: Insights into its lignocellulolytic structure and secondary metabolite profile. <i>Genomics</i> , 2020, 112, 2794-2803.	1.3	7
1540	Transcriptome profiles reveal that gibberellin-related genes regulate weeping traits in crape myrtle. <i>Horticulture Research</i> , 2020, 7, 54.	2.9	17
1541	c-di-AMP hydrolysis by the phosphodiesterase AtaC promotes differentiation of multicellular bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7392-7400.	3.3	32
1542	Horizontal gene transfer of <i>Fhb7</i> from fungus underlies <i>Fusarium</i> head blight resistance in wheat. <i>Science</i> , 2020, 368, .	6.0	398
1543	LysM Proteins Regulate Fungal Development and Contribute to Hyphal Protection and Biocontrol Traits in <i>Clonostachys rosea</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 679.	1.5	32
1544	Heat stress response in the closest algal relatives of land plants reveals conserved stress signaling circuits. <i>Plant Journal</i> , 2020, 103, 1025-1048.	2.8	65
1545	Comparison of Transcriptome Profiles of the Fungus <i>Botrytis cinerea</i> and Insect Pest <i>Bradysia odoriphaga</i> in Response to Benzothiazole. <i>Frontiers in Microbiology</i> , 2020, 11, 1043.	1.5	9
1546	Chromosome-Level Assembly of the <i>Caenorhabditis remanei</i> Genome Reveals Conserved Patterns of Nematode Genome Organization. <i>Genetics</i> , 2020, 214, 769-780.	1.2	28
1547	<i>Pseudomonas</i> Can Survive Tailocin Killing via Persistence-Like and Heterogenous Resistance Mechanisms. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	16
1548	Transcriptomic analysis of sea cucumber ( <i>Holothuria leucospilota</i> ) coelomocytes revealed the echinoderm cytokine response during immune challenge. <i>BMC Genomics</i> , 2020, 21, 306.	1.2	10
1549	Deletion of S-Layer Associated Ig-Like Domain Protein Disrupts the <i>Lactobacillus acidophilus</i> Cell Surface. <i>Frontiers in Microbiology</i> , 2020, 11, 345.	1.5	14
1550	Identification and in vitro Characterization of a Novel Phage Endolysin that Targets Gram-Negative Bacteria. <i>Microorganisms</i> , 2020, 8, 447.	1.6	14
1551	A comprehensive analysis of the lysine acetylome reveals diverse functions of acetylated proteins during de-etiolation in <i>Zea mays</i> . <i>Journal of Plant Physiology</i> , 2020, 248, 153158.	1.6	9
1552	Characterization of bacteriophage VP001 and its application for the inhibition of <i>Vibrio vulnificus</i> causing seafood-borne diseases. <i>Food Microbiology</i> , 2021, 94, 103630.	2.1	25
1553	Identification and analysis of small proteins and short open reading frame encoded peptides in Hep3B cell. <i>Journal of Proteomics</i> , 2021, 230, 103965.	1.2	17
1554	Functional Genomics Platform, A Cloud-Based Platform for Studying Microbial Life at Scale. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 940-952.	1.9	18
1555	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.	2.2	28
1556	Little parallelism in genomic signatures of local adaptation in two sympatric, cryptic sister species. <i>Journal of Evolutionary Biology</i> , 2021, 34, 937-952.	0.8	9

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1557	Novel black yeast-like species in chaetothyriales with ant-associated life styles. <i>Fungal Biology</i> , 2021, 125, 276-284.	1.1	9
1558	Metabolic versatility of the nitrite-oxidizing bacterium <i>Nitrospira marina</i> and its proteomic response to oxygen-limited conditions. <i>ISME Journal</i> , 2021, 15, 1025-1039.	4.4	62
1559	Identification of ACC synthetase genes in <i>Volvariella volvacea</i> and analysis of their response to ethephon and 1-methylcyclopropene treatments. <i>Scientia Horticulturae</i> , 2021, 278, 109848.	1.7	5
1560	Development of an endolysin enzyme and its cell wall-binding domain protein and their applications for biocontrol and rapid detection of <i>Clostridium perfringens</i> in food. <i>Food Chemistry</i> , 2021, 345, 128562.	4.2	22
1561	Proteomics analysis of <i>Cyclobalanopsis gilva</i> provides new insights of low seed germination. <i>Biochimie</i> , 2021, 180, 68-78.	1.3	14
1562	GhN/AINV13 positively regulates cotton stress tolerance by interacting with the 14 <sup>3-3</sup> protein. <i>Genomics</i> , 2021, 113, 44-56.	1.3	10
1563	The Function and Evolution of Motile DNA Replication Systems in Ciliates. <i>Current Biology</i> , 2021, 31, 66-76.e6.	1.8	76
1564	A chromosome-level genome assembly provides insights into ascorbic acid accumulation and fruit softening in guava ( <i>Psidium guajava</i> ). <i>Plant Biotechnology Journal</i> , 2021, 19, 717-730.	4.1	52
1565	Expression and functional analysis of cytochrome P450 genes in the integument of the oriental armyworm, <i>Mythimna separata</i> (Walker). <i>Pest Management Science</i> , 2021, 77, 577-587.	1.7	11
1566	Inhibition of Maize Caffeate 3-O-Methyltransferase by Nitecapone as a Possible Approach to Reduce Lignocellulosic Biomass Recalcitrance. <i>Plant Molecular Biology Reporter</i> , 2021, 39, 179-191.	1.0	5
1567	Identifying the causes and consequences of assembly gaps using a multiplatform genome assembly of a bird's paradise. <i>Molecular Ecology Resources</i> , 2021, 21, 263-286.	2.2	103
1568	<i>Apolygus lucorum</i> genome provides insights into omnivorousness and mesophyll feeding. <i>Molecular Ecology Resources</i> , 2021, 21, 287-300.	2.2	31
1569	In Silico Characterization of a Hypothetical Protein from <i>Shigella dysenteriae</i> ATCC 12039 Reveals a Pathogenesis-Related Protein of the Type-VI Secretion System. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110111.	1.0	10
1570	Sinbase 2.0: An Updated Database to Study Multi-Omics in <i>Sesamum indicum</i> . <i>Plants</i> , 2021, 10, 272.	1.6	6
1571	Genome-wide investigation of malate dehydrogenase gene family in poplar ( <i>Populus trichocarpa</i> ) and their expression analysis under salt stress. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	1.0	9
1572	Genome Sequence and Adaptation Analysis of the Human and Rice Pathogenic Strain <i>Burkholderia glumae</i> AU6208. <i>Pathogens</i> , 2021, 10, 87.	1.2	5
1574	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. <i>BMC Bioinformatics</i> , 2021, 22, 11.	1.2	61
1576	Genome-wide identification and classification of Lipxygenase gene family and their roles in sorghum-aphid interaction. <i>Plant Molecular Biology</i> , 2021, 105, 527-541.	2.0	18



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1577	The enzymology of oxazolone and thioamide synthesis in methanobactin. <i>Methods in Enzymology</i> , 2021, 656, 341-373.	0.4	3
1578	Phylogenetic analyses suggest centipede venom arsenals were repeatedly stocked by horizontal gene transfer. <i>Nature Communications</i> , 2021, 12, 818.	5.8	15
1579	De novo assembly of the <i>Mylia taylorii</i> transcriptome and identification of sesquiterpene synthases. <i>Archives of Biochemistry and Biophysics</i> , 2021, 698, 108742.	1.4	2
1580	Deciphering a Marine Bone-Degrading Microbiome Reveals a Complex Community Effort. <i>MSystems</i> , 2021, 6, .	1.7	10
1581	Gene family amplification facilitates adaptation in freshwater unionid bivalve <i>Megaloniais nervosa</i> . <i>Molecular Ecology</i> , 2021, 30, 1155-1173.	2.0	19
1582	Experimental increase in fecundity causes upregulation of fecundity and body maintenance genes in the fat body of ant queens. <i>Biology Letters</i> , 2021, 17, 20200909.	1.0	8
1583	A bacteriophage infecting <i>Mesorhizobium</i> species has a prolate capsid and shows similarities to a family of <i>Caulobacter crescentus</i> phages. <i>Canadian Journal of Microbiology</i> , 2021, 67, 147-160.	0.8	3
1584	Identification of genes associated with the biosynthesis of unsaturated fatty acid and oil accumulation in herbaceous peony "Hangshao" ( <i>Paeonia lactiflora</i> "Hangshao") seeds based on transcriptome analysis. <i>BMC Genomics</i> , 2021, 22, 94.	1.2	17
1585	Plant Co-expression Annotation Resource: a web server for identifying targets for genetically modified crop breeding pipelines. <i>BMC Bioinformatics</i> , 2021, 22, 46.	1.2	0
1587	Proteomic analysis of decidua in patients with recurrent pregnancy loss (RPL) reveals mitochondrial oxidative stress dysfunction. <i>Clinical Proteomics</i> , 2021, 18, 9.	1.1	18
1588	The First Whole Genome Sequence and Characterisation of Avian Nephritis Virus Genotype 3. <i>Viruses</i> , 2021, 13, 235.	1.5	7
1589	Deciphering the dynamic gene expression patterns of pollen abortion in a male sterile line of <i>Avena sativa</i> through transcriptome analysis at different developmental stages. <i>BMC Plant Biology</i> , 2021, 21, 101.	1.6	2
1590	RNA sequencing-based exploration of the effects of far-red light on lncRNAs involved in the shade-avoidance response of <i>D. officinale</i> . <i>PeerJ</i> , 2021, 9, e10769.	0.9	10
1591	Integrated Full-Length Transcriptome and RNA-Seq to Identify Immune System Genes from the Skin of Sperm Whale ( <i>Physeter macrocephalus</i> ). <i>Genes</i> , 2021, 12, 233.	1.0	4
1592	geneRFinder: gene finding in distinct metagenomic data complexities. <i>BMC Bioinformatics</i> , 2021, 22, 87.	1.2	6
1593	Cytochrome P450 monooxygenase genes in the wild silkworm, <i>Bombyx mandarina</i> . <i>PeerJ</i> , 2021, 9, e10818.	0.9	6
1594	Genome Sequencing of <i>Kocuria varians</i> Strain 80, Isolated from Starter Culture for Dry Sausage. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
1595	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.	2.9	23

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1596	TaNAC032 transcription factor regulates lignin-biosynthetic genes to combat Fusarium head blight in wheat. <i>Plant Science</i> , 2021, 304, 110820.	1.7	23
1597	Structural characterization and functional annotation of microbial proteases mined from solid tannery waste metagenome. <i>Biologia (Poland)</i> , 2021, 76, 1829-1842.	0.8	4
1598	The Redox Proteome of Thiol Proteins in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 648894.	1.5	4
1599	The effect of environmental stress on ageing in a termite species with low social complexity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20190739.	1.8	15
1600	The Crown Pearl: a draft genome assembly of the European freshwater pearl mussel <i>Margaritifera margaritifera</i> (Linnaeus, 1758). <i>DNA Research</i> , 2021, 28, .	1.5	15
1602	Use of data-independent acquisition mass spectrometry for comparative proteomics analyses of sera from pregnant women with intrahepatic cholestasis of pregnancy. <i>Journal of Proteomics</i> , 2021, 236, 104124.	1.2	7
1603	A multi-omic characterization of temperature stress in a halotolerant <i>Scenedesmus</i> strain for algal biotechnology. <i>Communications Biology</i> , 2021, 4, 333.	2.0	22
1604	Novelty and Convergence in Adaptation to Whole Genome Duplication. <i>Molecular Biology and Evolution</i> , 2021, 38, 3910-3924.	3.5	22
1605	Chromosome-level reference genome of the soursop ( <i>Annona muricata</i> ): A new resource for Magnoliid research and tropical pomology. <i>Molecular Ecology Resources</i> , 2021, 21, 1608-1619.	2.2	18
1606	Transcriptional Analyses of Acute Exposure to Methylmercury on Erythrocytes of Loggerhead Sea Turtle. <i>Toxics</i> , 2021, 9, 70.	1.6	2
1607	Hybrid genome de novo assembly with methylome analysis of the anaerobic thermophilic subsurface bacterium <i>Thermanaerosceptrum fracticalcis</i> strain DRI-13T. <i>BMC Genomics</i> , 2021, 22, 209.	1.2	3
1608	Transcriptome analyses and weighted gene coexpression network analysis reveal key pathways and genes involved in the rapid cold resistance of the Chinese white wax scale insect. <i>Archives of Insect Biochemistry and Physiology</i> , 2021, 107, e21781.	0.6	11
1609	Asgard archaea in the haima cold seep: Spatial distribution and genomic insights. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103489.	0.6	11
1610	The consensus N glyco X <sub>1</sub> Y/T motif and a previously unknown N glyco N-linked glycosylation are necessary for growth and pathogenicity of <i>Phytophthora</i> . <i>Environmental Microbiology</i> , 2021, 23, 5147-5163.	1.8	5
1611	The Asgard Archaeal-Unique Contribution to Protein Families of the Eukaryotic Common Ancestor Was 0.3%. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
1612	Identification of Novel Toxin Genes from the Stinging Nettle Caterpillar <i>Parasa lepida</i> (Cramer, 1799): Insights into the Evolution of Lepidoptera Toxins. <i>Insects</i> , 2021, 12, 396.	1.0	2
1613	De novo Genome Assembly of the Raccoon Dog ( <i>Nyctereutes procyonoides</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 658256.	1.1	11
1615	Chromosome-scale assembly and analysis of biomass crop <i>Miscanthus lutarioriparius</i> genome. <i>Nature Communications</i> , 2021, 12, 2458.	5.8	25

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1616	GCG inhibits SARS-CoV-2 replication by disrupting the liquid phase condensation of its nucleocapsid protein. <i>Nature Communications</i> , 2021, 12, 2114.	5.8	70
1618	Integration of Transcriptomic and Proteomic Data Reveals the Possible Action Mechanism of the Antimicrobial Zhongshengmycin Against <i>Didymella segeticola</i> , the Causal Agent of Tea Leaf Spot. <i>Phytopathology</i> , 2021, 111, 2238-2249.	1.1	7
1621	Genome Expression Dynamics Reveal the Parasitism Regulatory Landscape of the Root-Knot Nematode <i>Meloidogyne incognita</i> and a Promoter Motif Associated with Effector Genes. <i>Genes</i> , 2021, 12, 771.	1.0	24
1622	The identification of a transposon affecting the asexual reproduction of the wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 800-816.	2.0	17
1623	Vulture Genomes Reveal Molecular Adaptations Underlying Obligate Scavenging and Low Levels of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 3649-3663.	3.5	9
1624	Computational discovery and ex-vivo validation study of novel antigenic vaccine candidates against tuberculosis. <i>Acta Tropica</i> , 2021, 217, 105870.	0.9	6
1625	Building a reference transcriptome for the hexaploid hard fescue turfgrass ( <i>Festuca brevipila</i> ) using a combination of PacBio Isoseq and Illumina sequencing. <i>Crop Science</i> , 2021, 61, 2798-2811.	0.8	3
1626	CmMLO17 and its partner CmKIC potentially support <i>Alternaria alternata</i> growth in <i>Chrysanthemum morifolium</i> . <i>Horticulture Research</i> , 2021, 8, 101.	2.9	13
1627	Chitin Deacetylases Are Required for <i>Epichloa festucae</i> Endophytic Cell Wall Remodeling During Establishment of a Mutualistic Symbiotic Interaction with <i>Lolium perenne</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1181-1192.	1.4	12
1628	CRISPR-Cas9-Based Discovery of the Verrucosidin Biosynthesis Gene Cluster in <i>Penicillium polonicum</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 660871.	1.5	10
1629	The macronuclear genome of anaerobic ciliate <i>Entodinium caudatum</i> reveals its biological features adapted to the distinct rumen environment. <i>Genomics</i> , 2021, 113, 1416-1427.	1.3	20
1630	Comparative proteomic analysis to annotate the structural and functional association of the hypothetical proteins of <i>S. maltophilia</i> k279a and predict potential T and B cell targets for vaccination. <i>PLoS ONE</i> , 2021, 16, e0252295.	1.1	5
1631	De novo genome assembly of the land snail <i>Candidula unifasciata</i> (Mollusca: Gastropoda). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	8
1632	RNA-seq derived identification of coronatine-regulated genes putatively involved in terpenoid biosynthetic pathway in the rubber tree <i>Hevea brasiliensis</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2021, 749, 012033.	0.2	1
1633	Not just shades of grey: life is full of colour for the ocellate river stingray ( <i>Potamotrygon motoro</i> ). <i>Journal of Experimental Biology</i> , 2021, 224, .	0.8	8
1634	Molecular Insights into the Role of Cysteine-Rich Peptides in Induced Resistance to <i>Fusarium oxysporum</i> Infection in Tomato Based on Transcriptome Profiling. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5741.	1.8	10
1635	Identification and Analysis of bZIP Family Genes in Potato and Their Potential Roles in Stress Responses. <i>Frontiers in Plant Science</i> , 2021, 12, 637343.	1.7	20
1636	Comparative transcriptome and methylome analysis of the hindbrain in olive flounder ( <i>Paralichthys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlaid Physiology Part D: Genomics and Proteomics, 2021, 38, 100799.	0.4	2

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1637	The Chromosome-Level Genome of <i>Triplophysa dalaica</i> (Cypriniformes: Cobitidae) Provides Insights into Its Survival in Extremely Alkaline Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
1638	Geographical, Molecular, and Computational Analysis of Migraine-Causing Genes. <i>Journal of Computational Biophysics and Chemistry</i> , 2021, 20, 391-403.	1.0	6
1639	Postmating gene expression of Mexican fruit fly females: disentangling the effects of the male accessory glands. <i>Insect Molecular Biology</i> , 2021, 30, 480-496.	1.0	10
1640	Genomic Analysis of Prophages Recovered from <i>Listeria monocytogenes</i> Lysogens Found in Seafood and Seafood-Related Environment. <i>Microorganisms</i> , 2021, 9, 1354.	1.6	5
1641	Identification and analysis of olfactory genes in <i>Dioryctria abietella</i> based on the antennal transcriptome. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100814.	0.4	12
1642	De novo genome assembly of a foxtail millet cultivar Huagu11 uncovered the genetic difference to the cultivar Yugu1, and the genetic mechanism of imazethapyr tolerance. <i>BMC Plant Biology</i> , 2021, 21, 271.	1.6	9
1643	Pangenomics reveals alternative environmental lifestyles among chlamydiae. <i>Nature Communications</i> , 2021, 12, 4021.	5.8	29
1644	Characterisation of Bacteriophage-Encoded Depolymerases Selective for Key <i>Klebsiella pneumoniae</i> Capsular Exopolysaccharides. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 686090.	1.8	14
1645	TopDomain: Exhaustive Protein Domain Boundary Metaprediction Combining Multisource Information and Deep Learning. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 4599-4613.	2.3	5
1646	Zetaproteobacteria Pan-Genome Reveals Candidate Gene Cluster for Twisted Stalk Biosynthesis and Export. <i>Frontiers in Microbiology</i> , 2021, 12, 679409.	1.5	9
1647	A chromosome-level <i>Amaranthus cruentus</i> genome assembly highlights gene family evolution and biosynthetic gene clusters that may underpin the nutritional value of this traditional crop. <i>Plant Journal</i> , 2021, 107, 613-628.	2.8	30
1649	Exposure to dexamethasone modifies transcriptomic responses of free-living stages of <i>Strongyloides stercoralis</i> . <i>PLoS ONE</i> , 2021, 16, e0253701.	1.1	4
1650	Identification and analysis of the structure, expression and nucleotide polymorphism of the GPAT gene family in rice. <i>Plant Gene</i> , 2021, 26, 100290.	1.4	7
1651	Combined transcriptomic and metabolic analyses reveal potential mechanism for fruit development and quality control of Chinese raspberry ( <i>Rubus chingii</i> Hu). <i>Plant Cell Reports</i> , 2021, 40, 1923-1946.	2.8	10
1652	Chromosome-level genome assembly of Sichuan pepper provides insights into apomixis, drought tolerance, and alkaloid biosynthesis. <i>Molecular Ecology Resources</i> , 2021, 21, 2533-2545.	2.2	30
1653	Genome-Wide Patterns of Bracovirus Chromosomal Integration into Multiple Host Tissues during Parasitism. <i>Journal of Virology</i> , 2021, 95, e0068421.	1.5	6
1655	The transcriptional dynamics during <i>de novo</i> shoot organogenesis of Ma bamboo ( <i>Dendrocalamus latiflorus</i> Munro): implication of the contributions of the abiotic stress response in this process. <i>Plant Journal</i> , 2021, 107, 1513-1532.	2.8	10
1656	Identification and Expression Profile of Chemosensory Genes in the Small Hive Beetle <i>Aethina tumida</i> . <i>Insects</i> , 2021, 12, 661.	1.0	8

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1658	Draft genome assembly of the Aral barbell <i>Luciobarbus brachycephalus</i> using PacBio sequencing. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	0
1659	Comparative Transcriptome Analyses of the Developmental Stages of <i>Taenia multiceps</i> . <i>Frontiers in Veterinary Science</i> , 2021, 8, 677045.	0.9	5
1660	Computational Structural Genomics Unravels Common Folds and Novel Families in the Secretome of Fungal Phytopathogen <i>Magnaporthe oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1267-1280.	1.4	49
1662	Haplotype-resolved genome assembly and allele-specific gene expression in cultivated ginger. <i>Horticulture Research</i> , 2021, 8, 188.	2.9	31
1663	A high-quality draft genome for <i>Melaleuca alternifolia</i> (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. <i>GigaByte</i> , 0, 2021, 1-15.	0.0	11
1664	Identification and expression pattern of lentil HSPs under different abiotic stresses. <i>Plant Biotechnology Reports</i> , 2021, 15, 609-625.	0.9	4
1666	Nicastrin-Like, a Novel Transmembrane Protein from <i>Trypanosoma cruzi</i> Associated to the Flagellar Pocket. <i>Microorganisms</i> , 2021, 9, 1750.	1.6	1
1669	Potentiators of Disease During Barley Infection by <i>Pyrenophora teres</i> f. <i>teres</i> in a Susceptible Interaction. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 779-792.	1.4	5
1670	The chromosome-scale reference genome of <i>Rubus chingii</i> Hu provides insight into the biosynthetic pathway of hydrolyzable tannins. <i>Plant Journal</i> , 2021, 107, 1466-1477.	2.8	26
1671	<i>Candidatus Chloroploca mongolica</i> sp. nov. a new mesophilic filamentous anoxygenic phototrophic bacterium. <i>FEMS Microbiology Letters</i> , 2021, 368, .	0.7	2
1672	Comparative Genomic Analysis Reveals Genetic Variation and Adaptive Evolution in the Pathogenicity-Related Genes of <i>Phytophthora capsici</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 694136.	1.5	4
1673	Modern transcriptome data processing algorithms: a review of methods and results of approbation. <i>Sistemnyj Analiz I Prikladnaya Informatika</i> , 2021, , 54-62.	0.1	1
1674	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	27
1675	Whole-Genome and Transcriptome Sequencing of <i>Phlebopus portentosus</i> Reveals Its Associated Ectomycorrhizal Niche and Conserved Pathways Involved in Fruiting Body Development. <i>Frontiers in Microbiology</i> , 2021, 12, 732458.	1.5	8
1676	Comparative genomic analysis reveals metabolic flexibility of Woesearchaeota. <i>Nature Communications</i> , 2021, 12, 5281.	5.8	25
1677	A vast pool of lineage-specific microproteins encoded by long non-coding RNAs in plants. <i>Nucleic Acids Research</i> , 2021, 49, 10328-10346.	6.5	33
1678	Genome-wide identification studies – A primer to explore new genes in plant species. <i>Plant Biology</i> , 2022, 24, 9-22.	1.8	5
1679	Comprehensive analysis and expression profiles of cassava UDP-glycosyltransferases (UGT) family reveal their involvement in development and stress responses in cassava. <i>Genomics</i> , 2021, 113, 3415-3429.	1.3	13

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1680	Genomic Insights into the Ecological Role and Evolution of a Novel <i>Thermoplasmata</i> Order, <i>Candidatus</i> <i>Sysuiplasmatales</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0106521.	1.4	3
1681	High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, <i>Sciara coprophila</i> , using single-molecule sequencing. <i>BMC Genomics</i> , 2021, 22, 643.	1.2	17
1682	De novo Assembly, Annotation, and Analysis of Transcriptome Data of the Ladakh Ground Skink Provide Genetic Information on High-Altitude Adaptation. <i>Genes</i> , 2021, 12, 1423.	1.0	0
1683	The reduced ARF regulatory system in <i>Giardia intestinalis</i> pre-dates the transition to parasitism in the lineage Fornicata. <i>International Journal for Parasitology</i> , 2021, 51, 825-839.	1.3	5
1684	Viviparity and habitat restrictions may influence the evolution of male reproductive genes in tsetse fly ( <i>Glossina</i> ) species. <i>BMC Biology</i> , 2021, 19, 211.	1.7	5
1685	Genomic analysis unveils mechanisms of northward invasion and signatures of plateau adaptation in the Asian house rat. <i>Molecular Ecology</i> , 2021, 30, 6596-6610.	2.0	10
1686	The first chromosome-level genome assembly of a green lacewing <i>Chrysopa pallens</i> and its implication for biological control. <i>Molecular Ecology Resources</i> , 2022, 22, 755-767.	2.2	7
1687	Pan-Genome of the Genus <i>Streptomyces</i> and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. <i>Frontiers in Microbiology</i> , 2021, 12, 677558.	1.5	21
1688	Protocol for HSDFinder: Identifying, annotating, categorizing, and visualizing duplicated genes in eukaryotic genomes. <i>STAR Protocols</i> , 2021, 2, 100619.	0.5	8
1689	Identification, evolution and expression analysis of WRKY gene family in <i>Eucommia ulmoides</i> . <i>Genomics</i> , 2021, 113, 3294-3309.	1.3	20
1690	Vorinostat targets UBE2C to reverse epithelial-mesenchymal transition and control cervical cancer growth through the ubiquitination pathway. <i>European Journal of Pharmacology</i> , 2021, 908, 174399.	1.7	10
1691	De novo transcriptome sequencing of triton shell <i>Charonia lampas sauliae</i> : Identification of genes related to neurotoxins and discovery of genetic markers. <i>Marine Genomics</i> , 2021, 59, 100862.	0.4	5
1692	Novel Corneal Protein Biomarker Candidates Reveal Iron Metabolic Disturbance in High Myopia Eyes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 689917.	1.8	2
1693	Proteomic screening of potential N-glycoprotein biomarkers for colorectal cancer by TMT labeling combined with LC-MS/MS. <i>Clinica Chimica Acta</i> , 2021, 521, 122-130.	0.5	5
1694	Discovery of a fucoidan endo-4O-sulfatase: Regioselective 4O-desulfation of fucoidans and its effect on anticancer activity in vitro. <i>Carbohydrate Polymers</i> , 2021, 271, 118449.	5.1	19
1695	ATF6-DGAT pathway is involved in TLR7-induced innate immune response in <i>Ctenopharyngodon idellus</i> kidney cells. <i>Developmental and Comparative Immunology</i> , 2021, 124, 104197.	1.0	3
1696	Transcriptome-wide study in the green microalga <i>Messastrum gracile</i> SE-MC4 identifies prominent roles of photosynthetic integral membrane protein genes during exponential growth stage. <i>Phytochemistry</i> , 2021, 192, 112936.	1.4	4
1697	Genes involved in the Type I pheromone biosynthesis pathway and chemoreception from the sex pheromone gland transcriptome of <i>Dioryctria abietella</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 40, 100892.	0.4	1

#	ARTICLE	IF	CITATIONS
1698	Draft genome analysis, poly-phasic study and lipid biosynthesis pathway of <i>Scenedesmus</i> sp. SVMIICT1. <i>Bioresource Technology</i> , 2021, 341, 125809.	4.8	4
1699	Chromosome-level reference genome of the European wasp spider <i>Argiope bruennichi</i> : a resource for studies on range expansion and evolutionary adaptation. <i>GigaScience</i> , 2021, 10, .	3.3	35
1700	Comparative genomics of opportunistic <i>Phialophora</i> species involved in divergent disease types. <i>Mycoses</i> , 2021, 64, 555-568.	1.8	7
1701	Label-free proteomic analysis of serum exosomes from paroxysmal atrial fibrillation patients. <i>Clinical Proteomics</i> , 2021, 18, 1.	1.1	17
1703	In Silico Characterization of Toxin-Antitoxin Systems in <i>Campylobacter</i> Isolates Recovered from Food Sources and Sporadic Human Illness. <i>Genes</i> , 2021, 12, 72.	1.0	1
1705	Mapping genomes by using bioinformatics data and tools. , 2021, , 245-278.		3
1706	Genome-Wide Mining of Disease Resistance Gene Analogs Using Conserved Domains. <i>Methods in Molecular Biology</i> , 2020, 2107, 365-375.	0.4	1
1707	Methods for Plant Genome Annotation. , 2014, , 1-7.		1
1708	In Sffamily Identification of Genes in Bacteriophage DNA. <i>Methods in Molecular Biology</i> , 2009, 502, 57-89.	0.4	25
1709	Computational Identification of Plant Transcription Factors and the Construction of the PlantTFDB Database. <i>Methods in Molecular Biology</i> , 2010, 674, 351-368.	0.4	16
1710	Integration of Proteomic and Metabolomic Profiling as well as Metabolic Modeling for the Functional Analysis of Metabolic Networks. <i>Methods in Molecular Biology</i> , 2011, 694, 341-363.	0.4	10
1711	Exploiting Complex Protein Domain Networks for Protein Function Annotation. <i>Studies in Computational Intelligence</i> , 2019, , 598-610.	0.7	7
1712	Bayesian Data Integration and Enrichment Analysis for Predicting Gene Function in Malaria. <i>Lecture Notes in Computer Science</i> , 2009, , 457-466.	1.0	1
1713	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
1714	Characterization of DNA methylation variations during fruit development and ripening of <i>Vitis vinifera</i> (cv. "Fujiminori"). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 617-637.	1.4	13
1715	Unraveling the Genetic Complexities in Gene Set of Sugarcane Red Rot Pathogen <i>Colletotrichum falcatum</i> Through Transcriptomic Approach. <i>Sugar Tech</i> , 2017, 19, 604-615.	0.9	22
1716	Tench ( <i>Tinca tinca</i> ) high-throughput transcriptomics reveal feed dependent gut profiles. <i>Aquaculture</i> , 2017, 479, 200-207.	1.7	1
1717	Building an octaploid genome and transcriptome of the medicinal plant <i>Pogostemon cablin</i> from Lamiales. <i>Scientific Data</i> , 2018, 5, 180274.	2.4	17

#	ARTICLE	IF	CITATIONS
1718	iTRAQ-based proteomics analysis on insomnia rats treated with Mongolian medical warm acupuncture. <i>Bioscience Reports</i> , 2020, 40, .	1.1	17
1719	Origin, genomic diversity and microevolution of the <i>Clostridium difficile</i> B1/NAP1/RT027/ST01 strain in Costa Rica, Chile, Honduras and Mexico. <i>Microbial Genomics</i> , 2020, 6, .	1.0	6
1720	Identifying glycoside hydrolase family 18 genes in the mycoparasitic fungal species <i>Clonostachys rosea</i> . <i>Microbiology (United Kingdom)</i> , 2015, 161, 1407-1419.	0.7	86
1721	Variation in genome content and predatory phenotypes between <i>Bdellovibrio</i> sp. NC01 isolated from soil and <i>B. bacteriovorus</i> type strain HD100. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1315-1330.	0.7	11
1743	Draft Genome Sequences of <i>Acinetobacter</i> sp. Strain EKM10A, <i>Enterobacter hormaechei</i> EKM10E, and <i>Enterobacter hormaechei</i> EKM11E (Phylum Proteobacteria ) Colonizing the Seed Surface Biogel of <i>Echinocystis lobata</i> (Wild Cucumber). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
1744	Draft Genome Sequences of <i>Pantoea agglomerans</i> , <i>Paenibacillus polymyxa</i> , and <i>Pseudomonas</i> sp. Strains, Seed Biogel-Associated Endophytes of <i>Cucumis sativus</i> L. (Cucumber) and <i>Cucumis melo</i> L. (Cantaloupe). <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
1745	Circular Single-Stranded DNA Virus ( <i>Microviridae</i> : <i>Gokushovirinae</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 507 Td ( <i>Jodre depressus</i> ). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
1746	Comprehensive analysis of the <i>Gossypium hirsutum</i> L. respiratory burst oxidase homolog (Ghrboh) gene family. <i>BMC Genomics</i> , 2020, 21, 91.	1.2	22
1747	Galaxy and Apollo as a biologist-friendly interface for high-quality cooperative phage genome annotation. <i>PLoS Computational Biology</i> , 2020, 16, e1008214.	1.5	96
1748	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen <i>Candida metapsilosis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005626.	1.5	139
1749	Interacting networks of resistance, virulence and core machinery genes identified by genome-wide epistasis analysis. <i>PLoS Genetics</i> , 2017, 13, e1006508.	1.5	85
1750	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e301.	1.3	44
1751	Stage- and Gender-Specific Proteomic Analysis of <i>Brugia malayi</i> Excretory-Secretory Products. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e326.	1.3	134
1752	Exploiting Amino Acid Composition for Predicting Protein-Protein Interactions. <i>PLoS ONE</i> , 2009, 4, e7813.	1.1	61
1753	In Silico Identification of Carboxylate Clamp Type Tetratricopeptide Repeat Proteins in <i>Arabidopsis</i> and Rice As Putative Co-Chaperones of Hsp90/Hsp70. <i>PLoS ONE</i> , 2010, 5, e12761.	1.1	76
1754	Specificity of the <i>E. coli</i> LysR-Type Transcriptional Regulators. <i>PLoS ONE</i> , 2010, 5, e15189.	1.1	25
1755	Gene Expression Rhythms in the Mussel <i>Mytilus galloprovincialis</i> (Lam.) across an Annual Cycle. <i>PLoS ONE</i> , 2011, 6, e18904.	1.1	89
1756	Transcriptome-Based Differentiation of Closely-Related <i>Miscanthus</i> Lines. <i>PLoS ONE</i> , 2012, 7, e29850.	1.1	24



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1757	Alternative Splicing of a Multi-Drug Transporter from <i>Pseudoperonospora cubensis</i> Generates an RXLR Effector Protein That Elicits a Rapid Cell Death. <i>PLoS ONE</i> , 2012, 7, e34701.	1.1	57
1758	Genes for the Major Structural Components of Thermotogales Speciesâ€™™ Togas Revealed by Proteomic and Evolutionary Analyses of OmpA and OmpB Homologs. <i>PLoS ONE</i> , 2012, 7, e40236.	1.1	22
1759	Tyrosinase Degradation Is Prevented when EDEM1 Lacks the Intrinsically Disordered Region. <i>PLoS ONE</i> , 2012, 7, e42998.	1.1	34
1760	Development, Characterization and Experimental Validation of a Cultivated Sunflower ( <i>Helianthus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook	1.1	28
1761	Hybrid Sequencing Approach Applied to Human Fecal Metagenomic Clone Libraries Revealed Clones with Potential Biotechnological Applications. <i>PLoS ONE</i> , 2012, 7, e47654.	1.1	16
1762	Identification of Novel and Differentially Expressed MicroRNAs of Dairy Goat Mammary Gland Tissues Using Solexa Sequencing and Bioinformatics. <i>PLoS ONE</i> , 2012, 7, e49463.	1.1	70
1763	Sequencing and Comparative Analysis of the Straw Mushroom ( <i>Volvariella volvacea</i> ) Genome. <i>PLoS ONE</i> , 2013, 8, e58294.	1.1	143
1764	Comparative Transcriptional Profiling of the Axolotl Limb Identifies a Tripartite Regeneration-Specific Gene Program. <i>PLoS ONE</i> , 2013, 8, e61352.	1.1	107
1765	Developmental Gene Discovery in a Hemimetabolous Insect: De Novo Assembly and Annotation of a Transcriptome for the Cricket <i>Gryllus bimaculatus</i> . <i>PLoS ONE</i> , 2013, 8, e61479.	1.1	41
1766	Transcriptional Response of the Mussel <i>Mytilus galloprovincialis</i> (Lam.) following Exposure to Heat Stress and Copper. <i>PLoS ONE</i> , 2013, 8, e66802.	1.1	91
1767	Secretome Analysis of the Pine Wood Nematode <i>Bursaphelenchus xylophilus</i> Reveals the Tangled Roots of Parasitism and Its Potential for Molecular Mimicry. <i>PLoS ONE</i> , 2013, 8, e67377.	1.1	98
1768	Detection of <i>Escherichia coli</i> and Associated Î²-Lactamases Genes from Diabetic Foot Ulcers by Multiplex PCR and Molecular Modeling and Docking of SHV-1, TEM-1, and OXA-1 Î²-Lactamases with Clindamycin and Piperacillin-Tazobactam. <i>PLoS ONE</i> , 2013, 8, e68234.	1.1	23
1769	Identification and Characterization of Cancer Mutations in Japanese Lung Adenocarcinoma without Sequencing of Normal Tissue Counterparts. <i>PLoS ONE</i> , 2013, 8, e73484.	1.1	41
1770	Generation and Analysis of a Large-Scale Expressed Sequence Tag Database from a Full-Length Enriched cDNA Library of Developing Leaves of <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2013, 8, e76443.	1.1	10
1771	Development of Reference Transcriptomes for the Major Field Insect Pests of Cowpea: A Toolbox for Insect Pest Management Approaches in West Africa. <i>PLoS ONE</i> , 2013, 8, e79929.	1.1	23
1772	Mating Type Gene Homologues and Putative Sex Pheromone-Sensing Pathway in Arbuscular Mycorrhizal Fungi, a Presumably Asexual Plant Root Symbiont. <i>PLoS ONE</i> , 2013, 8, e80729.	1.1	40
1773	RNA-Seq Transcriptome Profiling of Upland Cotton ( <i>Gossypium hirsutum</i> L.) Root Tissue under Water-Deficit Stress. <i>PLoS ONE</i> , 2013, 8, e82634.	1.1	53
1774	Functional Annotation of Conserved Hypothetical Proteins from <i>Haemophilus influenzae</i> Rd KW20. <i>PLoS ONE</i> , 2013, 8, e84263.	1.1	93

#	ARTICLE	IF	CITATIONS
1775	Genomic Evolution of 11 Type Strains within Family Planctomycetaceae. PLoS ONE, 2014, 9, e86752.	1.1	18
1776	Identification of MicroRNAs in the Coral <i>Stylophora pistillata</i> . PLoS ONE, 2014, 9, e91101.	1.1	49
1777	Genome-Wide Survey and Expression Analysis of Calcium-Dependent Protein Kinase in <i>Gossypium raimondii</i> . PLoS ONE, 2014, 9, e98189.	1.1	77
1778	A Survey of Innovation through Duplication in the Reduced Genomes of Twelve Parasites. PLoS ONE, 2014, 9, e99213.	1.1	7
1779	A Comprehensive Reference Transcriptome Resource for the Common House Spider <i>Parasteatoda tepidariorum</i> . PLoS ONE, 2014, 9, e104885.	1.1	57
1780	A Comprehensive Analysis of the Cupin Gene Family in Soybean ( <i>Glycine max</i> ). PLoS ONE, 2014, 9, e110092.	1.1	20
1781	Comparative Analysis of Predicted Plastid-Targeted Proteomes of Sequenced Higher Plant Genomes. PLoS ONE, 2014, 9, e112870.	1.1	8
1782	Genome-Based Identification of Active Prophage Regions by Next Generation Sequencing in <i>Bacillus licheniformis</i> DSM13. PLoS ONE, 2015, 10, e0120759.	1.1	22
1783	Structural Models of Zebrafish ( <i>Danio rerio</i> ) NOD1 and NOD2 NACHT Domains Suggest Differential ATP Binding Orientations: Insights from Computational Modeling, Docking and Molecular Dynamics Simulations. PLoS ONE, 2015, 10, e0121415.	1.1	31
1784	An Interspecies Comparative Analysis of the Predicted Secretomes of the Necrotrophic Plant Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . PLoS ONE, 2015, 10, e0130534.	1.1	72
1785	The Immunoreactive Exo-1,3- $\beta$ -Glucanase from the Pathogenic Oomycete <i>Pythium insidiosum</i> Is Temperature Regulated and Exhibits Glycoside Hydrolase Activity. PLoS ONE, 2015, 10, e0135239.	1.1	12
1786	Complete Genome Sequence of a High Lipid-Producing Strain of <i>Mucor circinelloides</i> WJ11 and Comparative Genome Analysis with a Low Lipid-Producing Strain CBS 277.49. PLoS ONE, 2015, 10, e0137543.	1.1	52
1787	The Prediction and Validation of Small CDSs Expand the Gene Repertoire of the Smallest Known Eukaryotic Genomes. PLoS ONE, 2015, 10, e0139075.	1.1	3
1788	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. PLoS ONE, 2016, 11, e0146423.	1.1	23
1789	Insight into the Salivary Gland Transcriptome of <i>Lygus lineolaris</i> (Palisot de Beauvois). PLoS ONE, 2016, 11, e0147197.	1.1	23
1790	Identifying Aspects of the Post-Transcriptional Program Governing the Proteome of the Green Alga <i>Micromonas pusilla</i> . PLoS ONE, 2016, 11, e0155839.	1.1	7
1791	Comparative Genome-Wide Analysis of the Malate Dehydrogenase Gene Families in Cotton. PLoS ONE, 2016, 11, e0166341.	1.1	21
1792	<i>Agrobacterium tumefaciens</i> estC, Encoding an Enzyme Containing Esterase Activity, Is Regulated by EstR, a Regulator in the MarR Family. PLoS ONE, 2016, 11, e0168791.	1.1	4

#	ARTICLE	IF	CITATIONS
1793	Assessing the Genotypic Differences between Strains of <i>Corynebacterium pseudotuberculosis</i> biovar equi through Comparative Genomics. <i>PLoS ONE</i> , 2017, 12, e0170676.	1.1	26
1794	Comparative genomic study of ALDH gene superfamily in <i>Gossypium</i> : A focus on <i>Gossypium hirsutum</i> under salt stress. <i>PLoS ONE</i> , 2017, 12, e0176733.	1.1	21
1795	The first transcriptome of Italian wall lizard, a new tool to infer about the Island Syndrome. <i>PLoS ONE</i> , 2017, 12, e0185227.	1.1	5
1796	Comparative proteomic analysis of pituitary glands from Huoyan geese between pre-laying and laying periods using an iTRAQ-based approach. <i>PLoS ONE</i> , 2017, 12, e0185253.	1.1	6
1797	Comparative transcriptomics revealed enhanced light responses, energy transport and storage in domestication of cassava ( <i>Manihot esculenta</i> ). <i>Frontiers of Agricultural Science and Engineering</i> , 2016, 3, 295.	0.9	1
1798	De novo Analysis of <i>Heortia vitessoides</i> (Lepidoptera: Crambidae) Transcriptome and Identification of Putative Cytochrome P450 Monooxygenase Genes. <i>Journal of Entomological Science</i> , 2019, 54, 293.	0.2	2
1799	Analysis of <i>Bos taurus</i> and <i>Sus scrofa</i> X and Y chromosome transcriptome highlights reproductive driver genes. <i>Oncotarget</i> , 2017, 8, 54416-54433.	0.8	6
1801	Current Advances in the Identification and Characterization of Putative Drug and Vaccine Targets in the Bacterial Genomes. <i>Current Topics in Medicinal Chemistry</i> , 2015, 16, 1040-1069.	1.0	35
1802	Identification of a novel plasmid-mediated colistin-resistance gene, <i>mcr-2</i> , in <i>Escherichia coli</i> , Belgium, June 2016. <i>Eurosurveillance</i> , 2016, 21, .	3.9	648
1803	Genome-wide identification and characterization of TCP family genes associated with flower and fruit development in <i>Fragaria vesca</i> . <i>Pakistan Journal of Botany</i> , 2019, 51, .	0.2	8
1804	Alternative splice variants, a new class of protein cancer biomarker candidates: findings in pancreatic cancer and breast cancer with systems biology implications. <i>Disease Markers</i> , 2010, 28, 241-51.	0.6	36
1805	Functional Prediction and Assignment of <i>Methanobrevibacter ruminantium</i> M1 Operome Using a Combined Bioinformatics Approach. <i>Frontiers in Genetics</i> , 2020, 11, 593990.	1.1	12
1806	In Silico Identification of Dual Ability of <i>N. gonorrhoeae</i> <i>ddl</i> for Developing Drug and Vaccine Against Pathogenic <i>Neisseria</i> and Other Human Pathogens. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 082-090.	0.4	10
1807	Mechanisms of Radiation Resistance in <i>Deinococcus radiodurans</i> R1 Revealed by the Reconstruction of Gene Regulatory Network Using Bayesian Network Approach. <i>Journal of Proteomics and Bioinformatics</i> , 2013, 01, .	0.4	4
1808	Transcriptome Analysis of Ten-DPA Fiber in an Upland Cotton (&lt;i&gt; <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 187 American Journal of Plant Sciences, 2017, 08, 2530-2553.	0.3	8
1809	The draft genome assembly of the critically endangered <i>Nyssa yunnanensis</i> , a plant species with extremely small populations endemic to Yunnan Province, China. <i>GigaByte</i> , 0, 2020, 1-12.	0.0	3
1810	Functional Prediction of Hypothetical Proteins from <i>Shigella flexneri</i> and Validation of the Predicted Models by Using ROC Curve Analysis. <i>Genomics and Informatics</i> , 2018, 16, e26.	0.4	11
1811	Designing a Novel Multi-epitope DNA- Based Vaccine Against Tuberculosis: In Silico Approach. <i>Jundishapur Journal of Microbiology</i> , 2017, 10, .	0.2	11

#	ARTICLE	IF	CITATIONS
1812	Homology modeling of an antifungal metabolite plipastatin synthase from the bacillus subtilis 168. <i>Bioinformatics</i> , 2011, 7, 384-387.	0.2	14
1813	Mining for SSRs and FDMs from expressed sequence tags of <i>Camellia sinensis</i> . <i>Bioinformatics</i> , 2012, 8, 260-266.	0.2	19
1814	Computer aided gene mining for gingerol biosynthesis. <i>Bioinformatics</i> , 2015, 11, 316-321.	0.2	3
1815	Optimizing k-mer size using a variant grid search to enhance de novo genome assembly. <i>Bioinformatics</i> , 2016, 12, 36-40.	0.2	5
1816	Networking of predicted post-translational modification (PTM) sites in human EGFR. <i>Bioinformatics</i> , 2019, 15, 448-454.	0.2	2
1817	Analysis of methyltransferase (MTase) domain from Zika virus (ZIKV). <i>Bioinformatics</i> , 2020, 16, 229-235.	0.2	3
1818	Genome streamlining in a minute herbivore that manipulates its host plant. <i>ELife</i> , 2020, 9, .	2.8	33
1819	Structures of diverse poxin cGAMP nucleases reveal a widespread role for cGAS-STING evasion in host-pathogen conflict. <i>ELife</i> , 2020, 9, .	2.8	34
1820	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. <i>PeerJ</i> , 2016, 4, e1616.	0.9	56
1821	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. <i>PeerJ</i> , 2013, 1, e167.	0.9	159
1822	The scavenger receptor repertoire in six cnidarian species and its putative role in cnidarian-dinoflagellate symbiosis. <i>PeerJ</i> , 2016, 4, e2692.	0.9	57
1823	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015, 3, e740.	0.9	157
1824	The sugarcane mitochondrial genome: assembly, phylogenetics and transcriptomics. <i>PeerJ</i> , 2019, 7, e7558.	0.9	15
1825	Identification and characterization of hirudin-HN, a new thrombin inhibitor, from the salivary glands of <i>Hirudo nipponia</i> . <i>PeerJ</i> , 2019, 7, e7716.	0.9	18
1826	Identification and expression pattern of chemosensory genes in the transcriptome of <i>Propiloscerus akamusi</i> . <i>PeerJ</i> , 2020, 8, e9584.	0.9	5
1829	Genomic and Transcriptomic Insight of Giant Sclerotium Formation of Wood-Decay Fungi. <i>Frontiers in Microbiology</i> , 2021, 12, 746121.	1.5	7
1830	Evolutionary history and pan-genome dynamics of strawberry ( <i>Fragaria</i> spp.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	43
1832	Characterization of a novel phage depolymerase specific to <i>Escherichia coli</i> O157:H7 and biofilm control on abiotic surfaces. <i>Journal of Microbiology</i> , 2021, 59, 1002-1009.	1.3	6

#	ARTICLE	IF	CITATIONS
1833	Genome-Wide Analysis of Major Facilitator Superfamily and Its Expression in Response of Poplar to <i>Fusarium oxysporum</i> . <i>Frontiers in Genetics</i> , 2021, 12, 769888.	1.1	3
1834	Depside and Depsidone Synthesis in Lichenized Fungi Comes into Focus through a Genome-Wide Comparison of the Olivetoric Acid and Physodic Acid Chemotypes of <i>Pseudevernia furfuracea</i> . <i>Biomolecules</i> , 2021, 11, 1445.	1.8	27
1835	High-quality reference genome of <i>Fasciola gigantica</i> : Insights into the genomic signatures of transposon-mediated evolution and specific parasitic adaptation in tropical regions. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009750.	1.3	12
1836	Trends in biological data integration for the selection of enzymes and transcription factors related to cellulose and hemicellulose degradation in fungi. <i>3 Biotech</i> , 2021, 11, 475.	1.1	3
1837	Complete genomes of the eukaryotic poultry parasite <i>Histomonas meleagridis</i> : linking sequence analysis with virulence / attenuation. <i>BMC Genomics</i> , 2021, 22, 753.	1.2	17
1839	Protocol for using NoBadWordsCombiner to merge and minimize "bad words" from BLAST hits against multiple eukaryotic gene annotation databases. <i>STAR Protocols</i> , 2021, 2, 100888.	0.5	1
1840	Musarin, a novel protein with tyrosine kinase inhibitory activity from <i>Trametes versicolor</i> , inhibits colorectal cancer stem cell growth. <i>Biomedicine and Pharmacotherapy</i> , 2021, 144, 112339.	2.5	7
1842	Methods for Gene Ontology Annotation. , 2007, 406, 495-520.		8
1843	An automated protein annotation filter for integrating web-based annotation tools. <i>Bioinformatics</i> , 2007, 2, 76-77.	0.2	0
1845	Expressed sequence tags from the midgut of <i>Epiphyas postvittana</i> (Walker) (Lepidoptera: Tortricidae). <i>Insect Molecular Biology</i> , 2007, .	1.0	0
1846	Resources for functional annotation. , 2008, , 139-164.		0
1847	Structure to function. , 2008, , 239-262.		0
1848	System Design and Implementation for the Efficient Management and Automatic Update of Protein-Protein Interaction Data.. <i>Journal of Life Science</i> , 2008, 18, 318-322.	0.2	0
1849	A pattern mining approach toward discovering generalized sequence signatures. , 2008, , .		1
1850	A Bioinformatics Resource for Crop Functional Genomics: GFSelector Module in Automated Annotation System, RiceGAAS. <i>Japan Agricultural Research Quarterly</i> , 2009, 43, 103-113.	0.1	0
1851	A Visualization ToolKit Based Application for Representing Macromolecular Surfaces. <i>Lecture Notes in Computer Science</i> , 2009, , 284-292.	1.0	0
1852	A database for human Y chromosome protein data. <i>Bioinformatics</i> , 2009, 4, 184-186.	0.2	0
1853	Practical Guide: Genomic Techniques and How to Apply Them to Marine Questions. , 2010, , 315-378.		0

#	ARTICLE	IF	CITATIONS
1854	Whole-Genome Sequence Characterization of Primary Auxin-Responsive <math>IAA</math> Gene Family in Sorghum (<math>Sorghum bicolor</math> L.). Acta Agronomica Sinica(China), 2010, 36, 688-694.	0.1	1
1855	Functional Inference in Microbial Genomics Based on Large-Scale Comparative Analysis. , 2011, , 55-92.		0
1857	Research paper In silico prediction and characterization of three-dimensional structure of Actin-1 of Arabidopsis thaliana. Biotechnologia, 2013, 4, 432-443.	0.3	1
1858	Identificaci3n in silico de un grupo de secuencias ort3logas conservadas (COS) de Ipomoea batatas. Revista Peruana De Biologia, 2013, 15, .	0.1	0
1859	Bioinformatics Analysis Of Novel Non-Coding Motifs In Pathogenic Bacterial Genome. Journal of the Asiatic Society of Bangladesh Science, 2013, 39, 9-20.	0.1	0
1860	PCR Amplification, Sequencing, and In Silico Characterization of Pectin Lyase Genes from Aspergillus flavus NIIICC8142. , 2014, , 413-421.		2
1861	Functional Annotation of Proteins by a Novel Method Using Weight and Feature Selection. Lecture Notes in Electrical Engineering, 2014, , 785-797.	0.3	0
1862	Human Microbiome Project, Reference Genomes, Rationale, Selection, Acquisition, Sequencing, and Annotation. , 2014, , 1-4.		0
1866	The Human Microbiome. , 0, , 226-237.		1
1873	Plant Genome Annotation, Methods for. , 2018, , 887-893.		0
1874	Identification of coding sequence and its use for functional and structural characterization of catalase from Phyllanthus emblica. Bioinformation, 2018, 14, 008-014.	0.2	3
1876	GENOME-WIDE IDENTIFICATION AND CHARACTERIZATION OF THE SBP GENE FAMILY IN EUCALYPTUS GRANDIS. Applied Ecology and Environmental Research, 2018, 16, 6181-6193.	0.2	0
1882	Eucalyptus grandis YABBY Transkripsiyon Fakt3rlerinin Genom Baz3nda Analizi. T3rkiye Tar3msal AraŸt3rmalar Dergisi, 2018, 5, 158-166.	0.5	5
1885	Transcriptome profiling in the spathe of Anthurium andraeanum "Albama"™ and its anthocyanin-loss mutant "Xueyu"™. Scientific Data, 2018, 5, 180247.	2.4	2
1888	IN SILICO STRUCTURAL CHARACTERIZATION OF L. lactis subsp. cremoris MG1363 FFH-FTSY COMPLEX IN PROTEIN TARGETING INTERACTION. Jurnal Teknologi (Sciences and Engineering), 2019, 81, .	0.3	0
1891	Development and Validation of a Transcriptome-Based Simple Sequence Repeats Markers in Coilia nasus. Pakistan Journal of Zoology, 2019, 51, .	0.1	2
1895	From EST to structure models for functional inference of APP, BACE1, PSEN1, PSEN2 genes. Bioinformation, 2019, 15, 760-771.	0.2	0
1899	Analysis of predicted proteasomal cleavages in the methyltransferase domain from JEV. Bioinformation, 2020, 16, 223-228.	0.2	1

#	ARTICLE	IF	CITATIONS
1903	Sorghum bicolor CAMTA Transkripsiyon Faktörlerinin Genom Açıklama Analizi. Atatürk Üniversitesi Ziraat Fakültesi Dergisi, 0, , .	0.7	1
1907	Use of Chou's 5-steps rule to predict the subcellular localization of gram-negative and gram-positive bacterial proteins by multi-label learning based on gene ontology annotation and profile alignment. Journal of Integrative Bioinformatics, 2021, 18, 51-79.	1.0	7
1908	From sequence analysis of DPP-4 to molecular docking based searching of its inhibitors. Bioinformation, 2020, 16, 444-451.	0.2	2
1909	Multi-species transcriptomics reveals evolutionary diversity in the mechanisms regulating shrimp tail muscle excitation-contraction coupling. Gene, 2020, 752, 144765.	1.0	4
1911	Draft Genome Sequences of Seven Strains of Paenibacillus spp. (Phylum Firmicutes ) Inhabiting the Seeds of Cucumis melo L. (Cantaloupe) and Exhibiting Plant Probiotic Traits. Microbiology Resource Announcements, 2020, 9, .	0.3	1
1912	Variability and evolution of NBS-LRR genes in Agave tequilana and their differential response to Lasiodiplodia infection. European Journal of Plant Pathology, 0, , 1.	0.8	1
1913	Quantitative phosphoproteomic analysis reveals chemoresistance-related proteins and signaling pathways induced by rhIL-6 in human osteosarcoma cells. Cancer Cell International, 2021, 21, 581.	1.8	5
1916	Transcriptome analyses of Ditylenchus destructor in responses to cold and desiccation stress. Genetics and Molecular Biology, 2020, 43, e20180057.	0.6	0
1917	De novo assembly, annotation, marker discovery, and genetic diversity of the Stipa breviflora Griseb. (Poaceae) response to grazing. PLoS ONE, 2020, 15, e0244222.	1.1	4
1921	Sequencing and Assembling the Nuclear and Organelle Genomes of North American Spruces. Compendium of Plant Genomes, 2020, , 1-8.	0.3	0
1922	In silico detection tools to identify fungal secondary metabolites and their biosynthetic gene clusters. , 2020, , 23-35.		0
1925	Unraveling the role of male reproductive tract and haemolymph in cantharidin-exuding Lydus trimaculatus and Mylabris variabilis (Coleoptera: Meloidae): a comparative transcriptomics approach. BMC Genomics, 2021, 22, 808.	1.2	7
1926	Candidate Effectors of Plasmodiophora brassicae Pathotype 5X During Infection of Two Brassica napus Genotypes. Frontiers in Microbiology, 2021, 12, 742268.	1.5	7
1928	Integrated Servers for Structure-Informed Function Prediction. , 2009, , 251-272.		0
1929	Case Study: Structure and Function Prediction of a Protein with No Functionally Characterized Homolog. Studies in Computational Intelligence, 2008, , 379-395.	0.7	0
1931	Sorghum [Sorghum bicolor (L.) Moench] Genomunda BES1 Transkripsiyon Faktör Ailesinin Genom Açıklama Analizi. Atatürk Tarımsal Araştırmalar Dergisi, 2020, 7, 85-95.	0.5	7
1933	REP27, a tetratricopeptide repeat nuclear-encoded and chloroplast-localized protein, functions in D1/32-kD reaction center protein turnover and photosystem II repair from photodamage. Plant Physiology, 2007, 143, 1547-60.	2.3	18
1934	Identification and differential expression of microRNAs in 1, 25-dihydroxyvitamin D3-induced osteogenic differentiation of human adipose-derived mesenchymal stem cells. American Journal of Translational Research (discontinued), 2017, 9, 4856-4871.	0.0	8

#	ARTICLE	IF	CITATIONS
1935	Chloranthus genome provides insights into the early diversification of angiosperms. <i>Nature Communications</i> , 2021, 12, 6930.	5.8	44
1937	Identification and Expression Analysis of G Protein-Coupled Receptors in the Miridae Insect <i>Apolygus lucorum</i> . <i>Frontiers in Endocrinology</i> , 2021, 12, 773669.	1.5	10
1938	<i>Enterococcus faecium</i> Regulates Honey Bee Developmental Genes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12105.	1.8	12
1939	Identification and functional annotation of hypothetical proteins of uropathogenic <i>Escherichia coli</i> strain CFT073 towards designing antimicrobial drug targets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 14084-14095.	2.0	4
1940	The draft chromosome-level genome assembly of tetraploid ground cherry ( <i>Prunus fruticosa</i> Pall.) from long reads. <i>Genomics</i> , 2021, 113, 4173-4183.	1.3	14
1942	Transcriptomic Response to <i>Perkinsus marinus</i> in Two <i>Crassostrea</i> Oysters Reveals Evolutionary Dynamics of Host-Parasite Interactions. <i>Frontiers in Genetics</i> , 2021, 12, 795706.	1.1	6
1943	Ciliary photoreceptors in sea urchin larvae indicate pan-deuterostome cell type conservation. <i>BMC Biology</i> , 2021, 19, 257.	1.7	7
1944	Histone acetylation regulates the expression of genes involved in worker reproduction in the ant <i>Temnothorax rugatulus</i> . <i>BMC Genomics</i> , 2021, 22, 871.	1.2	10
1945	A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6301-6314.	1.9	80
1947	A global phosphoproteomics analysis of adult <i>Fasciola gigantica</i> by LC-MS/MS. <i>Parasitology Research</i> , 2022, , 1.	0.6	1
1948	Highly diverged lineages of <i>Saccharomyces paradoxus</i> in temperate to subtropical climate zones in China. <i>Yeast</i> , 2021, , .	0.8	8
1951	A novel phage indirectly regulates diatom growth by infecting diatom-associated biofilm-forming bacterium. <i>Applied and Environmental Microbiology</i> , 2022, , AEM0213821.	1.4	2
1952	Carbohydrate active enzymes (CAZy) regulate cellulolytic and pectinolytic enzymes in <i>Colletotrichum falcatum</i> causing red rot in sugarcane. <i>3 Biotech</i> , 2022, 12, 48.	1.1	5
1953	Discovery and Evolutionary Analysis of a Novel Bat-Borne Paramyxovirus. <i>Viruses</i> , 2022, 14, 288.	1.5	8
1954	Genetic characterisation of an Iflavirus associated with a vomiting disease in the Indian tropical tasar silkworm, <i>Antheraea mylitta</i> . <i>Virus Research</i> , 2022, 311, 198703.	1.1	5
1955	Identification of Phosphorus Stress Related Proteins in the Seedlings of Dongxiang Wild Rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF 5	1.0	7
1956	Genomic insight into the scale specialization of the biological control agent <i>Novius pumilus</i> (Weise,) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5	1.2	6
1957	Genome-wide identification, characterization, and expression analysis of aluminum-activated malate transporter genes (ALMTs) in <i>Gossypium hirsutum</i> L. <i>Biocell</i> , 2022, 46, 1347-1356.	0.4	0



#	ARTICLE	IF	CITATIONS
1958	Improved 93-11 Genome and Time-Course Transcriptome Expand Resources for Rice Genomics. <i>Frontiers in Plant Science</i> , 2021, 12, 769700.	1.7	4
1959	Tracking Down the Functional Potential of the Core Genome between <i>Ralstonia solanacearum</i> Strains Across Different Plant Hosts. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1961	Genome-Wide Analysis Indicates a Complete Prostaglandin Pathway from Synthesis to Inactivation in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 1654.	1.8	0
1962	Ubiquitylomes and proteomes analyses provide a new interpretation of the molecular mechanisms of rice leaf senescence. <i>Planta</i> , 2022, 255, 43.	1.6	2
1963	Partitiã-like viruses from African armyworm increase larval and pupal mortality of a novel host: the Egyptian cotton leafworm. <i>Pest Management Science</i> , 2022, 78, 1529-1537.	1.7	4
1964	Evolution of host-microbe cell adherence by receptor domain shuffling. <i>ELife</i> , 2022, 11, .	2.8	4
1965	Characterization of Two Novel EF-Hand Proteins Identifies a Clade of Putative Ca <sup>2+</sup> -Binding Protein Specific to the Ambulacraria. <i>Journal of Bioinformatics and Systems Biology</i> , 2022, 05, .	0.2	1
1967	Genomic Characterization of the Titan-like Cell Producing <i>Naganishia tulchinskyi</i> , the First Novel Eukaryote Isolated from the International Space Station. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 165.	1.5	5
1968	Comprehensive Analysis of Arabinogalactan Protein-Encoding Genes Reveals the Involvement of Three BrFLA Genes in Pollen Germination in <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 13142.	1.8	4
1969	HSDFinder: A BLAST-Based Strategy for Identifying Highly Similar Duplicated Genes in Eukaryotic Genomes. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	5
1970	Genome-wide characterization of the sorghum JAZ gene family and their responses to phytohormone treatments and aphid infestation. <i>Scientific Reports</i> , 2022, 12, 3238.	1.6	8
1971	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	1.7	1
1972	Comparative proteome analysis reveals the role of negative floral regulators and defense-related genes in phytoplasma infected sesame. <i>Protoplasma</i> , 2022, 259, 1441-1453.	1.0	4
1973	Genomic insights into longan evolution from a chromosome-level genome assembly and population genomics of longan accessions. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
1974	Genome-wide evolution and expression analysis of the <i>MYB-CC</i> gene family in <i>Brassica</i> spp.. <i>PeerJ</i> , 2022, 10, e12882.	0.9	2
1975	Enhanced antibacterial effect of a novel Friunavirus phage vWU2001 in combination with colistin against carbapenem-resistant <i>Acinetobacter baumannii</i> . <i>Scientific Reports</i> , 2022, 12, 2633.	1.6	12
1976	Identification of Microproteins in Hep3B Cells at Different Cell Cycle Stages. <i>Journal of Proteome Research</i> , 2022, 21, 1052-1060.	1.8	3
1977	Multi-Omics Analysis Reveals that the Antimicrobial Kasugamycin Potential Targets Nitrate Reductase in <i>Didymella segeticola</i> to Achieve Control of Tea Leaf Spot. <i>Phytopathology</i> , 2022, 112, 1894-1906.	1.1	5

#	ARTICLE	IF	CITATIONS
1978	Fasulye bitkisinde phospholipase D gen ailesinin tuz ve kuraklık stresi altında genom analiz karakterizasyonu. European Journal of Science and Technology, 0, , .	0.5	0
1979	Pangenome Analysis of the Soilborne Fungal Phytopathogen <i>Rhizoctonia solani</i> and Development of a Comprehensive Web Resource: RsolaniDB. <i>Frontiers in Microbiology</i> , 2022, 13, 839524.	1.5	14
1980	Identification of the LOX Gene Family in Peanut and Functional Characterization of AhLOX29 in Drought Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 832785.	1.7	16
1981	Fasulye Genotiplerinde Tuz ve Kuraklık Stresleri Altında VPE Gen Ailesinin Genom Analizi ve Karakterizasyonu. European Journal of Science and Technology, 0, , .	0.5	1
1982	PvTLP genlerinin genom analiz tespit ve karakterizasyonu. European Journal of Science and Technology, 0, , .	0.5	0
1984	Evolution of the recombination regulator PRDM9 in minke whales. <i>BMC Genomics</i> , 2022, 23, 212.	1.2	4
1985	BURP domain-containing genes in legumes: genome-wide identification, structure, and expression analysis under stresses and development. <i>Plant Biotechnology Reports</i> , 2022, 16, 369-388.	0.9	4
1986	Selection drives convergent gene expression changes during transitions to co-sexuality in haploid sexual systems. <i>Nature Ecology and Evolution</i> , 2022, 6, 579-589.	3.4	12
1988	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.	1.6	5
1989	Proteomic Analysis Reveals Enzymes for Î <sup>2</sup> -D-Glucan Formation and Degradation in <i>Levilactobacillus brevis</i> TMW 1.2112. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3393.	1.8	2
1990	Multi-omics reveal differentiation and maintenance of dimorphic flowers in an alpine plant on the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2023, 32, 1411-1424.	2.0	7
1991	Comparative transcriptomics reveals altered species interaction between the bioeroding sponge <i>Cliona varians</i> and the coral <i>Porites furcata</i> under ocean acidification. <i>Molecular Ecology</i> , 2022, 31, 3002-3017.	2.0	2
1992	NBS-LRR-WRKY genes and protease inhibitors (PIs) seem essential for cowpea resistance to root-knot nematode. <i>Journal of Proteomics</i> , 2022, 261, 104575.	1.2	4
1994	Whole-Genome Sequencing of <i>Acer catalpifolium</i> Reveals Evolutionary History of Endangered Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
1996	Genomic characterization of ZIP genes in pigeonpea (CcZIP) and their expression analysis among the genotypes with contrasting host response to pod borer. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2787-2804.	1.4	0
1998	INTERMEDIUM-C mediates the shade-induced bud growth arrest in barley. <i>Journal of Experimental Botany</i> , 2022, 73, 1963-1977.	2.4	0
1999	Proteomic Screening and Verification of Biomarkers in Different Stages of Mycosis Fungoides: A pilot Study. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 747017.	1.8	1
2000	Discovery of a Polyamino Acid Antibiotic Solely Comprising Î <sup>2</sup> -Lysine by Potential Producer Prioritization-Guided Genome Mining. <i>ACS Chemical Biology</i> , 2022, 17, 171-180.	1.6	3

#	ARTICLE	IF	CITATIONS
2001	Paraneptunicella aestuarii gen. nov., sp. nov., a member of the family Alteromonadaceae isolated from seawater in East China Sea. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	7
2003	The hidden genomic diversity of ciliated protists revealed by single-cell genome sequencing. BMC Biology, 2021, 19, 264.	1.7	11
2004	Genome sequencing and transcriptome analyses provide insights into the origin and domestication of water caltrop (<i>Trapa</i> spp., Lythraceae). Plant Biotechnology Journal, 2022, 20, 761-776.	4.1	16
2005	Chromosome-level genome assembly and characterization of <i>Sophora Japonica</i>. DNA Research, 2022, 29, .	1.5	3
2006	Role of APOA1 in the resistance to platinum-based chemotherapy in squamous cervical cancer. BMC Cancer, 2022, 22, 411.	1.1	3
2007	Phylogeny and Metabolic Potential of the Candidate Phylum SAR324. Biology, 2022, 11, 599.	1.3	8
2009	Global Transcriptomic Analysis of Bacteriophage-Host Interactions between a Kayvirus Therapeutic Phage and Staphylococcus aureus. Microbiology Spectrum, 2022, 10, e0012322.	1.2	3
2010	A chromosome-level genome of the kuruma shrimp (Marsupenaeus japonicus) provides insights into its evolution and cold-resistance mechanism. Genomics, 2022, 114, 110373.	1.3	8
2011	Find My Way to You: A Comparative Study of Antennal Sensilla and Olfactory Genes in Slug Moth With Different Diet Ranges (Lepidoptera: Limacodidae). Frontiers in Ecology and Evolution, 2022, 10, .	1.1	0
2192	GOBlet: annotation of anonymous sequence data with gene ontology and pathway terms. Journal of Integrative Bioinformatics, 2008, 5, .	1.0	2
2194	Systemic necrosis induced by overexpression of wheat yellow mosaic virus 14KÅsuppresses the replication of other viruses in Nicotiana benthamiana. Phytopathology Research, 2022, 4, .	0.9	1
2195	A Blueprint of Microstructures and Stage-Specific Transcriptome Dynamics of Cuticle Formation in Bombyx mori. International Journal of Molecular Sciences, 2022, 23, 5155.	1.8	3
2196	ProtPathDB: A Web-based Resource of Parasite Proteases. Current Bioinformatics, 2022, 17, 710-722.	0.7	0
2199	Genome-wide characterization of the TALE homeodomain family and the KNOX-BLH interaction network in tomato. Plant Molecular Biology, 2022, 109, 799-821.	2.0	14
2200	Comparative proteomic analysis identifies differentially expressed proteins and reveals potential mechanisms of traumatic heterotopic ossification progression. Journal of Orthopaedic Translation, 2022, 34, 42-59.	1.9	6
2201	Characterization of NRPS and PKS genes involved in the biosynthesis of SMs in Alternaria dauci including the phytotoxic polyketide aldaulactone. Scientific Reports, 2022, 12, 8155.	1.6	10
2202	Variation in leaf transcriptome responses to elevated ozone corresponds with physiological sensitivity to ozone across maize inbred lines. Genetics, 2022, 221, .	1.2	1
2203	The assembled and annotated genome of the masked palm civet (<i>Paguma larvata</i>). GigaScience, 2022, 11, .	3.3	2

#	ARTICLE	IF	CITATIONS
2204	Bactericidal Effect of Cecropin A Fused Endolysin on Drug-Resistant Gram-Negative Pathogens. <i>Journal of Microbiology and Biotechnology</i> , 2022, 32, 816-823.	0.9	13
2205	Symbiosis with Dinoflagellates Alters Cnidarian Cell-Cycle Gene Expression. <i>Cellular Microbiology</i> , 2022, 2022, 1-20.	1.1	4
2206	A chromosome-level genome assembly of the pollinating fig wasp <i>Valisia javana</i> . <i>DNA Research</i> , 2022, 29, .	1.5	3
2207	Eradication of drug-resistant <i>Acinetobacter baumannii</i> by cell-penetrating peptide fused endolysin. <i>Journal of Microbiology</i> , 2022, 60, 859-866.	1.3	5
2209	Extreme freeze-tolerance in cryophilic tardigrades relies on controlled ice formation but does not involve significant change in transcription. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2022, 271, 111245.	0.8	8
2212	In silico Structural and Functional Characterization of a Hypothetical Protein from <i>Stenotrophomonas maltophilia</i> SRM01. <i>Journal of Pure and Applied Microbiology</i> , 2022, 16, 1167-1178.	0.3	2
2214	Genome of <i>Varanus salvator macromaculatus</i> (Asian Water Monitor) Reveals Adaptations in the Blood Coagulation and Innate Immune System. <i>Frontiers in Ecology and Evolution</i> , 2022, 10, .	1.1	0
2215	A telomere-to-telomere gap-free reference genome of watermelon and its mutation library provide important resources for gene discovery and breeding. <i>Molecular Plant</i> , 2022, 15, 1268-1284.	3.9	74
2216	Cultivated hawthorn ( <i>Crataegus pinnatifida</i> var. <i>major</i> ) genome sheds light on the evolution of Maleae (apple tribe). <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1487-1501.	4.1	12
2217	Co-Expression Analysis Reveals Differential Expression of Homologous Genes Associated with Specific Terpenoid Biosynthesis in <i>Rehmannia glutinosa</i> . <i>Genes</i> , 2022, 13, 1092.	1.0	3
2218	Genome-Wide Identification and Analysis of the Class III Peroxidase Gene Family in Tobacco ( <i>Nicotiana glauca</i> ). <i>Plant Physiology</i> , 2022, 170, 1117-1128.	1.1	9
2220	Iterative analysis of metabolic modulation in the cyanobacterium <i>Aphanizomenon flos-aquae</i> 2012 KM1/D3 upon nitric oxide synthase derived NO induction. <i>Environmental and Experimental Botany</i> , 2022, 201, 104967.	2.0	8
2221	Conserved secreted effectors contribute to endophytic growth and multihost plant compatibility in a vascular wilt fungus. <i>Plant Cell</i> , 2022, 34, 3214-3232.	3.1	20
2222	Tandem mass tagging combined with liquid chromatography-tandem mass spectrometry technique to detect protein markers in gastroesophageal junction adenocarcinoma. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, .	0.7	3
2225	A de novo assembled high-quality chromosome-scale <i>Trifolium pratense</i> genome and fine-scale phylogenetic analysis. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
2226	A Chromosome-Scale Genome Assembly of the Okapi ( <i>Okapia johnstoni</i> ). <i>Journal of Heredity</i> , 2022, 113, 568-576.	1.0	2
2227	A Candidate Gene Cluster for the Bioactive Natural Product Gyrophoric Acid in Lichen-Forming Fungi. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12
2228	Comparative genomic analysis of <i>Babesia duncani</i> responsible for human babesiosis. <i>BMC Biology</i> , 2022, 20, .	1.7	11

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2229	<i>In silico</i> homology modeling, docking and sequence analysis of some bacterial laccases to unravel enzymatic specificity towards lignin biodegradation. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-19.	2.0	4
2230	A chromosome-level genome assembly of <i>Neotoxoptera formosana</i> (Takahashi, 1921) (Hemiptera: Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 5 0.8	1.0	7
2231	Comparative bioinformatics analysis and abiotic stress responses of expansin proteins in Cucurbitaceae members: watermelon and melon. <i>Protoplasma</i> , 2023, 260, 509-527.	1.0	7
2232	Identification of Microproteins in <i>Saccharomyces cerevisiae</i> under Different Stress Conditions. <i>Journal of Proteome Research</i> , 0, , .	1.8	2
2233	A pan-genome and chromosome-length reference genome of narrow-leaved lupin ( <i>Lupinus</i> ) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 5 2.8	2.8	9
2234	Emerging Computational Approaches for Antimicrobial Peptide Discovery. <i>Antibiotics</i> , 2022, 11, 936.	1.5	12
2235	Phylogenies of the 16S rRNA gene and its hypervariable regions lack concordance with core genome phylogenies. <i>Microbiome</i> , 2022, 10, .	4.9	43
2236	Pan-Cancer Analysis Reveals Recurrent <i>BCAR4</i> Gene Fusions across Solid Tumors. <i>Molecular Cancer Research</i> , 2022, 20, 1481-1488.	1.5	3
2237	Genomic divergence of <i>Stellera chamaejasme</i> through local selection across the Qinghai-Tibet plateau and northern China. <i>Molecular Ecology</i> , 2022, 31, 4782-4796.	2.0	15
2238	Genome-Wide Identification and Expression Analysis of DGK (Diacylglycerol Kinase) Genes in Common Bean. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 2558-2569.	2.8	4
2240	Genome-wide identification, characterization, and expression profiling of 14-3-3 genes in legumes. <i>Plant Biotechnology Reports</i> , 2022, 16, 579-597.	0.9	3
2241	Multi-omics profiling of the cold tolerant <i>Monoraphidium minutum</i> 26B-AM in response to abiotic stress. <i>Algal Research</i> , 2022, 66, 102794.	2.4	3
2242	A lipopolysaccharide-dependent phage infects a pseudomonad phytopathogen and can evolve to evade phage resistance. <i>Environmental Microbiology</i> , 2022, 24, 4834-4852.	1.8	9
2243	Less hairy leaf 1, an RNaseH-like protein, regulates trichome formation in rice through auxin. <i>Journal of Integrative Agriculture</i> , 2023, 22, 31-40.	1.7	3
2244	A Polyketide Synthetase Gene Cluster Is Responsible for Antibacterial Activity of <i>Burkholderia contaminans</i> MS14. <i>Phytopathology</i> , 2023, 113, 11-20.	1.1	2
2245	AMPK Is Involved in Regulating the Utilization of Carbon Sources, Conidiation, Pathogenicity, and Stress Response of the Nematode-Trapping Fungus <i>Arthrobotrys oligospora</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	13
2248	Functional Analysis of Conserved Hypothetical Proteins from the Antarctic Bacterium, <i>Pedobacter cryoconitis</i> Strain BG5 Reveals Protein Cold Adaptation and Thermal Tolerance Strategies. <i>Microorganisms</i> , 2022, 10, 1654.	1.6	0
2249	The Improved Biocontrol Agent, F1-35, Protects Watermelon against Fusarium Wilt by Triggering Jasmonic Acid and Ethylene Pathways. <i>Microorganisms</i> , 2022, 10, 1710.	1.6	4

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2250	Multi-omics analyses reveal <i>MdMYB10</i> hypermethylation being responsible for a bud sport of apple fruit color. <i>Horticulture Research</i> , 2022, 9, .	2.9	4
2251	Fucoidan-active $\alpha$ -L-fucosidases of the GH29 and GH95 families from a fucoidan degrading cluster of the marine bacterium <i>Wenyngzhuangia fucanilytica</i> . <i>Archives of Biochemistry and Biophysics</i> , 2022, 728, 109373.	1.4	12
2252	Characterization and expression profiling of G protein-coupled receptors (GPCRs) in <i>Spodoptera litura</i> (Lepidoptera: Noctuidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 44, 101018.	0.4	2
2253	DGPD: a knowledge database of dense granule proteins of the Apicomplexa. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	4
2254	Chromosome-level Genomes Reveal the Genetic Basis of Descending Dysploidy and Sex Determination in <i>Morus</i> Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1119-1137.	3.0	6
2255	Proteome-wide analysis of lysine 2-hydroxyisobutyrylation in <i>Frankliniella occidentalis</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	0
2256	Global-Scale Profiling of Differential Expressed Lysine-Lactylated Proteins in the Cerebral Endothelium of Cerebral Ischemia-“Reperfusion Injury Rats. <i>Cellular and Molecular Neurobiology</i> , 2023, 43, 1989-2004.	1.7	9
2257	Biocomputational characterisation of MBO_200107 protein of <i>Mycobacterium tuberculosis</i> variant <i>caprae</i> : a molecular docking and simulation study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 7204-7223.	2.0	2
2259	Effects of Acclimation, Population, and Sex on Behavioral Thermoregulation, CTMax, Symptoms of Heat Stress, and Gene Expression of <i>Melanoplus differentialis</i> , a Generalist Grasshopper-“Does Temporal Thermal Heterogeneity Prepare Populations for a Warming World?. <i>Journal of Insect Behavior</i> , 0, .	0.4	0
2260	Host-delivered RNAi-mediated silencing of the root-knot nematode ( <i>Meloidogyne incognita</i> ) effector genes, Mi-msp10 and Mi-msp23, confers resistance in <i>Arabidopsis</i> and impairs reproductive ability of the root-knot nematode. <i>Planta</i> , 2022, 256, .	1.6	1
2261	Genomic adaptation of the picoeukaryote <i>Pelagomonas calceolata</i> to iron-poor oceans revealed by a chromosome-scale genome sequence. <i>Communications Biology</i> , 2022, 5, .	2.0	6
2262	<i>Enterobacteria</i> Phage Ac3's Genome Annotation and Host Range Analysis Against the ECOR Reference Library. <i>Phage</i> , 2022, 3, 165-170.	0.8	1
2263	Integrated Transcriptome and Proteome Analysis Reveals that the Antimicrobial Griseofulvin Targets <i>Didymella segeticola</i> beta-Tubulin to Control Tea Leaf Spot. <i>Phytopathology</i> , 0, .	1.1	1
2264	Chromosome-level genome assembly of <i>Amomum tsao-ko</i> provides insights into the biosynthesis of flavor compounds. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
2265	Comparative study of neuropeptide signaling systems in Hemiptera. <i>Insect Science</i> , 2023, 30, 705-724.	1.5	2
2266	Identification and Characterization of Malate Dehydrogenases in Tomato ( <i>Solanum lycopersicum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 10028.	1.8	8
2267	Chromosome-scale assemblies of <i>Acanthamoeba castellanii</i> genomes provide insights into <i>Legionella pneumophila</i> infection-“related chromatin reorganization. <i>Genome Research</i> , 2022, 32, 1698-1710.	2.4	13
2268	A High-Quality Genome of <i>Rhizoctonia solani</i> , a Devastating Fungal Pathogen with a Wide Host Range. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 954-958.	1.4	5

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2269	Transcriptome analysis of mangrove-isolated <i>Chlorella vulgaris</i> UMT-M1 reveals insights for vigorous growth and lipid accumulation through reduced salinity. <i>Algal Research</i> , 2022, 67, 102833.	2.4	3
2270	Omics data unveil early molecular response underlying limb regeneration in the Chinese mitten crab, <i>Eriocheir sinensis</i> . <i>Science Advances</i> , 2022, 8, .	4.7	9
2271	Nuclear Functions of KaeA, a Subunit of the KEOPS Complex in <i>Aspergillus nidulans</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 11138.	1.8	0
2272	Microbial communities of stratified aquatic ecosystems of Kandalaksha Bay (White Sea) shed light on the evolutionary history of green and brown morphotypes of <i>Chlorobiota</i> . <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	3
2273	Integration of genome and transcriptome reveal molecular regulation mechanism of early flowering trait in <i>Prunus</i> genus ( <i>Prunus mume</i> and <i>Prunus persica</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2274	Molecular and expression analysis indicate the role of CBL interacting protein kinases (CIPKs) in abiotic stress signaling and development in chickpea. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
2276	HSDatabase” a database of highly similar duplicate genes from plants, animals, and algae. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	2
2277	IAAnimal: a cross-species omics knowledgebase for animals. <i>Nucleic Acids Research</i> , 2023, 51, D1312-D1324.	6.5	6
2278	The pangenome of the wheat pathogen <i>Pyrenophora tritici-repentis</i> reveals novel transposons associated with necrotrophic effectors ToxA and ToxB. <i>BMC Biology</i> , 2022, 20, .	1.7	15
2279	A New Expression System Based on Psychrotolerant <i>Debaryomyces hansenii</i> Yeast and Its Application to the Production of Cold-Active $\beta$ -D-Galactosidase from <i>Paracoccus</i> sp. 32d. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11691.	1.8	2
2280	Exosomal DNAJB11 promotes the development of pancreatic cancer by modulating the EGFR/MAPK pathway. <i>Cellular and Molecular Biology Letters</i> , 2022, 27, .	2.7	7
2281	The genome and lifestage-specific transcriptomes of a plant-parasitic nematode and its host reveal susceptibility genes involved in trans-kingdom synthesis of vitamin B5. <i>Nature Communications</i> , 2022, 13, .	5.8	28
2283	Identification and expression analysis of G protein-coupled receptors in the cotton aphid, <i>Aphis gossypii</i> Glover. <i>International Journal of Biological Macromolecules</i> , 2023, 224, 115-124.	3.6	3
2284	Epichloa seed transmission efficiency is influenced by plant defense response mechanisms. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2285	Genome-wide identification of biotin carboxyl carrier subunits of acetyl-CoA carboxylase in <i>Brassica</i> and their role in stress tolerance in oilseed <i>Brassica napus</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	9
2286	Fasulyede Tuz ve Kuraklık Stresi Altında PIF Gen Ailesinin Genomunda Analizi ve Karakterizasyonu. <i>Türkiye Tarımsal Araştırmalar Dergisi</i> , 0, , .	0.5	0
2287	SNARE Protein DdVam7 of the Nematode-Trapping Fungus <i>Drechlerella dactyloides</i> Regulates Vegetative Growth, Conidiation, and the Predatory Process via Vacuole Assembly. <i>Microbiology Spectrum</i> , 0, , .	1.2	5
2288	A global pangenome for the wheat fungal pathogen <i>Pyrenophora tritici-repentis</i> and prediction of effector protein structural homology. <i>Microbial Genomics</i> , 2022, 8, .	1.0	5

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2289	Thirteen Dipteroocarpoideae genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464.	3.6	6
2290	Genome-Wide Analysis and Characterization of SABATH Gene Family in <i>Phaseolus vulgaris</i> Genotypes Subject to Melatonin under Drought and Salinity Stresses. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 242-259.	1.0	5
2291	Genomic profiling of climate adaptation in <i>Aedes aegypti</i> along an altitudinal gradient in Nepal indicates nongradual expansion of the disease vector. <i>Molecular Ecology</i> , 2023, 32, 350-368.	2.0	3
2292	Functional characterization of <i>MANNANOSE-BINDING LECTIN 1</i> , a G-type lectin gene family member, in response to fungal pathogens of strawberry. <i>Journal of Experimental Botany</i> , 2023, 74, 149-161.	2.4	8
2293	Genomic insights into phage-host interaction in the deep-sea chemolithoautotrophic <i>Campylobacterota</i> , <i>Nitratiruptor</i> . <i>ISME Communications</i> , 2022, 2, .	1.7	1
2294	Olfactory and gustatory receptor genes in fig wasps: Evolutionary insights from comparative studies. <i>Gene</i> , 2023, 850, 146953.	1.0	6
2295	The whole-genome assembly of an endangered Salicaceae species: <i>Chosenia arbutifolia</i> (Pall.) A. Skv. <i>GigaScience</i> , 2022, 11, .	3.3	1
2296	The Soursop Genome ( <i>Annona muricata</i> L., Annonaceae). <i>Compendium of Plant Genomes</i> , 2022, , 149-174.	0.3	0
2297	Structural and Functional Annotation of Hypothetical Protein P9WIB9 of <i>Mycobacterium tuberculosis</i> H37Rv: An In-Silico Approach. , 2022, , .		0
2298	<i>Pectobacterium carotovorum</i> Phage vB_PcaM_P7_Pc Is a New Member of the Genus <i>Certvirus</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
2302	<i>MeGATA</i> s, functional generalists in interactions between cassava growth and development, and abiotic stresses. <i>AoB PLANTS</i> , 0, , .	1.2	0
2303	Combined analysis of transcriptomics and metabolomics revealed complex metabolic genes for diterpenoids biosynthesis in different organs of <i>Anoectochilus roxburghii</i> . <i>Chinese Herbal Medicines</i> , 2022, , .	1.2	0
2306	A Novel <i>Aeromonas popoffii</i> Phage AerP_220 Proposed to Be a Member of a New Tolavirus Genus in the Autographiviridae Family. <i>Viruses</i> , 2022, 14, 2733.	1.5	6
2307	Harnessing the genomic diversity of <i>Pseudomonas</i> strains against lettuce bacterial pathogens. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
2308	Temperature-Dependent Structure-Function Properties of Bacterial Xylose Isomerase Enzyme for Food Applications: An In Silico Study. <i>Clean Technologies</i> , 2022, 4, 1317-1329.	1.9	1
2309	ggMOB: Elucidation of genomic conjugative features and associated cargo genes across bacterial genera using genus-genus mobilization networks. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
2310	Genome of <i>Paspalum vaginatum</i> and the role of trehalose mediated autophagy in increasing maize biomass. <i>Nature Communications</i> , 2022, 13, .	5.8	4
2312	Does integument arise de novo or from pre-existing structures? Insights from the key regulatory genes controlling integument development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3



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2313	Genome Characterization of Bacteriophage KPP-1, a Novel Member in the Subfamily Vequintavirinae, and Use of Its Endolysin for the Lysis of Multidrug-Resistant <i>Klebsiella variicola</i> In Vitro. <i>Microorganisms</i> , 2023, 11, 207.	1.6	1
2315	Transcriptional and Physiological Analysis Reveal New Insights into the Regulation of Fertilization (N) Tj ETQq1 1 0.784314 rgBT /Ove Journal of Molecular Sciences, 2023, 24, 1522.	1.8	3
2316	The putative metal-binding proteome of the Coronaviridae family. <i>Metallomics</i> , 2023, 15, .	1.0	3
2317	Chromosome-level genome of black cutworm provides novel insights into polyphagy and seasonal migration in insects. <i>BMC Biology</i> , 2023, 21, .	1.7	6
2318	A draft <i>Diabrotica virgifera virgifera</i> genome: insights into control and host plant adaption by a major maize pest insect. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
2320	Marmesin and Marmelosin Interact with the Heparan Sulfatase-2 Active Site: Potential Mechanism for Phytochemicals from Bael Fruit Extract as Antitumor Therapeutics. <i>Oxidative Medicine and Cellular Longevity</i> , 2023, 2023, 1-19.	1.9	0
2321	<i>coth</i> Genes Are Necessary for Normal Spore Formation and Virulence in <i>Mucor lusitanicus</i> . <i>MBio</i> , 2023, 14, .	1.8	10
2322	Annotation of the <i>Turnera subulata</i> (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of Turneroideae from Passifloroideae in a Stepwise Manner. <i>Plants</i> , 2023, 12, 286.	1.6	2
2323	Label-free quantitative proteomics of arbuscular mycorrhizal <i>Elaeagnus angustifolia</i> seedlings provides insights into salt-stress tolerance mechanisms. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2324	Identification of potential proteins translated from circular RNA splice variants. <i>European Journal of Cell Biology</i> , 2023, 102, 151286.	1.6	3
2325	Two haplotype-resolved, gap-free genome assemblies for <i>Actinidia latifolia</i> and <i>Actinidia chinensis</i> shed light on the regulatory mechanisms of vitamin C and sucrose metabolism in kiwifruit. <i>Molecular Plant</i> , 2023, 16, 452-470.	3.9	19
2327	Chromosome-level genome and the identification of sex chromosomes in <i>Uloborus diversus</i> . <i>GigaScience</i> , 2022, 12, .	3.3	6
2328	Functional Characterization of Potato UBC13-UEV1s Genes Required for Ubiquitin Lys63 Chain to Polyubiquitination. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2412.	1.8	0
2330	Genome wide identification and evolutionary analysis of vat like NBS-LRR genes potentially associated with resistance to aphids in cotton. <i>Genetica</i> , 0, , .	0.5	0
2331	A chromosome-scale reference genome assembly of the great sand eel, <i>Hyperoplus lanceolatus</i> . <i>Journal of Heredity</i> , 2023, 114, 189-194.	1.0	2
2332	Phylogenomic analysis of <i>Wolbachia</i> genomes from the Darwin Tree of Life biodiversity genomics project. <i>PLoS Biology</i> , 2023, 21, e3001972.	2.6	13
2333	Genome wide Analysis and Characterization of <i>Eucalyptus grandis</i> TCP Transcription Factors. <i>Tarim Bilimleri Dergisi</i> , 0, , .	0.4	2
2334	Genome-wide identification and expression analysis of the HD2 protein family and its response to drought and salt stress in <i>Gossypium</i> species. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1

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2335	Characterization of KMSP1, a newly isolated virulent bacteriophage infecting <i>Staphylococcus aureus</i> , and its application to dairy products. <i>International Journal of Food Microbiology</i> , 2023, 390, 110119.	2.1	3
2336	Chromosome-level genome of the bean bug <i>Megacopta cribraria</i> in native range, provides insights into adaptation and pest management. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 123989.	3.6	0
2337	Genome sequencing of <i>Cladophialophora exuberans</i> , a novel candidate for bioremediation of hydrocarbon and heavy metal polluted habitats. <i>Fungal Biology</i> , 2023, 127, 1032-1042.	1.1	3
2338	Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity. <i>IScience</i> , 2023, 26, 106024.	1.9	6
2339	Computational models for prediction of protein-protein interaction in rice and <i>Magnaporthe grisea</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
2340	Pangenomic analysis of <i>Wolbachia</i> provides insight into the evolution of host adaptation and cytoplasmic incompatibility factor genes. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	2
2341	A chromosome-level genome assembly of the beet armyworm <i>Spodoptera exigua</i> . <i>Genomics</i> , 2023, 115, 110571.	1.3	4
2342	All3048, a DnaJ III homolog of <i>Anabaena</i> sp. PCC7120 mediates heat shock response in <i>E. coli</i> and its N-terminus J-domain stimulates DnaK ATPase activity. <i>International Journal of Biological Macromolecules</i> , 2023, 233, 123563.	3.6	0
2343	Evolution of the WRKY66 Gene Family and Its Mutations Generated by the CRISPR/Cas9 System Increase the Sensitivity to Salt Stress in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3071.	1.8	5
2344	Identification of AHL Synthase in <i>Desulfovibrio vulgaris</i> Hildenborough Using an In-Silico Methodology. <i>Catalysts</i> , 2023, 13, 364.	1.6	1
2345	Wound healing and regeneration in the reef building coral <i>Acropora millepora</i> . <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
2346	Comparative Modeling and Analysis of Extremophilic D-Ala-D-Ala Carboxypeptidases. <i>Biomolecules</i> , 2023, 13, 328.	1.8	0
2347	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, .	1.6	1
2349	<i>GUN</i> Mutants: New Weapons To Unravel Ascospore Germination Regulation in the Model Fungus <i>Podospira anserina</i> . <i>Microbiology Spectrum</i> , 2023, 11, .	1.2	0
2350	Genome-Wide Identification of G Protein-Coupled Receptors in Ciliated Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3869.	1.8	2
2351	Early antitermination in the atypical coliphage mEp021 mediated by the Gp17 protein. <i>Archives of Virology</i> , 2023, 168, .	0.9	0
2352	A novel binary pesticidal protein from <i>Chryseobacterium arthrosphaerae</i> controls western corn rootworm by a different mode of action to existing commercial pesticidal proteins. <i>PLoS ONE</i> , 2023, 18, e0267220.	1.1	2
2354	Genomics of Secondarily Temperate Adaptation in the Only Non-Antarctic Icefish. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	4

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2355	Diversity of the Antimicrobial Peptide Genes in Collembola. <i>Insects</i> , 2023, 14, 215.	1.0	1
2356	The expansin gene <i>CsLIEXP1</i> is a direct target of CsLOB1 in citrus. <i>Phytopathology</i> , 0, , .	1.1	1
2358	Genome-Wide Identification and Characterisation of Abiotic Stress Responsive mTERF Gene Family in <i>Amaranthus hypochondriacus</i> . <i>Phyton</i> , 2023, 92, 1649-1664.	0.4	1
2359	Chromosome-level reference genome of <i>Tetrastigma hemsleyanum</i> (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. <i>Plant Journal</i> , 2023, 114, 805-823.	2.8	5
2360	A chromosome-scale high-contiguity genome assembly of the cheetah ( <i>Acinonyx jubatus</i> ). <i>Journal of Heredity</i> , 0, , .	1.0	0
2361	Comparison of Plasma Exosome Proteomes Between Obese and Non-Obese Patients with Type 2 Diabetes Mellitus. <i>Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy</i> , 0, Volume 16, 629-642.	1.1	1
2364	Comprehensive Analysis of Universal Stress Protein Family Genes and Their Expression in <i>Fusarium oxysporum</i> Response of <i>Populus davidiana</i> – <i>P. alba</i> var. <i>pyramidalis</i> Louche Based on the Transcriptome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5405.	1.8	4
2365	Functional metagenomics uncovers nitrile-hydrolysing enzymes in a coal metagenome. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	1.6	3
2366	Axenic in vitro cultivation and genome diploidization of the moss <i>Vesicularia montagnei</i> for horticulture utilization. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
2367	Comprehensive Analysis of Calcium Sensor Families, CBL and CIPK, in <i>Aeluropus littoralis</i> and Their Expression Profile in Response to Salinity. <i>Genes</i> , 2023, 14, 753.	1.0	4
2368	Gene abundance linked to climate zone: Parallel evolution of gene content along elevation gradients in lichenized fungi. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
2370	Cotton <i>scp4</i> coumarate-CoA ligase 3 enhanced plant resistance to <i>Verticillium dahliae</i> by promoting jasmonic acid signaling-mediated vascular lignification and metabolic flux. <i>Plant Journal</i> , 2023, 115, 190-204.	2.8	9
2371	Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. <i>GigaScience</i> , 2022, 12, .	3.3	3
2372	Genome-wide characterization and comparative analysis of the OSCA gene family and identification of its potential stress-responsive members in legumes. <i>Scientific Reports</i> , 2023, 13, .	1.6	4
2373	Standing genetic variation fuels rapid evolution of herbicide resistance in blackgrass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	7
2374	Stable endocytic structures navigate the complex pellicle of apicomplexan parasites. <i>Nature Communications</i> , 2023, 14, .	5.8	13
2375	Evolution and expression analysis of the caffeoyl-CoA 3-O-methyltransferase (CCoAOMT) gene family in jute ( <i>Corchorus L.</i> ). <i>BMC Genomics</i> , 2023, 24, .	1.2	3
2376	Identification and analysis of the secretome of plant pathogenic fungi reveals lifestyle adaptation. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	3

#	ARTICLE	IF	CITATIONS
2377	First draft genome and transcriptome of <i>Cercosporidium personatum</i> , causal agent of late leaf spot disease of peanut. <i>BMC Research Notes</i> , 2023, 16, .	0.6	3
2462	Computational Genomics Approaches for Livestock Improvement and Management. <i>Livestock Diseases and Management</i> , 2023, , 351-376.	0.5	0
2470	Identification and Functional Annotation of circRNAs in Neuroblastoma Based on Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2023, , 351-363.	1.0	0
2546	How Does Bioinformatics Play a Role in Fungal Drug Discovery?. , 2024, , 725-742.		0