

The Pfam protein families database

Nucleic Acids Research

36, D281-D288

DOI: [10.1093/nar/gkm960](https://doi.org/10.1093/nar/gkm960)

Citation Report

#	ARTICLE	IF	CITATIONS
1	A Random Sequencing Approach for the Analysis of the Trypanosoma cruzi Genome: General Structure, Large Gene and Repetitive DNA Families, and Gene Discovery. Genome Research, 2000, 10, 1996-2005.	5.5	49
2	Divergent human and mouse orthologs of a novel gene (WBCSR15/ <i>Wbscr15</i>) reside within the genomic interval commonly deleted in Williams syndrome. Cytogenetic and Genome Research, 2000, 90, 285-290.	1.1	14
3	InterPro (The Integrated Resource of Protein Domains and Functional Sites). Yeast, 2000, 1, 327-334.	1.7	10
4	Gene Ontology: tool for the unification of biology. Nature Genetics, 2000, 25, 25-29.	21.4	34,499
5	Microbial genome sequencing. Nature, 2000, 406, 799-803.	27.8	164
6	Prediction of amino acid sequence from structure. Protein Science, 2000, 9, 1106-1119.	7.6	78
7	Improving the quality of twilight-zone alignments. Protein Science, 2000, 9, 1487-1496.	7.6	120
8	Crystal structure of FadR, a fatty acid-responsive transcription factor with a novel acyl coenzyme A-binding fold. EMBO Journal, 2000, 19, 5167-5177.	7.8	125
9	Genomewide insertional mutagenesis in Streptomyces coelicolor reveals additional genes involved in morphological differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9642-9647.	7.1	67
10	Reengineering the glutathione S-transferase scaffold: A rational design strategy pays off. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10298-10300.	7.1	27
11	Genome sequence of Halobacterium species NRC-1. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 12176-12181.	7.1	672
12	IE-Kb: intron exon knowledge base. Bioinformatics, 2000, 16, 1151-1152.	4.1	13
13	GeneRAGE: a robust algorithm for sequence clustering and domain detection. Bioinformatics, 2000, 16, 451-457.	4.1	186
14	SMART: a web-based tool for the study of genetically mobile domains. Nucleic Acids Research, 2000, 28, 231-234.	14.5	1,159
15	Functional studies of the BTB domain in the Drosophila GAGA and Mod(mdg4) proteins. Nucleic Acids Research, 2000, 28, 3864-3870.	14.5	24
16	Alternative splicing at the MEFV locus involved in familial Mediterranean fever regulates translocation of the marenostin/pyrin protein to the nucleus. Human Molecular Genetics, 2000, 9, 3001-3009.	2.9	63
17	Prediction of the Coding Sequences of Unidentified Human Genes. XIX. The complete Sequences of 100 New cDNA Clones from Brain Which Code for Large Proteins in vitro. DNA Research, 2000, 7, 347-355.	3.4	80
18	Proteomic databases and software on the web. Briefings in Bioinformatics, 2000, 1, 250-259.	6.5	15

#	ARTICLE	IF	CITATIONS
19	Classification of Transmembrane Protein Families in the <i>Caenorhabditis elegans</i> Genome and Identification of Human Orthologs. <i>Genome Research</i> , 2000, 10, 1679-1689.	5.5	29
20	Complete Nucleotide Sequence of Ubiquitous Plasmid pEA29 from <i>Erwinia amylovora</i> Strain Ea88: Gene Organization and Intraspecies Variation. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4897-4907.	3.1	102
21	Characterization of Long cDNA Clones from Human Adult Spleen. <i>DNA Research</i> , 2000, 7, 357-366.	3.4	8
22	Protein structure prediction methods for drug design. <i>Briefings in Bioinformatics</i> , 2000, 1, 275-288.	6.5	14
23	PANAL: an integrated resource for Protein sequence ANALysis. <i>Bioinformatics</i> , 2000, 16, 1157-1158.	4.1	12
24	Identification of a novel protein interacting with RPCR. <i>Human Molecular Genetics</i> , 2000, 9, 2085-2093.	2.9	114
25	Crystal structure of yeast initiation factor 4A, a DEAD-box RNA helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13080-13085.	7.1	258
26	A search for reverse transcriptase-coding sequences reveals new non-LTR retrotransposons in the genome of <i>Drosophila melanogaster</i> . <i>Genome Biology</i> , 2000, 1, research0012.1.	9.6	34
27	Analysis of the <i>Thermotoga maritima</i> genome combining a variety of sequence similarity and genome context tools. <i>Nucleic Acids Research</i> , 2000, 28, 4573-4576.	14.5	24
28	Genome Annotation Assessment in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2000, 10, 483-501.	5.5	172
29	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000, 16, 1145-1150.	4.1	301
30	Functional and phylogenetic analysis of the ubiquitylation system in <i>Caenorhabditis elegans</i> : ubiquitin-conjugating enzymes, ubiquitin-activating enzymes, and ubiquitin-like proteins. <i>Genome Biology</i> , 2001, 3, research0002.1.	9.6	106
31	Tools and resources for identifying protein families, domains and motifs. <i>Genome Biology</i> , 2001, 3, reviews2001.1.	9.6	23
32	Computational prediction of membrane-tethered transcription factors. <i>Genome Biology</i> , 2001, 2, research0050.1.	9.6	32
33	Prediction of co-regulated genes in <i>Bacillus subtilis</i> on the basis of upstream elements conserved across three closely related species. <i>Genome Biology</i> , 2001, 2, research0048.1.	9.6	15
34	The adaptive evolution database (TAED). <i>Genome Biology</i> , 2001, 2, research0028.1.	9.6	35
35	Genome cartography through domain annotation. <i>Genome Biology</i> , 2001, 2, comment2006.1.	9.6	9
36	Identification of conserved C2H2 zinc-finger gene families in the Bilateria. <i>Genome Biology</i> , 2001, 2, research0016.1.	9.6	33

#	ARTICLE	IF	CITATIONS
37	The Adaptive Evolution Database (TAED). Genome Biology, 2001, 2, preprint0003.1.	9.6	37
38	The cohesin complex: sequence homologies, interaction networks and shared motifs. Genome Biology, 2001, 2, research0009.1.	9.6	31
39	BAlIbASE (Benchmark Alignment dataBASE): enhancements for repeats, transmembrane sequences and circular permutations. Nucleic Acids Research, 2001, 29, 323-326.	14.5	148
40	Predicting proteinâ€“protein interactions from primary structure. Bioinformatics, 2001, 17, 455-460.	4.1	491
41	The human genome: an immuno-centric view of evolutionary strategies. Trends in Immunology, 2001, 22, 227-229.	6.8	11
42	Microbial disease in humans: A genomic perspective. Molecular Diagnosis and Therapy, 2001, 6, 243-252.	1.1	10
43	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. Nucleic Acids Research, 2001, 29, 37-40.	14.5	928
44	InterProScan â€“ an integration platform for the signature-recognition methods in InterPro. Bioinformatics, 2001, 17, 847-848.	4.1	2,580
45	Hidden Markov models in biological sequence analysis. IBM Journal of Research and Development, 2001, 45, 449-454.	3.1	63
46	PSST... the probabilistic sequence search tool. , 2001, , .		2
47	Functional Analysis of Genes for Biosynthesis of Pyocyanin and Phenazine-1-Carboxamide from Pseudomonas aeruginosa PAO1. Journal of Bacteriology, 2001, 183, 6454-6465.	2.2	665
48	Genome sequence of an industrial microorganism <i>Streptomyces avermitilis</i> : Deducing the ability of producing secondary metabolites. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 12215-12220.	7.1	784
49	Toward more intelligent annotation tools: a prototype. IEEE Intelligent Systems, 2001, 16, 42-51.	4.0	5
50	Phylogenetic Relationships within Cation Transporter Families of Arabidopsis. Plant Physiology, 2001, 126, 1646-1667.	4.8	1,110
51	Sequence Analysis of the Human Genome. Archives of Neurology, 2001, 58, 1772.	4.5	29
52	A large family of endosome-localized proteins related to sorting nexin 1. Biochemical Journal, 2001, 358, 7.	3.7	104
53	What is bioinformatics? An introduction and overview. Yearbook of Medical Informatics, 2001, 10, 83-100.	1.0	68
54	Sequence, expression, and characterization of the first archaeal ATP-dependent 6-phosphofructokinase, a non-allosteric enzyme related to the phosphofructokinase-B sugar kinase family, from the hyperthermophilic crenarchaeote Aeropyrum pernix. Archives of Microbiology, 2001, 177, 62-69.	2.2	35

#	ARTICLE	IF	CITATIONS
55	Isolation and characterization of the UBASH3A gene on 21q22.3 encoding a potential nuclear protein with a novel combination of domains. Human Genetics, 2001, 108, 140-147.	3.8	47
56	Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. Journal of Biosciences, 2001, 26, 277-284.	1.1	5
57	Review of the TEIRESIAS-Based Tools of the IBM Bioinformatics and Pattern Discovery Group. Metabolic Engineering, 2001, 3, 285-288.	7.0	4
58	Complete genome sequence of <i>Caulobacter crescentus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 4136-4141.	7.1	489
59	An alpha-L-fucosidase from <i>Thermus</i> sp. with unusually broad specificity. Glycoconjugate Journal, 2001, 18, 827-834.	2.7	31
60	A combination of the F-box motif and kelch repeats defines a large Arabidopsis family of F-box proteins. Plant Molecular Biology, 2001, 46, 603-614.	3.9	52
61	<i>Synechocystis</i> sp. PCC 6803 - a useful tool in the study of the genetics of cyanobacteria. Photosynthesis Research, 2001, 70, 73-83.	2.9	137
62	The PYRIN domain: A member of the death domain-fold superfamily. Protein Science, 2001, 10, 1911-1918.	7.6	144
63	Sialidase-like Asp-boxes: Sequence-similar structures within different protein folds. Protein Science, 2001, 10, 285-292.	7.6	70
64	Evolutionary relationships among G protein-coupled receptors using a clustered database approach. AAPS PharmSci, 2001, 3, 25-42.	1.3	50
65	The <i>Saccharomyces cerevisiae</i> Set1 complex includes an Ash2 homologue and methylates histone 3 lysine 4. EMBO Journal, 2001, 20, 7137-7148.	7.8	519
66	Completeness in structural genomics. Nature Structural Biology, 2001, 8, 559-566.	9.7	336
67	Evolutionary expansion of CRIB-containing Cdc42 effector proteins. Trends in Genetics, 2001, 17, 370-373.	6.7	49
68	Evolution, language and analogy in functional genomics. Trends in Genetics, 2001, 17, 414-418.	6.7	24
69	Integrative data mining: the new direction in bioinformatics. IEEE Engineering in Medicine and Biology Magazine, 2001, 20, 33-40.	0.8	32
70	Using genomics to understand the nervous system. Drug Discovery Today, 2001, 6, 81-85.	6.4	2
71	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2001, 29, 11-16.	14.5	204
72	The MetaFam Server: a comprehensive protein family resource. Nucleic Acids Research, 2001, 29, 49-51.	14.5	16

#	ARTICLE	IF	CITATIONS
73	MetaFam: a unified classification of protein families. II. Schema and query capabilities. <i>Bioinformatics</i> , 2001, 17, 262-271.	4.1	17
74	Molecular Characterization of Thermoduced Immunogenic Proteins Q1p42 and Hsp15 of <i>Leptospira interrogans</i> . <i>Infection and Immunity</i> , 2001, 69, 7616-7624.	2.2	56
75	HUNT: launch of a full-length cDNA database from the Helix Research Institute. <i>Nucleic Acids Research</i> , 2001, 29, 185-188.	14.5	42
76	Mendel-GFDb and Mendel-ESTS: databases of plant gene families and ESTs annotated with gene family numbers and gene family names. <i>Nucleic Acids Research</i> , 2001, 29, 120-122.	14.5	4
77	HOMSTRAD: adding sequence information to structure-based alignments of homologous protein families. <i>Bioinformatics</i> , 2001, 17, 748-749.	4.1	49
78	EASY--an Expert Analysis SYstem for interpreting database search outputs. <i>Bioinformatics</i> , 2001, 17, 105-106.	4.1	6
79	NIFAS: visual analysis of domain evolution in proteins. <i>Bioinformatics</i> , 2001, 17, 343-348.	4.1	20
80	MetaFam: a unified classification of protein families. I. Overview and statistics. <i>Bioinformatics</i> , 2001, 17, 249-261.	4.1	25
81	BETAWRAP: Successful prediction of parallel α -helices from primary sequence reveals an association with many microbial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14819-14824.	7.1	109
82	Genomic and genetic dissection of an archaeal regulon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 2521-2525.	7.1	63
83	trEST, trGEN and Hits: access to databases of predicted protein sequences. <i>Nucleic Acids Research</i> , 2001, 29, 148-151.	14.5	27
84	Proteome Analysis Database: online application of InterPro and CluSTr for the functional classification of proteins in whole genomes. <i>Nucleic Acids Research</i> , 2001, 29, 44-48.	14.5	84
85	Identification and Characterization of a Developmentally Regulated Protein, EshA, Required for Sporogenic Hyphal Branches in <i>Streptomyces griseus</i> . <i>Journal of Bacteriology</i> , 2001, 183, 3004-3015.	2.2	23
86	Analysis of smu-1 , a Gene That Regulates the Alternative Splicing of unc-52 Pre-mRNA in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Biology</i> , 2001, 21, 4985-4995.	2.3	48
87	Prediction of Protein Functional Domains from Sequences Using Artificial Neural Networks. <i>Genome Research</i> , 2001, 11, 1410-1417.	5.5	33
88	A simple algorithm to infer gene duplication and speciation events on a gene tree. <i>Bioinformatics</i> , 2001, 17, 821-828.	4.1	186
89	Divergence of Function in Sequence-Related Groups of <i>Escherichia coli</i> Proteins. <i>Genome Research</i> , 2001, 11, 1375-1381.	5.5	32
90	Complete genome sequence of an M1 strain of <i>Streptococcus pyogenes</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 4658-4663.	7.1	861

#	ARTICLE	IF	CITATIONS
91	A thermostable endonuclease III homolog from the archaeon <i>Pyrobaculum aerophilum</i> . <i>Nucleic Acids Research</i> , 2001, 29, 604-613.	14.5	13
92	ATV: display and manipulation of annotated phylogenetic trees. <i>Bioinformatics</i> , 2001, 17, 383-384.	4.1	251
93	Strain-specific genes of <i>Helicobacter pylori</i> : distribution, function and dynamics. <i>Nucleic Acids Research</i> , 2001, 29, 4395-4404.	14.5	43
94	iProClass: an integrated, comprehensive and annotated protein classification database. <i>Nucleic Acids Research</i> , 2001, 29, 52-54.	14.5	32
95	Sequence and structural aspects of functional diversification in class I α -mannosidase evolution. <i>Bioinformatics</i> , 2001, 17, 965-976.	4.1	13
96	Neuropeptides and Neuropeptide Receptors in the <i>Drosophila melanogaster</i> Genome. <i>Genome Research</i> , 2001, 11, 1126-1142.	5.5	505
97	Phylogenetic footprinting of transcription factor binding sites in proteobacterial genomes. <i>Nucleic Acids Research</i> , 2001, 29, 774-782.	14.5	235
98	The SBASE protein domain library, release 8.0: a collection of annotated protein sequence segments. <i>Nucleic Acids Research</i> , 2001, 29, 58-60.	14.5	21
99	Expression of hsp16 in response to nucleotide depletion is regulated via the spc1 MAPK pathway in <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 2001, 29, 3030-3040.	14.5	35
100	Birth of scale-free molecular networks and the number of distinct DNA and protein domains per genome. <i>Bioinformatics</i> , 2001, 17, 988-996.	4.1	130
101	nag Genes of <i>Ralstonia</i> (Formerly <i>Pseudomonas</i>) sp. Strain U2 Encoding Enzymes for Gentisate Catabolism. <i>Journal of Bacteriology</i> , 2001, 183, 700-708.	2.2	203
102	CluSTR: a database of clusters of SWISS-PROT+TrEMBL proteins. <i>Nucleic Acids Research</i> , 2001, 29, 33-36.	14.5	99
103	Novel Motility Mutants of <i>Synechocystis</i> Strain PCC 6803 Generated by In Vitro Transposon Mutagenesis. <i>Journal of Bacteriology</i> , 2001, 183, 6140-6143.	2.2	63
104	Domain homologues of dopamine beta-hydroxylase and ferric reductase: roles for iron metabolism in neurodegenerative disorders?. <i>Human Molecular Genetics</i> , 2001, 10, 1853-1858.	2.9	54
105	DBAli: a database of protein structure alignments. <i>Bioinformatics</i> , 2001, 17, 746-747.	4.1	49
106	Protein Information Resource: a community resource for expert annotation of protein data. <i>Nucleic Acids Research</i> , 2001, 29, 29-32.	14.5	72
107	Making sense of score statistics for sequence alignments. <i>Briefings in Bioinformatics</i> , 2001, 2, 51-67.	6.5	46
108	<i>Yersinia pestis</i> pFra Shows Biovar-Specific Differences and Recent Common Ancestry with a <i>Salmonella enterica</i> Serovar Typhi Plasmid. <i>Journal of Bacteriology</i> , 2001, 183, 2586-2594.	2.2	56

#	ARTICLE	IF	CITATIONS
109	Implications of the Human Genome for Understanding Human Biology and Medicine. JAMA - Journal of the American Medical Association, 2001, 286, 2296.	7.4	122
110	The HIB database of annotated UniGene clusters. Bioinformatics, 2001, 17, 571-572.	4.1	4
111	Increased bone density in sclerosteosis is due to the deficiency of a novel secreted protein (SOST). Human Molecular Genetics, 2001, 10, 537-543.	2.9	1,009
112	Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9883-9888.	7.1	278
113	Functional and structural genomics using PEDANT. Bioinformatics, 2001, 17, 44-57.	4.1	191
114	The Bordetella bhu Locus Is Required for Heme Iron Utilization. Journal of Bacteriology, 2001, 183, 4278-4287.	2.2	68
115	The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis. Nucleic Acids Research, 2001, 29, 2145-2153.	14.5	241
116	Combining multiple structure and sequence alignments to improve sequence detection and alignment: Application to the SH2 domains of Janus kinases. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14796-14801.	7.1	60
117	ERB1, the yeast homolog of mammalian Bop1, is an essential gene required for maturation of the 25S and 5.8S ribosomal RNAs. Nucleic Acids Research, 2001, 29, 3621-3630.	14.5	65
118	mmsearch: a motif arrangement language and search program. Bioinformatics, 2001, 17, 1234-1235.	4.1	7
119	Functional information in SWISS-PROT: The basis for large-scale characterisation of protein sequences. Briefings in Bioinformatics, 2001, 2, 9-18.	6.5	53
120	Peptide-N-glycanases and DNA repair proteins, Xp-C/Rad4, are, respectively, active and inactivated enzymes sharing a common transglutaminase fold. Human Molecular Genetics, 2001, 10, 1627-1630.	2.9	45
121	Proteins of Mycobacterium bovis BCG Induced in the Wayne Dormancy Model. Journal of Bacteriology, 2001, 183, 2672-2676.	2.2	111
122	TIGRFAMs: a protein family resource for the functional identification of proteins. Nucleic Acids Research, 2001, 29, 41-43.	14.5	445
123	DBTBS: a database of Bacillus subtilis promoters and transcription factors. Nucleic Acids Research, 2001, 29, 278-280.	14.5	70
124	Estimation of P-values for global alignments of protein sequences. Bioinformatics, 2001, 17, 1158-1167.	4.1	33
125	Genome Sequencing and Annotation. , 2001, 67, 215-230.		0
126	The Zebrafish Thrombospondin 3 and 4 Genes (thbs3 and thbs4): cDNA and Protein Structure. DNA Sequence, 2002, 13, 277-285.	0.7	6

#	ARTICLE	IF	CITATIONS
127	The Protein Information Resource: an integrated public resource of functional annotation of proteins. <i>Nucleic Acids Research</i> , 2002, 30, 35-37.	14.5	186
128	The KEGG databases at GenomeNet. <i>Nucleic Acids Research</i> , 2002, 30, 42-46.	14.5	1,202
129	A Combinatorial Toolbox for Protein Sequence Design and Landscape Analysis in the Grand Canonical Model. <i>Journal of Computational Biology</i> , 2002, 9, 721-741.	1.6	1
130	Relatedness of Chromosomal and Plasmid DNAs of <i>Erwinia pyrifoliae</i> and <i>Erwinia amylovora</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 6182-6192.	3.1	49
131	FANTOM DB: database of Functional Annotation of RIKEN Mouse cDNA Clones. <i>Nucleic Acids Research</i> , 2002, 30, 116-118.	14.5	55
132	Systematic Identification of Novel Protein Domain Families Associated with Nuclear Functions. <i>Genome Research</i> , 2002, 12, 47-56.	5.5	527
133	Structural Characterization of the Human Proteome. <i>Genome Research</i> , 2002, 12, 1625-1641.	5.5	66
134	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between <i>Arabidopsis</i> and Rice. <i>Genome Research</i> , 2002, 12, 1792-1801.	5.5	127
135	HMM-based databases in InterPro. <i>Briefings in Bioinformatics</i> , 2002, 3, 236-245.	6.5	28
136	DBC2, a candidate for a tumor suppressor gene involved in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13647-13652.	7.1	202
137	Novel domains and orthologues of eukaryotic transcription elongation factors. <i>Nucleic Acids Research</i> , 2002, 30, 3643-3652.	14.5	101
138	Disease mechanism for retinitis pigmentosa (RP11) caused by mutations in the splicing factor gene PRPF31. <i>Human Molecular Genetics</i> , 2002, 11, 3209-3219.	2.9	75
139	Target Selection for Structural Genomics: A Single Genome Approach. <i>OMICS A Journal of Integrative Biology</i> , 2002, 6, 349-362.	2.0	4
140	Consensus-derived structural determinants of the ankyrin repeat motif. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16029-16034.	7.1	320
141	<i>Arabidopsis</i> disrupted in SQD2 encoding sulfolipid synthase is impaired in phosphate-limited growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5732-5737.	7.1	306
142	Cloning and characterization of a cAMP-specific phosphodiesterase (TbPDE2B) from <i>Trypanosoma brucei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4714-4719.	7.1	48
143	The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14422-14427.	7.1	874
144	Identification of 113 conserved essential genes using a high-throughput gene disruption system in <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2002, 30, 3152-3162.	14.5	203

#	ARTICLE	IF	CITATIONS
145	A fragment of human TrpRS as a potent antagonist of ocular angiogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 178-183.	7.1	151
146	A human aminoacyl-tRNA synthetase as a regulator of angiogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 173-177.	7.1	257
147	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13148-13153.	7.1	422
148	DATABASES AND TOOLS FOR BROWSING GENOMES. Annual Review of Genomics and Human Genetics, 2002, 3, 293-310.	6.2	23
149	PathFinder: reconstruction and dynamic visualization of metabolic pathways. Bioinformatics, 2002, 18, 124-129.	4.1	66
150	Evolutionary Clues to the Molecular Function of Fanconi Anemia Genes. Acta Haematologica, 2002, 108, 231-236.	1.4	12
151	Functional domains involved in the interaction between Orc1 and transcriptional repressor AIF-C that bind to an origin/promoter of the rat aldolase B gene. Nucleic Acids Research, 2002, 30, 5205-5212.	14.5	20
152	A Novel Nucleus-Targeted Protein Is Expressed in Barley Leaves during Senescence and Pathogen Infection. Plant Physiology, 2002, 130, 1172-1180.	4.8	53
153	Database resources of the National Center for Biotechnology Information: 2002 update. Nucleic Acids Research, 2002, 30, 13-16.	14.5	184
154	Domain Fishing: a first step in protein comparative modelling. Bioinformatics, 2002, 18, 1141-1142.	4.1	152
155	PRINTS and PRINTS-S shed light on protein ancestry. Nucleic Acids Research, 2002, 30, 239-241.	14.5	93
156	The SBASE protein domain library, release 9.0: an online resource for protein domain identification. Nucleic Acids Research, 2002, 30, 273-275.	14.5	17
157	A comparison of profile hidden Markov model procedures for remote homology detection. Nucleic Acids Research, 2002, 30, 4321-4328.	14.5	137
158	Tolerating some redundancy significantly speeds up clustering of large protein databases. Bioinformatics, 2002, 18, 77-82.	4.1	475
159	TranScout: prediction of gene expression regulatory proteins from their sequences. Bioinformatics, 2002, 18, 597-607.	4.1	9
160	Identification of four candidate cGMP targets in Dictyostelium. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6749-6754.	7.1	88
161	Crystal structure of conserved hypothetical protein Aq1575 from Aquifex aeolicus. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7980-7985.	7.1	30
162	Positional cloning of the murine flavivirus resistance gene. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9322-9327.	7.1	245

#	ARTICLE	IF	CITATIONS
163	Nonlinear partial differential equations and applications: An exchanger-like protein underlies the large Mg ²⁺ current in <i>Paramecium</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15717-15722.	7.1	25
164	Automated De Novo Identification of Repeat Sequence Families in Sequenced Genomes. Genome Research, 2002, 12, 1269-1276.	5.5	776
165	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155
166	Dictionary-driven prokaryotic gene finding. Nucleic Acids Research, 2002, 30, 2710-2725.	14.5	31
167	The POPPs: clustering and searching using peptide probability profiles. Bioinformatics, 2002, 18, S38-S45.	4.1	20
168	Identification of New Herpesvirus Gene Homologs in the Human Genome. Genome Research, 2002, 12, 1739-1748.	5.5	86
169	Sentra, a database of signal transduction proteins. Nucleic Acids Research, 2002, 30, 349-350.	14.5	16
170	QuickTree: building huge Neighbour-Joining trees of protein sequences. Bioinformatics, 2002, 18, 1546-1547.	4.1	249
171	Comprehensive gene expression analysis by transcript profiling. , 2002, , 75-97.		28
172	Inferring Domain-Domain Interactions From Protein-Protein Interactions. Genome Research, 2002, 12, 1540-1548.	5.5	376
173	Association of nucleotide patterns with gene function classes: application to human 3' untranslated sequences. Bioinformatics, 2002, 18, 182-189.	4.1	56
174	PFDB: a generic protein family database integrating the CATH domain structure database with sequence based protein family resources. Bioinformatics, 2002, 18, 1666-1672.	4.1	15
175	DRAGON View: information visualization for annotated microarray data. Bioinformatics, 2002, 18, 323-324.	4.1	37
176	ProClust: improved clustering of protein sequences with an extended graph-based approach. Bioinformatics, 2002, 18, S182-S191.	4.1	70
177	Metallo-beta-lactamase fold within nucleic acids processing enzymes: the beta-CASP family. Nucleic Acids Research, 2002, 30, 3592-3601.	14.5	288
178	POTE, a highly homologous gene family located on numerous chromosomes and expressed in prostate, ovary, testis, placenta, and prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16975-16980.	7.1	75
179	TreeWiz: interactive exploration of huge trees. Bioinformatics, 2002, 18, 109-114.	4.1	25
180	A motif of a microbial starch-binding domain found in human genethonin. Bioinformatics, 2002, 18, 1534-1537.	4.1	40

#	ARTICLE	IF	CITATIONS
181	Signatures of Domain Shuffling in the Human Genome. <i>Genome Research</i> , 2002, 12, 1642-1650.	5.5	91
182	SCOP database in 2002: refinements accommodate structural genomics. <i>Nucleic Acids Research</i> , 2002, 30, 264-267.	14.5	403
183	Diversity in Nucleotide Binding Site-Leucine-Rich Repeat Genes in Cereals. <i>Genome Research</i> , 2002, 12, 1871-1884.	5.5	292
184	An efficient algorithm for large-scale detection of protein families. <i>Nucleic Acids Research</i> , 2002, 30, 1575-1584.	14.5	3,173
185	Interrogating protein interaction networks through structural biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5896-5901.	7.1	330
186	Annotating the human proteome: the Human Proteome Survey Database (HumanPSDTM) and an in-depth target database for G protein-coupled receptors (GPCR-PDTM) from Incyte Genomics. <i>Nucleic Acids Research</i> , 2002, 30, 137-141.	14.5	65
187	SKIP is an indispensable factor for <i>Caenorhabditis elegans</i> development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9254-9259.	7.1	27
188	The complete genomic sequence of <i>Mycoplasma penetrans</i> , an intracellular bacterial pathogen in humans. <i>Nucleic Acids Research</i> , 2002, 30, 5293-5300.	14.5	178
189	Identification of a Novel Type of cGMP Phosphodiesterase That Is Defective in the ChemotacticstmFMutants. <i>Molecular Biology of the Cell</i> , 2002, 13, 3870-3877.	2.1	29
190	Proteome analysis based on motif statistics. <i>Bioinformatics</i> , 2002, 18, S161-S171.	4.1	9
191	EXProt: a database for proteins with an experimentally verified function. <i>Nucleic Acids Research</i> , 2002, 30, 50-51.	14.5	12
192	Predicting Gene Ontology Functions from ProDom and CDD Protein Domains. <i>Genome Research</i> , 2002, 12, 648-655.	5.5	81
193	CDD: a database of conserved domain alignments with links to domain three-dimensional structure. <i>Nucleic Acids Research</i> , 2002, 30, 281-283.	14.5	609
194	Target space for structural genomics revisited. <i>Bioinformatics</i> , 2002, 18, 922-933.	4.1	71
195	Diversity of TITAN Functions in Arabidopsis Seed Development. <i>Plant Physiology</i> , 2002, 128, 38-51.	4.8	101
196	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
197	The Complement of Protein Phosphatase Catalytic Subunits Encoded in the Genome of Arabidopsis. <i>Plant Physiology</i> , 2002, 129, 908-925.	4.8	242
198	A Strategy to Retrieve the Whole Set of Protein Modules in Microbial Proteomes. <i>Genome Research</i> , 2002, 12, 1961-1973.	5.5	10

#	ARTICLE	IF	CITATIONS
199	SYSTERS, GeneNest, SpliceNest: exploring sequence space from genome to protein. Nucleic Acids Research, 2002, 30, 299-300.	14.5	54
200	The EBI SRS server--recent developments. Bioinformatics, 2002, 18, 368-373.	4.1	119
201	Gene3D: Structural Assignment for Whole Genes and Genomes Using the CATH Domain Structure Database. Genome Research, 2002, 12, 503-514.	5.5	55
202	Clustering of proximal sequence space for the identification of protein families. Bioinformatics, 2002, 18, 908-921.	4.1	58
203	Short Integuments1/suspensor1/carpel Factory, a Dicer Homolog, Is a Maternal Effect Gene Required for Embryo Development in Arabidopsis. Plant Physiology, 2002, 130, 808-822.	4.8	171
204	SUPFAM--a database of potential protein superfamily relationships derived by comparing sequence-based and structure-based families: implications for structural genomics and function annotation in genomes. Nucleic Acids Research, 2002, 30, 289-293.	14.5	40
205	Folding free energy function selects native-like protein sequences in the core but not on the surface. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13554-13559.	7.1	63
206	Predicting Protein Cellular Localization Using a Domain Projection Method. Genome Research, 2002, 12, 1168-1174.	5.5	97
207	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. Genome Research, 2002, 12, 367-378.	5.5	21
208	GTOP: a database of protein structures predicted from genome sequences. Nucleic Acids Research, 2002, 30, 294-298.	14.5	69
209	SUPERFAMILY: HMMs representing all proteins of known structure. SCOP sequence searches, alignments and genome assignments. Nucleic Acids Research, 2002, 30, 268-272.	14.5	252
210	Comparison of the Small Molecule Metabolic Enzymes of Escherichia coli and Saccharomyces cerevisiae. Genome Research, 2002, 12, 916-929.	5.5	24
211	Frequent oligonucleotide motifs in genomes of three streptococci. Nucleic Acids Research, 2002, 30, 4216-4221.	14.5	26
212	Noncoding RNA genes identified in AT-rich hyperthermophiles. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7542-7547.	7.1	154
213	CDART: Protein Homology by Domain Architecture. Genome Research, 2002, 12, 1619-1623.	5.5	622
214	MODBASE, a database of annotated comparative protein structure models. Nucleic Acids Research, 2002, 30, 255-259.	14.5	114
215	The use of structure information to increase alignment accuracy does not aid homologue detection with profile HMMs. Bioinformatics, 2002, 18, 1243-1249.	4.1	19
216	A male-specific (cysteine-rich) protein of Oesophagostomum dentatum (Strongylida) with structural characteristics of a serine protease inhibitor containing two trypsin inhibitor-like domains. Parasitology, 2002, 125, 445-455.	1.5	16

#	ARTICLE	IF	CITATIONS
217	Characterization of a putative α -mannosyltransferase involved in phosphatidylinositol trimannoside biosynthesis in <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2002, 363, 437.	3.7	65
218	Comparative Genome Analysis. <i>Methods of Biochemical Analysis</i> , 2002, 43, 359-392.	0.2	13
219	From sequence to consequence: In silico hypothesis generation and testing. <i>Methods in Microbiology</i> , 2002, , 27-48.	0.8	3
220	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V<i>Streptococcus agalactiae</i>. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12391-12396.	7.1	447
221	Sequence Analysis of LRPPRC and Its SEC1 Domain Interaction Partners Suggests Roles in Cytoskeletal Organization, Vesicular Trafficking, Nucleocytosolic Shuttling, and Chromosome Activity. <i>Genomics</i> , 2002, 79, 124-136.	2.9	69
222	Comparative Analysis of Human Genome Assemblies Reveals Genome-Level Differences. <i>Genomics</i> , 2002, 80, 138-139.	2.9	12
223	Identification of protein superfamily from structure-based sequence motif. <i>Science Bulletin</i> , 2002, 47, 1377.	1.7	2
224	The repertoire of protein kinases encoded in the draft version of the human genome: atypical variations and uncommon domain combinations. <i>Genome Biology</i> , 2002, 3, research0066.1.	9.6	42
225	Membrane-bound progesterone receptors contain a cytochrome b5-like ligand-binding domain. <i>Genome Biology</i> , 2002, 3, research0068.1.	9.6	117
226	Genomic functional annotation using co-evolution profiles of gene clusters. <i>Genome Biology</i> , 2002, 3, research0060.1.	9.6	63
227	Conservation of long-range synteny and microsynteny between the genomes of two distantly related nematodes. <i>Genome Biology</i> , 2002, 3, research0057.1.	9.6	46
228	Genomic analysis of membrane protein families: abundance and conserved motifs. <i>Genome Biology</i> , 2002, 3, research0054.1.	9.6	65
229	NEAT: a domain duplicated in genes near the components of a putative Fe ³⁺ siderophore transporter from Gram-positive pathogenic bacteria. <i>Genome Biology</i> , 2002, 3, research0047.1.	9.6	129
230	ORMDL proteins are a conserved new family of endoplasmic reticulum membrane proteins. <i>Genome Biology</i> , 2002, 3, research0027.1.	9.6	148
231	Mouse Crossveinless-2 is the vertebrate homolog of a <i>Drosophila</i> extracellular regulator of BMP signaling. <i>Mechanisms of Development</i> , 2002, 119, S179-S184.	1.7	39
232	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. <i>Bioinformatics</i> , 2002, 18, S71-S77.	4.1	536
233	Proteome-scale purification of human proteins from bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2654-2659.	7.1	256
234	Clustering Patterns of Cytotoxic T-Lymphocyte Epitopes in Human Immunodeficiency Virus Type 1 (HIV-1) Proteins Reveal Imprints of Immune Evasion on HIV-1 Global Variation. <i>Journal of Virology</i> , 2002, 76, 8757-8768.	3.4	241

#	ARTICLE	IF	CITATIONS
235	Identification of a family of group II introns encoding LAGLIDADG ORFs typical of group I introns. <i>Rna</i> , 2002, 8, 1373-1377.	3.5	64
236	Identification and characterization of subfamily-specific signatures in a large protein superfamily by a hidden Markov model approach. <i>BMC Bioinformatics</i> , 2002, 3, 1.	2.6	99
237	RIO: analyzing proteomes by automated phylogenomics using resampled inference of orthologs. <i>BMC Bioinformatics</i> , 2002, 3, 14.	2.6	160
238	A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure. <i>BMC Bioinformatics</i> , 2002, 3, 18.	2.6	206
239	Visualizing the genome: techniques for presenting human genome data and annotations. <i>BMC Bioinformatics</i> , 2002, 3, 19.	2.6	30
240	The SGS3 protein involved in PTGS finds a family. <i>BMC Bioinformatics</i> , 2002, 3, 21.	2.6	27
241	SeqHound: biological sequence and structure database as a platform for bioinformatics research. <i>BMC Bioinformatics</i> , 2002, 3, 32.	2.6	40
242	FunSpec: a web-based cluster interpreter for yeast. <i>BMC Bioinformatics</i> , 2002, 3, 35.	2.6	367
243	Birth and death of protein domains: a simple model of evolution explains power law behavior. <i>BMC Evolutionary Biology</i> , 2002, 2, 18.	3.2	158
244	Structural, functional, and evolutionary analysis of moeZ, a gene encoding an enzyme required for the synthesis of the <i>Pseudomonas</i> metabolite, pyridine-2,6-bis(thiocarboxylic acid). <i>BMC Evolutionary Biology</i> , 2002, 2, 8.	3.2	17
245	Molecular diversity of phospholipase D in angiosperms. <i>BMC Genomics</i> , 2002, 3, 2.	2.8	97
246	Domain-oriented functional analysis based on expression profiling. <i>BMC Genomics</i> , 2002, 3, 32.	2.8	6
247	The methionine salvage pathway in <i>Bacillus subtilis</i> . <i>BMC Microbiology</i> , 2002, 2, 8.	3.3	83
248	Correct Assignment of Homology is Crucial When Genomics Meets Molecular Evolution. <i>Comparative and Functional Genomics</i> , 2002, 3, 488-493.	2.0	1
249	Molecular analysis of a major locus for resistance to downy mildew in sunflower with specific PCR-based markers. <i>Theoretical and Applied Genetics</i> , 2002, 104, 592-600.	3.6	64
250	Ribonucleotide Reductases: Divergent Evolution of an Ancient Enzyme. <i>Journal of Molecular Evolution</i> , 2002, 55, 138-152.	1.8	88
251	Identification and characterization of SF2000 and SF2001, two new members of the immune receptor SLAM/CD2 family. <i>Immunogenetics</i> , 2002, 53, 843-850.	2.4	55
252	The <i>Drosophila</i> Pipsqueak protein defines a new family of helix-turn-helix DNA-binding proteins. <i>Development Genes and Evolution</i> , 2002, 212, 152-157.	0.9	68

#	ARTICLE	IF	CITATIONS
253	Yeast genomic databases and the challenge of the post-genomic era. <i>Functional and Integrative Genomics</i> , 2002, 2, 212-237.	3.5	19
254	Crystal structure of <i>Escherichia coli</i> EC1530, a glyoxylate induced protein YgbM. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 427-430.	2.6	3
255	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
256	Novel tools for the study of class I α -mannosidases: a chromogenic substrate and a substrate-analog inhibitor. <i>Analytical Biochemistry</i> , 2002, 307, 361-367.	2.4	6
257	Possible structure and active site residues of starch, glycogen, and sucrose synthases. <i>The Protein Journal</i> , 2002, 21, 297-306.	1.1	15
258	The cadherin superfamily database. <i>Journal of Structural and Functional Genomics</i> , 2002, 2, 135-143.	1.2	8
259	The Nogo receptor, its ligands and axonal regeneration in the spinal cord; a review. <i>Journal of Neurocytology</i> , 2002, 31, 93-120.	1.5	117
260	Lipopolysaccharide phosphorylating enzymes encoded in the genomes of Gram-negative bacteria are related to the eukaryotic protein kinases. <i>Protein Science</i> , 2002, 11, 1580-1584.	7.6	24
261	Structural similarity to link sequence space: New potential superfamilies and implications for structural genomics. <i>Protein Science</i> , 2002, 11, 1101-1116.	7.6	20
262	A model of the replication fork blocking protein Fob1p based on the catalytic core domain of retroviral integrases. <i>Protein Science</i> , 2002, 11, 1274-1277.	7.6	14
263	A complex prediction: three-dimensional model of the yeast exosome. <i>EMBO Reports</i> , 2002, 3, 628-635.	4.5	89
264	Genomic expansion and clustering of ZAD-containing C2H2 zinc-finger genes in <i>Drosophila</i> . <i>EMBO Reports</i> , 2002, 3, 1158-1162.	4.5	95
265	The structure of the Dead ringer-DNA complex reveals how AT-rich interaction domains (ARIDs) recognize DNA. <i>EMBO Journal</i> , 2002, 21, 1197-1209.	7.8	59
266	Bioinformatics Methods to Predict Protein Structure and Function: A Practical Approach. <i>Molecular Biotechnology</i> , 2003, 23, 139-166.	2.4	34
267	Multiple sequence alignment with the Clustal series of programs. <i>Nucleic Acids Research</i> , 2003, 31, 3497-3500.	14.5	4,221
268	The Unique FaeI Restriction Modification System: Cloning and Protein Sequence Comparisons. <i>Molecular Biology</i> , 2003, 37, 524-528.	1.3	3
269	Characteristics and prediction of domain linker sequences in multi-domain proteins. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 79-85.	1.2	27
270	Structure-based functional inference in structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 129-135.	1.2	60

#	ARTICLE	IF	CITATIONS
271	Computational approaches to protein-protein interaction. <i>Journal of Structural and Functional Genomics</i> , 2003, 4, 245-255.	1.2	11
272	Identification of differentially expressed cDNA sequences in ovaries of sexual and apomictic plants of <i>Brachiaria brizantha</i> . <i>Plant Molecular Biology</i> , 2003, 53, 745-757.	3.9	66
273	Structural genomics: Computational methods for structure analysis. <i>Protein Science</i> , 2003, 12, 1813-1821.	7.6	104
274	A semiautomated approach to gene discovery through expressed sequence tag data mining: Discovery of new human transporter genes. <i>AAPS PharmSci</i> , 2003, 5, 1-18.	1.3	15
275	Target Selection and Determination of Function in Structural Genomics. <i>IUBMB Life</i> , 2003, 55, 249-255.	3.4	22
276	A novel sensor of NADH/NAD ⁺ redox poise in <i>Streptomyces coelicolor</i> A3(2). <i>EMBO Journal</i> , 2003, 22, 4856-4865.	7.8	214
277	Transcriptional activation of known and novel apoptotic pathways by Nur77 orphan steroid receptor. <i>EMBO Journal</i> , 2003, 22, 6526-6536.	7.8	114
278	Sequence analysis corresponding to the PPE and PE proteins in <i>Mycobacterium tuberculosis</i> and other genomes. <i>Journal of Biosciences</i> , 2003, 28, 169-179.	1.1	49
279	Bioinformatical study on the proteomics and evolution of SARS-CoV. <i>Science Bulletin</i> , 2003, 48, 1277-1287.	1.7	2
280	Neurotoxin Gene Clusters in <i>Clostridium botulinum</i> Type A Strains: Sequence Comparison and Evolutionary Implications. <i>Current Microbiology</i> , 2003, 46, 345-352.	2.2	86
281	Evolution, biochemistry and genetics of protein kinase C in fungi. <i>Current Genetics</i> , 2003, 43, 245-254.	1.7	49
282	Lytic transglycosylases in macromolecular transport systems of Gram-negative bacteria. <i>Cellular and Molecular Life Sciences</i> , 2003, 60, 2371-2388.	5.4	192
283	Automatic prediction of protein function. <i>Cellular and Molecular Life Sciences</i> , 2003, 60, 2637-2650.	5.4	225
284	Specificity of Cellular Expression of <i>C. variopedatus</i> Polychaete Innexin in the Developing Embryo: Evolutionary Aspects of Innexins? Heterogeneous Gene Structures. <i>Journal of Molecular Evolution</i> , 2003, 57, S165-S173.	1.8	8
285	Standardized Phylogenetic Tree: A Reference to Discover Functional Evolution. <i>Journal of Molecular Evolution</i> , 2003, 57, S174-S181.	1.8	1
286	Comparisons of Two Large Phaeoviral Genomes and Evolutionary Implications. <i>Journal of Molecular Evolution</i> , 2003, 57, 613-622.	1.8	33
287	Presence of dUTPase in the Various Human Endogenous Retrovirus K (HERV-K) Families. <i>Journal of Molecular Evolution</i> , 2003, 57, 642-649.	1.8	19
288	Evolution of the proto-MHC ancestral region: more evidence for the plesiomorphic organisation of human chromosome 9q34 region. <i>Immunogenetics</i> , 2003, 55, 429-436.	2.4	23

#	ARTICLE	IF	CITATIONS
289	Positional cloning of jcpk/bpk locus of the mouse. <i>Mammalian Genome</i> , 2003, 14, 242-249.	2.2	85
290	PepPat, a pattern-based oligopeptide homology search method and the identification of a novel tachykinin-like peptide. <i>Mammalian Genome</i> , 2003, 14, 341-349.	2.2	17
291	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 213-221.	0.9	129
292	A genomewide survey of developmentally relevant genes in <i>Ciona intestinalis</i> . <i>Development Genes and Evolution</i> , 2003, 213, 303-313.	0.9	99
293	Gene expression profiles of microdissected pancreatic ductal adenocarcinoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2003, 443, 508-517.	2.8	103
294	A large scale analysis of resistance gene homologues in <i>Arachis</i> . <i>Molecular Genetics and Genomics</i> , 2003, 270, 34-45.	2.1	69
295	Evolution and microsynteny of the apyrase gene family in three legume genomes. <i>Molecular Genetics and Genomics</i> , 2003, 270, 347-361.	2.1	50
296	No evidence for PHD fingers as ubiquitin ligases. <i>Trends in Cell Biology</i> , 2003, 13, 285-287.	7.9	53
297	Bioinformatics: not just for sequences anymore. <i>Biosilico</i> , 2003, 1, 103-111.	0.5	2
298	The CW domain, a structural module shared amongst vertebrates, vertebrate-infecting parasites and higher plants. <i>Trends in Biochemical Sciences</i> , 2003, 28, 576-580.	7.5	83
299	Domain fusion analysis by applying relational algebra to protein sequence and domain databases. <i>BMC Bioinformatics</i> , 2003, 4, 16.	2.6	15
300	A comparison of Pfam and MEROPS: two databases, one comprehensive, and one specialised. <i>BMC Bioinformatics</i> , 2003, 4, 17.	2.6	7
301	ELISA: structure-function inferences based on statistically significant and evolutionarily inspired observations. <i>BMC Bioinformatics</i> , 2003, 4, 34.	2.6	15
302	Molecular phylogeny of the kelch-repeat superfamily reveals an expansion of BTB/kelch proteins in animals. <i>BMC Bioinformatics</i> , 2003, 4, 42.	2.6	142
303	The TROVE module: a common element in Telomerase, Ro and Vault ribonucleoproteins. <i>BMC Bioinformatics</i> , 2003, 4, 49.	2.6	28
304	A knowledge discovery object model API for Java. <i>BMC Bioinformatics</i> , 2003, 4, 51.	2.6	1
305	LEAPing to conclusions: a computational reanalysis of late embryogenesis abundant proteins and their possible roles. <i>BMC Bioinformatics</i> , 2003, 4, 52.	2.6	211
306	Reannotation of the CELO genome characterizes a set of previously unassigned open reading frames and points to novel modes of host interaction in avian adenoviruses. <i>BMC Bioinformatics</i> , 2003, 4, 55.	2.6	22

#	ARTICLE	IF	CITATIONS
307	The PAM domain, a multi-protein complex-associated module with an all-alpha-helix fold. BMC Bioinformatics, 2003, 4, 64.	2.6	15
308	Application of comparative genomics in the identification and analysis of novel families of membrane-associated receptors in bacteria. BMC Genomics, 2003, 4, 34.	2.8	83
309	PCAS – a precomputed proteome annotation database resource. BMC Genomics, 2003, 4, 42.	2.8	6
310	Phylogenomic identification of five new human homologs of the DNA repair enzyme AlkB. BMC Genomics, 2003, 4, 48.	2.8	180
311	The WD-repeat protein superfamily in Arabidopsis: conservation and divergence in structure and function. BMC Genomics, 2003, 4, 50.	2.8	256
312	Metabolic reconstruction of sulfur assimilation in the extremophile Acidithiobacillus ferrooxidans based on genome analysis. BMC Genomics, 2003, 4, 51.	2.8	67
313	Annotation and evolutionary relationships of a small regulatory RNA gene micF and its target ompF in Yersinia species. BMC Microbiology, 2003, 3, 13.	3.3	15
314	A DNA element recognised by the molybdenum-responsive transcription factor ModE is conserved in Proteobacteria, green sulphur bacteria and Archaea. BMC Microbiology, 2003, 3, 24.	3.3	31
315	New knowledge from old: in silico discovery of novel protein domains in Streptomyces coelicolor. BMC Microbiology, 2003, 3, 3.	3.3	98
316	Cloning and characterization of Plasmodium falciparum homologs of nuclear import factors, karyopherin β and karyopherin β ² . Molecular and Biochemical Parasitology, 2003, 127, 199-203.	1.1	9
317	SARS associated coronavirus has a recombinant polymerase and coronaviruses have a history of host-shifting. Infection, Genetics and Evolution, 2003, 3, 219-225.	2.3	88
318	The Escherichia coli amidase AmiC is a periplasmic septal ring component exported via the twin-arginine transport pathway. Molecular Microbiology, 2003, 48, 1171-1182.	2.5	299
319	Pathogenic Leptospira species express surface-exposed proteins belonging to the bacterial immunoglobulin superfamily. Molecular Microbiology, 2003, 49, 929-946.	2.5	239
320	Prediction of human protein function according to Gene Ontology categories. Bioinformatics, 2003, 19, 635-642.	4.1	233
321	Prediction of protein function from protein sequence and structure. Quarterly Reviews of Biophysics, 2003, 36, 307-340.	5.7	376
322	Metagenomes of Complex Microbial Consortia Derived from Different Soils as Sources for Novel Genes Conferring Formation of Carbonyls from Short-Chain Polyols on <i>Escherichia coli</i> . Journal of Molecular Microbiology and Biotechnology, 2003, 5, 46-56.	1.0	83
323	Crystal structure of the conserved protein TT1542 from <i>Thermus thermophilus</i> HB8. Protein Science, 2003, 12, 1621-1632.	7.6	32
324	Homology modeling and molecular dynamics simulations of the N-terminal domain of wheat high molecular weight glutenin subunit 10. Protein Science, 2003, 12, 34-43.	7.6	14

#	ARTICLE	IF	CITATIONS
325	<i>Vibrio cholerae</i> cytolysin is composed of an alpha-hemolysin-like core. <i>Protein Science</i> , 2003, 12, 379-383.	7.6	42
326	Three monophyletic superfamilies account for the majority of the known glycosyltransferases. <i>Protein Science</i> , 2003, 12, 1418-1431.	7.6	196
327	Crystal structure of a phosphatase with a unique substrate binding domain from <i>Thermotoga maritima</i> . <i>Protein Science</i> , 2003, 12, 1464-1472.	7.6	35
328	Construction of a sequence motif characteristic of aminergic G protein-coupled receptors. <i>Protein Science</i> , 2003, 12, 1360-1367.	7.6	57
329	Asymmetric mutation rates at enzyme-inhibitor interfaces: Implications for the protein-protein docking problem. <i>Protein Science</i> , 2003, 12, 2099-2103.	7.6	20
330	Exploring the nonlinear geometry of protein homology. <i>Protein Science</i> , 2003, 12, 1604-1612.	7.6	14
331	Analysis of Structure and Function of Putative Surface-Exposed Proteins Encoded in the <i>Streptococcus pneumoniae</i> Genome: A Bioinformatics-Based Approach to Vaccine and Drug Design. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2003, 38, 143-168.	5.2	54
332	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	7.1	506
333	The 2.2Å... Resolution Structure of RpiB/AlsB from <i>Escherichia coli</i> Illustrates a New Approach to the Ribose-5-phosphate Isomerase Reaction. <i>Journal of Molecular Biology</i> , 2003, 332, 1083-1094.	4.2	71
334	Glycosylphosphatidylinositol Lipid Anchoring of Plant Proteins. Sensitive Prediction from Sequence- and Genome-Wide Studies for <i>Arabidopsis</i> and Rice. <i>Plant Physiology</i> , 2003, 133, 1691-1701.	4.8	185
335	Engineering Vitamin E Content: From <i>Arabidopsis</i> Mutant to Soy Oil. <i>Plant Cell</i> , 2003, 15, 3007-3019.	6.6	231
336	Assessment of putative protein targets derived from the SARS genome. <i>FEBS Letters</i> , 2003, 554, 257-263.	2.8	19
337	<i>Aplysia</i> mollusk-derived growth factor is a mitogen with adenosine deaminase activity and is expressed in the developing central nervous system. <i>Molecular Brain Research</i> , 2003, 117, 228-236.	2.3	15
338	Exploring the immunogenome with bioinformatics. <i>Seminars in Immunology</i> , 2003, 15, 233-238.	5.6	1
339	Bioinformatics approaches for the classification of G-protein-coupled receptors. <i>Current Opinion in Pharmacology</i> , 2003, 3, 114-120.	3.5	38
340	Tools for comparative protein structure modeling and analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3375-3380.	14.5	406
341	CDD: a curated Entrez database of conserved domain alignments. <i>Nucleic Acids Research</i> , 2003, 31, 383-387.	14.5	673
342	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment. <i>Genome Research</i> , 2003, 13, 2265-2270.	5.5	305

#	ARTICLE	IF	CITATIONS
343	Practical Bioinformatics for Proteomics. , 2003, 141, 79-92.		9
344	Pilot survey of expressed sequence tags (ESTs) from the asexual blood stages of Plasmodium vivax in human patients. Malaria Journal, 2003, 2, 21.	2.3	7
345	Identifying biological themes within lists of genes with EASE. Genome Biology, 2003, 4, R70.	8.8	1,664
346	A comparative proteomics resource: proteins of Arabidopsis thaliana. Genome Biology, 2003, 4, R51.	9.6	25
347	THoR: a tool for domain discovery and curation of multiple alignments. Genome Biology, 2003, 4, R52.	9.6	3
348	Horizontally transferred genes in plant-parasitic nematodes: a high-throughput genomic approach. Genome Biology, 2003, 4, R39.	9.6	134
349	Protein prenyltransferases. Genome Biology, 2003, 4, 212.	9.6	106
350	Latent Periodicity of 21 Bases Typical for MCP II Gene is Widely Present in Various Bacterial Genes. DNA Sequence, 2003, 14, 33-52.	0.7	5
351	Development of Human Protein Reference Database as an Initial Platform for Approaching Systems Biology in Humans. Genome Research, 2003, 13, 2363-2371.	5.5	954
352	The complete genome sequence of the <i>Arabidopsis</i> and tomato pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10181-10186.	7.1	785
353	Rfam: an RNA family database. Nucleic Acids Research, 2003, 31, 439-441.	14.5	1,296
354	Enzyme-specific profiles for genome annotation: PRIAM. Nucleic Acids Research, 2003, 31, 6633-6639.	14.5	323
355	PANTHER: A Library of Protein Families and Subfamilies Indexed by Function. Genome Research, 2003, 13, 2129-2141.	5.5	2,703
356	The Nuclear Protein Database (NPD): sub-nuclear localisation and functional annotation of the nuclear proteome. Nucleic Acids Research, 2003, 31, 328-330.	14.5	85
357	A cluster-based solution for high performance hmmpfam using EARTH execution model. , 2003, , .		6
358	Inference of protein-protein interactions by unlikely profile pair. , 0, , .		1
359	RNA Expression Profiles and Data Mining of Sugarcane Response to Low Temperature. Plant Physiology, 2003, 132, 1811-1824.	4.8	155
360	The sequence and analysis of Trypanosoma brucei chromosome II. Nucleic Acids Research, 2003, 31, 4856-4863.	14.5	59

#	ARTICLE	IF	CITATIONS
361	DC3, the 21-kDa Subunit of the Outer Dynein Arm-Docking Complex (ODA-DC), Is a Novel EF-Hand Protein Important for Assembly of Both the Outer Arm and the ODA-DC. <i>Molecular Biology of the Cell</i> , 2003, 14, 3650-3663.	2.1	95
362	Parallel Evolution of Ligand Specificity Between LacI/GalR Family Repressors and Periplasmic Sugar-Binding Proteins. <i>Molecular Biology and Evolution</i> , 2003, 20, 267-277.	8.9	55
363	REBASE: restriction enzymes and methyltransferases. <i>Nucleic Acids Research</i> , 2003, 31, 418-420.	14.5	205
364	Scansite 2.0: proteome-wide prediction of cell signaling interactions using short sequence motifs. <i>Nucleic Acids Research</i> , 2003, 31, 3635-3641.	14.5	1,455
365	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	5.5	254
366	The Gene Ontology Annotation (GOA) Project: Implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003, 13, 662-672.	5.5	297
367	GlobPlot: exploring protein sequences for globularity and disorder. <i>Nucleic Acids Research</i> , 2003, 31, 3701-3708.	14.5	869
368	Pandit: a database of protein and associated nucleotide domains with inferred trees. <i>Bioinformatics</i> , 2003, 19, 1556-1563.	4.1	44
369	Phydbac (phylogenomic display of bacterial genes): an interactive resource for the annotation of bacterial genomes. <i>Nucleic Acids Research</i> , 2003, 31, 3720-3722.	14.5	12
370	Using structural motif templates to identify proteins with DNA binding function. <i>Nucleic Acids Research</i> , 2003, 31, 2811-2823.	14.5	57
371	RTKdb: database of receptor tyrosine kinase. <i>Nucleic Acids Research</i> , 2003, 31, 353-358.	14.5	35
372	Complete sequence of the mitochondrial genome of <i>Tetrahymena thermophila</i> and comparative methods for identifying highly divergent genes. <i>Nucleic Acids Research</i> , 2003, 31, 1673-1682.	14.5	64
373	Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: II. The Complete Nucleotide Sequences of 400 Mouse KIAA-homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-fractionated Libraries. <i>DNA Research</i> , 2003, 10, 35-48.	3.4	43
374	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. <i>Nucleic Acids Research</i> , 2003, 31, 6516-6523.	14.5	285
375	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003, 31, 365-370.	14.5	3,096
376	A comparative analysis of HGSC and Celera human genome assemblies and gene sets. <i>Bioinformatics</i> , 2003, 19, 1597-1605.	4.1	8
377	MBGD: microbial genome database for comparative analysis. <i>Nucleic Acids Research</i> , 2003, 31, 58-62.	14.5	113
378	Comprehensive Analysis of Orthologous Protein Domains Using the HOPS Database. <i>Genome Research</i> , 2003, 13, 2353-2362.	5.5	40

#	ARTICLE	IF	CITATIONS
379	Using multiple interdependency to separate functional from phylogenetic correlations in protein alignments. <i>Bioinformatics</i> , 2003, 19, 750-755.	4.1	118
380	Cytokine-Related Genes Identified From the RIKEN Full-Length Mouse cDNA Data Set. <i>Genome Research</i> , 2003, 13, 1307-1317.	5.5	2
381	Mapping the Proteome of Barrel Medic (<i>Medicago truncatula</i>),. <i>Plant Physiology</i> , 2003, 131, 1104-1123.	4.8	217
382	The TIGR rice genome annotation resource: annotating the rice genome and creating resources for plant biologists. <i>Nucleic Acids Research</i> , 2003, 31, 229-233.	14.5	128
383	Identification and Analysis of Chromodomain-Containing Proteins Encoded in the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1416-1429.	5.5	50
384	E-MSD: the European Bioinformatics Institute Macromolecular Structure Database. <i>Nucleic Acids Research</i> , 2003, 31, 458-462.	14.5	93
385	Efficient estimation of emission probabilities in profile hidden Markov models. <i>Bioinformatics</i> , 2003, 19, 2359-2368.	4.1	8
386	Crystal structure of human Î±-tocopherol transfer protein bound to its ligand: Implications for ataxia with vitamin E deficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14713-14718.	7.1	121
387	GANESH: Software for Customized Annotation of Genome Regions. <i>Genome Research</i> , 2003, 13, 2195-2202.	5.5	2
388	Mpi recombinase globally modulates the surface architecture of a human commensal bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10446-10451.	7.1	111
389	Maintaining epithelial integrity. <i>Journal of Cell Biology</i> , 2003, 162, 1305-1315.	5.2	59
390	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. <i>Nucleic Acids Research</i> , 2003, 31, 4864-4873.	14.5	56
391	3MATRIX and 3MOTIF: a protein structure visualization system for conserved sequence motifs. <i>Nucleic Acids Research</i> , 2003, 31, 3328-3332.	14.5	10
392	The SBASE domain sequence library, release 10: domain architecture prediction. <i>Nucleic Acids Research</i> , 2003, 31, 403-405.	14.5	11
393	SEARCHPKS: a program for detection and analysis of polyketide synthase domains. <i>Nucleic Acids Research</i> , 2003, 31, 3654-3658.	14.5	103
394	iSPOT: a web tool to infer the interaction specificity of families of protein modules. <i>Nucleic Acids Research</i> , 2003, 31, 3709-3711.	14.5	30
395	Genome-Wide Analysis of NBS-LRR-Encoding Genes in Arabidopsis[W]. <i>Plant Cell</i> , 2003, 15, 809-834.	6.6	1,457
396	Kinase Pathway Database: An Integrated Protein-Kinase and NLP-Based Protein-Interaction Resource. <i>Genome Research</i> , 2003, 13, 1231-1243.	5.5	50

#	ARTICLE	IF	CITATIONS
397	Arabidopsis Proteins Containing Similarity to the Universal Stress Protein Domain of Bacteria. <i>Plant Physiology</i> , 2003, 131, 1209-1219.	4.8	89
398	Structure of the GAT domain of human GGA1: A syntaxin amino-terminal domain fold in an endosomal trafficking adaptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4451-4456.	7.1	42
399	The PEDANT genome database. <i>Nucleic Acids Research</i> , 2003, 31, 207-211.	14.5	110
400	PRINTS and its automatic supplement, prePRINTS. <i>Nucleic Acids Research</i> , 2003, 31, 400-402.	14.5	345
401	Integration of related sequences with protein three-dimensional structural families in an updated version of PALI database. <i>Nucleic Acids Research</i> , 2003, 31, 486-488.	14.5	38
402	InterDom: a database of putative interacting protein domains for validating predicted protein interactions and complexes. <i>Nucleic Acids Research</i> , 2003, 31, 251-254.	14.5	130
403	The PSSH database of alignments between protein sequences and tertiary structures. <i>Nucleic Acids Research</i> , 2003, 31, 494-498.	14.5	11
404	NetAffx: Affymetrix probesets and annotations. <i>Nucleic Acids Research</i> , 2003, 31, 82-86.	14.5	438
405	Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. <i>Nucleic Acids Research</i> , 2003, 31, 790-797.	14.5	35
406	Evolution of transcription factors and the gene regulatory network in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2003, 31, 1234-1244.	14.5	283
407	The structure of full-length LysR-type transcriptional regulators. Modeling of the full-length OxyR transcription factor dimer. <i>Nucleic Acids Research</i> , 2003, 31, 1444-1454.	14.5	68
408	Genome sequence of <i>Chlamydomonas reinhardtii</i> (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , 2003, 31, 2134-2147.	14.5	266
409	The SV40 T antigen modulates CBP histone acetyltransferase activity. <i>Nucleic Acids Research</i> , 2003, 31, 3114-3122.	14.5	34
410	SEGID: Identifying Interesting Segments in (Multiple) Sequence Alignments. <i>Bioinformatics</i> , 2003, 19, 297-298.	4.1	27
411	Learning to predict protein-protein interactions from protein sequences. <i>Bioinformatics</i> , 2003, 19, 1875-1881.	4.1	140
412	Complete Genome Structure of <i>Gloeobacter violaceus</i> PCC 7421, a Cyanobacterium that Lacks Thylakoids. <i>DNA Research</i> , 2003, 10, 137-145.	3.4	269
413	Phylogenomic Analysis of the <i>Giardia intestinalis</i> Transcarboxylase Reveals Multiple Instances of Domain Fusion and Fission in the Evolution of Biotin-Dependent Enzymes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 172-189.	1.0	15
414	Conservation of structure and function among tyrosine recombinases: homology-based modeling of the lambda integrase core-binding domain. <i>Nucleic Acids Research</i> , 2003, 31, 805-818.	14.5	27

#	ARTICLE	IF	CITATIONS
415	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	14.5	56
416	The Esterase and PHD Domains in CR1-Like Non-LTR Retrotransposons. <i>Molecular Biology and Evolution</i> , 2003, 20, 38-46.	8.9	71
417	Single Eubacterial Origin of Eukaryotic Sulfide:Quinone Oxidoreductase, a Mitochondrial Enzyme Conserved from the Early Evolution of Eukaryotes During Anoxic and Sulfidic Times. <i>Molecular Biology and Evolution</i> , 2003, 20, 1564-1574.	8.9	184
418	Bioverse: functional, structural and contextual annotation of proteins and proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 3736-3737.	14.5	23
419	iProClass: an integrated database of protein family, function and structure information. <i>Nucleic Acids Research</i> , 2003, 31, 390-392.	14.5	41
420	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
421	Amassin, an olfactomedin protein, mediates the massive intercellular adhesion of sea urchin coelomocytes. <i>Journal of Cell Biology</i> , 2003, 160, 597-604.	5.2	72
422	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	14.5	555
423	TRAIT (TRANscript Integrated Table): a knowledgebase of human skeletal muscle transcripts. <i>Bioinformatics</i> , 2003, 19, 661-662.	4.1	4
424	Pyranose oxidase identified as a member of the GMC oxidoreductase family. <i>Bioinformatics</i> , 2003, 19, 1216-1220.	4.1	24
425	Mining and interpretation of association rules among protein sequence motifs. , 0, , .		1
426	Database resources of the National Center for Biotechnology. <i>Nucleic Acids Research</i> , 2003, 31, 28-33.	14.5	879
427	What's in the genome of a filamentous fungus? Analysis of the <i>Neurospora</i> genome sequence. <i>Nucleic Acids Research</i> , 2003, 31, 1944-1954.	14.5	59
428	MASE1 and MASE2: Two Novel Integral Membrane Sensory Domains. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2003, 5, 11-16.	1.0	68
429	The <i>Tre2</i> (<i>USP6</i>) oncogene is a hominoid-specific gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2507-2511.	7.1	134
430	Gene3D: structural assignments for the biologist and bioinformaticist alike. <i>Nucleic Acids Research</i> , 2003, 31, 469-473.	14.5	23
431	Involvement of Sialoadhesin in Entry of Porcine Reproductive and Respiratory Syndrome Virus into Porcine Alveolar Macrophages. <i>Journal of Virology</i> , 2003, 77, 8207-8215.	3.4	238
432	Enhanced protein domain discovery by using language modeling techniques from speech recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4516-4520.	7.1	47

#	ARTICLE	IF	CITATIONS
433	ASAP, a systematic annotation package for community analysis of genomes. <i>Nucleic Acids Research</i> , 2003, 31, 147-151.	14.5	152
434	The first completed genome sequence from a teleost fish (<i>Fugu rubripes</i>) adds significant diversity to the nuclear receptor superfamily. <i>Nucleic Acids Research</i> , 2003, 31, 4051-4058.	14.5	137
435	Bayesian gene/species tree reconciliation and orthology analysis using MCMC. <i>Bioinformatics</i> , 2003, 19, i7-i15.	4.1	137
436	Integrated Mapping, Chromosomal Sequencing and Sequence Analysis of <i>Cryptosporidium parvum</i> . <i>Genome Research</i> , 2003, 13, 1787-99.	5.5	60
437	NONSYNDROMICSEIZUREDISORDERS: Epilepsy and the Use of the Internet to Advance Research. <i>Annual Review of Genomics and Human Genetics</i> , 2003, 4, 437-457.	6.2	1
438	ProtoNet: hierarchical classification of the protein space. <i>Nucleic Acids Research</i> , 2003, 31, 348-352.	14.5	70
439	PDP: protein domain parser. <i>Bioinformatics</i> , 2003, 19, 429-430.	4.1	152
440	SVM-Prot: web-based support vector machine software for functional classification of a protein from its primary sequence. <i>Nucleic Acids Research</i> , 2003, 31, 3692-3697.	14.5	515
441	InterPreTS: protein Interaction Prediction through Tertiary Structure. <i>Bioinformatics</i> , 2003, 19, 161-162.	4.1	214
442	Convergent neofunctionalization by positive Darwinian selection after ancient recurrent duplications of the xanthine dehydrogenase gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13413-13417.	7.1	124
443	Expression of the Apyrase-Like APY1 Genes in Roots of <i>Medicago truncatula</i> Is Induced Rapidly and Transiently by Stress and Not by <i>Sinorhizobium meliloti</i> or Nod Factors. <i>Plant Physiology</i> , 2003, 131, 1124-1136.	4.8	24
444	Identifying residue-residue clashes in protein hybrids by using a second-order mean-field approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5091-5096.	7.1	50
445	Amino acids determining enzyme-substrate specificity in prokaryotic and eukaryotic protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4463-4468.	7.1	84
446	The ERGOTM genome analysis and discovery system. <i>Nucleic Acids Research</i> , 2003, 31, 164-171.	14.5	207
447	A profile hidden Markov model for signal peptides generated by HMMER. <i>Bioinformatics</i> , 2003, 19, 307-308.	4.1	85
448	Using multiple sequence correlation analysis to characterize functionally important protein regions. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 397-406.	2.1	32
449	Inferring strengths of protein-protein interactions from experimental data using linear programming. <i>Bioinformatics</i> , 2003, 19, ii58-ii65.	4.1	23
450	The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.	5.6	812

#	ARTICLE	IF	CITATIONS
451	Retroids in Archaea: Phylogeny and Lateral Origins. <i>Molecular Biology and Evolution</i> , 2003, 20, 1134-1142.	8.9	71
452	Protein families and TRIBES in genome sequence space. <i>Nucleic Acids Research</i> , 2003, 31, 4632-4638.	14.5	113
453	tRNAHis maturation: An essential yeast protein catalyzes addition of a guanine nucleotide to the 5' end of tRNAHis. <i>Genes and Development</i> , 2003, 17, 2889-2901.	5.9	104
454	Integrative approach for computationally inferring protein domain interactions. <i>Bioinformatics</i> , 2003, 19, 923-929.	4.1	159
455	PRECIS: Protein reports engineered from concise information in SWISS-PROT. <i>Bioinformatics</i> , 2003, 19, 1664-1671.	4.1	12
456	Implementing parallel hmm-pfam on the EARTH multithreaded architecture. , 0, , .		9
457	Is prokaryotic complexity limited by accelerated growth in regulatory overhead?. <i>Genome Biology</i> , 2003, 5, P2.	9.6	22
458	EST Pipeline System: Detailed and Automated EST Data Processing and Mining. <i>Genomics, Proteomics and Bioinformatics</i> , 2003, 1, 236-242.	6.9	12
459	Retrieval-independent localization of lysyl hydroxylase in the endoplasmic reticulum via a peptide fold in its iron-binding domain. <i>Biochemical Journal</i> , 2003, 370, 913-920.	3.7	18
460	Inhibition of Plant-Pathogenic Fungi by the Barley Cystatin Hv-CPI (Gene Icy) Is Not Associated with Its Cysteine-Proteinase Inhibitory Properties. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 876-883.	2.6	68
461	Genlight: Interactive high-throughput sequence analysis and comparative genomics. <i>Journal of Integrative Bioinformatics</i> , 2004, 1, 90-107.	1.5	7
462	Bioinformatic Approaches to Assigning Protein Function From Novel Sequence Data. , 2005, 104, 313-332.		0
463	Cathepsin L-like cysteine proteases from <i>Brugia malayi</i> : cDNA cloning and comparison with <i>Caenorhabditis elegans</i> . <i>Biomedical Research</i> , 2004, 25, 287-293.	0.9	3
464	Segmentally Variable Genes: A New Perspective on Adaptation. <i>PLoS Biology</i> , 2004, 2, e81.	5.6	22
465	The ProDom database of protein domain families: more emphasis on 3D. <i>Nucleic Acids Research</i> , 2004, 33, D212-D215.	14.5	305
466	SPD--a web-based secreted protein database. <i>Nucleic Acids Research</i> , 2004, 33, D169-D173.	14.5	172
467	Prediction of <i>Saccharomyces cerevisiae</i> protein functional class from functional domain composition. <i>Bioinformatics</i> , 2004, 20, 1292-1300.	4.1	49
468	The MAPPER database: a multi-genome catalog of putative transcription factor binding sites. <i>Nucleic Acids Research</i> , 2004, 33, D91-D97.	14.5	111

#	ARTICLE	IF	CITATIONS
469	Improved techniques for the identification of pseudogenes. <i>Bioinformatics</i> , 2004, 20, i94-i100.	4.1	21
470	Using column dependency to compress tables. , 0, , .		2
471	3did: interacting protein domains of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2004, 33, D413-D417.	14.5	160
472	FamClash: A method for ranking the activity of engineered enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4142-4147.	7.1	70
473	CHOP: parsing proteins into structural domains. <i>Nucleic Acids Research</i> , 2004, 32, W569-W571.	14.5	30
474	ADDA: a domain database with global coverage of the protein universe. <i>Nucleic Acids Research</i> , 2004, 33, D188-D191.	14.5	39
475	Detecting distant homology with Meta-BASIC. <i>Nucleic Acids Research</i> , 2004, 32, W576-W581.	14.5	92
476	PRISM: protein integration of sequence metrics. , 2004, 2004, 2991-4.		0
477	Phylogenomic inference of protein molecular function: advances and challenges. <i>Bioinformatics</i> , 2004, 20, 170-179.	4.1	184
478	The Evolutionary Repertoires of the Eukaryotic-Type ABC Transporters in Terms of the Phylogeny of ATP-binding Domains in Eukaryotes and Prokaryotes. <i>Molecular Biology and Evolution</i> , 2004, 21, 2149-2160.	8.9	29
479	Genomic and Proteomic Analysis of Thirty-Nine Structural Proteins of Shrimp White Spot Syndrome Virus. <i>Journal of Virology</i> , 2004, 78, 11360-11370.	3.4	219
480	Structural Basis of Protein-Protein Interactions. , 2004, 261, 003-014.		19
481	A Novel Virulence Gene in <i>Klebsiella pneumoniae</i> Strains Causing Primary Liver Abscess and Septic Metastatic Complications. <i>Journal of Experimental Medicine</i> , 2004, 199, 697-705.	8.5	609
482	A Gateway-Compatible Yeast One-Hybrid System. <i>Genome Research</i> , 2004, 14, 2093-2101.	5.5	189
483	EyeSite: a semi-automated database of protein families in the eye. <i>Nucleic Acids Research</i> , 2004, 32, 148D-152.	14.5	7
484	Analysis of the LAGLIDADG interface of the monomeric homing endonuclease I-Dmol. <i>Nucleic Acids Research</i> , 2004, 32, 3156-3168.	14.5	29
485	Sequence-based prediction of protein domains. <i>Nucleic Acids Research</i> , 2004, 32, 3522-3530.	14.5	73
486	Geminate Structures of African Cassava Mosaic Virus. <i>Journal of Virology</i> , 2004, 78, 6758-6765.	3.4	107

#	ARTICLE	IF	CITATIONS
487	Functional clues for hypothetical proteins based on genomic context analysis in prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 6321-6326.	14.5	57
488	Database resources of the National Center for Biotechnology Information: update. <i>Nucleic Acids Research</i> , 2004, 32, 35D-40.	14.5	4,118
489	Comparative Analysis of Apicomplexa and Genomic Diversity in Eukaryotes. <i>Genome Research</i> , 2004, 14, 1686-1695.	5.5	172
490	HOMSTRAD: recent developments of the Homologous Protein Structure Alignment Database. <i>Nucleic Acids Research</i> , 2004, 32, 203D-207.	14.5	85
491	LEON: multiple aLignment Evaluation Of Neighbours. <i>Nucleic Acids Research</i> , 2004, 32, 1298-1307.	14.5	24
492	The Jalview Java alignment editor. <i>Bioinformatics</i> , 2004, 20, 426-427.	4.1	1,342
493	Arabidopsis HMA2, a Divalent Heavy Metal-Transporting PIB-Type ATPase, Is Involved in Cytoplasmic Zn ²⁺ Homeostasis. <i>Plant Physiology</i> , 2004, 136, 3712-3723.	4.8	206
494	Complete Genome Sequence of <i>Rickettsia typhi</i> and Comparison with Sequences of Other <i>Rickettsiae</i> . <i>Journal of Bacteriology</i> , 2004, 186, 5842-5855.	2.2	223
495	Cloning and expression of an inhibitor of microbial metalloproteinases from insects contributing to innate immunity. <i>Biochemical Journal</i> , 2004, 382, 315-322.	3.7	70
496	The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome. <i>Nucleic Acids Research</i> , 2004, 32, 3977-3983.	14.5	77
497	PIRSF: family classification system at the Protein Information Resource. <i>Nucleic Acids Research</i> , 2004, 32, 112D-114.	14.5	193
498	The Noc proteins involved in ribosome synthesis and export contain divergent HEAT repeats. <i>Rna</i> , 2004, 10, 351-354.	3.5	15
499	Enhanced homology searching through genome reading frame predetermination. <i>Bioinformatics</i> , 2004, 20, 1416-1427.	4.1	4
500	Predicting functional family of novel enzymes irrespective of sequence similarity: a statistical learning approach. <i>Nucleic Acids Research</i> , 2004, 32, 6437-6444.	14.5	90
501	Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. <i>Genome Research</i> , 2004, 14, 1516-1529.	5.5	79
502	From quantitative microscopy to automated image understanding. <i>Journal of Biomedical Optics</i> , 2004, 9, 893.	2.6	101
503	Detection and evaluation of intron retention events in the human transcriptome. <i>Rna</i> , 2004, 10, 757-765.	3.5	193
504	<i>Bacillus subtilis</i> YhcR, a High-Molecular-Weight, Nonspecific Endonuclease with a Unique Domain Structure. <i>Journal of Bacteriology</i> , 2004, 186, 5376-5383.	2.2	15

#	ARTICLE	IF	CITATIONS
505	Occurrence and Consequences of Coding Sequence Insertions and Deletions in Mammalian Genomes. <i>Genome Research</i> , 2004, 14, 555-566.	5.5	114
506	Domainal organization of the lower eukaryotic homologs of the yeast RNA polymerase II core subunit Rpb7 reflects functional conservation. <i>Nucleic Acids Research</i> , 2004, 32, 201-210.	14.5	14
507	Characterization of the 3' exonuclease subunit DP1 of <i>Methanococcus jannaschii</i> replicative DNA polymerase D. <i>Nucleic Acids Research</i> , 2004, 32, 2430-2440.	14.5	30
508	AplA, a Member of a New Class of Phycobiliproteins Lacking a Traditional Role in Photosynthetic Light Harvesting. <i>Journal of Bacteriology</i> , 2004, 186, 7420-7428.	2.2	20
509	From Endonucleases to Transcription Factors: Evolution of the AP2 DNA Binding Domain in Plants[W]. <i>Plant Cell</i> , 2004, 16, 2265-2277.	6.6	227
510	CoPS: Comprehensive Peptide Signature Database. <i>Bioinformatics</i> , 2004, 20, 2886-2888.	4.1	11
511	Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. <i>Genome Research</i> , 2004, 14, 580-590.	5.5	187
512	Large-scale assessment of the utility of low-resolution protein structures for biochemical function assignment. <i>Bioinformatics</i> , 2004, 20, 1087-1096.	4.1	51
513	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon <i>Halobacterium</i> NRC-1. <i>Genome Research</i> , 2004, 14, 1025-1035.	5.5	130
514	Molecular Evolution of PAS Domain-Containing Proteins of Filamentous Cyanobacteria Through Domain Shuffling and Domain Duplication. <i>DNA Research</i> , 2004, 11, 69-81.	3.4	20
515	Pattern of Sequence Variation Across 213 Environmental Response Genes. <i>Genome Research</i> , 2004, 14, 1821-1831.	5.5	157
516	Cloning and Expression of <i>afpA</i> , a Gene Encoding an Antifreeze Protein from the Arctic Plant Growth-Promoting Rhizobacterium <i>Pseudomonas putida</i> GR12-2. <i>Journal of Bacteriology</i> , 2004, 186, 5661-5671.	2.2	82
517	Functional classification of proteins and protein variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6576-6581.	7.1	23
518	Optimizing substitution matrices by separating score distributions. <i>Bioinformatics</i> , 2004, 20, 863-873.	4.1	13
519	Cloning and Characterization of Two NAD Kinases from Arabidopsis. Identification of a Calmodulin Binding Isoform. <i>Plant Physiology</i> , 2004, 135, 1243-1255.	4.8	116
520	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. <i>Nucleic Acids Research</i> , 2004, 32, 245D-250.	14.5	14
521	EFICAz: a comprehensive approach for accurate genome-scale enzyme function inference. <i>Nucleic Acids Research</i> , 2004, 32, 6226-6239.	14.5	107
522	Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2004, 33, D39-D45.	14.5	369

#	ARTICLE	IF	CITATIONS
523	Quality of alignment comparison by COMPASS improves with inclusion of diverse confident homologs. <i>Bioinformatics</i> , 2004, 20, 818-828.	4.1	28
524	Comparative Analysis of Protein Domain Organization. <i>Genome Research</i> , 2004, 14, 343-353.	5.5	80
525	Visualizing Sequence Similarity of Protein Families. <i>Genome Research</i> , 2004, 14, 1160-1169.	5.5	5
526	Identification and Transcriptional Control of <i>Caulobacter crescentus</i> Genes Encoding Proteins Containing a Cold Shock Domain. <i>Journal of Bacteriology</i> , 2004, 186, 5603-5613.	2.2	16
527	Identifying DNA-binding proteins using structural motifs and the electrostatic potential. <i>Nucleic Acids Research</i> , 2004, 32, 4732-4741.	14.5	100
528	Prokaryotic diversity of the <i>Saccharomyces cerevisiae</i> Atx1p-mediated copper pathway. <i>Bioinformatics</i> , 2004, 20, 2644-2655.	4.1	12
529	The Evolutionary Gain of Spliceosomal Introns: Sequence and Phase Preferences. <i>Molecular Biology and Evolution</i> , 2004, 21, 1252-1263.	8.9	115
530	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2004, 32, 160D-164.	14.5	355
531	Plasmodium interspersed repeats: the major multigene superfamily of malaria parasites. <i>Nucleic Acids Research</i> , 2004, 32, 5712-5720.	14.5	100
532	Sequence and Comparative Analysis of the Maize NB Mitochondrial Genome. <i>Plant Physiology</i> , 2004, 136, 3486-3503.	4.8	279
533	THE REPRESENTATION, COMPARISON, AND PREDICTION OF PROTEIN PATHWAYS. Lecture Notes Series, Institute for Mathematical Sciences, 2004, , 25-63.	0.2	0
534	Sinuous is a <i>Drosophila</i> claudin required for septate junction organization and epithelial tube size control. <i>Journal of Cell Biology</i> , 2004, 164, 313-323.	5.2	191
535	SPrCY: comparison of structural predictions in the <i>Saccharomyces cerevisiae</i> genome. <i>Bioinformatics</i> , 2004, 20, 2312-2314.	4.1	14
536	Proteins associated with diseases show enhanced sequence correlation between charged residues. <i>Bioinformatics</i> , 2004, 20, 2345-2354.	4.1	23
537	Homing Endonucleases Encoded by Germ Line-Limited Genes in <i>Tetrahymena thermophila</i> Have APETELA2 DNA Binding Domains. <i>Eukaryotic Cell</i> , 2004, 3, 685-694.	3.4	37
538	Synthesis of the Heteropolysaccharide O Antigen of <i>Escherichia coli</i> O52 Requires an ABC Transporter: Structural and Genetic Evidence. <i>Journal of Bacteriology</i> , 2004, 186, 4510-4519.	2.2	58
539	Crystal Structures of <i>Escherichia coli</i> ATP-Dependent Glucokinase and Its Complex with Glucose. <i>Journal of Bacteriology</i> , 2004, 186, 6915-6927.	2.2	75
540	Identification of <i>Escherichia coli</i> O114 O-Antigen Gene Cluster and Development of an O114 Serogroup-Specific PCR Assay. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3799-3804.	3.9	60

#	ARTICLE	IF	CITATIONS
541	Comparative Genomics of Transcriptional Control in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2004, 14, 1548-1554.	5.5	221
542	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004, 32, 142D-144.	14.5	892
543	Comparative analysis of complete genomes reveals gene loss, acquisition and acceleration of evolutionary rates in Metazoa, suggests a prevalence of evolution via gene acquisition and indicates that the evolutionary rates in animals tend to be conserved. <i>Nucleic Acids Research</i> , 2004, 32, 5029-5035.	14.5	14
544	CDD: a Conserved Domain Database for protein classification. <i>Nucleic Acids Research</i> , 2004, 33, D192-D196.	14.5	976
545	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	7.1	251
546	Identification of core amino acids stabilizing rhodopsin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7246-7251.	7.1	156
547	Coenzyme A Biosynthesis: Reconstruction of the Pathway in Archaea and an Evolutionary Scenario Based on Comparative Genomics. <i>Molecular Biology and Evolution</i> , 2004, 21, 1242-1251.	8.9	114
548	KinG: a database of protein kinases in genomes. <i>Nucleic Acids Research</i> , 2004, 32, 153D-155.	14.5	75
549	Characterization of the <i>Saccharomyces cerevisiae</i> Foli Protein: Starvation for C1 Carrier Induces Pseudohyphal Growth. <i>Molecular Biology of the Cell</i> , 2004, 15, 3811-3828.	2.1	39
550	Prediction of RNA-binding proteins from primary sequence by a support vector machine approach. <i>Rna</i> , 2004, 10, 355-368.	3.5	109
551	PGTdb: a database providing growth temperatures of prokaryotes. <i>Bioinformatics</i> , 2004, 20, 276-278.	4.1	58
552	Highly specific prediction of phosphorylation sites in proteins. <i>Bioinformatics</i> , 2004, 20, 3620-3627.	4.1	23
553	WILMA--automated annotation of protein sequences. <i>Bioinformatics</i> , 2004, 20, 127-128.	4.1	9
554	Identification of Candidate Disease Genes by EST Alignments, Synteny, and Expression and Verification of Ensembl Genes on Rat Chromosome 1q43-54. <i>Genome Research</i> , 2004, 14, 640-650.	5.5	17
555	MyHits: a new interactive resource for protein annotation and domain identification. <i>Nucleic Acids Research</i> , 2004, 32, W332-W335.	14.5	82
556	GeneFarm, structural and functional annotation of Arabidopsis gene and protein families by a network of experts. <i>Nucleic Acids Research</i> , 2004, 33, D641-D646.	14.5	16
557	How Unique Is the Rice Transcriptome?. <i>Science</i> , 2004, 303, 168b-168.	12.6	4
558	Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors <i>Aedes aegypti</i> and <i>Armigeres subalbatus</i> . <i>Infection and Immunity</i> , 2004, 72, 4114-4126.	2.2	144

#	ARTICLE	IF	CITATIONS
559	MitoProteome: mitochondrial protein sequence database and annotation system. Nucleic Acids Research, 2004, 32, 463D-467.	14.5	144
560	High-throughput protein analysis integrating bioinformatics and experimental assays. Nucleic Acids Research, 2004, 32, 742-748.	14.5	17
561	SledgeHMMER: a web server for batch searching the Pfam database. Nucleic Acids Research, 2004, 32, W542-W544.	14.5	26
562	Public web-based services from the European Bioinformatics Institute. Nucleic Acids Research, 2004, 32, W3-W9.	14.5	34
563	PRED-GPCR: GPCR recognition and family classification server. Nucleic Acids Research, 2004, 32, W380-W382.	14.5	49
564	BLAST Filter and GraphAlign: rule-based formation and analysis of sets of related DNA and protein sequences. Nucleic Acids Research, 2004, 32, W26-W32.	14.5	14
565	The PEDANT genome database in 2005. Nucleic Acids Research, 2004, 33, D308-D310.	14.5	50
566	The CATH Domain Structure Database and related resources Gene3D and DHS provide comprehensive domain family information for genome analysis. Nucleic Acids Research, 2004, 33, D247-D251.	14.5	226
567	The SYSTERS Protein Family Database in 2005. Nucleic Acids Research, 2004, 33, D226-D229.	14.5	37
568	PDB-Ligand: a ligand database based on PDB for the automated and customized classification of ligand-binding structures. Nucleic Acids Research, 2004, 33, D238-D241.	14.5	49
569	eBLOCKs: enumerating conserved protein blocks to achieve maximal sensitivity and specificity. Nucleic Acids Research, 2004, 33, D178-D182.	14.5	23
570	FunShift: a database of function shift analysis on protein subfamilies. Nucleic Acids Research, 2004, 33, D197-D200.	14.5	39
571	SNPeffect: a database mapping molecular phenotypic effects of human non-synonymous coding SNPs. Nucleic Acids Research, 2004, 33, D527-D532.	14.5	136
572	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	14.5	478
573	The SBASE domain sequence resource, release 12: prediction of protein domain-architecture using support vector machines. Nucleic Acids Research, 2004, 33, D223-D225.	14.5	25
574	CandidaDB: a genome database for Candida albicans pathogenomics. Nucleic Acids Research, 2004, 33, D353-D357.	14.5	79
575	The Vertebrate Genome Annotation (Vega) database. Nucleic Acids Research, 2004, 33, D459-D465.	14.5	125
576	pyramus and thisbe: FGF genes that pattern the mesoderm of Drosophila embryos. Genes and Development, 2004, 18, 687-699.	5.9	163

#	ARTICLE	IF	CITATIONS
577	Genome sequence of the enterobacterial phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> and characterization of virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11105-11110.	7.1	366
578	The GATA Family of Transcription Factors in <i>Arabidopsis</i> and Rice. <i>Plant Physiology</i> , 2004, 134, 1718-1732.	4.8	331
579	Graph-based clustering for finding distant relationships in a large set of protein sequences. <i>Bioinformatics</i> , 2004, 20, 243-252.	4.1	39
580	The Immediate-Early 63 Protein of Varicella-Zoster Virus: Analysis of Functional Domains Required for Replication In Vitro and for T-Cell and Skin Tropism in the SCIDhu Model In Vivo. <i>Journal of Virology</i> , 2004, 78, 1181-1194.	3.4	51
581	Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234.	5.5	268
582	Identification of β -Dependent Genes in <i>Bacillus cereus</i> by Proteome and In Vitro Transcription Analysis. <i>Journal of Bacteriology</i> , 2004, 186, 4100-4109.	2.2	26
583	Protein structure prediction for the male-specific region of the human Y chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2305-2310.	7.1	46
584	The <i>Schizosaccharomyces pombe</i> HIRA-Like Protein Hip1 Is Required for the Periodic Expression of Histone Genes and Contributes to the Function of Complex Centromeres. <i>Molecular and Cellular Biology</i> , 2004, 24, 4309-4320.	2.3	71
585	Identification of Genes Required for Embryo Development in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 135, 1206-1220.	4.8	440
586	Analysis of Curated and Predicted Plastid Subproteomes of <i>Arabidopsis</i> . Subcellular Compartmentalization Leads to Distinctive Proteome Properties. <i>Plant Physiology</i> , 2004, 135, 723-734.	4.8	73
587	A Complementary Bioinformatics Approach to Identify Potential Plant Cell Wall Glycosyltransferase-Encoding Genes. <i>Plant Physiology</i> , 2004, 136, 2609-2620.	4.8	67
588	The RD1 virulence locus of <i>Mycobacterium tuberculosis</i> regulates DNA transfer in <i>Mycobacterium smegmatis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12598-12603.	7.1	126
589	Variation in sequence and organization of splicing regulatory elements in vertebrate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15700-15705.	7.1	208
590	Direct Physical and Functional Interaction of the NuA4 Complex Components Yaf9p and Swc4p. <i>Eukaryotic Cell</i> , 2004, 3, 976-983.	3.4	28
591	Conserved Repeat Motifs and Glucan Binding by Glucanases of Oral Streptococci and <i>Leuconostoc mesenteroides</i> . <i>Journal of Bacteriology</i> , 2004, 186, 8301-8308.	2.2	44
592	ConSeq: the identification of functionally and structurally important residues in protein sequences. <i>Bioinformatics</i> , 2004, 20, 1322-1324.	4.1	458
593	The nonconserved wrapping of conserved protein folds reveals a trend toward increasing connectivity in proteomic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2823-2827.	7.1	35
594	The $\alpha 2$ Subunit of GABAA Receptors Is a Substrate for Palmitoylation by GODZ. <i>Journal of Neuroscience</i> , 2004, 24, 5881-5891.	3.6	225

#	ARTICLE	IF	CITATIONS
595	The Diatom EST Database. <i>Nucleic Acids Research</i> , 2004, 33, D344-D347.	14.5	75
596	A novel method for multiple alignment of sequences with repeated and shuffled elements. <i>Genome Research</i> , 2004, 14, 2336-2346.	5.5	106
597	Introns and Splicing Elements of Five Diverse Fungi. <i>Eukaryotic Cell</i> , 2004, 3, 1088-1100.	3.4	246
598	ESTHER, the database of the \hat{A}/\hat{A} -hydrolase fold superfamily of proteins. <i>Nucleic Acids Research</i> , 2004, 32, 145D-147.	14.5	150
599	Islander: a database of integrative islands in prokaryotic genomes, the associated integrases and their DNA site specificities. <i>Nucleic Acids Research</i> , 2004, 32, 55D-58.	14.5	100
600	Nematode.net: a tool for navigating sequences from parasitic and free-living nematodes. <i>Nucleic Acids Research</i> , 2004, 32, 423D-426.	14.5	76
601	Complete Nucleotide Sequence of the Conjugative Tetracycline Resistance Plasmid pFBAOT6, a Member of a Group of IncU Plasmids with Global Ubiquity. <i>Applied and Environmental Microbiology</i> , 2004, 70, 7497-7510.	3.1	71
602	Comparative genomics of the methionine metabolism in Gram-positive bacteria: a variety of regulatory systems. <i>Nucleic Acids Research</i> , 2004, 32, 3340-3353.	14.5	159
603	Computational Identification and Characterization of Novel Genes from Legumes \hat{A} . <i>Plant Physiology</i> , 2004, 135, 1179-1197.	4.8	175
604	Human protein reference database as a discovery resource for proteomics. <i>Nucleic Acids Research</i> , 2004, 32, 497D-501.	14.5	534
605	'Conserved hypothetical' proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , 2004, 32, 5452-5463.	14.5	346
606	In-Depth Analysis of the Thylakoid Membrane Proteome of <i>Arabidopsis thaliana</i> Chloroplasts: New Proteins, New Functions, and a Plastid Proteome Database[W]. <i>Plant Cell</i> , 2004, 16, 478-499.	6.6	444
607	E-MSD: an integrated data resource for bioinformatics. <i>Nucleic Acids Research</i> , 2004, 32, 211D-216.	14.5	90
608	PCOAT: positional correlation analysis using multiple methods. <i>Bioinformatics</i> , 2004, 20, 3697-3699.	4.1	6
609	MITOPRED: a genome-scale method for prediction of nucleus-encoded mitochondrial proteins. <i>Bioinformatics</i> , 2004, 20, 1785-1794.	4.1	130
610	FLAGdb++: a database for the functional analysis of the <i>Arabidopsis</i> genome. <i>Nucleic Acids Research</i> , 2004, 32, 347D-350.	14.5	64
611	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	14.5	1,681
612	Large-scale analysis of non-synonymous coding region single nucleotide polymorphisms. <i>Bioinformatics</i> , 2004, 20, 1006-1014.	4.1	70

#	ARTICLE	IF	CITATIONS
613	CD-Search: protein domain annotations on the fly. <i>Nucleic Acids Research</i> , 2004, 32, W327-W331.	14.5	1,785
614	The PredictProtein server. <i>Nucleic Acids Research</i> , 2004, 32, W321-W326.	14.5	1,246
615	A Putative Polyketide Synthase/Peptide Synthetase from <i>Magnaporthe grisea</i> Signals Pathogen Attack to Resistant Rice[W]. <i>Plant Cell</i> , 2004, 16, 2499-2513.	6.6	334
616	Delineation of modular proteins: Domain boundary prediction from sequence information. <i>Briefings in Bioinformatics</i> , 2004, 5, 179-192.	6.5	26
617	RHM2 Is Involved in Mucilage Pectin Synthesis and Is Required for the Development of the Seed Coat in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 134, 286-295.	4.8	127
618	QuickJoin-fast neighbour-joining tree reconstruction. <i>Bioinformatics</i> , 2004, 20, 3261-3262.	4.1	34
619	Transmembrane protein domains rarely use covalent domain recombination as an evolutionary mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3495-3497.	7.1	38
620	fog-2 and the Evolution of Self-Fertile Hermaphroditism in <i>Caenorhabditis</i> . <i>PLoS Biology</i> , 2004, 3, e6.	5.6	106
621	The ASTRAL Compendium in 2004. <i>Nucleic Acids Research</i> , 2004, 32, 189D-192.	14.5	480
622	Bacterial signal transduction network in a genomic perspective^{â€‹}. <i>Environmental Microbiology</i> , 2004, 6, 552-567.	3.8	318
623	A novel sensor kinase-response regulator hybrid regulates type III secretion and is required for virulence in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2004, 54, 1090-1103.	2.5	98
624	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004, 4, 177-183.	28.4	2,868
625	Screening for synthetic lethal mutants in <i>Escherichia coli</i> and identification of EnvC (YibP) as a periplasmic septal ring factor with murein hydrolase activity. <i>Molecular Microbiology</i> , 2004, 52, 1255-1269.	2.5	192
626	Bioinformatics tools to understand human diseases. <i>Surgery</i> , 2004, 135, 579-585.	1.9	5
627	NERD: a DNA processing-related domain present in the anthrax virulence plasmid, pXO1. <i>Trends in Biochemical Sciences</i> , 2004, 29, 106-110.	7.5	15
628	NCD3G: a novel nine-cysteine domain in family 3 GPCRs. <i>Trends in Biochemical Sciences</i> , 2004, 29, 458-461.	7.5	27
629	ECEPE proteins: a novel family of eukaryotic cysteine proteinases. <i>Trends in Biochemical Sciences</i> , 2004, 29, 524-526.	7.5	3
630	The BACK domain in BTB-kelch proteins. <i>Trends in Biochemical Sciences</i> , 2004, 29, 634-637.	7.5	146

#	ARTICLE	IF	CITATIONS
631	Global analysis of bacterial transcription factors to predict cellular target processes. Trends in Genetics, 2004, 20, 126-131.	6.7	12
632	Protein domains correlate strongly with exons in multiple eukaryotic genomes – evidence of exon shuffling?. Trends in Genetics, 2004, 20, 399-403.	6.7	121
633	LCCL proteins of apicomplexan parasites. Trends in Parasitology, 2004, 20, 102-108.	3.3	42
634	Comparative sequence analysis of the icm/dot genes in Legionella. Plasmid, 2004, 51, 127-147.	1.4	48
635	The Hotdog fold: wrapping up a superfamily of thioesterases and dehydratases. BMC Bioinformatics, 2004, 5, 109.	2.6	158
636	IdentiCS – Identification of coding sequence and in silico reconstruction of the metabolic network directly from unannotated low-coverage bacterial genome sequence. BMC Bioinformatics, 2004, 5, 112.	2.6	40
637	Automatic annotation of protein motif function with Gene Ontology terms. BMC Bioinformatics, 2004, 5, 122.	2.6	26
638	cuticleDB: a relational database of Arthropod cuticular proteins. BMC Bioinformatics, 2004, 5, 138.	2.6	62
639	Implications for domain fusion protein-protein interactions based on structural information. BMC Bioinformatics, 2004, 5, 161.	2.6	12
640	SS-Wrapper: a package of wrapper applications for similarity searches on Linux clusters. BMC Bioinformatics, 2004, 5, 171.	2.6	7
641	prot4EST: translating expressed sequence tags from neglected genomes. BMC Bioinformatics, 2004, 5, 187.	2.6	118
642	DEDB: a database of Drosophila melanogaster exons in splicing graph form. BMC Bioinformatics, 2004, 5, 189.	2.6	31
643	Optimal cDNA microarray design using expressed sequence tags for organisms with limited genomic information. BMC Bioinformatics, 2004, 5, 191.	2.6	21
644	Using 3D Hidden Markov Models that explicitly represent spatial coordinates to model and compare protein structures. BMC Bioinformatics, 2004, 5, 2.	2.6	20
645	SUPFAM: a database of sequence superfamilies of protein domains. BMC Bioinformatics, 2004, 5, 28.	2.6	36
646	A hybrid clustering approach to recognition of protein families in 114 microbial genomes. BMC Bioinformatics, 2004, 5, 45.	2.6	40
647	A structural study for the optimisation of functional motifs encoded in protein sequences. BMC Bioinformatics, 2004, 5, 50.	2.6	6
648	Enhanced protein domain discovery using taxonomy. BMC Bioinformatics, 2004, 5, 56.	2.6	18

#	ARTICLE	IF	CITATIONS
649	HMM Logos for visualization of protein families. BMC Bioinformatics, 2004, 5, 7.	2.6	195
650	Interaction profile-based protein classification of death domain. BMC Bioinformatics, 2004, 5, 75.	2.6	1
651	SPOC: a widely distributed domain associated with cancer, apoptosis and transcription. BMC Bioinformatics, 2004, 5, 91.	2.6	33
652	Reconstruction of ancestral protein sequences and its applications. BMC Evolutionary Biology, 2004, 4, 33.	3.2	98
653	The iron-sulfur cluster assembly genes iscS and iscU of Entamoeba histolytica were acquired by horizontal gene transfer. BMC Evolutionary Biology, 2004, 4, 7.	3.2	65
654	Conservation, diversification and expansion of C2H2 zinc finger proteins in the Arabidopsis thaliana genome. BMC Genomics, 2004, 5, 39.	2.8	355
655	Novel conserved domains in proteins with predicted roles in eukaryotic cell-cycle regulation, decapping and RNA stability. BMC Genomics, 2004, 5, 45.	2.8	72
656	Protein kinases of the human malaria parasite Plasmodium falciparum: the kinome of a divergent eukaryote. BMC Genomics, 2004, 5, 79.	2.8	440
657	Functional characterization in Caenorhabditis elegans of transmembrane worm-human orthologs. BMC Genomics, 2004, 5, 85.	2.8	15
658	Expression of a novel gene, gluP, is essential for normal Bacillus subtilis cell division and contributes to glucose export. BMC Microbiology, 2004, 4, 13.	3.3	26
659	Analysis of the lambdoid prophage element e14 in the E. coli K-12 genome. BMC Microbiology, 2004, 4, 4.	3.3	50
660	The roles of segmental and tandem gene duplication in the evolution of large gene families in Arabidopsis thaliana. BMC Plant Biology, 2004, 4, 10.	3.6	1,523
661	ACRATA: a novel electron transfer domain associated to apoptosis and cancer. BMC Cancer, 2004, 4, 98.	2.6	37
662	Putative lipoproteins of Streptococcus agalactiae identified by bioinformatic genome analysis. Antonie Van Leeuwenhoek, 2004, 85, 305-315.	1.7	23
663	Structural and Functional Characterization of Gene Products Encoded in the Human Genome by Homology Detection. IUBMB Life, 2004, 56, 317-331.	3.4	7
664	Protein structure prediction and analysis using the Robetta server. Nucleic Acids Research, 2004, 32, W526-W531.	14.5	1,683
665	Rapid evolution in conformational space: A study of loop regions in a ubiquitous GTP binding domain. Protein Science, 2004, 13, 608-616.	7.6	27
666	Similar active sites in lysostaphins and D-Ala-D-Ala metalloproteases. Protein Science, 2004, 13, 854-861.	7.6	66

#	ARTICLE	IF	CITATIONS
667	The ankyrin repeat as molecular architecture for protein recognition. <i>Protein Science</i> , 2004, 13, 1435-1448.	7.6	782
668	Proteome-wide functional classification and identification of prokaryotic transmembrane proteins by transmembrane topology similarity comparison. <i>Protein Science</i> , 2004, 13, 2170-2183.	7.6	7
669	Letter to the Editor: NMR assignment of the hypothetical rhodanese domain At4g01050 from <i>Arabidopsis thaliana</i> . <i>Journal of Biomolecular NMR</i> , 2004, 29, 207-208.	2.8	12
670	Letter to the Editor: Solution Structure of the Hypothetical Protein SAV1595 from <i>Staphylococcus Aureus</i> , a Putative RNA Binding Protein. <i>Journal of Biomolecular NMR</i> , 2004, 29, 391-394.	2.8	3
671	Expression screening, protein purification and NMR analysis of human protein domains for structural genomics. <i>Journal of Structural and Functional Genomics</i> , 2004, 5, 119-131.	1.2	45
672	The PROF_PAT Protein Pattern Database: Assessment of Efficiency. <i>Molecular Biology</i> , 2004, 38, 210-217.	1.3	0
673	Sulfur Assimilation and the Role of Sulfur in Plant Metabolism: A Survey. <i>Photosynthesis Research</i> , 2004, 79, 331-348.	2.9	196
674	Identification and functional analysis of 'hypothetical' genes expressed in <i>Haemophilus influenzae</i> . <i>Nucleic Acids Research</i> , 2004, 32, 2353-2361.	14.5	75
675	Visualization for genomics: the Microbial Genome Viewer. <i>Bioinformatics</i> , 2004, 20, 1812-1814.	4.1	67
676	Estimating the Frequency of Events That Cause Multiple-Nucleotide Changes. <i>Genetics</i> , 2004, 167, 2027-2043.	2.9	81
677	Determinants of Adaptive Evolution at the Molecular Level: the Extended Complexity Hypothesis. <i>Molecular Biology and Evolution</i> , 2004, 22, 200-209.	8.9	56
678	C-Terminal 23kDa polypeptide of soybean Glycine max is a potential allergen. <i>Planta</i> , 2004, 220, 56-63.		40
679	A description of the Mei2-like protein family; structure, phylogenetic distribution and biological context. <i>Development Genes and Evolution</i> , 2004, 214, 149-158.	0.9	27
680	Naturally mosaic operons for secondary metabolite biosynthesis: variability and putative horizontal transfer of discrete catalytic domains of the epothilone polyketide synthase locus. <i>Molecular Genetics and Genomics</i> , 2004, 270, 420-431.	2.1	33
681	ADP-dependent 6-phosphofructokinase, an extremely thermophilic, non-allosteric enzyme from the hyperthermophilic, sulfate-reducing archaeon <i>Archaeoglobus fulgidus</i> strain 7324. <i>Extremophiles</i> , 2004, 8, 29-35.	2.3	19
682	Molecular modeling of the von Willebrand factor A2 Domain and the effects of associated type 2A von Willebrand disease mutations. <i>Journal of Molecular Modeling</i> , 2004, 10, 259-270.	1.8	71
683	Molecular modeling of the interleukin-19 receptor complex. <i>Journal of Molecular Modeling</i> , 2004, 10, 290-6.	1.8	6
684	Modeling the helicase domain of Brome mosaic virus 1a replicase. <i>Journal of Molecular Modeling</i> , 2004, 10, 382-392.	1.8	5

#	ARTICLE	IF	CITATIONS
685	Isolation from Cochlea of a Novel Human Intronless Gene with Predominant Fetal Expression. JARO - Journal of the Association for Research in Otolaryngology, 2004, 5, 185-202.	1.8	48
686	The anthracnose resistance locus Co-4 of common bean is located on chromosome 3 and contains putative disease resistance-related genes. Theoretical and Applied Genetics, 2004, 109, 690-699.	3.6	50
687	Cloning and Characterization of the Gene Encoding for OMP-PD Porin: The Major Photobacterium damsela Outer Membrane Protein. Current Microbiology, 2004, 48, 167-174.	2.2	9
688	The transcriptional program of synchronous gametogenesis in Chlamydomonas reinhardtii. Current Genetics, 2004, 46, 304-315.	1.7	53
689	Assembly of MHC class I peptide complexes from the perspective of disulfide bond formation. Cellular and Molecular Life Sciences, 2004, 61, 547-556.	5.4	33
690	Glucose-6-phosphate isomerase from the hyperthermophilic archaeon Methanococcus jannaschii: characterization of the first archaeal member of the phosphoglucose isomerase superfamily. Archives of Microbiology, 2004, 181, 82-87.	2.2	18
691	A Plant Orthologue of RNase L Inhibitor (RLI) Is Induced in Plants Showing RNA Interference. Journal of Molecular Evolution, 2004, 59, 20-30.	1.8	32
692	Phylogenetic Analysis of Proteins Associated in the Four Major Energy Metabolism Systems: Photosynthesis, Aerobic Respiration, Denitrification, and Sulfur Respiration. Journal of Molecular Evolution, 2004, 59, 158-176.	1.8	21
693	The DY genes of the cattle MHC: expression and comparative analysis of an unusual class II MHC gene pair. Immunogenetics, 2004, 55, 748-755.	2.4	26
694	Bioinformatic discovery and initial characterisation of nine novel antimicrobial peptide genes in the chicken. Immunogenetics, 2004, 56, 170-177.	2.4	197
695	Crystallization and preliminary X-ray analysis of 5â€²-methylthioribose kinase from Bacillus subtilis and Arabidopsis thaliana. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 116-119.	2.5	10
696	Crystallization and preliminary X-ray crystallographic analysis of the N-terminal domain of XpsE protein from Xanthomonas campestris, an essential component of the type II protein-secretion machinery. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 129-131.	2.5	1
697	Purification and crystallization of Escherichia coli oligoribonuclease. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 736-739.	2.5	14
698	Structure of OsmC from Escherichia coli: a salt-shock-induced protein. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 903-911.	2.5	32
699	Structure of serine acetyltransferase from Haemophilus influenzae Rd. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1600-1605.	2.5	31
700	Production of soluble mammalian proteins in Escherichia coli: identification of protein features that correlate with successful expression. BMC Biotechnology, 2004, 4, 32.	3.3	215
701	Crystal structure of the YffB protein from Pseudomonas aeruginosa suggests a glutathione-dependent thiol reductase function. BMC Structural Biology, 2004, 4, 5.	2.3	6
702	The solution structure of ChaB, a putative membrane ion antiporter regulator from Escherichia coli. BMC Structural Biology, 2004, 4, 9.	2.3	17

#	ARTICLE	IF	CITATIONS
703	A Survey of Nucleotide Cyclases in Actinobacteria: Unique Domain Organization and Expansion of the Class III Cyclase Family in <i>Mycobacterium tuberculosis</i> . <i>Comparative and Functional Genomics</i> , 2004, 5, 17-38.	2.0	48
704	Identification and Analysis of Novel Tandem Repeats in the Cell Surface Proteins of Archaeal and Bacterial Genomes Using Computational Tools. <i>Comparative and Functional Genomics</i> , 2004, 5, 2-16.	2.0	35
705	Comparative Analysis of the Testis and Ovary Transcriptomes in Zebrafish by Combining Experimental and Computational Tools. <i>Comparative and Functional Genomics</i> , 2004, 5, 403-418.	2.0	48
706	Integral and differential form of the protein folding problem. <i>Physics of Life Reviews</i> , 2004, 1, 103-127.	2.8	5
707	Structural and functional anatomy of the globular domain of complement protein C1q. <i>Immunology Letters</i> , 2004, 95, 113-128.	2.5	166
708	MoDEL: an efficient strategy for ungapped local multiple alignment. <i>Computational Biology and Chemistry</i> , 2004, 28, 119-128.	2.3	8
709	Parallel RNA sequence-structure alignment. , 0, , .		3
710	Protein seer: a Web server for protein homology detection. , 2004, 2004, 3064-7.		0
711	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	14.5	2,994
712	Discovering novel interacting motif pairs from large protein-protein interaction datasets. , 0, , .		0
713	CADRE: the Central <i>Aspergillus</i> Data REpository. <i>Nucleic Acids Research</i> , 2004, 32, 401D-405.	14.5	60
714	Identification and proteomic profiling of exosomes in human urine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13368-13373.	7.1	1,875
715	Xpro: database of eukaryotic protein-encoding genes. <i>Nucleic Acids Research</i> , 2004, 32, 59D-63.	14.5	21
716	Protein family classification using structural and sequence information. , 0, , .		1
717	SIBIOS: a system for the integration of bioinformatics services. , 0, , .		2
718	Prediction of protein-protein interactions using support vector machines. , 0, , .		10
719	Systematic analysis and nomenclature of mammalian F-box proteins. <i>Genes and Development</i> , 2004, 18, 2573-2580.	5.9	589
720	Focus on Fungi. <i>American Biology Teacher</i> , 2004, 66, 377-382.	0.2	3

#	ARTICLE	IF	CITATIONS
721	The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website. British Journal of Cancer, 2004, 91, 355-358.	6.4	1,118
722	SCOP database in 2004: refinements integrate structure and sequence family data. Nucleic Acids Research, 2004, 32, 226D-229.	14.5	815
723	Identification of Mammalian microRNA Host Genes and Transcription Units. Genome Research, 2004, 14, 1902-1910.	5.5	1,704
724	A new native EcHsp31 structure suggests a key role of structural flexibility for chaperone function. Protein Science, 2004, 13, 269-277.	7.6	25
725	Denaturation of replication protein A reveals an alternative conformation with intact domain structure and oligonucleotide binding activity. Protein Science, 2004, 13, 1365-1378.	7.6	11
726	New enzymes from environmental cassette arrays: Functional attributes of a phosphotransferase and an RNA-methyltransferase. Protein Science, 2004, 13, 1651-1659.	7.6	30
727	Evolutionary families of peptidase inhibitors. Biochemical Journal, 2004, 378, 705-716.	3.7	528
728	The Complete Genome Sequence of <i>Bacillus licheniformis</i> DSM13, an Organism with Great Industrial Potential. Journal of Molecular Microbiology and Biotechnology, 2004, 7, 204-211.	1.0	284
729	Homology-Modeled Structure of the Yeast Mitochondrial Citrate Transport Protein. Biophysical Journal, 2004, 87, 907-911.	0.5	31
730	GeneDB: a resource for prokaryotic and eukaryotic organisms. Nucleic Acids Research, 2004, 32, 339D-343.	14.5	199
731	Structural flexibility in the <i>Burkholderia mallei</i> genome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14246-14251.	7.1	366
732	Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis. Genome Biology, 2004, 6, R6.	9.6	101
733	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. Genome Biology, 2004, 5, R90.	9.6	162
734	A comprehensive transcript index of the human genome generated using microarrays and computational approaches. Genome Biology, 2004, 5, R73.	9.6	92
735	Alternative splicing of mouse transcription factors affects their DNA-binding domain architecture and is tissue specific. Genome Biology, 2004, 5, R75.	9.6	67
736	Complete genome sequence of the industrial bacterium <i>Bacillus licheniformis</i> and comparisons with closely related <i>Bacillus</i> species. Genome Biology, 2004, 5, r77.	9.6	319
737	Comprehensive analysis of pseudogenes in prokaryotes: widespread gene decay and failure of putative horizontally transferred genes. Genome Biology, 2004, 5, R64.	9.6	143
738	Large-scale exploration of growth inhibition caused by overexpression of genomic fragments in <i>Saccharomyces cerevisiae</i> . Genome Biology, 2004, 5, R72.	9.6	36

#	ARTICLE	IF	CITATIONS
739	Comprehensive de novo structure prediction in a systems-biology context for the archaea <i>Halobacterium</i> sp. NRC-1. <i>Genome Biology</i> , 2004, 5, R52.	9.6	45
740	START lipid/sterol-binding domains are amplified in plants and are predominantly associated with homeodomain transcription factors. <i>Genome Biology</i> , 2004, 5, R41.	9.6	233
741	Progress towards mapping the universe of protein folds. <i>Genome Biology</i> , 2004, 5, 107.	9.6	72
742	MYRbase: analysis of genome-wide glycine myristoylation enlarges the functional spectrum of eukaryotic myristoylated proteins. <i>Genome Biology</i> , 2004, 5, R21.	9.6	76
743	Development of a PCR-based mating-type assay for. <i>FEMS Microbiology Letters</i> , 2004, 237, 205-212.	1.8	29
744	The new genes of rice: a closer look. <i>Trends in Plant Science</i> , 2004, 9, 281-285.	8.8	33
745	The promise of functional genomics: completing the encyclopedia of a cell. <i>Current Opinion in Microbiology</i> , 2004, 7, 546-554.	5.1	44
746	Rfam: annotating non-coding RNAs in complete genomes. <i>Nucleic Acids Research</i> , 2004, 33, D121-D124.	14.5	1,255
747	Computational Prediction of Protein-Protein Interactions. , 2004, 261, 445-468.		57
748	Computational analysis of evolution and conservation in a protein superfamily. <i>Methods</i> , 2004, 32, 73-92.	3.8	11
749	Genome fingerprint scanning for protein identification and gene finding. <i>Drug Discovery Today: TARGETS</i> , 2004, 3, 56-62.	0.5	1
750	MODBASE, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2004, 32, 217D-222.	14.5	256
751	WebLogo: A Sequence Logo Generator: Figure 1. <i>Genome Research</i> , 2004, 14, 1188-1190.	5.5	10,751
752	Parasite Genome Databases and Web-Based Resources. , 2004, 270, 045-074.		6
753	Identification of 51 Novel Exons of the Usher Syndrome Type 2A (USH2A) Gene That Encode Multiple Conserved Functional Domains and That Are Mutated in Patients with Usher Syndrome Type II. <i>American Journal of Human Genetics</i> , 2004, 74, 738-744.	6.2	176
754	Allelic Heterogeneity in the COH1 Gene Explains Clinical Variability in Cohen Syndrome. <i>American Journal of Human Genetics</i> , 2004, 75, 138-145.	6.2	72
755	Structural Proteomics: Inferring Function from Protein Structure. <i>Current Proteomics</i> , 2004, 1, 59-65.	0.3	15
756	BacMap: an interactive picture atlas of annotated bacterial genomes. <i>Nucleic Acids Research</i> , 2004, 33, D317-D320.	14.5	48

#	ARTICLE	IF	CITATIONS
757	A novel omega3-fatty acid desaturase involved in the biosynthesis of eicosapentaenoic acid. Biochemical Journal, 2004, 378, 665-671.	3.7	75
758	Computational analysis of membrane proteins: genomic occurrence, structure prediction and helix interactions. Quarterly Reviews of Biophysics, 2004, 37, 121-146.	5.7	62
759	A cluster-based solution for high performance hmmpfam using EARTH execution model. International Journal of High Performance Computing and Networking, 2004, 2, 66.	0.4	0
760	Identification of an orphan guanylate cyclase receptor selectively expressed in mouse testis. Biochemical Journal, 2004, 379, 385-393.	3.7	28
761	Modelling and bioinformatics studies of the human Kappa-class glutathione transferase predict a novel third glutathione transferase family with similarity to prokaryotic 2-hydroxychromene-2-carboxylate isomerases. Biochemical Journal, 2004, 379, 541-552.	3.7	89
762	Identification of the actin-binding domain of Ins(1,4,5)P3 3-kinase isoform B (IP3K-B). Biochemical Journal, 2004, 382, 353-362.	3.7	24
763	Isolation and functional expression of human COQ2, a gene encoding a polyprenyl transferase involved in the synthesis of CoQ. Biochemical Journal, 2004, 382, 519-526.	3.7	110
764	The Path to Enlightenment: Making Sense of Genomic and Proteomic Information. Genomics, Proteomics and Bioinformatics, 2004, 2, 123-131.	6.9	7
765	Predicting Protein Subcellular Localization: Past, Present, and Future. Genomics, Proteomics and Bioinformatics, 2004, 2, 209-215.	6.9	95
766	Development of an integrated genome informatics, data management and workflow infrastructure: A toolbox for the study of complex disease genetics. Human Genomics, 2004, 1, 98.	2.9	15
767	Seasonal migration pattern of owls at Bukowo-KopaÅ,, station (N Poland) in 2000-2003. Ring, 2004, 26, 13-21.	0.4	3
768	'A variant of uncertain significance' and the proliferation of human disease gene databases. Human Genomics, 2005, 2, 70.	2.9	4
769	GNARE: an environment for grid-based high-throughput genome analysis. , 2005, , .		16
770	Microarray analysis of gene expression following preparation of sterile intestinal œloops•in calves. Canadian Journal of Animal Science, 2005, 85, 13-22.	1.5	10
771	Signal processing for functional analysis of protein mutants. International Journal of Bioinformatics Research and Applications, 2005, 1, 102.	0.2	2
772	An overview of protein-folding techniques: issues and perspectives. International Journal of Bioinformatics Research and Applications, 2005, 1, 121.	0.2	23
773	PolnTree: A Polar and Interactive Phylogenetic Tree. Genomics, Proteomics and Bioinformatics, 2005, 3, 58-60.	6.9	2
774	The Evolutionary Relationship of the Domain Architectures in the RhoGEF-containing Proteins. Genomics, Proteomics and Bioinformatics, 2005, 3, 94-106.	6.9	2

#	ARTICLE	IF	CITATIONS
775	In silico characterization of LZTS3, a potential tumor suppressor. <i>Oncology Reports</i> , 2005, 14, 547.	2.6	5
776	Genome sequence of <i>Blochmannia pennsylvanicus</i> indicates parallel evolutionary trends among bacterial mutualists of insects. <i>Genome Research</i> , 2005, 15, 1023-1033.	5.5	169
778	Non-EST based prediction of exon skipping and intron retention events using Pfam information. <i>Nucleic Acids Research</i> , 2005, 33, 5611-5621.	14.5	25
779	DNA-binding properties of ARID family proteins. <i>Nucleic Acids Research</i> , 2005, 33, 66-80.	14.5	195
780	Plasmin alters the activity and quaternary structure of human plasma carboxypeptidase N. <i>Biochemical Journal</i> , 2005, 388, 81-91.	3.7	13
781	Identification, molecular cloning and functional characterization of a novel NADH kinase from <i>Arabidopsis thaliana</i> (thale cress). <i>Biochemical Journal</i> , 2005, 385, 217-223.	3.7	67
782	Calcium-induced tertiary structure modifications of endo- β -1,3-glucanase from <i>Pyrococcus furiosus</i> in 7.9ÅM guanidinium chloride. <i>Biochemical Journal</i> , 2005, 386, 515-524.	3.7	6
784	A proteome-wide analysis of domain architectures of prokaryotic single-spanning transmembrane proteins. <i>Computational Biology and Chemistry</i> , 2005, 29, 379-387.	2.3	1
785	Determining Structure and Function of Steroid Dehydrogenase Enzymes by Sequence Analysis, Homology Modeling, and Rational Mutational Analysis. <i>Annals of the New York Academy of Sciences</i> , 2005, 1061, 135-148.	3.8	19
786	Structure and mechanism of ADP-ribose-1''-monophosphatase (Appr-1''-pase), a ubiquitous cellular processing enzyme. <i>Protein Science</i> , 2005, 14, 719-726.	7.6	36
787	Structural similarity to bridge sequence space: Finding new families on the bridges. <i>Protein Science</i> , 2005, 14, 1305-1314.	7.6	11
788	Solution structure of the PWWP domain of the hepatoma-derived growth factor family. <i>Protein Science</i> , 2005, 14, 756-764.	7.6	48
789	Improved membrane protein topology prediction by domain assignments. <i>Protein Science</i> , 2005, 14, 1723-1728.	7.6	40
790	Rv0216, a conserved hypothetical protein from <i>Mycobacterium tuberculosis</i> that is essential for bacterial survival during infection, has a double hotdog fold. <i>Protein Science</i> , 2005, 14, 1850-1862.	7.6	26
791	Structure of the B3 domain from <i>Arabidopsis thaliana</i> protein At1g16640. <i>Protein Science</i> , 2005, 14, 2478-2483.	7.6	55
792	COG3926 and COG5526: A tale of two new lysozyme-like protein families. <i>Protein Science</i> , 2005, 14, 2574-2581.	7.6	23
793	Complete reannotation of the <i>Arabidopsis</i> genome: methods, tools, protocols and the final release. <i>BMC Biology</i> , 2005, 3, 7.	3.8	149
794	Conservation and Variation of Gene Regulation in Embryonic Stem Cells Assessed by Comparative Genomics. <i>Cell Biochemistry and Biophysics</i> , 2005, 43, 379-406.	1.8	19

#	ARTICLE	IF	CITATIONS
795	<i>Pseudomonas aeruginosa</i> fimL regulates multiple virulence functions by intersecting with Vfr-modulated pathways. <i>Molecular Microbiology</i> , 2005, 55, 1357-1378.	2.5	85
796	Identification of a ferriredutase required for efficient transferrin-dependent iron uptake in erythroid cells. <i>Nature Genetics</i> , 2005, 37, 1264-1269.	21.4	575
797	Maintenance of structure and function of mitochondrial Hsp70 chaperones requires the chaperone Hep1. <i>EMBO Journal</i> , 2005, 24, 1046-1056.	7.8	89
798	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	27.8	985
799	Fast Fourier Transform-based Support Vector Machine for Prediction of G-protein Coupled Receptor Subfamilies. <i>Acta Biochimica Et Biophysica Sinica</i> , 2005, 37, 759-766.	2.0	15
800	Finding the biologically optimal alignment of multiple sequences. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 9-18.	6.5	10
801	Gene Discovery in the Genome. <i>Protist</i> , 2005, 156, 203-214.	1.5	74
802	MSP domain proteins. <i>Trends in Parasitology</i> , 2005, 21, 224-231.	3.3	40
803	The limits of protein sequence comparison?. <i>Current Opinion in Structural Biology</i> , 2005, 15, 254-260.	5.7	81
804	A recurring theme in protein engineering: the design, stability and folding of repeat proteins. <i>Current Opinion in Structural Biology</i> , 2005, 15, 464-471.	5.7	119
805	Filtering high-throughput protein-protein interaction data using a combination of genomic features. <i>BMC Bioinformatics</i> , 2005, 6, 100.	2.6	138
806	A method for the prediction of GPCRs coupling specificity to G-proteins using refined profile Hidden Markov Models. <i>BMC Bioinformatics</i> , 2005, 6, 104.	2.6	44
807	Large scale hierarchical clustering of protein sequences. <i>BMC Bioinformatics</i> , 2005, 6, 15.	2.6	62
808	AutoFACT: an automatic functional annotation and classification tool. <i>BMC Bioinformatics</i> , 2005, 6, 151.	2.6	189
809	The PD-(D/E)XK superfamily revisited: identification of new members among proteins involved in DNA metabolism and functional predictions for domains of (hitherto) unknown function. <i>BMC Bioinformatics</i> , 2005, 6, 172.	2.6	84
810	FIGENIX: intelligent automation of genomic annotation: expertise integration in a new software platform. <i>BMC Bioinformatics</i> , 2005, 6, 198.	2.6	109
811	JACOP: a simple and robust method for the automated classification of protein sequences with modular architecture. <i>BMC Bioinformatics</i> , 2005, 6, 216.	2.6	22
812	Clustering the annotation space of proteins. <i>BMC Bioinformatics</i> , 2005, 6, 24.	2.6	16

#	ARTICLE	IF	CITATIONS
813	Phydbac "Gene Function Predictor": a gene annotation tool based on genomic context analysis. BMC Bioinformatics, 2005, 6, 247.	2.6	59
814	Kalign—an accurate and fast multiple sequence alignment algorithm. BMC Bioinformatics, 2005, 6, 298.	2.6	615
815	Prediction of a common structural scaffold for proteasome lid, COP9-signalosome and eIF3 complexes. BMC Bioinformatics, 2005, 6, 71.	2.6	80
816	Comparative mapping of sequence-based and structure-based protein domains. BMC Bioinformatics, 2005, 6, 77.	2.6	16
817	MAPPER: a search engine for the computational identification of putative transcription factor binding sites in multiple genomes. BMC Bioinformatics, 2005, 6, 79.	2.6	178
818	Improved profile HMM performance by assessment of critical algorithmic features in SAM and HMMER. BMC Bioinformatics, 2005, 6, 99.	2.6	45
819	A new decoding algorithm for hidden Markov models improves the prediction of the topology of all-beta membrane proteins. BMC Bioinformatics, 2005, 6, S12.	2.6	54
820	Evolutionary cores of domain co-occurrence networks. BMC Evolutionary Biology, 2005, 5, 24.	3.2	90
821	Genome wide survey of G protein-coupled receptors in Tetraodon nigroviridis. BMC Evolutionary Biology, 2005, 5, 41.	3.2	31
822	Bioinformatic mapping of AlkB homology domains in viruses. BMC Genomics, 2005, 6, 1.	2.8	166
823	Prediction of the general transcription factors associated with RNA polymerase II in Plasmodium falciparum: conserved features and differences relative to other eukaryotes. BMC Genomics, 2005, 6, 100.	2.8	114
824	Functional genomics and expression analysis of the Corynebacterium glutamicum fpr2-cysIXHDNYZ gene cluster involved in assimilatory sulphate reduction. BMC Genomics, 2005, 6, 121.	2.8	61
825	Comparative analysis of the kinomes of three pathogenic trypanosomatids: Leishmania major, Trypanosoma brucei and Trypanosoma cruzi. BMC Genomics, 2005, 6, 127.	2.8	310
826	Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. BMC Genomics, 2005, 6, 129.	2.8	65
827	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. BMC Genomics, 2005, 6, 144.	2.8	119
828	The EH1 motif in metazoan transcription factors. BMC Genomics, 2005, 6, 169.	2.8	67
829	Protein domains and architectural innovation in plant-associated Proteobacteria. BMC Genomics, 2005, 6, 17.	2.8	13
830	Bacterial genome adaptation to niches: Divergence of the potential virulence genes in three Burkholderia species of different survival strategies. BMC Genomics, 2005, 6, 174.	2.8	142

#	ARTICLE	IF	CITATIONS
831	The PECACE domain: a new family of enzymes with potential peptidoglycan cleavage activity in Gram-positive bacteria. BMC Genomics, 2005, 6, 19.	2.8	14
832	Gene fusions and gene duplications: relevance to genomic annotation and functional analysis. BMC Genomics, 2005, 6, 33.	2.8	11
833	A novel firmicute protein family related to the actinobacterial resuscitation-promoting factors by non-orthologous domain displacement. BMC Genomics, 2005, 6, 39.	2.8	66
834	A census of membrane-bound and intracellular signal transduction proteins in bacteria: bacterial IQ, extroverts and introverts. BMC Microbiology, 2005, 5, 35.	3.3	398
835	The influence of acetyl phosphate on DspA signalling in the Cyanobacterium Synechocystis sp. PCC6803. BMC Microbiology, 2005, 5, 47.	3.3	14
836	Bioinformatics analysis of the locus for enterocyte effacement provides novel insights into type-III secretion. BMC Microbiology, 2005, 5, 9.	3.3	100
837	A7DB: a relational database for mutational, physiological and pharmacological data related to the alpha7 nicotinic acetylcholine receptor. BMC Neuroscience, 2005, 6, 2.	1.9	3
838	Floral gene resources from basal angiosperms for comparative genomics research. BMC Plant Biology, 2005, 5, 5.	3.6	100
839	Distribution of immunodeficiency fact files with XML “ from Web to WAP. BMC Medical Informatics and Decision Making, 2005, 5, 21.	3.0	5
840	Identification of novel mutations in patients with Shwachman-Diamond syndrome. Human Mutation, 2005, 25, 410-410.	2.5	52
841	Phylogenetic Differences in Content and Intensity of Periodic Proteins. Journal of Molecular Evolution, 2005, 60, 447-461.	1.8	4
842	Positively Selected Sites in the Arabidopsis Receptor-Like Kinase Gene Family. Journal of Molecular Evolution, 2005, 61, 325-332.	1.8	10
843	Signs of Ancient and Modern Exon-Shuffling Are Correlated to the Distribution of Ancient and Modern Domains Along Proteins. Journal of Molecular Evolution, 2005, 61, 341-350.	1.8	36
844	Origin and evolution of the Ig-like domains present in mammalian leukocyte receptors: insights from chicken, frog, and fish homologues. Immunogenetics, 2005, 57, 151-157.	2.4	36
845	Organization, alternative splicing, polymorphism, and phylogenetic position of lamprey CD45 gene. Immunogenetics, 2005, 57, 607-617.	2.4	10
846	A family of putative transcription termination factors shared amongst metazoans and plants. Current Genetics, 2005, 48, 265-269.	1.7	116
847	The HERC proteins: functional and evolutionary insights. Cellular and Molecular Life Sciences, 2005, 62, 1826-1838.	5.4	74
848	Arabidopsis emb175 and other ppr knockout mutants reveal essential roles for pentatricopeptide repeat (PPR) proteins in plant embryogenesis. Planta, 2005, 221, 424-436.	3.2	137

#	ARTICLE	IF	CITATIONS
849	Elicitin genes in <i>Phytophthora infestans</i> are clustered and interspersed with various transposon-like elements. <i>Molecular Genetics and Genomics</i> , 2005, 273, 20-32.	2.1	42
850	A candidate autonomous version of the wheat MITE Hikkoshi is present in the rice genome. <i>Molecular Genetics and Genomics</i> , 2005, 273, 404-414.	2.1	11
851	Cooperative function of the CHD5-like protein Mdm39p with a P-type ATPase Spf1p in the maintenance of ER homeostasis in <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 2005, 273, 497-506.	2.1	19
852	The genome of BCJA1c: a bacteriophage active against the alkaliphilic bacterium, <i>Bacillus clarkii</i> . <i>Extremophiles</i> , 2005, 9, 99-109.	2.3	12
853	Domain-based homology modeling and mapping of the conformational epitopes of envelope glycoprotein of west nile virus. <i>Journal of Molecular Modeling</i> , 2005, 11, 248-255.	1.8	5
854	Letter to the Editor: NMR structure note ? Solution structure of a bacterial BOLA-like protein XC975 from a plant pathogen <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Journal of Biomolecular NMR</i> , 2005, 31, 167-172.	2.8	12
855	Gnare: Automated System For High-Throughput Genome Analysis With Grid Computational Backend. <i>Journal of Clinical Monitoring and Computing</i> , 2005, 19, 361-369.	1.6	19
856	MLH1 and MSH2 Mutations in Colombian Families with Hereditary Nonpolyposis Colorectal Cancer (Lynch syndrome) – Description of Four Novel Mutations. <i>Familial Cancer</i> , 2005, 4, 285-290.	1.9	21
857	High-throughput Limited Proteolysis/Mass Spectrometry for Protein Domain Elucidation. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 129-134.	1.2	55
858	Protein Production and Crystallization at SECSG – An Overview. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 233-243.	1.2	14
859	Structural Genomics of Minimal Organisms and Protein Fold Space. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 63-70.	1.2	29
860	A Dynamic Workflow Approach for the Integration of Bioinformatics Services. <i>Cluster Computing</i> , 2005, 8, 279-291.	5.0	11
861	The Last Common Ancestor: What's in a name?. <i>Origins of Life and Evolution of Biospheres</i> , 2005, 35, 537-554.	1.9	69
862	OsPPR1, a pentatricopeptide repeat protein of rice is essential for the chloroplast biogenesis. <i>Plant Molecular Biology</i> , 2005, 58, 421-433.	3.9	118
863	Transcription Factors in Rice: A Genome-wide Comparative Analysis between Monocots and Eudicots. <i>Plant Molecular Biology</i> , 2005, 59, 191-203.	3.9	186
864	Structure of a putative trans-editing enzyme for prolyl-tRNA synthetase from <i>Aeropyrum pernix</i> K1 at 1.7 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 26-29.	0.7	10
865	The structure at 1.7 Å resolution of the protein product of the At2g17340 gene from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 630-635.	0.7	6
866	Preparation, crystallization and preliminary X-ray characterization of a conserved hypothetical protein XC1692 from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 691-693.	0.7	0

#	ARTICLE	IF	CITATIONS
867	Cloning, purification, crystallization and preliminary X-ray analysis of XC229, a conserved hypothetical protein from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 694-696.	0.7	0
868	Cloning, expression, crystallization and preliminary X-ray analysis of a putative multiple antibiotic resistance repressor protein (MarR) from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 706-708.	0.7	1
869	Structure of a NAD kinase from <i>Thermotoga maritima</i> at 2.3 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 640-646.	0.7	10
870	Structure of a class II TrmH tRNA-modifying enzyme from <i>Aquifex aeolicus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 722-728.	0.7	23
871	The structure at 2.5 Å resolution of human basophilic leukemia-expressed protein BLES03. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 812-817.	0.7	2
872	Cloning, purification, crystallization and preliminary X-ray crystallographic analysis of XC847, a 3'-5' oligoribonuclease from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 902-905.	0.7	19
873	Crystallization and preliminary X-ray analysis of the RAD protein from <i>Antirrhinum majus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 885-888.	0.7	4
874	The ybeY protein from <i>Escherichia coli</i> is a metalloprotein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 959-963.	0.7	38
875	A comprehensive update of the sequence and structure classification of kinases. <i>BMC Structural Biology</i> , 2005, 5, 6.	2.3	105
876	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , 2005, 3, 20.	3.8	158
877	Human Lsg1 defines a family of essential GTPases that correlates with the evolution of compartmentalization. <i>BMC Biology</i> , 2005, 3, 21.	3.8	49
878	A study of archaeal enzymes involved in polar lipid synthesis linking amino acid sequence information, genomic contexts and lipid composition. <i>Archaea</i> , 2005, 1, 399-410.	2.3	50
879	Bioinformatics Methods for Microbial Detection and Forensic Diagnostic Design. , 2005, , 313-353.		0
880	A Bioinformatics Analysis of Protein Tyrosine Phosphatases in Humans. <i>DNA Research</i> , 2005, 12, 79-89.	3.4	18
881	Detecting coevolving amino acid sites using Bayesian mutational mapping. <i>Bioinformatics</i> , 2005, 21, i126-i135.	4.1	61
882	Endoplasmic Reticulum Glucosidase II Is Required for Pathogenicity of <i>Ustilago maydis</i> [W]. <i>Plant Cell</i> , 2005, 17, 3532-3543.	6.6	71
883	Systematic Discovery of New Recognition Peptides Mediating Protein Interaction Networks. <i>PLoS Biology</i> , 2005, 3, e405.	5.6	310
884	Protein Molecular Function Prediction by Bayesian Phylogenomics. <i>PLoS Computational Biology</i> , 2005, 1, e45.	3.2	162

#	ARTICLE	IF	CITATIONS
885	Structural Evolution of the Protein Kinase-“Like Superfamily. PLoS Computational Biology, 2005, 1, e49.	3.2	234
886	Functional Coverage of the Human Genome by Existing Structures, Structural Genomics Targets, and Homology Models. PLoS Computational Biology, 2005, 1, e31.	3.2	63
887	Lineage-specific gene loss following mitochondrial endosymbiosis and its potential for function prediction in eukaryotes. Bioinformatics, 2005, 21, ii144-ii150.	4.1	26
888	The Histidine Kinase Hik34 Is Involved in Thermotolerance by Regulating the Expression of Heat Shock Genes in Synechocystis. Plant Physiology, 2005, 138, 1409-1421.	4.8	89
889	A Human-Curated Annotation of the Candida albicans Genome. PLoS Genetics, 2005, 1, e1.	3.5	293
890	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. PLoS Computational Biology, 2005, 1, e55.	3.2	260
891	lin-8, Which Antagonizes Caenorhabditis elegans Ras-Mediated Vulval Induction, Encodes a Novel Nuclear Protein That Interacts With the LIN-35 Rb Protein. Genetics, 2005, 171, 1017-1031.	2.9	18
892	Novel Virulence Gene of Pseudomonas syringae pv. tomato Strain DC3000. Journal of Bacteriology, 2005, 187, 7805-7814.	2.2	21
893	Crystal Structure of the “PhoU-Like” Phosphate Uptake Regulator from Aquifex aeolicus. Journal of Bacteriology, 2005, 187, 4238-4244.	2.2	29
894	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. Genome Research, 2005, 15, 1284-1291.	5.5	73
895	The expression of wild-type pendrin (SLC26A4) in human embryonic kidney (HEK 293 Phoenix) cells leads to the activation of cationic currents. European Journal of Endocrinology, 2005, 153, 693-699.	3.7	18
896	Esf2p, a U3-Associated Factor Required for Small-Subunit Processome Assembly and Compaction. Molecular and Cellular Biology, 2005, 25, 5523-5534.	2.3	33
897	Reciprocal Regulation of Pyoluteorin Production with Membrane Transporter Gene Expression in Pseudomonas fluorescens Pf-5. Applied and Environmental Microbiology, 2005, 71, 6900-6909.	3.1	36
898	Exploring relationships and mining data with the UCSC Gene Sorter. Genome Research, 2005, 15, 737-741.	5.5	77
899	Plant Protein Annotation in the UniProt Knowledgebase. Plant Physiology, 2005, 138, 59-66.	4.8	42
900	Complete genome sequencing of Anaplasma marginale reveals that the surface is skewed to two superfamilies of outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 844-849.	7.1	238
901	Pectin Methylesterases and Pectin Dynamics in Pollen Tubes. Plant Cell, 2005, 17, 3219-3226.	6.6	309
902	The Initial Enzyme for Glycosylphosphatidylinositol Biosynthesis Requires PIC-Y, a Seventh Component. Molecular Biology of the Cell, 2005, 16, 5236-5246.	2.1	53

#	ARTICLE	IF	CITATIONS
903	The barley cystatin gene (lcy) is regulated by DOF transcription factors in aleurone cells upon germination. <i>Journal of Experimental Botany</i> , 2005, 56, 547-556.	4.8	38
904	Functional Analysis of All Aminotransferase Proteins Inferred from the Genome Sequence of <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2005, 187, 7639-7646.	2.2	88
905	Exploring <i>Lactobacillus plantarum</i> Genome Diversity by Using Microarrays. <i>Journal of Bacteriology</i> , 2005, 187, 6119-6127.	2.2	229
906	Four-helix bundle: a ubiquitous sensory module in prokaryotic signal transduction. <i>Bioinformatics</i> , 2005, 21, iii45-iii48.	4.1	60
907	The Genome of <i>Sulfolobus acidocaldarius</i> , a Model Organism of the Crenarchaeota. <i>Journal of Bacteriology</i> , 2005, 187, 4992-4999.	2.2	262
908	Complete Nucleotide Sequence of the LE1 Prophage from the Spirochete <i>Leptospira biflexa</i> and Characterization of Its Replication and Partition Functions. <i>Journal of Bacteriology</i> , 2005, 187, 3931-3940.	2.2	34
909	Functional insights from the distribution and role of homopeptide repeat-containing proteins. <i>Genome Research</i> , 2005, 15, 537-551.	5.5	189
910	Hag Directly Mediates the Adherence of <i>Moraxella catarrhalis</i> to Human Middle Ear Cells. <i>Infection and Immunity</i> , 2005, 73, 5127-5136.	2.2	47
911	Defining Genes in the Genome of the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> : Implications for All Microbial Genomes. <i>Journal of Bacteriology</i> , 2005, 187, 7325-7332.	2.2	41
912	Universal Stress Proteins in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6253-6254.	2.2	83
913	Genome Cluster Database. A Sequence Family Analysis Platform for Arabidopsis and Rice. <i>Plant Physiology</i> , 2005, 138, 47-54.	4.8	45
914	The Common Viral Insertion Site Evi12 Is Located in the 5' Noncoding Region of Gnn, a Novel Gene with Enhanced Expression in Two Subclasses of Human Acute Myeloid Leukemia. <i>Journal of Virology</i> , 2005, 79, 5249-5258.	3.4	5
915	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. <i>Journal of Bacteriology</i> , 2005, 187, 6488-6498.	2.2	301
916	Novel specificities emerge by stepwise duplication of functional modules. <i>Genome Research</i> , 2005, 15, 552-559.	5.5	78
917	Reconstitution of uridine-deletion precleaved RNA editing with two recombinant enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1017-1022.	7.1	59
918	Sequence Analysis of the <i>Escherichia coli</i> O15 Antigen Gene Cluster and Development of a PCR Assay for Rapid Detection of Intestinal and Extraintestinal Pathogenic <i>E. coli</i> O15 Strains. <i>Journal of Clinical Microbiology</i> , 2005, 43, 703-710.	3.9	27
919	Decomposing protein networks into domain-domain interactions. <i>Bioinformatics</i> , 2005, 21, ii220-ii221.	4.1	19
920	Genome-Wide Detection and Analysis of Cell Wall-Bound Proteins with LPxTG-Like Sorting Motifs. <i>Journal of Bacteriology</i> , 2005, 187, 4928-4934.	2.2	134

#	ARTICLE	IF	CITATIONS
921	The Arabidopsis Peroxisomal Targeting Signal Type 2 Receptor PEX7 Is Necessary for Peroxisome Function and Dependent on PEX5. Molecular Biology of the Cell, 2005, 16, 573-583.	2.1	136
922	Identification of genomic features using microsynteny of domains: Domain teams. Genome Research, 2005, 15, 867-874.	5.5	37
923	Evolutionary Algorithm for Noun Phrase Detection in Natural Language Processing. , 0, , .		3
924	Design and evaluation of CATPA. , 2005, , .		0
925	AnoEST: Toward A. gambiae functional genomics. Genome Research, 2005, 15, 893-899.	5.5	19
926	Structural and Genetic Characterization of Enterohemorrhagic Escherichia coli O145 O Antigen and Development of an O145 Serogroup-Specific PCR Assay. Journal of Bacteriology, 2005, 187, 758-764.	2.2	61
927	Mining sequence annotation databanks for association patterns. Bioinformatics, 2005, 21, iii49-iii57.	4.1	32
928	The MicrobesOnline Web site for comparative genomics. Genome Research, 2005, 15, 1015-1022.	5.5	176
929	The Receptor for the Subgroup C Avian Sarcoma and Leukosis Viruses, Tvc, Is Related to Mammalian Butyrophilins, Members of the Immunoglobulin Superfamily. Journal of Virology, 2005, 79, 10408-10419.	3.4	88
930	Specificity prediction of adenylation domains in nonribosomal peptide synthetases (NRPS) using transductive support vector machines (TSVMs). Nucleic Acids Research, 2005, 33, 5799-5808.	14.5	388
931	Protein length in eukaryotic and prokaryotic proteomes. Nucleic Acids Research, 2005, 33, 3390-3400.	14.5	342
932	The importance of being divisible by three in alternative splicing. Nucleic Acids Research, 2005, 33, 5574-5582.	14.5	58
933	<i>In Silico</i> Analysis of ORF1ab in Coronavirus HKU1 Genome Reveals a Unique Putative Cleavage Site of Coronavirus HKU1 3C ^{pro} -Like Protease. Microbiology and Immunology, 2005, 49, 899-908.	1.4	33
934	Bioinformatic Tools for Gene and Protein Sequence Analysis. , 2005, , 387-407.		1
935	Gene Ontology Automatic Annotation Using a Domain Based Gene Product Similarity Measure. , 0, , .		5
936	Finding Protein Domain Boundaries: An Automated, Non-Homology-Based Method. IEEE Intelligent Systems, 2005, 20, 26-33.	4.0	2
937	MAFFT version 5: improvement in accuracy of multiple sequence alignment. Nucleic Acids Research, 2005, 33, 511-518.	14.5	4,184
938	DIAL: a web-based server for the automatic identification of structural domains in proteins. Nucleic Acids Research, 2005, 33, W130-W132.	14.5	25

#	ARTICLE	IF	CITATIONS
939	Reduced Proteolysis of Secreted Gelatin and Yps1-Mediated Î±-Factor Leader Processing in a <i>Pichia pastoris</i> <i>kex2</i> Disruptant. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2310-2317.	3.1	50
940	The genome of the heartwater agent <i>Ehrlichia ruminantium</i> contains multiple tandem repeats of actively variable copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 838-843.	7.1	158
941	Genomic characterization of non-O1, non-O139 <i>Vibrio cholerae</i> reveals genes for a type III secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3465-3470.	7.1	217
942	Prophage-Like Elements in <i>Bifidobacteria</i> : Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	3.1	70
943	Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen <i>Corynebacterium jeikeium</i> K411, a Lipid-Requiring Bacterium of the Human Skin Flora. <i>Journal of Bacteriology</i> , 2005, 187, 4671-4682.	2.2	189
944	Detecting remotely related proteins by their interactions and sequence similarity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7151-7156.	7.1	26
945	Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7315-7320.	7.1	553
946	Identification of a nematode chemosensory gene family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 146-151.	7.1	51
947	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10913-10918.	7.1	529
948	Characterization of <i>Mycobacterium tuberculosis</i> Rv3676 (CRP Mt), a Cyclic AMP Receptor Protein-Like DNA Binding Protein. <i>Journal of Bacteriology</i> , 2005, 187, 7795-7804.	2.2	115
949	The <i>Chlamydomonas reinhardtii</i> genome sequence reveals an array of variable proteins that contribute to interspecies variation. <i>Genome Research</i> , 2005, 15, 629-640.	5.5	158
950	ProbCons: Probabilistic consistency-based multiple sequence alignment. <i>Genome Research</i> , 2005, 15, 330-340.	5.5	982
951	GlnD Is Essential for NifA Activation, NtrB/NtrC-Regulated Gene Expression, and Posttranslational Regulation of Nitrogenase Activity in the Photosynthetic, Nitrogen-Fixing Bacterium <i>Rhodospirillum rubrum</i> . <i>Journal of Bacteriology</i> , 2005, 187, 1254-1265.	2.2	58
952	Role of Unc104/KIF1-related Motor Proteins in Mitochondrial Transport in <i>Neurospora crassa</i> . <i>Molecular Biology of the Cell</i> , 2005, 16, 153-161.	2.1	34
953	Web-based toolkits for topology prediction of transmembrane helical proteins, fold recognition, structure and binding scoring, folding-kinetics analysis and comparative analysis of domain combinations. <i>Nucleic Acids Research</i> , 2005, 33, W193-W197.	14.5	17
954	A data integration methodology for systems biology: Experimental verification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17302-17307.	7.1	124
955	BioFilter: An Architecture for Parallel Deployment and Dynamic Chaining of Standalone Bioinformatics Tools. , 0, , .		0
956	Truncated Profile Hidden Markov Models. , 2005, , .		0

#	ARTICLE	IF	CITATIONS
957	Systematic Targeted Mutagenesis of <i>Brucella melitensis</i> 16M Reveals a Major Role for GntR Regulators in the Control of Virulence. <i>Infection and Immunity</i> , 2005, 73, 5578-5586.	2.2	92
958	<i>Sulfolobus tengchongensis</i> Spindle-Shaped Virus STSV1: Virus-Host Interactions and Genomic Features. <i>Journal of Virology</i> , 2005, 79, 8677-8686.	3.4	119
959	Evidence for Diversifying Selection at the Pyoverdine Locus of <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2005, 187, 2138-2147.	2.2	164
960	Phylogenetic Analysis of the Formin Homology 2 Domain. <i>Molecular Biology of the Cell</i> , 2005, 16, 1-13.	2.1	249
961	Effective function annotation through catalytic residue conservation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12299-12304.	7.1	55
962	Identification of gmhA, a <i>Yersinia pestis</i> Gene Required for Flea Blockage, by Using a <i>Caenorhabditis elegans</i> Biofilm System. <i>Infection and Immunity</i> , 2005, 73, 7236-7242.	2.2	75
963	Statistical signals in bioinformatics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13355-13362.	7.1	28
964	A selenocysteine tRNA and SECIS element in <i>Plasmodium falciparum</i> . <i>Rna</i> , 2005, 11, 119-122.	3.5	32
965	Characterization of a Resistance-Nodulation-Cell Division Transporter System Associated with the syr-syp Genomic Island of <i>Pseudomonas syringae</i> pv. <i>syringae</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 5056-5065.	3.1	49
966	Genetic Analysis of the HAMP Domain of the Aer Aerotaxis Sensor Localizes Flavin Adenine Dinucleotide-Binding Determinants to the AS-2 Helix. <i>Journal of Bacteriology</i> , 2005, 187, 193-201.	2.2	26
967	H2B Ubiquitin Protease Ubp8 and Sgf11 Constitute a Discrete Functional Module within the <i>Saccharomyces cerevisiae</i> SAGA Complex. <i>Molecular and Cellular Biology</i> , 2005, 25, 1162-1172.	2.3	126
968	Levels and Activity of the <i>Pseudomonas putida</i> Global Regulatory Protein Crc Vary According to Growth Conditions. <i>Journal of Bacteriology</i> , 2005, 187, 3678-3686.	2.2	54
969	Novel Activator of Mannose-Specific Phosphotransferase System Permease Expression in <i>Listeria innocua</i> , Identified by Screening for Pediocin AcH Resistance. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1283-1290.	3.1	26
970	The Terminal Phase of Cytokinesis in the <i>Caenorhabditis elegans</i> Early Embryo Requires Protein Glycosylation. <i>Molecular Biology of the Cell</i> , 2005, 16, 4202-4213.	2.1	23
971	Global profiling of <i>Shewanella oneidensis</i> MR-1: Expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2099-2104.	7.1	113
972	Origin and evolution of the chicken leukocyte receptor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4057-4062.	7.1	36
973	Glycoprotein gp130 of <i>Dictyostelium discoideum</i> Influences Macropinocytosis and Adhesion. <i>Molecular Biology of the Cell</i> , 2005, 16, 2681-2693.	2.1	11
974	Molecular Analysis of the O-Antigen Gene Cluster of <i>Escherichia coli</i> O86:B7 and Characterization of the Chain Length Determinant Gene (wzz). <i>Applied and Environmental Microbiology</i> , 2005, 71, 7995-8001.	3.1	47

#	ARTICLE	IF	CITATIONS
975	Complete Sequences of Four Plasmids of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> SK11 Reveal Extensive Adaptation to the Dairy Environment. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8371-8382.	3.1	150
976	RasA Is Required for <i>Myxococcus xanthus</i> Development and Social Motility. <i>Journal of Bacteriology</i> , 2005, 187, 6845-6848.	2.2	6
977	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. <i>Genome Research</i> , 2005, 16, 66-77.	5.5	92
978	The Institute for Genomic Research Osa1 Rice Genome Annotation Database. <i>Plant Physiology</i> , 2005, 138, 18-26.	4.8	201
979	Repressor- and Activator-Type Ethylene Response Factors Functioning in Jasmonate Signaling and Disease Resistance Identified via a Genome-Wide Screen of Arabidopsis Transcription Factor Gene Expression. <i>Plant Physiology</i> , 2005, 139, 949-959.	4.8	540
980	Arabidopsis Has Two Redundant Cullin3 Proteins That Are Essential for Embryo Development and That Interact with RBX1 and BTB Proteins to Form Multisubunit E3 Ubiquitin Ligase Complexes in Vivo. <i>Plant Cell</i> , 2005, 17, 1180-1195.	6.6	153
981	Characterization and functional investigation of an Arabidopsis cDNA encoding a homologue to the d-PGMase superfamily. <i>Journal of Experimental Botany</i> , 2005, 56, 1129-1142.	4.8	8
982	Identification of nine human-specific frameshift mutations by comparative analysis of the human and the chimpanzee genome sequences. <i>Bioinformatics</i> , 2005, 21, i186-i194.	4.1	53
983	Gene and Genome Duplication in <i>Acanthamoeba polyphaga</i> Mimivirus. <i>Journal of Virology</i> , 2005, 79, 14095-14101.	3.4	85
984	Identification of a novel class of mammalian phosphoinositol-specific phospholipase C enzymes. <i>International Journal of Molecular Medicine</i> , 2005, 15, 117.	4.0	9
985	Significant expansion of exon-bordering protein domains during animal proteome evolution. <i>Nucleic Acids Research</i> , 2005, 33, 95-105.	14.5	48
986	Protein coding potential of retroviruses and other transposable elements in vertebrate genomes. <i>Nucleic Acids Research</i> , 2005, 33, 946-954.	14.5	47
987	Detecting DNA-binding helix-turn-helix structural motifs using sequence and structure information. <i>Nucleic Acids Research</i> , 2005, 33, 2129-2140.	14.5	21
988	MAVL/StickWRLD for protein: visualizing protein sequence families to detect non-consensus features. <i>Nucleic Acids Research</i> , 2005, 33, W315-W319.	14.5	9
989	REPPER--repeats and their periodicities in fibrous proteins. <i>Nucleic Acids Research</i> , 2005, 33, W239-W243.	14.5	118
990	Current Comparative Table (CCT) automates customized searches of dynamic biological databases. <i>Nucleic Acids Research</i> , 2005, 33, W770-W773.	14.5	1
991	enoLOGOS: a versatile web tool for energy normalized sequence logos. <i>Nucleic Acids Research</i> , 2005, 33, W389-W392.	14.5	199
992	One-Block CYRCA: an automated procedure for identifying multiple-block alignments from single block queries. <i>Nucleic Acids Research</i> , 2005, 33, W281-W283.	14.5	3

#	ARTICLE	IF	CITATIONS
993	QuasiMotiFinder: protein annotation by searching for evolutionarily conserved motif-like patterns. Nucleic Acids Research, 2005, 33, W255-W261.	14.5	35
994	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. Nucleic Acids Research, 2005, 33, 3598-3605.	14.5	83
995	SNEV is an evolutionarily conserved splicing factor whose oligomerization is necessary for spliceosome assembly. Nucleic Acids Research, 2005, 33, 6868-6883.	14.5	46
996	A sequence sub-sampling algorithm increases the power to detect distant homologues. Nucleic Acids Research, 2005, 33, 3772-3778.	14.5	1
997	PhyloDome-visualization of taxonomic distributions of domains occurring in eukaryote protein sequence sets. Nucleic Acids Research, 2005, 33, W121-W125.	14.5	3
998	Evidence that the Tfg1/Tfg2 dimer interface of TFIIF lies near the active center of the RNA polymerase II initiation complex. Nucleic Acids Research, 2005, 33, 5045-5052.	14.5	41
999	Searching for Protein Classification Features. , 0, , .		0
1000	FFAS03: a server for profile-profile sequence alignments. Nucleic Acids Research, 2005, 33, W284-W288.	14.5	522
1001	Predicting protein-protein interactions based on protein-domain relationships. , 0, , .		3
1002	Ankyrin-G in skeletal muscle: Tissue-specific alternative splicing contributes to the complexity of the sarcolemmal cytoskeleton†. Experimental Cell Research, 2005, 309, 86-98.	2.6	33
1003	Characterization and Complete Genome Sequence of a Novel Coronavirus, Coronavirus HKU1, from Patients with Pneumonia. Journal of Virology, 2005, 79, 884-895.	3.4	1,269
1004	Fuzzy Profile Hidden Markov Models for Protein Sequence Analysis. , 2005, , .		1
1005	Protein-Protein Interaction Prediction Based on Sequence Data by Support Vector Machine with Probability Assignment. , 2005, , .		1
1006	Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14040-14045.	7.1	1,322
1007	Crystal Structure of the Bacterial YhcH Protein Indicates a Role in Sialic Acid Catabolism. Journal of Bacteriology, 2005, 187, 5520-5527.	2.2	21
1008	miRU: an automated plant miRNA target prediction server. Nucleic Acids Research, 2005, 33, W701-W704.	14.5	324
1009	Structural and Biochemical Characterization of Gun4 Suggests a Mechanism for Its Role in Chlorophyll Biosynthesisâ€¦. Biochemistry, 2005, 44, 7603-7612.	2.5	126
1010	Practical lessons from protein structure prediction. Nucleic Acids Research, 2005, 33, 1874-1891.	14.5	109

#	ARTICLE	IF	CITATIONS
1011	Sequence-based Protein-Protein Interaction Prediction Optimized for Target Selection in Biological Experiments. , 2005, 2006, 236-9.		1
1012	Expectations from Structural Genomics Revisited. Molecular Diagnosis and Therapy, 2005, 5, 339-342.	3.3	3
1013	Prediction of Putative Adverse Drug Reaction-Related Proteins from Primary Sequence by Support Vector Machines. Pharmaceutical Medicine, 2005, 19, 317-322.	0.4	1
1014	A case study of instant workbench for InterProScan by Knoppix high throughput computing edition. , 0, , .		0
1015	The TetR Family of Transcriptional Repressors. Microbiology and Molecular Biology Reviews, 2005, 69, 326-356.	6.6	989
1016	InterProScan: protein domains identifier. Nucleic Acids Research, 2005, 33, W116-W120.	14.5	2,556
1017	The evolution of vertebrate Toll-like receptors. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9577-9582.	7.1	1,026
1018	BASys: a web server for automated bacterial genome annotation. Nucleic Acids Research, 2005, 33, W455-W459.	14.5	290
1019	Interaction of Heterochromatin Protein 2 with HP1 Defines a Novel HP1-Binding Domain. Biochemistry, 2005, 44, 13394-13403.	2.5	22
1020	Pathway to Synthesis and Processing of Mycolic Acids in Mycobacterium tuberculosis. Clinical Microbiology Reviews, 2005, 18, 81-101.	13.6	577
1021	SlmA, a Nucleoid-Associated, FtsZ Binding Protein Required for Blocking Septal Ring Assembly over Chromosomes in E. coli. Molecular Cell, 2005, 18, 555-564.	9.7	472
1022	Cloning of a glycosylphosphatidylinositol-anchored alpha-2-macroglobulin cDNA from the ascidian, , and its possible role in immunity. Molecular Immunology, 2005, 42, 683-694.	2.2	13
1023	Evolutionary rate variation in eukaryotic lineage specific human intronless proteins. Biochemical and Biophysical Research Communications, 2005, 337, 1192-1197.	2.1	9
1024	Structural Basis for Endosomal Targeting by the Bro1 Domain. Developmental Cell, 2005, 8, 937-947.	7.0	171
1025	Development of PLEX, a plasmid-based expression system for production of heterologous gene products by the gram-positive bacteria Streptococcus gordonii. Protein Expression and Purification, 2005, 40, 319-326.	1.3	3
1026	Nucleotide sequence and phylogenetic analyses of the DNA polymerase gene of Anticarsia gemmatilis nucleopolyhedrovirus. Virus Research, 2005, 110, 99-109.	2.2	2
1027	Nomenclature of the ARID family of DNA-binding proteins. Genomics, 2005, 86, 242-251.	2.9	133
1028	One-component systems dominate signal transduction in prokaryotes. Trends in Microbiology, 2005, 13, 52-56.	7.7	461

#	ARTICLE	IF	CITATIONS
1029	Bioinformatics in microbial biotechnology--a mini review. <i>Microbial Cell Factories</i> , 2005, 4, 19.	4.0	73
1030	Comparative modelling of protein structure and its impact on microbial cell factories. <i>Microbial Cell Factories</i> , 2005, 4, 20.	4.0	19
1031	Assessing strategies for improved superfamily recognition. <i>Protein Science</i> , 2005, 14, 1800-1810.	7.6	20
1032	EDD, a novel phosphotransferase domain common to mannose transporter EIIA, dihydroxyacetone kinase, and DegV. <i>Protein Science</i> , 2005, 14, 360-367.	7.6	16
1033	Crystal structure of a predicted phosphoribosyltransferase (TT1426) from <i>Thermus thermophilus</i> HB8 at 2.01 Å resolution. <i>Protein Science</i> , 2005, 14, 823-827.	7.6	6
1034	The P5 protein from bacteriophage phi-6 is a distant homolog of lytic transglycosylases. <i>Protein Science</i> , 2005, 14, 1370-1374.	7.6	11
1035	Computational Protein Design Is a Challenge for Implicit Solvation Models. <i>Biophysical Journal</i> , 2005, 88, 156-171.	0.5	54
1036	A Guild of 45 CRISPR-Associated (Cas) Protein Families and Multiple CRISPR/Cas Subtypes Exist in Prokaryotic Genomes. <i>PLoS Computational Biology</i> , 2005, 1, e60.	3.2	835
1037	Structural relatedness of plant food allergens with specific reference to cross-reactive allergens: An in silico analysis. <i>Journal of Allergy and Clinical Immunology</i> , 2005, 115, 163-170.	2.9	245
1038	Chapter 11 Protein bioinformatics. <i>Comprehensive Analytical Chemistry</i> , 2005, , 487-500.	1.3	0
1039	ROCPLLOT. <i>Applied Bioinformatics</i> , 2005, 4, 131-135.	1.6	3
1040	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	2.2	321
1041	Computational prediction of SEG (single exon gene) function in humans. <i>Frontiers in Bioscience - Landmark</i> , 2005, 10, 1382.	3.0	27
1042	Soilborne wheat mosaic virus (SBWMV) 19K protein belongs to a class of cysteine rich proteins that suppress RNA silencing. <i>Virology Journal</i> , 2005, 2, 18.	3.4	34
1043	A new example of viral intein in Mimivirus. <i>Virology Journal</i> , 2005, 2, 8.	3.4	40
1044	Inferring protein domain interactions from databases of interacting proteins. <i>Genome Biology</i> , 2005, 6, R89.	9.6	128
1045	Sequence and structural analysis of BTB domain proteins. <i>Genome Biology</i> , 2005, 6, R82.	9.6	575
1046	The SET-domain protein superfamily: protein lysine methyltransferases. <i>Genome Biology</i> , 2005, 6, 227.	9.6	661

#	ARTICLE	IF	CITATIONS
1047	Creation and disruption of protein features by alternative splicing -- a novel mechanism to modulate function. <i>Genome Biology</i> , 2005, 6, R58.	9.6	28
1048	The rarity of gene shuffling in conserved genes. <i>Genome Biology</i> , 2005, 6, R50.	9.6	16
1049	Novel G-protein-coupled receptor-like proteins in the plant pathogenic fungus <i>Magnaporthe grisea</i> . <i>Genome Biology</i> , 2005, 6, R24.	9.6	182
1050	The 'permeome' of the malaria parasite: an overview of the membrane transport proteins of <i>Plasmodium falciparum</i> . <i>Genome Biology</i> , 2005, 6, R26.	9.6	154
1051	Genomic sequence and analysis of a vaccinia virus isolate from a patient with a smallpox vaccine-related complication. <i>Virology Journal</i> , 2006, 3, 88.	3.4	24
1052	Genetic diversity among five T4-like bacteriophages. <i>Virology Journal</i> , 2006, 3, 30.	3.4	93
1053	Multiple independent evolutionary solutions to core histone gene regulation. <i>Genome Biology</i> , 2006, 7, R122.	9.6	47
1054	Predicting domain-domain interactions using a parsimony approach. <i>Genome Biology</i> , 2006, 7, R104.	9.6	73
1055	Mining the <i>Arabidopsis thaliana</i> genome for highly-divergent seven transmembrane receptors. <i>Genome Biology</i> , 2006, 7, R96.	9.6	80
1056	PhyloFacts: an online structural phylogenomic encyclopedia for protein functional and structural classification. <i>Genome Biology</i> , 2006, 7, R83.	9.6	50
1057	The cnidarian-bilaterian ancestor possessed at least 56 homeoboxes: evidence from the starlet sea anemone, <i>Nematostella vectensis</i> . <i>Genome Biology</i> , 2006, 7, R64.	9.6	162
1058	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. <i>Genome Biology</i> , 2006, 7, R36.	9.6	456
1059	GENCODE: producing a reference annotation for ENCODE. <i>Genome Biology</i> , 2006, 7, S4.	9.6	533
1060	A gold standard set of mechanistically diverse enzyme superfamilies. <i>Genome Biology</i> , 2006, 7, R8.	9.6	62
1061	SEQOPTICS: A Protein Sequence Clustering Method. , 2006, , .		7
1062	Structural Classification of Bacterial Response Regulators: Diversity of Output Domains and Domain Combinations. <i>Journal of Bacteriology</i> , 2006, 188, 4169-4182.	2.2	436
1063	Evolution of Circular Permutations in Multidomain Proteins. <i>Molecular Biology and Evolution</i> , 2006, 23, 734-743.	8.9	71
1064	Support vector machines for predicting protein-protein interactions using domains and hydrophobicity features. , 2006, , .		3

#	ARTICLE	IF	CITATIONS
1065	Assigning Schema Labels Using Ontology And Hueristics. , 2006, , .		1
1066	Using multiple grid resources for bioinformatics applications in GADU. , 2006, , .		3
1067	Characterization of myo -Inositol Utilization by Corynebacterium glutamicum : the Stimulon, Identification of Transporters, and Influence on l -Lysine Formation. Journal of Bacteriology, 2006, 188, 8054-8061.	2.2	94
1068	Sparse Logistic Classifiers for Interpretable Protien Homology Detection. , 2006, , .		0
1069	Escherichia coli K-12: a cooperatively developed annotation snapshot--2005. Nucleic Acids Research, 2006, 34, 1-9.	14.5	606
1070	A hitchhiker's guide to expressed sequence tag (EST) analysis. Briefings in Bioinformatics, 2006, 8, 6-21.	6.5	235
1071	Genome-Wide Survey of Transcription Factors in Prokaryotes Reveals Many Bacteria-Specific Families Not Found in Archaea. DNA Research, 2006, 12, 269-280.	3.4	67
1072	Sequence Homology Search Based on Database Indexing Using the Profile Hidden Markov Model. , 2006, , .		2
1073	The Methanosarcina barkeri Genome: Comparative Analysis with Methanosarcina acetivorans and Methanosarcina mazei Reveals Extensive Rearrangement within Methanosarcinal Genomes. Journal of Bacteriology, 2006, 188, 7922-7931.	2.2	158
1074	Application of New Multiresolution Methods for the Comparison of Biomolecular Electrostatic Properties in the Absence of Global Structural Similarity. Multiscale Modeling and Simulation, 2006, 5, 1196-1213.	1.6	32
1075	Identification of putative domain linkers by a neural network - application to a large sequence database. BMC Bioinformatics, 2006, 7, 323.	2.6	16
1076	A statistical score for assessing the quality of multiple sequence alignments. BMC Bioinformatics, 2006, 7, 484.	2.6	41
1077	Molecular cloning and functional characterization of Î²-N-acetylglucosaminidase genes from Sf9 cells. Protein Expression and Purification, 2006, 47, 571-590.	1.3	35
1078	Localizome: a server for identifying transmembrane topologies and TM helices of eukaryotic proteins utilizing domain information. Nucleic Acids Research, 2006, 34, W99-W103.	14.5	27
1079	IPro: An Iterative Computational Protein Library Redesign and Optimization Procedure. Biophysical Journal, 2006, 90, 4167-4180.	0.5	54
1080	Computer-aided NMR assay for detecting natively folded structural domains. Protein Science, 2006, 15, 871-883.	7.6	27
1081	The signaling helix: a common functional theme in diverse signaling proteins. Biology Direct, 2006, 1, 25.	4.6	117
1082	Modelling proteinâ€“protein interaction networks via a stickiness index. Journal of the Royal Society Interface, 2006, 3, 711-716.	3.4	76

#	ARTICLE	IF	CITATIONS
1083	Pollen allergens are restricted to few protein families and show distinct patterns of species distribution. <i>Journal of Allergy and Clinical Immunology</i> , 2006, 117, 141-147.	2.9	194
1084	Comparative Analysis of the Heat Stable Proteome of Radicles of <i>Medicago truncatula</i> Seeds during Germination Identifies Late Embryogenesis Abundant Proteins Associated with Desiccation Tolerance. <i>Plant Physiology</i> , 2006, 140, 1418-1436.	4.8	189
1085	TRANSFAC(R) and its module TRANSCompel(R): transcriptional gene regulation in eukaryotes. <i>Nucleic Acids Research</i> , 2006, 34, D108-D110.	14.5	2,015
1086	A profile-based protein sequence alignment algorithm for a domain clustering database. , 2006, , .		0
1087	Molecular and phylogenetic analyses reveal mammalian-like clockwork in the honey bee (<i>Apis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 2006, 16, 1352-1365.	5.5	223
1088	Automated protein function prediction--the genomic challenge. <i>Briefings in Bioinformatics</i> , 2006, 7, 225-242.	6.5	307
1089	GISMO--gene identification using a support vector machine for ORF classification. <i>Nucleic Acids Research</i> , 2006, 35, 540-549.	14.5	47
1090	Myo1c Binds Phosphoinositides through a Putative Pleckstrin Homology Domain. <i>Molecular Biology of the Cell</i> , 2006, 17, 4856-4865.	2.1	130
1091	Biochemical and Structural Domain Analysis of Xeroderma Pigmentosum Complementation Group C Protein. <i>Biochemistry</i> , 2006, 45, 14965-14979.	2.5	74
1092	Pentapeptide Repeat Proteinsâ€. <i>Biochemistry</i> , 2006, 45, 1-10.	2.5	160
1093	Structure of the DPS-Like Protein from <i>Sulfolobus solfataricus</i> Reveals a Bacterioferritin-Like Dimetal Binding Site within a DPS-Like Dodecameric Assemblyâ€,â€. <i>Biochemistry</i> , 2006, 45, 10815-10827.	2.5	61
1094	G-protein and cAMP-mediated signaling in aspergilli: A genomic perspective. <i>Fungal Genetics and Biology</i> , 2006, 43, 490-502.	2.1	131
1095	Functional insights from the structural modelling of a small Fe-hydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 277-283.	2.1	10
1096	Structural and genetic characterization of <i>Shigella boydii</i> type 17 O antigen and confirmation of two new genes involved in the synthesis of glucolactilic acid. <i>Biochemical and Biophysical Research Communications</i> , 2006, 349, 289-295.	2.1	9
1097	The Role of Domain Redundancy in Genetic Robustness Against Null Mutations. <i>Journal of Molecular Biology</i> , 2006, 362, 184-191.	4.2	31
1098	Co-evolutionary Analysis of Domains in Interacting Proteins Reveals Insights into Domainâ€Domain Interactions Mediating Proteinâ€Protein Interactions. <i>Journal of Molecular Biology</i> , 2006, 362, 861-875.	4.2	123
1099	MbIDGF, a novel member of the imaginal disc growth factor family in <i>Mamestra brassicae</i> , stimulates cell proliferation in two lepidopteran cell lines without insulin. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 536-546.	2.7	22
1100	The sialotranscriptome of adult male <i>Anopheles gambiae</i> mosquitoes. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 570-575.	2.7	45

#	ARTICLE	IF	CITATIONS
1101	A genome-wide survey of the evolutionarily conserved Wnt pathways in the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Developmental Biology</i> , 2006, 300, 121-131.	2.0	76
1102	Mutation Causing Self-Aggregation in Human \hat{I}^3 C-Crystallin Leading to Congenital Cataract. , 2006, 47, 5212.		23
1103	A New Family of Giardial Cysteine-Rich Non-VSP Protein Genes and a Novel Cyst Protein. <i>PLoS ONE</i> , 2006, 1, e44.	2.5	98
1104	Detection of Conjugation Related Type Four Secretion Machinery in <i>Aeromonas culicicola</i> . <i>PLoS ONE</i> , 2006, 1, e115.	2.5	13
1105	Lineage-specific partitions in archaeal transcription. <i>Archaea</i> , 2006, 2, 117-125.	2.3	11
1106	Distribution, structure and diversity of "bacterial" genes encoding two-component proteins in the Euryarchaeota. <i>Archaea</i> , 2006, 2, 11-30.	2.3	26
1107	Identification of SmtB/ArsRciselements and proteins in archaea using the Prokaryotic InterGenic Exploration Database (PIGED). <i>Archaea</i> , 2006, 2, 39-49.	2.3	8
1108	Two exo- \hat{I}^2 -D-glucosaminidases/exochitosanases from actinomycetes define a new subfamily within family 2 of glycoside hydrolases. <i>Biochemical Journal</i> , 2006, 394, 675-686.	3.7	48
1109	Functional analysis of a group A streptococcal glycoside hydrolase Spy1600 from family 84 reveals it is a \hat{I}^2 -N-acetylglucosaminidase and not a hyaluronidase. <i>Biochemical Journal</i> , 2006, 399, 241-247.	3.7	35
1110	Bioinformatic analysis of expressed sequence tags from sporophyte of <i>Porphyra yezoensis</i> (Bagiaceae,) Tj ETQq1 1 0.784314,rgBT /Over 4.4		
1111	The Role of the COG Database in Comparative and Functional Genomics. <i>Current Bioinformatics</i> , 2006, 1, 291-300.	1.5	16
1112	PUMA2-grid-based high-throughput analysis of genomes and metabolic pathways. <i>Nucleic Acids Research</i> , 2006, 34, D369-D372.	14.5	59
1113	BAG: a graph theoretic sequence clustering algorithm. <i>International Journal of Data Mining and Bioinformatics</i> , 2006, 1, 178.	0.1	27
1114	12 Reversible methylation of glutamate residues in the receptor proteins of bacterial sensory systems. <i>The Enzymes</i> , 2006, 24, 325-382.	1.7	9
1115	Structure of konkunitzin-S1, a neurotoxin and Kunitz-fold disulfide variant from cone snail. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 980-990.	2.5	40
1116	Expression, purification, crystallization and preliminary X-ray analysis of the olfactomedin domain from the sea urchin cell-adhesion protein amassin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 16-19.	0.7	4
1117	Structure of the conserved hypothetical protein MAL13P1.257 from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 180-185.	0.7	9
1118	Structure of Lmaj006129AAA, a hypothetical protein from <i>Leishmania major</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 175-179.	0.7	18

#	ARTICLE	IF	CITATIONS
1119	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of Rv2827c from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 753-756.	0.7	1
1120	Expression, purification, crystallization and preliminary crystallographic analysis of BipD, a component of the <i>Burkholderia pseudomallei</i> type III secretion system. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 861-864.	0.7	5
1121	Cloning, crystallization and preliminary X-ray study of XC1258, a CN-hydrolase superfamily protein from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 999-1002.	0.7	2
1122	The cloning, crystallization and preliminary X-ray analysis of XC2113, a YaeQ protein from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1046-1048.	0.7	1
1123	Cloning, crystallization and preliminary X-ray studies of XC2981 from <i>Xanthomonas campestris</i> , a putative CutA1 protein involved in copper-ion homeostasis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1113-1115.	0.7	3
1124	Structure of the second domain of the <i>Bacillus subtilis</i> DEAD-box RNA helicase YxiN. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1191-1195.	0.7	11
1125	Cloning, expression, crystallization and preliminary crystallographic analysis of a pentapeptide-repeat protein (Rfr23) from the bacterium <i>Cyanothece</i> 51142. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1251-1254.	0.7	5
1126	Crystallization and preliminary X-ray analysis of XC1015, a histidine triad-like protein from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1263-1265.	0.7	0
1127	Evidence that talin alternative splice variants from <i>Ciona intestinalis</i> have different roles in cell adhesion. <i>BMC Cell Biology</i> , 2006, 7, 40.	3.0	8
1128	Rtt107/Esc4 binds silent chromatin and DNA repair proteins using different BRCT motifs. <i>BMC Molecular Biology</i> , 2006, 7, 40.	3.0	27
1129	Structure of a conserved hypothetical protein SA1388 from <i>S. aureus</i> reveals a capped hexameric toroid with two PII domain lids and a dinuclear metal center. <i>BMC Structural Biology</i> , 2006, 6, 27.	2.3	14
1130	Exploring dynamics of protein structure determination and homology-based prediction to estimate the number of superfamilies and folds. , 2006, 6, 6.		23
1131	Structural proteomics of minimal organisms: conservation of protein fold usage and evolutionary implications. , 2006, 6, 7.		10
1132	Exopolysaccharide-associated protein sorting in environmental organisms: the PEP-CTERM/EpsH system. Application of a novel phylogenetic profiling heuristic. <i>BMC Biology</i> , 2006, 4, 29.	3.8	86
1133	EST-PAC a web package for EST annotation and protein sequence prediction. <i>Source Code for Biology and Medicine</i> , 2006, 1, 2.	1.7	9
1134	BISON: Bio-Interface for the Semi-global analysis Of Network patterns. <i>Source Code for Biology and Medicine</i> , 2006, 1, 8.	1.7	6
1135	Identification of latent periodicity in amino acid sequences of protein families. <i>Biochemistry (Moscow)</i> , 2006, 71, 18-31.	1.5	4
1136	Wza the translocon for <i>E. coli</i> capsular polysaccharides defines a new class of membrane protein. <i>Nature</i> , 2006, 444, 226-229.	27.8	321

#	ARTICLE	IF	CITATIONS
1137	The Nfs1 interacting protein Isd11 has an essential role in Fe/S cluster biogenesis in mitochondria. EMBO Journal, 2006, 25, 174-183.	7.8	208
1138	Structural and functional insights into the B30.2/SPRY domain. EMBO Journal, 2006, 25, 1353-1363.	7.8	139
1139	Two conformations of a crystalline human tRNA synthetaseâ€tRNA complex: implications for protein synthesis. EMBO Journal, 2006, 25, 2919-2929.	7.8	56
1140	Protein model refinement using structural fragment tessellation. Computational Biology and Chemistry, 2006, 30, 360-366.	2.3	10
1141	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. Protein Science, 2006, 15, 509-521.	7.6	158
1142	Determination of network of residues that regulate allostery in protein families using sequence analysis. Protein Science, 2006, 15, 258-268.	7.6	84
1143	The IclR family of transcriptional activators and repressors can be defined by a single profile. Protein Science, 2006, 15, 1207-1213.	7.6	45
1144	Crystal structure of the DUF16 domain of MPN010 from Mycoplasma pneumoniae. Protein Science, 2006, 15, 921-928.	7.6	7
1145	Crystal structure of trehalose-6-phosphate phosphatase-related protein: Biochemical and biological implications. Protein Science, 2006, 15, 1735-1744.	7.6	54
1146	A limited universe of membrane protein families and folds. Protein Science, 2006, 15, 1723-1734.	7.6	77
1147	The crystal structure of the E. coli stress protein YciF. Protein Science, 2006, 15, 2605-2611.	7.6	24
1148	Characterization of two potentially universal turn motifs that shape the repeated five-residues fold-Crystal structure of a luminal pentapeptide repeat protein from Cyanobacteria. Protein Science, 2006, 15, 2579-2595.	7.6	32
1149	Longin-like folds identified in CHiPS and DUF254 proteins: Vesicle trafficking complexes conserved in eukaryotic evolution. Protein Science, 2006, 15, 2669-2674.	7.6	32
1150	Genome-Wide Analysis and Experimentation of Plant Serine/ Threonine/Tyrosine-Specific Protein Kinases. Plant Molecular Biology, 2006, 60, 293-319.	3.9	120
1151	Light-dependent polyploidy control by a CUE protein variant in Arabidopsis. Plant Molecular Biology, 2006, 61, 817-828.	3.9	14
1152	Fine-tuning of protein domain boundary by minimizing potential coiled coil regions. Journal of Biomolecular NMR, 2006, 37, 53-63.	2.8	5
1153	Effect of N-terminal solubility enhancing fusion proteins on yield of purified target protein. Journal of Structural and Functional Genomics, 2006, 7, 1-14.	1.2	77
1154	The crystal structure of Rv0793, a hypothetical monooxygenase from M. tuberculosis. Journal of Structural and Functional Genomics, 2006, 6, 245-257.	1.2	12

#	ARTICLE	IF	CITATIONS
1155	Interrogating the druggable genome with structural informatics. <i>Molecular Diversity</i> , 2006, 10, 273-281.	3.9	49
1156	Identification and Characterization of LIW, a Novel Domain Involved in Animal NCKIPSDs and Some Uncharacterized Fungal Proteins. <i>Biochemical Genetics</i> , 2006, 44, 121-128.	1.7	0
1157	Structural model of an antistasin/notch-like fusion protein from the cocoon wall of the aquatic leech, <i>Theromyzon tessulatum</i> . <i>Journal of Molecular Modeling</i> , 2006, 12, 829-834.	1.8	7
1158	The functional analysis of Type I postplasmic/PEM mRNAs in embryos of the ascidian <i>Halocynthia roretzi</i> . <i>Development Genes and Evolution</i> , 2006, 216, 69-80.	0.9	22
1159	Some operations research methods for analyzing protein sequences and structures. <i>4or</i> , 2006, 4, 91-123.	1.6	11
1160	Organic Anion Transporting Polypeptides of the OATP/SLCO Superfamily: Identification of New Members in Nonmammalian Species, Comparative Modeling and a Potential Transport Mode. <i>Journal of Membrane Biology</i> , 2006, 208, 213-227.	2.1	121
1161	Efficient Methods for Estimating Amino Acid Replacement Rates. <i>Journal of Molecular Evolution</i> , 2006, 62, 663-673.	1.8	13
1162	Evolution and Diversification of RNA Silencing Proteins in Fungi. <i>Journal of Molecular Evolution</i> , 2006, 63, 127-135.	1.8	141
1163	Protein Superfamily Evolution and the Last Universal Common Ancestor (LUCA). <i>Journal of Molecular Evolution</i> , 2006, 63, 513-525.	1.8	105
1164	Variable domains in hagfish: NICIR is a polymorphic multigene family expressed preferentially in leukocytes and is related to lamprey TCR-like. <i>Immunogenetics</i> , 2006, 58, 216-225.	2.4	33
1165	A novel family of diversified immunoregulatory receptors in teleosts is homologous to both mammalian Fc receptors and molecules encoded within the leukocyte receptor complex. <i>Immunogenetics</i> , 2006, 58, 758-773.	2.4	61
1166	Comparative genomics of the HOG-signalling system in fungi. <i>Current Genetics</i> , 2006, 49, 137-151.	1.7	73
1167	Comparative analysis of HOG pathway proteins to generate hypotheses for functional analysis. <i>Current Genetics</i> , 2006, 49, 152-165.	1.7	52
1168	A secondary metabolite biosynthesis cluster in <i>Trichoderma virens</i> : evidence from analysis of genes underexpressed in a mutant defective in morphogenesis and antibiotic production. <i>Current Genetics</i> , 2006, 50, 193-202.	1.7	65
1169	Plant thionins – the structural perspective. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 1370-1385.	5.4	193
1170	Global analysis of gene transcription regulation in prokaryotes. <i>Cellular and Molecular Life Sciences</i> , 2006, 63, 2260-2290.	5.4	49
1171	A systematic bioinformatics approach for selection of epitope-based vaccine targets. <i>Cellular Immunology</i> , 2006, 244, 141-147.	3.0	78
1172	<i>Entamoeba histolytica</i> up-regulates the Cdc48-like protein, an AAA family member, during the activation of trophozoites with collagen type I and calcium. <i>Molecular and Biochemical Parasitology</i> , 2006, 146, 113-119.	1.1	6

#	ARTICLE	IF	CITATIONS
1173	The 3of5 web application for complex and comprehensive pattern matching in protein sequences. BMC Bioinformatics, 2006, 7, 144.	2.6	17
1174	Domain-based small molecule binding site annotation. BMC Bioinformatics, 2006, 7, 152.	2.6	25
1175	Automatic discovery of cross-family sequence features associated with protein function. BMC Bioinformatics, 2006, 7, 16.	2.6	10
1176	Classification of protein quaternary structure by functional domain composition. BMC Bioinformatics, 2006, 7, 187.	2.6	25
1177	An analysis of the Sargasso Sea resource and the consequences for database composition. BMC Bioinformatics, 2006, 7, 213.	2.6	18
1178	Statistical modeling of biomedical corpora: mining the Caenorhabditis Genetic Center Bibliography for genes related to life span. BMC Bioinformatics, 2006, 7, 250.	2.6	31
1179	An integrated approach to the prediction of domain-domain interactions. BMC Bioinformatics, 2006, 7, 269.	2.6	102
1180	EVEREST: automatic identification and classification of protein domains in all protein sequences. BMC Bioinformatics, 2006, 7, 277.	2.6	32
1181	Recrafting the neighbor-joining method. BMC Bioinformatics, 2006, 7, 29.	2.6	41
1182	Argument-predicate distance as a filter for enhancing precision in extracting predications on the genetic etiology of disease. BMC Bioinformatics, 2006, 7, 291.	2.6	27
1183	MACSIMS : multiple alignment of complete sequences information management system. BMC Bioinformatics, 2006, 7, 318.	2.6	38
1184	Tools for integrated sequence-structure analysis with UCSF Chimera. BMC Bioinformatics, 2006, 7, 339.	2.6	524
1185	Comparative assessment of performance and genome dependence among phylogenetic profiling methods. BMC Bioinformatics, 2006, 7, 420.	2.6	43
1186	Java GUI for InterProScan (IIPS): A tool to help process multiple InterProScans and perform ortholog analysis. BMC Bioinformatics, 2006, 7, 462.	2.6	7
1187	The accuracy of several multiple sequence alignment programs for proteins. BMC Bioinformatics, 2006, 7, 471.	2.6	122
1188	Integrating protein structures and precomputed genealogies in the Magnum database: examples with cellular retinoid binding proteins. BMC Bioinformatics, 2006, 7, 89.	2.6	2
1189	SEQOPTICS: a protein sequence clustering system. BMC Bioinformatics, 2006, 7, S10.	2.6	27
1190	Prediction of the functional class of metal-binding proteins from sequence derived physicochemical properties by support vector machine approach. BMC Bioinformatics, 2006, 7, S13.	2.6	58

#	ARTICLE	IF	CITATIONS
1191	Comparative genomics in cyprinids: common carp ESTs help the annotation of the zebrafish genome. BMC Bioinformatics, 2006, 7, S2.	2.6	40
1192	Eleven ancestral gene families lost in mammals and vertebrates while otherwise universally conserved in animals. BMC Evolutionary Biology, 2006, 6, 5.	3.2	33
1193	PHOG-BLAST—a new generation tool for fast similarity search of protein families. BMC Evolutionary Biology, 2006, 6, 51.	3.2	9
1194	Genetic structure and evolution of the Vps25 family, a yeast ESCRT-II component. BMC Evolutionary Biology, 2006, 6, 59.	3.2	9
1195	Molecular phylogenetics and comparative modeling of HEN1, a methyltransferase involved in plant microRNA biogenesis. BMC Evolutionary Biology, 2006, 6, 6.	3.2	46
1196	The monosaccharide transporter gene family in land plants is ancient and shows differential subfamily expression and expansion across lineages. BMC Evolutionary Biology, 2006, 6, 64.	3.2	58
1197	Tracing the origin of functional and conserved domains in the human proteome: implications for protein evolution at the modular level. BMC Evolutionary Biology, 2006, 6, 91.	3.2	12
1198	Topology and weights in a protein domain interaction network “a novel way to predict protein interactions. BMC Genomics, 2006, 7, 122.	2.8	28
1199	Lactobacillus plantarum gene clusters encoding putative cell-surface protein complexes for carbohydrate utilization are conserved in specific gram-positive bacteria. BMC Genomics, 2006, 7, 126.	2.8	96
1200	Identification and analysis of DNA-binding transcription factors in Bacillus subtilis and other Firmicutes- a genomic approach. BMC Genomics, 2006, 7, 147.	2.8	63
1201	Thirteen is enough: the myosins of Dictyostelium discoideum and their light chains. BMC Genomics, 2006, 7, 183.	2.8	30
1202	Generation, annotation and analysis of ESTs from Trichoderma harzianum CECT 2413. BMC Genomics, 2006, 7, 193.	2.8	60
1203	Cross genome comparisons of serine proteases in Arabidopsis and rice. BMC Genomics, 2006, 7, 200.	2.8	129
1204	Horizontal gene transfer from Bacteria to rumen Ciliates indicates adaptation to their anaerobic, carbohydrates-rich environment. BMC Genomics, 2006, 7, 22.	2.8	138
1205	RINGdb: An integrated database for G protein-coupled receptors and regulators of G protein signaling. BMC Genomics, 2006, 7, 317.	2.8	6
1206	Duplication and relocation of the functional DPY19L2 gene within low copy repeats. BMC Genomics, 2006, 7, 45.	2.8	28
1207	NovelFam3000 “Uncharacterized human protein domains conserved across model organisms. BMC Genomics, 2006, 7, 48.	2.8	5
1208	Bacterial repetitive extragenic palindromic sequences are DNA targets for Insertion Sequence elements. BMC Genomics, 2006, 7, 62.	2.8	87

#	ARTICLE	IF	CITATIONS
1209	Sex-dependent gene expression in early brain development of chicken embryos. BMC Neuroscience, 2006, 7, 12.	1.9	59
1210	StellaBase: The Nematostella vectensis Genomics Database. Nucleic Acids Research, 2006, 34, D495-D499.	14.5	101
1211	Gene3D: modelling protein structure, function and evolution. Nucleic Acids Research, 2006, 34, D281-D284.	14.5	59
1212	Comprehensive genome analysis of 203 genomes provides structural genomics with new insights into protein family space. Nucleic Acids Research, 2006, 34, 1066-1080.	14.5	65
1213	An experimental metagenome data management and analysis system. Bioinformatics, 2006, 22, e359-e367.	4.1	81
1214	Structural basis of yeast aminoacyl-tRNA synthetase complex formation revealed by crystal structures of two binary sub-complexes. Nucleic Acids Research, 2006, 34, 3968-3979.	14.5	67
1215	A Hidden Markov Model Approach to Model Protein Sequence and Structural Information: Identification of Helix-Turn-Helix DNA-Binding Motif. , 0, , .		0
1216	Autophagy and Related processes in Trypanosomatids: Insights from Genomic and Bioinformatic Analyses. Autophagy, 2006, 2, 107-118.	9.1	64
1217	OrthoMCL-DB: querying a comprehensive multi-species collection of ortholog groups. Nucleic Acids Research, 2006, 34, D363-D368.	14.5	802
1218	WormBase: better software, richer content. Nucleic Acids Research, 2006, 34, D475-D478.	14.5	74
1219	SGCEDb: a flexible database and web interface integrating experimental results and analysis for structural genomics focusing on Caenorhabditis elegans. Nucleic Acids Research, 2006, 34, D471-D474.	14.5	2
1220	The RNA Ontology Consortium: An open invitation to the RNA community. Rna, 2006, 12, 533-541.	3.5	59
1221	The CRAL/TRIO and GOLD Domain Protein CGR-1 Promotes Induction of Vulval Cell Fates in Caenorhabditis elegans and Interacts Genetically With the Ras Signaling Pathway. Genetics, 2006, 172, 929-942.	2.9	4
1222	Computational Prediction of Functionally Important Regions in Proteins. Current Bioinformatics, 2006, 1, 15-23.	1.5	28
1223	Phenotypic effects of membrane protein overexpression in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 11148-11153.	7.1	36
1224	NOPdb: Nucleolar Proteome Database. Nucleic Acids Research, 2006, 34, D218-D220.	14.5	93
1225	The integrated microbial genomes (IMG) system. Nucleic Acids Research, 2006, 34, D344-D348.	14.5	355
1226	VMD: a community annotation database for oomycetes and microbial genomes. Nucleic Acids Research, 2006, 34, D379-D381.	14.5	28

#	ARTICLE	IF	CITATIONS
1227	MuPSSM: a database of multiple position-specific scoring matrices of protein domain families. Nucleic Acids Research, 2006, 34, D243-D246.	14.5	29
1228	pSTIING: a 'systems' approach towards integrating signalling pathways, interaction and transcriptional regulatory networks in inflammation and cancer. Nucleic Acids Research, 2006, 34, D527-D534.	14.5	44
1229	Phytome: a platform for plant comparative genomics. Nucleic Acids Research, 2006, 34, D724-D730.	14.5	35
1230	LOCATE: a mouse protein subcellular localization database. Nucleic Acids Research, 2006, 34, D213-D217.	14.5	72
1231	PANDIT: an evolution-centric database of protein and associated nucleotide domains with inferred trees. Nucleic Acids Research, 2006, 34, D327-D331.	14.5	59
1232	The UCSC Archaeal Genome Browser. Nucleic Acids Research, 2006, 34, D407-D410.	14.5	107
1233	The tmRDB and SRPDB resources. Nucleic Acids Research, 2006, 34, D163-D168.	14.5	107
1234	The UCSC Genome Browser Database: update 2006. Nucleic Acids Research, 2006, 34, D590-D598.	14.5	1,156
1235	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
1236	The Molecular Biology Database Collection: 2006 update. Nucleic Acids Research, 2006, 34, D3-D5.	14.5	83
1237	A supersecondary structure library and search algorithm for modeling loops in protein structures. Nucleic Acids Research, 2006, 34, 2085-2097.	14.5	72
1238	ProKware: integrated software for presenting protein structural properties in protein tertiary structures. Nucleic Acids Research, 2006, 34, W89-W94.	14.5	2
1239	MAVL/StickWRLD: analyzing structural constraints using interpositional dependencies in biomolecular sequence alignments. Nucleic Acids Research, 2006, 34, W133-W136.	14.5	9
1240	Refining multiple sequence alignments with conserved core regions. Nucleic Acids Research, 2006, 34, 2598-2606.	14.5	33
1241	FISH--family identification of sequence homologues using structure anchored hidden Markov models. Nucleic Acids Research, 2006, 34, W10-W14.	14.5	5
1242	DOUTfinder--identification of distant domain outliers using subsignificant sequence similarity. Nucleic Acids Research, 2006, 34, W214-W218.	14.5	9
1243	AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. Nucleic Acids Research, 2006, 34, 3533-3545.	14.5	84
1244	Genomic scale sub-family assignment of protein domains. Nucleic Acids Research, 2006, 34, 3625-3633.	14.5	20

#	ARTICLE	IF	CITATIONS
1245	Multiple alignment of protein sequences with repeats and rearrangements. Nucleic Acids Research, 2006, 34, 5932-5942.	14.5	40
1246	Organization of chromosome ends in the rice blast fungus, <i>Magnaporthe oryzae</i> . Nucleic Acids Research, 2006, 34, 4685-4701.	14.5	98
1247	Inventory and analysis of the protein subunits of the ribonucleases P and MRP provides further evidence of homology between the yeast and human enzymes. Nucleic Acids Research, 2006, 34, 5145-5156.	14.5	67
1248	Genome design™ model and multicellular complexity: golden middle. Nucleic Acids Research, 2006, 34, 5906-5914.	14.5	34
1249	OryGenesDB: a database for rice reverse genetics. Nucleic Acids Research, 2006, 34, D736-D740.	14.5	82
1250	Mutations in the NB-ARC Domain of I-2 That Impair ATP Hydrolysis Cause Autoactivation. Plant Physiology, 2006, 140, 1233-1245.	4.8	276
1251	Integration of Biological Data with Semantic Networks. Current Bioinformatics, 2006, 1, 273-290.	1.5	6
1252	Panzea: a database and resource for molecular and functional diversity in the maize genome. Nucleic Acids Research, 2006, 34, D752-D757.	14.5	89
1253	Multiple Sequence Alignment as a Guideline for Protein Engineering Strategies. , 2006, 340, 171-182.		9
1254	Function and evolution of a gene family encoding odorant binding-like proteins in a social insect, the honey bee (<i>Apis mellifera</i>). Genome Research, 2006, 16, 1404-1413.	5.5	315
1255	INVHOGEN: a database of homologous invertebrate genes. Nucleic Acids Research, 2006, 34, D349-D353.	14.5	4
1256	Validating associations in biological databases. , 2006, , .		1
1257	A systems view of haloarchaeal strategies to withstand stress from transition metals. Genome Research, 2006, 16, 841-854.	5.5	101
1258	A graphical model for predicting protein molecular function. , 2006, , .		7
1259	Retention and Loss of Amino Acid Biosynthetic Pathways Based on Analysis of Whole-Genome Sequences. Eukaryotic Cell, 2006, 5, 272-276.	3.4	117
1260	Protein Homology Network Families Reveal Step-Wise Diversification of Type III and Type IV Secretion Systems. PLoS Computational Biology, 2006, 2, e173.	3.2	51
1261	Prioritizing Genomic Drug Targets in Pathogens: Application to <i>Mycobacterium tuberculosis</i> . PLoS Computational Biology, 2006, 2, e61.	3.2	133
1262	TreeFam: a curated database of phylogenetic trees of animal gene families. Nucleic Acids Research, 2006, 34, D572-D580.	14.5	465

#	ARTICLE	IF	CITATIONS
1263	Metabolism of Isovanillate, Vanillate, and Veratrate by <i>Comamonas testosteroni</i> Strain BR6020. <i>Journal of Bacteriology</i> , 2006, 188, 3862-3869.	2.2	31
1264	DBD: a transcription factor prediction database. <i>Nucleic Acids Research</i> , 2006, 34, D74-D81.	14.5	186
1265	Transcription Factor Map Alignment of Promoter Regions. <i>PLoS Computational Biology</i> , 2006, 2, e49.	3.2	50
1266	Functional Classification Using Phylogenomic Inference. <i>PLoS Computational Biology</i> , 2006, 2, e77.	3.2	61
1267	delayed flowering1 Encodes a Basic Leucine Zipper Protein That Mediates Floral Inductive Signals at the Shoot Apex in Maize. <i>Plant Physiology</i> , 2006, 142, 1523-1536.	4.8	161
1268	Two Membrane-Associated Tyrosine Phosphatase Homologs Potentiate <i>C. elegans</i> AKT-1/PKB Signaling. <i>PLoS Genetics</i> , 2006, 2, e99.	3.5	42
1269	An Integrative Genomic Approach to Uncover Molecular Mechanisms of Prokaryotic Traits. <i>PLoS Computational Biology</i> , 2006, 2, e159.	3.2	28
1270	The Malarial Host-Targeting Signal Is Conserved in the Irish Potato Famine Pathogen. <i>PLoS Pathogens</i> , 2006, 2, e50.	4.7	189
1271	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. <i>PLoS Genetics</i> , 2006, 2, e31.	3.5	661
1272	The <i>Pseudomonas aeruginosa</i> Universal Stress Protein PA4352 Is Essential for Surviving Anaerobic Energy Stress. <i>Journal of Bacteriology</i> , 2006, 188, 6529-6538.	2.2	55
1273	Bacterial regulatory networks are extremely flexible in evolution. <i>Nucleic Acids Research</i> , 2006, 34, 3434-3445.	14.5	207
1274	NikR Mediates Nickel-Responsive Transcriptional Repression of the <i>Helicobacter pylori</i> Outer Membrane Proteins FecA3 (HP1400) and FrpB4 (HP1512). <i>Infection and Immunity</i> , 2006, 74, 6821-6828.	2.2	78
1275	Active-Site Residues in the Type IV Prepilin Peptidase Homologue PibD from the Archaeon <i>Sulfolobus solfataricus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 1437-1443.	2.2	44
1276	A Ferroxidation/Permeation Iron Uptake System Is Required for Virulence in <i>Ustilago maydis</i> . <i>Plant Cell</i> , 2006, 18, 3332-3345.	6.6	154
1277	Analysis of the Lateral Flagellar Gene System of <i>Aeromonas hydrophila</i> AH-3. <i>Journal of Bacteriology</i> , 2006, 188, 852-862.	2.2	74
1278	Comparative and Functional Genomic Analyses of Iron Transport and Regulation in <i>Leptospira</i> spp. <i>Journal of Bacteriology</i> , 2006, 188, 7893-7904.	2.2	66
1279	Defenses against Oxidative Stress in <i>Neisseria gonorrhoeae</i> : a System Tailored for a Challenging Environment. <i>Microbiology and Molecular Biology Reviews</i> , 2006, 70, 344-361.	6.6	128
1280	The proteome: structure, function and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 441-451.	4.0	18

#	ARTICLE	IF	CITATIONS
1281	Exploiting protein structure data to explore the evolution of protein function and biological complexity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 425-440.	4.0	22
1282	DevA, a GntR-Like Transcriptional Regulator Required for Development in <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5014-5023.	2.2	51
1283	Function of the MAPK scaffold protein, Ste5, requires a cryptic PH domain. <i>Genes and Development</i> , 2006, 20, 1946-1958.	5.9	54
1284	The Locus Coding for the 3-Nitrobenzoate Dioxygenase of <i>Comamonas</i> sp. Strain JS46 Is Flanked by IS 1071 Elements and Is Subject to Deletion and Inversion Events. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2651-2660.	3.1	17
1285	indel-Seq-Gen: A New Protein Family Simulator Incorporating Domains, Motifs, and Indels. <i>Molecular Biology and Evolution</i> , 2006, 24, 640-649.	8.9	32
1286	Identification of a DNA Methyltransferase Gene Carried on a Pathogenicity Island-Like Element (VPAI) in <i>Vibrio parahaemolyticus</i> and Its Prevalence among Clinical and Environmental Isolates. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4455-4460.	3.1	28
1287	Innate Immune Responses in NF- κ B-Repressing Factor-Deficient Mice. <i>Molecular and Cellular Biology</i> , 2006, 26, 293-302.	2.3	17
1288	spe-10 Encodes a DHHC-CRD Zinc-Finger Membrane Protein Required for Endoplasmic Reticulum/Golgi Membrane Morphogenesis During <i>Caenorhabditis elegans</i> Spermatogenesis. <i>Genetics</i> , 2006, 172, 145-158.	2.9	33
1289	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251.	14.5	2,030
1290	Identification of RamA, a Novel LuxR-Type Transcriptional Regulator of Genes Involved in Acetate Metabolism of <i>Corynebacterium glutamicum</i> . <i>Journal of Bacteriology</i> , 2006, 188, 2554-2567.	2.2	104
1291	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D684-D688.	14.5	107
1292	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	5.5	138
1293	Identification and Characterization of a Novel ABC Iron Transport System, fit, in <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2006, 74, 6949-6956.	2.2	34
1294	Comparative and Functional Analysis of Sortase-Dependent Proteins in the Predicted Secretome of <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4143-4153.	3.1	145
1295	Evidence for Existence of <i>Mesotoga</i> Members of the Order Thermotogales Adapted to Low-Temperature Environments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5061-5068.	3.1	54
1296	Megx.net—database resources for marine ecological genomics. <i>Nucleic Acids Research</i> , 2006, 34, D390-D393.	14.5	34
1297	Sequence Analysis of the rfb Loci, Encoding Proteins Involved in the Biosynthesis of the <i>Salmonella enterica</i> O17 and O18 Antigens: Serogroup-Specific Identification by PCR. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7949-7953.	3.1	21
1298	A transcriptome analysis of the <i>Aedes aegypti</i> vitellogenic fat body. <i>Journal of Insect Science</i> , 2006, 6, 1-26.	1.5	18

#	ARTICLE	IF	CITATIONS
1299	Analysis of protein sequence and interaction data for candidate disease gene prediction. <i>Nucleic Acids Research</i> , 2006, 34, e130-e130.	14.5	138
1300	Identification of a Virulence-Associated Determinant, Dihydrolipoamide Dehydrogenase (Ipd), in <i>Mycoplasma gallisepticum</i> through In Vivo Screening of Transposon Mutants. <i>Infection and Immunity</i> , 2006, 74, 931-939.	2.2	61
1301	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.	4.8	33
1302	Crystal Structure of Neurotropism-Associated Variable Surface Protein 1 (Vsp1) of <i>Borrelia turicatae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4522-4530.	2.2	19
1303	Genetic and Molecular Characterization of the I Locus of <i>Phaseolus vulgaris</i> . <i>Genetics</i> , 2006, 172, 1229-1242.	2.9	80
1304	Isolation and functional analysis of human HMBOX1, a homeobox containing protein with transcriptional repressor activity. <i>Cytogenetic and Genome Research</i> , 2006, 114, 131-136.	1.1	44
1305	Human Herpesvirus 1 <i>UL24</i> Gene Encodes a Potential PD-(D/E)XK Endonuclease. <i>Journal of Virology</i> , 2006, 80, 2575-2577.	3.4	35
1306	The Homologous Putative GTPases Grn1p from Fission Yeast and the Human GNL3L Are Required for Growth and Play a Role in Processing of Nucleolar Pre-rRNA. <i>Molecular Biology of the Cell</i> , 2006, 17, 460-474.	2.1	43
1307	A <i>Holistic</i> Kinesin Phylogeny Reveals New Kinesin Families and Predicts Protein Functions. <i>Molecular Biology of the Cell</i> , 2006, 17, 1734-1743.	2.1	143
1308	Deletion of TolC orthologs in <i>Francisella tularensis</i> identifies roles in multidrug resistance and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12897-12902.	7.1	105
1309	A <i>Genome design</i> model: Evidence from conserved intronic sequence in human-mouse comparison. <i>Genome Research</i> , 2006, 16, 347-354.	5.5	64
1310	Bioinformatic, Genetic, and Biochemical Evidence that Some Glycoside Hydrolase Family 42 β -Galactosidases Are Arabinogalactan Type I Oligomer Hydrolases. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7730-7738.	3.1	44
1311	Isolation of Poly-3-Hydroxybutyrate Metabolism Genes from Complex Microbial Communities by Phenotypic Complementation of Bacterial Mutants. <i>Applied and Environmental Microbiology</i> , 2006, 72, 384-391.	3.1	60
1312	<i>Paenibacillus</i> sp. Strain JDR-2 and XynA 1 : a Novel System for Methylglucuronoxylan Utilization. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1496-1506.	3.1	57
1313	Mutational Analysis of RetS, an Unusual Sensor Kinase-Response Regulator Hybrid Required for <i>Pseudomonas aeruginosa</i> Virulence. <i>Infection and Immunity</i> , 2006, 74, 4462-4473.	2.2	75
1314	Global Gene Expression Analysis of the Heat Shock Response in the Phytopathogen <i>Xylella fastidiosa</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5821-5830.	2.2	37
1315	The Genome of the Novel Phage Rtp, with a Rosette-Like Tail Tip, Is Homologous to the Genome of Phage T1. <i>Journal of Bacteriology</i> , 2006, 188, 1419-1436.	2.2	44
1316	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	3.5	423

#	ARTICLE	IF	CITATIONS
1317	The <i>Arabidopsis thaliana</i> PARTING DANCERS Gene Encoding a Novel Protein Is Required for Normal Meiotic Homologous Recombination. <i>Molecular Biology of the Cell</i> , 2006, 17, 1331-1343.	2.1	92
1318	Comparative Genomic Evidence for a Close Relationship between the Dimorphic Prosthecate Bacteria <i>Hyphomonas neptunium</i> and <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 6841-6850.	2.2	57
1319	DILIMOT: discovery of linear motifs in proteins. <i>Nucleic Acids Research</i> , 2006, 34, W350-W355.	14.5	121
1320	Graph Theoretical Insights into Evolution of Multidomain Proteins. <i>Journal of Computational Biology</i> , 2006, 13, 351-363.	1.6	76
1321	Identification of a 709-Amino-Acid Internal Nonessential Region within the Essential Conserved Tegument Protein (p)UL36 of Pseudorabies Virus. <i>Journal of Virology</i> , 2006, 80, 9910-9915.	3.4	32
1322	Sequence Analysis of Two Cryptic Plasmids from <i>Bifidobacterium longum</i> DJO10A and Construction of a Shuttle Cloning Vector. <i>Applied and Environmental Microbiology</i> , 2006, 72, 527-535.	3.1	59
1323	Functional Domains of Murine Cytomegalovirus Nuclear Egress Protein M53/p38. <i>Journal of Virology</i> , 2006, 80, 73-84.	3.4	81
1324	Structures of wild-type and mutant human spermidine/spermineN1-acetyltransferase, a potential therapeutic drug target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2063-2068.	7.1	58
1325	The UDP N-Acetylgalactosamine 4-Epimerase Gene Is Essential for Mesophilic <i>Aeromonas hydrophila</i> Serotype O34 Virulence. <i>Infection and Immunity</i> , 2006, 74, 537-548.	2.2	29
1326	Crystal Structure of TDP-Fucosamine Acetyltransferase (WecD) from <i>Escherichia coli</i> , an Enzyme Required for Enterobacterial Common Antigen Synthesis. <i>Journal of Bacteriology</i> , 2006, 188, 5606-5617.	2.2	27
1327	Sequence Analysis and Organization of the Neodiprion abietis Nucleopolyhedrovirus Genome. <i>Journal of Virology</i> , 2006, 80, 6952-6963.	3.4	38
1328	Evolution of protein structural classes and protein sequence families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14056-14061.	7.1	72
1329	Evolution of sensory complexity recorded in a myxobacterial genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15200-15205.	7.1	424
1330	Formation of the <i>Arabidopsis</i> Pentatricopeptide Repeat Family. <i>Plant Physiology</i> , 2006, 141, 825-839.	4.8	85
1331	Characterization of a cancer/testis (CT) antigen gene family capable of eliciting humoral response in cancer patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18066-18071.	7.1	32
1332	Prevalence and Genetic Diversity of Coronaviruses in Bats from China. <i>Journal of Virology</i> , 2006, 80, 7481-7490.	3.4	301
1333	MotD of <i>Sinorhizobium meliloti</i> and Related α -Proteobacteria Is the Flagellar-Hook-Length Regulator and Therefore Reassigned as FliK. <i>Journal of Bacteriology</i> , 2006, 188, 2144-2153.	2.2	24
1334	Genomic Organization, Differential Expression, and Interaction of SQUAMOSA Promoter-Binding-Like Transcription Factors and microRNA156 in Rice. <i>Plant Physiology</i> , 2006, 142, 280-293.	4.8	595

#	ARTICLE	IF	CITATIONS
1335	SNP@Domain: a web resource of single nucleotide polymorphisms (SNPs) within protein domain structures and sequences. <i>Nucleic Acids Research</i> , 2006, 34, W642-W644.	14.5	21
1336	The Multifunctional \hat{I}^2 -Oxidation Enzyme Is Required for Full Symptom Development by the Biotrophic Maize Pathogen <i>Ustilago maydis</i> . <i>Eukaryotic Cell</i> , 2006, 5, 2047-2061.	3.4	38
1337	A New Immunoglobulin-Binding Protein, EibG, Is Responsible for the Chain-Like Adhesion Phenotype of Locus of Enterocyte Effacement-Negative, Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2006, 74, 5747-5755.	2.2	43
1338	Pertactin beta-helix folding mechanism suggests common themes for the secretion and folding of autotransporter proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4918-4923.	7.1	187
1339	The structural basis for regulated assembly and function of the transcriptional activator NtrC. <i>Genes and Development</i> , 2006, 20, 1485-1495.	5.9	109
1340	Cyanobacterial Two-Component Proteins: Structure, Diversity, Distribution, and Evolution. <i>Microbiology and Molecular Biology Reviews</i> , 2006, 70, 472-509.	6.6	123
1341	An Arabidopsis Basic Helix-Loop-Helix Leucine Zipper Protein Modulates Metal Homeostasis and Auxin Conjugate Responsiveness. <i>Genetics</i> , 2006, 174, 1841-1857.	2.9	98
1342	Lectin Receptor Kinases Participate in Protein-Protein Interactions to Mediate Plasma Membrane-Cell Wall Adhesions in Arabidopsis. <i>Plant Physiology</i> , 2006, 140, 81-90.	4.8	165
1343	The <i>Cryptococcus neoformans</i> Catalase Gene Family and Its Role in Antioxidant Defense. <i>Eukaryotic Cell</i> , 2006, 5, 1447-1459.	3.4	85
1344	The hmuQ and hmuD Genes from <i>Bradyrhizobium japonicum</i> Encode Heme-Degrading Enzymes. <i>Journal of Bacteriology</i> , 2006, 188, 6476-6482.	2.2	51
1345	Polar Flagellum Biogenesis in <i>Aeromonas hydrophila</i> . <i>Journal of Bacteriology</i> , 2006, 188, 542-555.	2.2	76
1346	SNAP: predict effect of non-synonymous polymorphisms on function. <i>Nucleic Acids Research</i> , 2007, 35, 3823-3835.	14.5	728
1347	Feature Extraction in Spatially-Conserved Regions and Protein Functional Classification. , 2007, , .		2
1348	G-protein Coupled Receptor Subfamilies Prediction Based on Nearest Neighbor Approach. , 2007, , .		0
1349	Evolution of the iron-responsive element. <i>Rna</i> , 2007, 13, 952-966.	3.5	138
1350	Global extent of horizontal gene transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4489-4494.	7.1	142
1351	Regulatory evolution in proteins by turnover and lineage-specific changes of cyclin-dependent kinase consensus sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17713-17718.	7.1	62
1352	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13913-13918.	7.1	72

#	ARTICLE	IF	CITATIONS
1353	Otopetrin 1 activation by purinergic nucleotides regulates intracellular calcium. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12023-12028.	7.1	37
1354	The protein that binds to DNA base J in trypanosomatids has features of a thymidine hydroxylase. Nucleic Acids Research, 2007, 35, 2107-2115.	14.5	84
1355	Comparisons Among Two Fertile and Three Male-Sterile Mitochondrial Genomes of Maize. Genetics, 2007, 177, 1173-1192.	2.9	210
1356	Approaching a complete repository of sequence-verified protein-encoding clones for <i>Saccharomyces cerevisiae</i> . Genome Research, 2007, 17, 536-543.	5.5	99
1357	Identification and Analysis of Novel Amino-Acid Sequence Repeats in <i>Bacillus anthracis</i> str. Ames Proteome Using Computational Tools. Comparative and Functional Genomics, 2007, 2007, 1-23.	2.0	5
1358	Novel Algorithms Reveal Streptococcal Transcriptomes and Clues about Undefined Genes. PLoS Computational Biology, 2007, 3, e132.	3.2	14
1359	Superfamily Assignments for the Yeast Proteome through Integration of Structure Prediction with the Gene Ontology. PLoS Biology, 2007, 5, e76.	5.6	48
1360	Proteomic and Immunoblot Analyses of <i>Bartonella quintana</i> Total Membrane Proteins Identify Antigens Recognized by Sera from Infected Patients. Infection and Immunity, 2007, 75, 2548-2561.	2.2	52
1361	Automated Protein Subfamily Identification and Classification. PLoS Computational Biology, 2007, 3, e160.	3.2	110
1362	The Undergraduate Genomics Research Initiative. PLoS Biology, 2007, 5, e141.	5.6	23
1363	Variants in a Novel Epidermal Collagen Gene (COL29A1) Are Associated with Atopic Dermatitis. PLoS Biology, 2007, 5, e242.	5.6	153
1364	PROMALS web server for accurate multiple protein sequence alignments. Nucleic Acids Research, 2007, 35, W649-W652.	14.5	61
1365	A Comparative and Phylogenetic Analysis of the α -Actinin Rod Domain. Molecular Biology and Evolution, 2007, 24, 2254-2265.	8.9	27
1366	Identification of <i>Escherichia coli</i> O157:H7 Genomic Regions Conserved in Strains with a Genotype Associated with Human Infection. Applied and Environmental Microbiology, 2007, 73, 22-31.	3.1	33
1367	ApiDB: integrated resources for the apicomplexan bioinformatics resource center. Nucleic Acids Research, 2007, 35, D427-D430.	14.5	94
1368	Challenges and Solutions in Proteomics. Current Genomics, 2007, 8, 21-28.	1.6	12
1369	Draft Crystal Structure of the Vault Shell at 9-Å... Resolution. PLoS Biology, 2007, 5, e318.	5.6	43
1370	An insight into the sialome of the oriental rat flea, <i>Xenopsylla cheopis</i> (Rots). BMC Genomics, 2007, 8, 102.	2.8	70

#	ARTICLE	IF	CITATIONS
1371	EVEREST: a collection of evolutionary conserved protein domains. Nucleic Acids Research, 2007, 35, D241-D246.	14.5	20
1372	Gating Rings Formed by RCK Domains: Keys to Gate Opening. Journal of General Physiology, 2007, 129, 101-107.	1.9	28
1373	Structural and Chemical Profiling of the Human Cytosolic Sulfotransferases. PLoS Biology, 2007, 5, e97.	5.6	187
1374	A Tree of Life Based on Protein Domain Organizations. Molecular Biology and Evolution, 2007, 24, 1181-1189.	8.9	47
1375	The Molecular Biology Database Collection: 2007 update. Nucleic Acids Research, 2007, 35, D3-D4.	14.5	80
1376	PROTCOM: searchable database of protein complexes enhanced with domain-domain structures. Nucleic Acids Research, 2007, 35, D575-D579.	14.5	43
1377	TBestDB: a taxonomically broad database of expressed sequence tags (ESTs). Nucleic Acids Research, 2007, 35, D445-D451.	14.5	81
1378	POGs/PlantRBP: a resource for comparative genomics in plants. Nucleic Acids Research, 2007, 35, D852-D856.	14.5	31
1379	SNAPPI-DB: a database and API of Structures, iNterfaces and Alignments for Protein-Protein Interactions. Nucleic Acids Research, 2007, 35, D580-D589.	14.5	58
1380	PATRIC: The VBI PathoSystems Resource Integration Center. Nucleic Acids Research, 2007, 35, D401-D406.	14.5	125
1381	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. Nucleic Acids Research, 2007, 35, D347-D353.	14.5	87
1382	Comparative DNA Analysis of Two vanA Plasmids from Enterococcus faecium Strains Isolated from Poultry and a Poultry Farmer in Norway. Antimicrobial Agents and Chemotherapy, 2007, 51, 736-739.	3.2	58
1383	Functional Similarity Analyzing of Protein Sequences with Empirical Mode Decomposition. , 2007, , .		10
1384	Comparative Analysis of Twelve Genomes of Three Novel Group 2c and Group 2d Coronaviruses Reveals Unique Group and Subgroup Features. Journal of Virology, 2007, 81, 1574-1585.	3.4	233
1385	PBB. , 2007, , .		1
1386	The identification of complete domains within protein sequences using accurate E-values for semi-global alignment. Nucleic Acids Research, 2007, 35, 4678-4685.	14.5	15
1387	TIGRFAMs and Genome Properties: tools for the assignment of molecular function and biological process in prokaryotic genomes. Nucleic Acids Research, 2007, 35, D260-D264.	14.5	266
1388	An Early Nodulin-Like Protein Accumulates in the Sieve Element Plasma Membrane of Arabidopsis. Plant Physiology, 2007, 143, 1576-1589.	4.8	65

#	ARTICLE	IF	CITATIONS
1389	A <i>Phytophthora infestans</i> Cystatin-Like Protein Targets a Novel Tomato Papain-Like Apoplastic Protease. <i>Plant Physiology</i> , 2007, 143, 364-377.	4.8	277
1390	Correlated substitution analysis and the prediction of amino acid structural contacts. <i>Briefings in Bioinformatics</i> , 2007, 9, 46-56.	6.5	58
1391	High Performance Database Searching with HMMer on FPGAs. , 2007, , .		14
1392	SUBA: the Arabidopsis Subcellular Database. <i>Nucleic Acids Research</i> , 2007, 35, D213-D218.	14.5	394
1393	Preliminary results in accelerating profile HMM search on FPGAs. , 2007, , .		17
1394	<i>Lactococcus lactis</i> Gene <i>yjgB</i> Encodes a $\hat{3}$ - <scp>d</scp>-Glutaminy- <scp>l</scp>-Lysyl-Endopeptidase Which Hydrolyzes Peptidoglycan. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5825-5831.	3.1	15
1395	empty pericarp4 Encodes a Mitochondrion-Targeted Pentatricopeptide Repeat Protein Necessary for Seed Development and Plant Growth in Maize. <i>Plant Cell</i> , 2007, 19, 196-210.	6.6	117
1396	The Nuclear-Encoded Factor HCF173 Is Involved in the Initiation of Translation of the <i>psbA</i> mRNA in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2007, 19, 1329-1346.	6.6	95
1397	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. <i>Briefings in Bioinformatics</i> , 2007, 9, 34-45.	6.5	4
1398	Identification of the Origin of Transfer (<i>oriT</i>) and DNA Relaxase Required for Conjugation of the Integrative and Conjugative Element ICE Bs1 of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2007, 189, 7254-7261.	2.2	79
1399	Nectin-like proteins mediate axon-Schwann cell interactions along the internode and are essential for myelination. <i>Journal of Cell Biology</i> , 2007, 178, 861-874.	5.2	158
1400	Identification of Diverse Archaeal Proteins with Class III Signal Peptides Cleaved by Distinct Archaeal Prepilin Peptidases. <i>Journal of Bacteriology</i> , 2007, 189, 772-778.	2.2	139
1401	Ecological Genomics of Marine Roseobacters. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4559-4569.	3.1	327
1402	DBAli tools: mining the protein structure space. <i>Nucleic Acids Research</i> , 2007, 35, W393-W397.	14.5	25
1403	Genetic Relatedness of the <i>Streptococcus pneumoniae</i> Capsular Biosynthetic Loci. <i>Journal of Bacteriology</i> , 2007, 189, 7841-7855.	2.2	118
1404	MPS3 mediates meiotic bouquet formation in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8863-8868.	7.1	139
1405	Characterization of a <i>Pseudomonas</i> 2-Nitrobenzoate Nitroreductase and Its Catabolic Pathway-Associated 2-Hydroxylaminobenzoate Mutase and a Chemoreceptor Involved in 2-Nitrobenzoate Chemotaxis. <i>Journal of Bacteriology</i> , 2007, 189, 3502-3514.	2.2	64
1406	Role of Gne and GalE in the Virulence of <i>Aeromonas hydrophila</i> Serotype O34. <i>Journal of Bacteriology</i> , 2007, 189, 540-550.	2.2	24

#	ARTICLE	IF	CITATIONS
1407	Discovering and detecting transposable elements in genome sequences. Briefings in Bioinformatics, 2007, 8, 382-392.	6.5	189
1408	The 3D structure of a periplasm-spanning platform required for assembly of group 1 capsular polysaccharides in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2390-2395.	7.1	139
1409	Role of the <i>rapA</i> Gene in Controlling Antibiotic Resistance of <i>Escherichia coli</i> Biofilms. Antimicrobial Agents and Chemotherapy, 2007, 51, 3650-3658.	3.2	90
1410	<i>Listeria monocytogenes</i> Surface Proteins: from Genome Predictions to Function. Microbiology and Molecular Biology Reviews, 2007, 71, 377-397.	6.6	230
1411	Proteome-Wide Prediction of Novel DNA/RNA-Binding Proteins Using Amino Acid Composition and Periodicity in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> . DNA Research, 2007, 14, 91-102.	3.4	16
1412	MyHits: improvements to an interactive resource for analyzing protein sequences. Nucleic Acids Research, 2007, 35, W433-W437.	14.5	185
1413	Berkeley Phylogenomics Group web servers: resources for structural phylogenomic analysis. Nucleic Acids Research, 2007, 35, W27-W32.	14.5	24
1414	CytoSVM: an advanced server for identification of cytokine-receptor interactions. Nucleic Acids Research, 2007, 35, W538-W542.	14.5	10
1415	Genome Sequence of Avery's Virulent Serotype 2 Strain D39 of <i>Streptococcus pneumoniae</i> and Comparison with That of Unencapsulated Laboratory Strain R6. Journal of Bacteriology, 2007, 189, 38-51.	2.2	429
1416	BioBayesNet: a web server for feature extraction and Bayesian network modeling of biological sequence data. Nucleic Acids Research, 2007, 35, W688-W693.	14.5	17
1417	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. Journal of Cell Biology, 2007, 178, 477-488.	5.2	140
1418	24 Bioinformatic Prediction of Yeast Gene Function. Methods in Microbiology, 2007, , 597-628.	0.8	4
1419	Gain-of-Function Mutations in the MEC-4 DEG/ENaC Sensory Mechanotransduction Channel Alter Gating and Drug Blockade. Journal of General Physiology, 2007, 129, 161-173.	1.9	37
1420	Adaptive Evolution Has Targeted the C-Terminal Domain of the RXLR Effectors of Plant Pathogenic Oomycetes. Plant Cell, 2007, 19, 2349-2369.	6.6	315
1421	High-throughput modeling and analysis of protein structural dynamics. Briefings in Bioinformatics, 2007, 8, 432-445.	6.5	8
1422	Diminished Redundancy of Outer Membrane Factor Proteins in Rhizobiales: A <i>nodT</i> Homolog Is Essential for Free-Living <i>Rhizobium etli</i> . Journal of Molecular Microbiology and Biotechnology, 2007, 13, 22-34.	1.0	13
1423	Enterococcal Leucine-Rich Repeat-Containing Protein Involved in Virulence and Host Inflammatory Response. Infection and Immunity, 2007, 75, 4463-4471.	2.2	50
1424	MALISAM: a database of structurally analogous motifs in proteins. Nucleic Acids Research, 2007, 36, D211-D217.	14.5	25

#	ARTICLE	IF	CITATIONS
1425	Comparative Genomics and Adaptive Selection of the ATP-Binding-Cassette Gene Family in <i>Caenorhabditis</i> Species. <i>Genetics</i> , 2007, 175, 1407-1418.	2.9	26
1426	LIN-61, One of Two <i>Caenorhabditis elegans</i> Malignant-Brain-Tumor-Repeat-Containing Proteins, Acts With the DRM and NuRD-Like Protein Complexes in Vulval Development but Not in Certain Other Biological Processes. <i>Genetics</i> , 2007, 176, 255-271.	2.9	36
1427	Identifying foldable regions in protein sequence from the hydrophobic signal. <i>Nucleic Acids Research</i> , 2007, 36, 578-588.	14.5	15
1428	ProtSweep, 2Dsweep and DomainSweep: protein analysis suite at DKFZ. <i>Nucleic Acids Research</i> , 2007, 35, W444-W450.	14.5	14
1429	Nickel-Resistant Determinant from <i>Leptospirillum ferriphilum</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 2364-2368.	3.1	28
1430	<i>Helicobacter pylori</i> EstV: Identification, Cloning, and Characterization of the First Lipase Isolated from an Epsilon-Proteobacterium. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2423-2431.	3.1	33
1431	Genomics and Proteomics of Foodborne Microorganisms. , 2007, , 935-951.		2
1432	Degradation of Î»-carrageenan by <i>Pseudoalteromonas carrageenovora</i> Î»-carrageenase: a new family of glycoside hydrolases unrelated to Îº- and Î¹-carrageenases. <i>Biochemical Journal</i> , 2007, 404, 105.	3.7	38
1433	A CBS domain-containing pyrophosphatase of <i>Moorella thermoacetica</i> is regulated by adenine nucleotides. <i>Biochemical Journal</i> , 2007, 408, 327-333.	3.7	28
1434	Multiple Graph Alignment for the Structural Analysis of Protein Active Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 310-320.	3.0	30
1435	Avl9p, a Member of a Novel Protein Superfamily, Functions in the Late Secretory Pathway. <i>Molecular Biology of the Cell</i> , 2007, 18, 1203-1219.	2.1	40
1436	The tify family previously known as ZIM. <i>Trends in Plant Science</i> , 2007, 12, 239-244.	8.8	283
1437	Diversity of olfactomedin proteins in the sea urchin. <i>Genomics</i> , 2007, 89, 721-730.	2.9	11
1438	Membrane protein prediction methods. <i>Methods</i> , 2007, 41, 460-474.	3.8	104
1439	Multiplex, Bead-Based Suspension Array for Molecular Determination of Common <i>Salmonella</i> Serogroups. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3323-3334.	3.9	150
1440	A fragmented aflatoxin-like gene cluster in the forest pathogen <i>Dothistroma septosporum</i> . <i>Fungal Genetics and Biology</i> , 2007, 44, 1342-1354.	2.1	35
1441	Immune gene discovery by expressed sequence tag analysis of spleen in the duck (<i>Anas platyrhynchos</i>). <i>Developmental and Comparative Immunology</i> , 2007, 31, 272-285.	2.3	23
1442	Acheron, a novel member of the Lupus Antigen family, is induced during the programmed cell death of skeletal muscles in the moth <i>Manduca sexta</i> . <i>Gene</i> , 2007, 393, 101-109.	2.2	34

#	ARTICLE	IF	CITATIONS
1443	Structural and thermodynamic consequences of b heme binding for monomeric apoglobins and other apoproteins. <i>Gene</i> , 2007, 398, 12-28.	2.2	29
1444	Modeling the Evolution of Protein Domain Architectures Using Maximum Parsimony. <i>Journal of Molecular Biology</i> , 2007, 366, 307-315.	4.2	104
1445	Exclusion of Glucosyl-Hydroxymethylcytosine DNA Containing Bacteriophages Is Overcome by the Injected Protein Inhibitor IPI*. <i>Journal of Molecular Biology</i> , 2007, 366, 779-789.	4.2	55
1446	HotPatch: A Statistical Approach to Finding Biologically Relevant Features on Protein Surfaces. <i>Journal of Molecular Biology</i> , 2007, 369, 863-879.	4.2	73
1447	An insight into the sialome of the adult female mosquito <i>Aedes albopictus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 107-127.	2.7	119
1448	An insight into the sialome of <i>Anopheles funestus</i> reveals an emerging pattern in anopheline salivary protein families. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 164-175.	2.7	101
1449	The sialotranscriptome of the blood-sucking bug <i>Triatoma brasiliensis</i> (Hemiptera, Triatominae). <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 702-712.	2.7	78
1450	An insight into the sialotranscriptome of the seed-feeding bug, <i>Oncopeltus fasciatus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 903-910.	2.7	29
1451	A cuticle protein gene in the honeybee: Expression during development and in relation to the ecdysteroid titer. <i>Insect Biochemistry and Molecular Biology</i> , 2007, 37, 1272-1282.	2.7	32
1452	Conservation of transcriptional sensing systems in prokaryotes: A perspective from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 2007, 581, 3499-3506.	2.8	6
1453	RestauRO-G: A Rapid Genome Re-Annotation System for Comparative Genomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 53-58.	6.9	17
1454	RiceDB: A Web-Based Integrated Database for Annotating Rice Microarray. <i>Rice Science</i> , 2007, 14, 256-264.	3.9	1
1455	Direct selection and phage display of a Gram-positive secretome. <i>Genome Biology</i> , 2007, 8, R266.	9.6	20
1456	Determinants of protein function revealed by combinatorial entropy optimization. <i>Genome Biology</i> , 2007, 8, R232.	9.6	262
1457	Using protein complexes to predict phenotypic effects of gene mutation. <i>Genome Biology</i> , 2007, 8, R252.	9.6	101
1458	Surprising complexity of the ancestral apoptosis network. <i>Genome Biology</i> , 2007, 8, R226.	9.6	77
1459	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	9.6	53
1460	Drawing the tree of eukaryotic life based on the analysis of 2,269 manually annotated myosins from 328 species. <i>Genome Biology</i> , 2007, 8, R196.	9.6	313

#	ARTICLE	IF	CITATIONS
1461	PHIDIAS: a pathogen-host interaction data integration and analysis system. <i>Genome Biology</i> , 2007, 8, R150.	9.6	63
1462	New genes in the evolution of the neural crest differentiation program. <i>Genome Biology</i> , 2007, 8, R36.	9.6	42
1463	Kappa-alpha plot derived structural alphabet and BLOSUM-like substitution matrix for rapid search of protein structure database. <i>Genome Biology</i> , 2007, 8, R31.	9.6	73
1464	A network perspective on the evolution of metabolism by gene duplication. <i>Genome Biology</i> , 2007, 8, R26.	9.6	51
1465	DiscoverySpace: an interactive data analysis application. <i>Genome Biology</i> , 2007, 8, R6.	9.6	41
1466	Three two-component transporters with channel-like properties have monovalent cation/proton antiport activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13289-13294.	7.1	59
1467	Complete Genome Sequence of the Prototype Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. <i>Journal of Bacteriology</i> , 2007, 189, 3256-3270.	2.2	362
1468	A Lazy Data Mining Approach for Protein Classification. <i>IEEE Transactions on Nanobioscience</i> , 2007, 6, 36-42.	3.3	13
1469	Prediction of protein interactions by combining genetic algorithm with SVM method. , 2007, , .		6
1470	Integration of Rotation and Piston Motions in Coiled-Coil Signal Transduction. <i>Journal of Bacteriology</i> , 2007, 189, 6048-6056.	2.2	30
1471	BioPM:An Efficient Algorithm for Protein Motif Mining. , 2007, , .		11
1472	Using Domain-Based Structural Ensemble to Improve Structure Modeling. , 2007, , .		0
1473	Protein Structure Prediction Based on a Domain Clustering Database. , 2007, , .		1
1474	The Early Response to Acid Shock in <i>Lactobacillus reuteri</i> Involves the ClpL Chaperone and a Putative Cell Wall-Altering Esterase. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3924-3935.	3.1	115
1475	Genome sequencing reveals complex secondary metabolome in the marine actinomycete <i>Salinispora tropica</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10376-10381.	7.1	502
1476	SmedGD: the <i>Schmidtea mediterranea</i> genome database. <i>Nucleic Acids Research</i> , 2007, 36, D599-D606.	14.5	251
1477	CPC: assess the protein-coding potential of transcripts using sequence features and support vector machine. <i>Nucleic Acids Research</i> , 2007, 35, W345-W349.	14.5	2,525
1478	Functional Analysis of Nine Putative Chemoreceptor Proteins in <i>Sinorhizobium meliloti</i> . <i>Journal of Bacteriology</i> , 2007, 189, 1816-1826.	2.2	51

#	ARTICLE	IF	CITATIONS
1479	pKaPS: prediction of protein kinase A phosphorylation sites with the simplified kinase-substrate binding model. <i>Biology Direct</i> , 2007, 2, 1.	4.6	131
1480	Amino-Acid Properties and Consequences of Substitutions. , 0, , 311-342.		88
1481	Recent Advances in Solving the Protein Threading Problem. , 0, , 325-356.		2
1482	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	5.6	736
1483	Plant Carbohydrate Scavenging through TonB-Dependent Receptors: A Feature Shared by Phytopathogenic and Aquatic Bacteria. <i>PLoS ONE</i> , 2007, 2, e224.	2.5	289
1484	The genome of <i>Hyperthermus butylicus</i> : a sulfur-reducing, peptide fermenting, neutrophilic Crenarchaeote growing up to 108 °C. <i>Archaea</i> , 2007, 2, 127-135.	2.3	41
1485	Disulfide bond disruption by a γ -Cys549Arg mutation in six Jordanian families with Glanzmann thrombasthenia causes diminished production of constitutively active β -tubulin. <i>Thrombosis and Haemostasis</i> , 2007, 98, 1257-1265.	3.4	37
1486	Computational methodologies for genome evolution and functional association. <i>Computers and Chemical Engineering</i> , 2007, 31, 943-949.	3.8	1
1487	Structure of a UPF0150-family protein from <i>Thermus thermophilus</i> HB8. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 173-177.	0.7	2
1488	The crystallization of apo-form UMP kinase from <i>Xanthomonas campestris</i> significantly improved in a strong magnetic field. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 438-442.	0.7	5
1489	Structure of O67745_AQUAE, a hypothetical protein from <i>Aquifex aeolicus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 369-374.	0.7	7
1490	Structure of the hypothetical protein PF0899 from <i>Pyrococcus furiosus</i> at 1.85 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 549-552.	0.7	6
1491	Domain selection combined with improved cloning strategy for high throughput expression of higher eukaryotic proteins. <i>BMC Biotechnology</i> , 2007, 7, 45.	3.3	6
1492	Realm of PD-(D/E)XK nuclease superfamily revisited: detection of novel families with modified transitive meta profile searches. <i>BMC Structural Biology</i> , 2007, 7, 40.	2.3	57
1493	Regulation of AMP-activated protein kinase by a pseudosubstrate sequence on the β subunit. <i>EMBO Journal</i> , 2007, 26, 806-815.	7.8	43
1494	An atypical receiver domain controls the dynamic polar localization of the <i>Myxococcus xanthus</i> social motility protein FrzS. <i>Molecular Microbiology</i> , 2007, 65, 319-332.	2.5	32
1495	Folds and activities of peptidoglycan amidases. <i>FEMS Microbiology Reviews</i> , 2007, 31, 676-691.	8.6	66
1496	Transcriptional Analysis of Three Major Putative Phosphatidylinositol Kinase Genes in a Parasitic Protozoan, <i>Giardia lamblia</i> . <i>Journal of Eukaryotic Microbiology</i> , 2007, 54, 29-32.	1.7	17

#	ARTICLE	IF	CITATIONS
1497	HMM-ModE – Improved classification using profile hidden Markov models by optimising the discrimination threshold and modifying emission probabilities with negative training sequences. BMC Bioinformatics, 2007, 8, 104.	2.6	31
1498	CGKB: an annotation knowledge base for cowpea (<i>Vigna unguiculata</i> L.) methylation filtered genomic genespace sequences. BMC Bioinformatics, 2007, 8, 129.	2.6	54
1499	Multiple non-collinear TF-map alignments of promoter regions. BMC Bioinformatics, 2007, 8, 138.	2.6	10
1500	Reconstruction of human protein interolog network using evolutionary conserved network. BMC Bioinformatics, 2007, 8, 152.	2.6	33
1501	A domain-based approach to predict protein-protein interactions. BMC Bioinformatics, 2007, 8, 199.	2.6	68
1502	Relationship between insertion/deletion (indel) frequency of proteins and essentiality. BMC Bioinformatics, 2007, 8, 227.	2.6	33
1503	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	2.6	68
1504	Efficacy of different protein descriptors in predicting protein functional families. BMC Bioinformatics, 2007, 8, 300.	2.6	66
1505	MaxAlign: maximizing usable data in an alignment. BMC Bioinformatics, 2007, 8, 312.	2.6	113
1506	Gene analogue finder: a GRID solution for finding functionally analogous gene products. BMC Bioinformatics, 2007, 8, 329.	2.6	6
1507	PathFinder: mining signal transduction pathway segments from protein-protein interaction networks. BMC Bioinformatics, 2007, 8, 335.	2.6	101
1508	Improving model construction of profile HMMs for remote homology detection through structural alignment. BMC Bioinformatics, 2007, 8, 435.	2.6	20
1509	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. BMC Bioinformatics, 2007, 8, 47.	2.6	23
1510	Blast sampling for structural and functional analyses. BMC Bioinformatics, 2007, 8, 62.	2.6	6
1511	False occurrences of functional motifs in protein sequences highlight evolutionary constraints. BMC Bioinformatics, 2007, 8, 68.	2.6	8
1512	Structural and evolutionary bioinformatics of the SPOUT superfamily of methyltransferases. BMC Bioinformatics, 2007, 8, 73.	2.6	137
1513	Towards a comprehensive structural coverage of completed genomes: a structural genomics viewpoint. BMC Bioinformatics, 2007, 8, 86.	2.6	45
1514	Linear array of conserved sequence motifs to discriminate protein subfamilies: study on pyridine nucleotide-disulfide reductases. BMC Bioinformatics, 2007, 8, 96.	2.6	9

#	ARTICLE	IF	CITATIONS
1515	A computational approach for detecting peptidases and their specific inhibitors at the genome level. BMC Bioinformatics, 2007, 8, S3.	2.6	5
1516	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
1517	Using structural motif descriptors for sequence-based binding site prediction. BMC Bioinformatics, 2007, 8, S5.	2.6	22
1518	Refining intra-protein contact prediction by graph analysis. BMC Bioinformatics, 2007, 8, S6.	2.6	6
1519	Multiple domain insertions and losses in the evolution of the Rab prenylation complex. BMC Evolutionary Biology, 2007, 7, 140.	3.2	22
1520	Horizontal gene transfer in chromalveolates. BMC Evolutionary Biology, 2007, 7, 173.	3.2	80
1521	The frontier between cell and organelle: genome analysis of <i>Candidatus Carsonella ruddii</i> . BMC Evolutionary Biology, 2007, 7, 181.	3.2	106
1522	Phylogenetic analysis of condensation domains in NRPS sheds light on their functional evolution. BMC Evolutionary Biology, 2007, 7, 78.	3.2	301
1523	FlowerPower: clustering proteins into domain architecture classes for phylogenomic inference of protein function. BMC Evolutionary Biology, 2007, 7, S12.	3.2	46
1524	Detecting non-coding selective pressure in coding regions. BMC Evolutionary Biology, 2007, 7, S9.	3.2	26
1525	The evolutionary conservation of the core components necessary for the extrinsic apoptotic signaling pathway, in Medaka fish. BMC Genomics, 2007, 8, 141.	2.8	32
1526	Phylogenetic distribution of translational GTPases in bacteria. BMC Genomics, 2007, 8, 15.	2.8	100
1527	The functional modulation of epigenetic regulators by alternative splicing. BMC Genomics, 2007, 8, 252.	2.8	14
1528	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. BMC Genomics, 2007, 8, 31.	2.8	64
1529	The extracellular Leucine-Rich Repeat superfamily; a comparative survey and analysis of evolutionary relationships and expression patterns. BMC Genomics, 2007, 8, 320.	2.8	147
1530	AphanoDB: a genomic resource for <i>Aphanomyces</i> pathogens. BMC Genomics, 2007, 8, 471.	2.8	43
1531	An annotated catalogue of salivary gland transcripts in the adult female mosquito, <i>Anopheles gambiae</i> . BMC Genomics, 2007, 8, 6.	2.8	219
1532	Spotted cotton oligonucleotide microarrays for gene expression analysis. BMC Genomics, 2007, 8, 81.	2.8	43

#	ARTICLE	IF	CITATIONS
1533	The actin multigene family of <i>Paramecium tetraurelia</i> . BMC Genomics, 2007, 8, 82.	2.8	28
1534	Gene function in early mouse embryonic stem cell differentiation. BMC Genomics, 2007, 8, 85.	2.8	123
1535	De novo identification of LTR retrotransposons in eukaryotic genomes. BMC Genomics, 2007, 8, 90.	2.8	73
1536	Structure and evolution of a proviral locus of <i>Glyptapanteles indiensis</i> bracovirus. BMC Microbiology, 2007, 7, 61.	3.3	45
1537	Plant SET domain-containing proteins: Structure, function and regulation. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2007, 1769, 316-329.	2.4	159
1538	Harnessing bioinformatics to discover new vaccines. Drug Discovery Today, 2007, 12, 389-395.	6.4	174
1539	Functional and Crystal Structure Analysis of Active Site Adaptations of a Potent Anti-Angiogenic Human tRNA Synthetase. Structure, 2007, 15, 793-805.	3.3	41
1540	An Empirical Codon Model for Protein Sequence Evolution. Molecular Biology and Evolution, 2007, 24, 1464-1479.	8.9	166
1541	Analysis and prediction of functionally important sites in proteins. Protein Science, 2007, 16, 4-13.	7.6	44
1542	DDOMAIN: Dividing structures into domains using a normalized domain-domain interaction profile. Protein Science, 2007, 16, 947-955.	7.6	67
1543	Atomic model of human Rcd-1 reveals an armadillo-like-repeat protein with in vitro nucleic acid binding properties. Protein Science, 2007, 16, 176-188.	7.6	54
1544	Solution structure of the zinc finger HIT domain in protein FON. Protein Science, 2007, 16, 1577-1587.	7.6	23
1545	The crystal structure of <i>M. leprae</i> ML2640c defines a large family of putative S-adenosylmethionine-dependent methyltransferases in mycobacteria. Protein Science, 2007, 16, 1896-1904.	7.6	14
1546	Robust recognition of zinc binding sites in proteins. Protein Science, 2008, 17, 54-65.	7.6	88
1547	Crystal structure of 5-methylthioribose 1-phosphate isomerase product complex from <i>Bacillus subtilis</i> : Implications for catalytic mechanism. Protein Science, 2007, 17, 126-135.	7.6	23
1548	Evolution of Gene Overlaps: Relative Reading Frame Bias in Prokaryotic Two-Component System Genes. Journal of Molecular Evolution, 2007, 64, 457-462.	1.8	25
1549	The <i>Arabidopsis thaliana</i> AT PRP39-1 gene, encoding a tetratricopeptide repeat protein with similarity to the yeast pre-mRNA processing protein PRP39, affects flowering time. Plant Cell Reports, 2007, 26, 1357-1366.	5.6	44
1550	The continuing conundrum of the LEA proteins. Die Naturwissenschaften, 2007, 94, 791-812.	1.6	629

#	ARTICLE	IF	CITATIONS
1551	Genetic and physical localization of an anthracnose resistance gene in <i>Medicago truncatula</i> . <i>Theoretical and Applied Genetics</i> , 2007, 116, 45-52.	3.6	22
1552	Cloning and Characterization of a Novel Crystal Protein from a Native <i>Bacillus thuringiensis</i> Isolate Highly Active Against <i>Aedes aegypti</i> . <i>Current Microbiology</i> , 2007, 54, 271-276.	2.2	10
1553	Computational protein function prediction: Are we making progress?. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 2505-2511.	5.4	46
1554	Structure-based inference of molecular functions of proteins of unknown function from Berkeley Structural Genomics Center. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 99-105.	1.2	26
1555	Molecular cloning and expression of the C-terminal domain of mouse NTE-related esterase. <i>Molecular and Cellular Biochemistry</i> , 2007, 306, 25-32.	3.1	11
1556	Cloning and expression of a novel human gene, Isl-2, encoded a LIM-homeodomain protein. <i>Molecular Biology Reports</i> , 2007, 34, 19-26.	2.3	8
1557	Complete nucleotide sequence of Nootka lupine vein-clearing virus. <i>Virus Genes</i> , 2007, 35, 807-814.	1.6	29
1558	A collection of 10,096 indica rice full-length cDNAs reveals highly expressed sequence divergence between <i>Oryza sativa indica</i> and <i>japonica</i> subspecies. <i>Plant Molecular Biology</i> , 2007, 65, 403-415.	3.9	55
1559	Isolation and characterization of shs1, a sugar-hypersensitive and ABA-insensitive mutant with multiple stress responses. <i>Plant Molecular Biology</i> , 2007, 65, 295-309.	3.9	10
1560	Hypothetical protein AF2241 from <i>Archaeoglobus fulgidus</i> adopts a cyclophilin-like fold. <i>Journal of Biomolecular NMR</i> , 2007, 38, 353-358.	2.8	2
1561	Modeling the Tertiary Structure of the Patatin Domain of Neuropathy Target Esterase. <i>Protein Journal</i> , 2007, 26, 165-172.	1.6	36
1562	Wheat VIN3-like PHD finger genes are up-regulated by vernalization. <i>Molecular Genetics and Genomics</i> , 2007, 277, 301-313.	2.1	56
1563	Microarray analysis of the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> exposed to gamma irradiation. <i>Extremophiles</i> , 2007, 11, 19-29.	2.3	83
1564	Structure-dependent relationships between growth temperature of prokaryotes and the amino acid frequency in their proteins. <i>Extremophiles</i> , 2007, 11, 585-596.	2.3	33
1565	Identification and characterization of human uracil phosphoribosyltransferase (UPRTase). <i>Journal of Human Genetics</i> , 2007, 52, 415-422.	2.3	30
1566	Genome inventory and analysis of nuclear hormone receptors in <i>Tetraodon nigroviridis</i> . <i>Journal of Biosciences</i> , 2007, 32, 43-50.	1.1	16
1567	Comparison of sequence-based and structure-based phylogenetic trees of homologous proteins: Inferences on protein evolution. <i>Journal of Biosciences</i> , 2007, 32, 83-96.	1.1	32
1568	The N-homologue LRR domain adopts a folding which explains the TMV-Cg-induced HR-like response in sensitive tobacco plants. <i>Journal of Molecular Graphics and Modelling</i> , 2008, 26, 850-860.	2.4	15

#	ARTICLE	IF	CITATIONS
1569	C2H2 zinc finger genes of the Gli, Zic, KLF, SP, Wilms's tumour, Hucbein, Snail, Ovo, Spalt, Odd, Blimp-1, Fez and related gene families from Branchiostoma floridae. Development Genes and Evolution, 2008, 218, 639-649.	0.9	30
1570	A method for probabilistic mapping between protein structure and function taxonomies through cross training. BMC Structural Biology, 2008, 8, 40.	2.3	1
1571	LRRML: a conformational database and an XML description of leucine-rich repeats (LRRs). BMC Structural Biology, 2008, 8, 47.	2.3	31
1572	Type II restriction endonuclease R.Hpy188I belongs to the GIY-YIG nuclease superfamily, but exhibits an unusual active site. BMC Structural Biology, 2008, 8, 48.	2.3	14
1573	Sequence alignment for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 25-32.	2.5	7
1574	Ultrafast pyrosequencing of Corynebacterium kroppenstedtii DSM44385 revealed insights into the physiology of a lipophilic corynebacterium that lacks mycolic acids. Journal of Biotechnology, 2008, 136, 22-30.	3.8	68
1575	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. Journal of Biotechnology, 2008, 136, 91-101.	3.8	202
1576	Mass spectrometric study of the Escherichia coli repressor proteins, IclR and GclR, and their complexes with DNA. Protein Science, 2008, 10, 1370-1380.	7.6	37
1577	Identification of a 2 Mb Human Ortholog of Drosophila eyes shut/spacemaker that is Mutated in Patients with Retinitis Pigmentosa. American Journal of Human Genetics, 2008, 83, 594-603.	6.2	141
1578	The Peroxisome RING-Finger Complex is Required for Meiosis in the Fungus Podospora anserina. Traffic, 2008, 9, 1998-2009.	2.7	54
1579	The genome of the simian and human malaria parasite Plasmodium knowlesi. Nature, 2008, 455, 799-803.	27.8	338
1580	The Pristionchus pacificus genome provides a unique perspective on nematode lifestyle and parasitism. Nature Genetics, 2008, 40, 1193-1198.	21.4	310
1581	Environmental genomics reveals a functional chlorite dismutase in the nitrite-oxidizing bacterium Candidatus Nitrospira defluvia. Environmental Microbiology, 2008, 10, 3043-3056.	3.8	102
1582	The novel Cladosporium fulvum lysin motif effector Ecp6 is a virulence factor with orthologues in other fungal species. Molecular Microbiology, 2008, 69, 119-136.	2.5	275
1583	A novel pathway of intercellular signalling in Bacillus subtilis involves a protein with similarity to a component of type III secretion channels. Molecular Microbiology, 2008, 69, 402-417.	2.5	90
1584	Functional characterization of cohesin subunit SCC1 in Trypanosoma brucei and dissection of mutant phenotypes in two life cycle stages. Molecular Microbiology, 2008, 69, 666-680.	2.5	37
1585	Interoperability of GADU in Using Heterogeneous Grid Resources for Bioinformatics Applications. IEEE Transactions on Information Technology in Biomedicine, 2008, 12, 241-246.	3.2	8
1586	NestedMICA as an ab initio protein motif discovery tool. BMC Bioinformatics, 2008, 9, 19.	2.6	32

#	ARTICLE	IF	CITATIONS
1587	PURE: A webserver for the prediction of domains in unassigned regions in proteins. BMC Bioinformatics, 2008, 9, 281.	2.6	11
1588	Comparison study on k-word statistical measures for protein: From sequence to 'sequence space'. BMC Bioinformatics, 2008, 9, 394.	2.6	34
1589	MetaMine – A tool to detect and analyse gene patterns in their environmental context. BMC Bioinformatics, 2008, 9, 459.	2.6	7
1590	Integrating biological data – the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	2.6	87
1591	Consistent and contrasting properties of lineage-specific genes in the apicomplexan parasites Plasmodium and Theileria. BMC Evolutionary Biology, 2008, 8, 108.	3.2	43
1592	Extreme primary and secondary protein structure variability in the chimeric male-transmitted cytochrome c oxidase subunit II protein in freshwater mussels: Evidence for an elevated amino acid substitution rate in the face of domain-specific purifying selection. BMC Evolutionary Biology, 2008, 8, 165.	3.2	37
1593	Phylogenetic analyses suggest multiple changes of substrate specificity within the Glycosyl hydrolase 20 family. BMC Evolutionary Biology, 2008, 8, 214.	3.2	51
1594	On the origins of arrestin and rhodopsin. BMC Evolutionary Biology, 2008, 8, 222.	3.2	200
1595	A phylogenomic profile of hemerythrins, the nonheme diiron binding respiratory proteins. BMC Evolutionary Biology, 2008, 8, 244.	3.2	47
1596	Unique genes in plants: specificities and conserved features throughout evolution. BMC Evolutionary Biology, 2008, 8, 280.	3.2	37
1597	Just how versatile are domains?. BMC Evolutionary Biology, 2008, 8, 285.	3.2	43
1598	Insight into the sialome of the castor bean tick, Ixodes ricinus. BMC Genomics, 2008, 9, 233.	2.8	77
1599	Transcriptome analysis of Loxosceles laeta (Araneae, Sicariidae) spider venomous gland using expressed sequence tags. BMC Genomics, 2008, 9, 279.	2.8	110
1600	A genome-wide 20 K citrus microarray for gene expression analysis. BMC Genomics, 2008, 9, 318.	2.8	49
1601	Characterization of expressed sequence tags from a full-length enriched cDNA library of Cryptomeria japonica male strobili. BMC Genomics, 2008, 9, 383.	2.8	70
1602	The protein-phosphatome of the human malaria parasite Plasmodium falciparum. BMC Genomics, 2008, 9, 412.	2.8	63
1603	NemaPath: online exploration of KEGG-based metabolic pathways for nematodes. BMC Genomics, 2008, 9, 525.	2.8	26
1604	Exploring the mialome of ticks: An annotated catalogue of midgut transcripts from the hard tick, Dermacentor variabilis (Acari: Ixodidae). BMC Genomics, 2008, 9, 552.	2.8	109

#	ARTICLE	IF	CITATIONS
1605	Evolutionary origin and genomic organisation of runt-domain containing genes in arthropods. BMC Genomics, 2008, 9, 558.	2.8	19
1606	Differential expression profiling of components associated with exoskeletal hardening in crustaceans. BMC Genomics, 2008, 9, 575.	2.8	56
1607	RICD: A rice indicacDNA database resource for rice functional genomics. BMC Plant Biology, 2008, 8, 118.	3.6	24
1608	Cloning, characterisation and comparative analysis of a starch synthase IV gene in wheat: functional and evolutionary implications. BMC Plant Biology, 2008, 8, 98.	3.6	109
1609	Protein subfamily assignment using the Conserved Domain Database. BMC Research Notes, 2008, 1, 114.	1.4	26
1610	A comparative analysis of metal transportomes from metabolically versatile Pseudomonas. BMC Research Notes, 2008, 1, 88.	1.4	12
1611	Genome Pool Strategy for Structural Coverage of Protein Families. Structure, 2008, 16, 1659-1667.	3.3	15
1612	MetaSim—A Sequencing Simulator for Genomics and Metagenomics. PLoS ONE, 2008, 3, e3373.	2.5	375
1614	cpRAS: a novel circularly permuted RAS-like GTPase domain with a highly scattered phylogenetic distribution. Biology Direct, 2008, 3, 21.	4.6	7
1615	Orphan SelD proteins and selenium-dependent molybdenum hydroxylases. Biology Direct, 2008, 3, 4.	4.6	40
1616	The evolution of domain-content in bacterial genomes. Biology Direct, 2008, 3, 51.	4.6	26
1617	Tv-RIO1 — an atypical protein kinase from the parasitic nematode Trichostrongylus vitrinus. Parasites and Vectors, 2008, 1, 34.	2.5	9
1618	Crystal structures of possible lysine decarboxylases from Thermus thermophilus HB8. Protein Science, 2008, 13, 3038-3042.	7.6	11
1619	Crystal structure of a dodecameric FMN-dependent UbiX-like decarboxylase (Pad1) from Escherichia coli O157: H7. Protein Science, 2008, 13, 3006-3016.	7.6	48
1620	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. Journal of the Royal Society Interface, 2008, 5, 151-170.	3.4	97
1621	Streptococcus iniae M-Like Protein Contributes to Virulence in Fish and Is a Target for Live Attenuated Vaccine Development. PLoS ONE, 2008, 3, e2824.	2.5	81
1622	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. Genome Biology, 2008, 9, R144.	9.6	75
1623	NetGrep: fast network schema searches in interactomes. Genome Biology, 2008, 9, R138.	9.6	34

#	ARTICLE	IF	CITATIONS
1624	Protein structure protection commits gene expression patterns. <i>Genome Biology</i> , 2008, 9, R107.	9.6	23
1625	Whole proteome identification of plant candidate G-protein coupled receptors in Arabidopsis, rice, and poplar: computational prediction and in-vivo protein coupling. <i>Genome Biology</i> , 2008, 9, R120.	9.6	81
1626	CPSARST: an efficient circular permutation search tool applied to the detection of novel protein structural relationships. <i>Genome Biology</i> , 2008, 9, R11.	9.6	36
1627	Inferring mouse gene functions from genomic-scale data using a combined functional network/classification strategy. <i>Genome Biology</i> , 2008, 9, S5.	9.6	66
1628	RBNBC: Repeat Based Naive Bayes Classifier for Biological Sequences. , 2008, , .		5
1629	HMMer-Cell: High Performance Protein Profile Searching on the Cell/B.E. Processor. , 2008, , .		8
1630	A Bioinformatician's Guide to Metagenomics. <i>Microbiology and Molecular Biology Reviews</i> , 2008, 72, 557-578.	6.6	361
1631	Isolation, endocrine regulation and transcript distribution of a putative primary JH-responsive gene from the pine engraver, <i>Ips pini</i> (Coleoptera: Scolytidae). <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 256-267.	2.7	4
1632	Nuclear receptors in <i>Bombyx mori</i> : Insights into genomic structure and developmental expression. <i>Insect Biochemistry and Molecular Biology</i> , 2008, 38, 1130-1137.	2.7	43
1633	Structures of open (R) and close (T) states of prephenate dehydratase (PDT)â€”Implication of allosteric regulation by l-phenylalanine. <i>Journal of Structural Biology</i> , 2008, 162, 94-107.	2.8	34
1634	Prediction of Interacting Single-Stranded RNA Bases by Protein-Binding Patterns. <i>Journal of Molecular Biology</i> , 2008, 379, 299-316.	4.2	35
1635	Structures and Functional Implications of an AMP-Binding Cystathionine Î²-Synthase Domain Protein from a Hyperthermophilic Archaeon. <i>Journal of Molecular Biology</i> , 2008, 380, 181-192.	4.2	24
1636	ribB and ribBA genes from <i>Acidithiobacillus ferrooxidans</i> : expression levels under different growth conditions and phylogenetic analysis. <i>Research in Microbiology</i> , 2008, 159, 423-431.	2.1	8
1637	The three adaptation systems of <i>Bacillus subtilis</i> chemotaxis. <i>Trends in Microbiology</i> , 2008, 16, 480-487.	7.7	103
1638	Identification and characterization of a splice variant of the catalytic domain of mouse NTE-related esterase. <i>Gene</i> , 2008, 417, 43-50.	2.2	6
1639	A Protein Domain-Based Interactome Network for <i>C. elegans</i> Early Embryogenesis. <i>Cell</i> , 2008, 134, 534-545.	28.9	196
1640	Hidden Markov Models Incorporating Fuzzy Measures and Integrals for Protein Sequence Identification and Alignment. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 98-110.	6.9	8
1641	Visualizing Domain Interaction Networks and the Impact of Alternative Splicing Events. , 2008, , .		1

#	ARTICLE	IF	CITATIONS
1642	Bacteriophage 2851 Is a Prototype Phage for Dissemination of the Shiga Toxin Variant Gene 2c in <i>Escherichia coli</i> O157:H7. <i>Infection and Immunity</i> , 2008, 76, 5466-5477.	2.2	64
1643	Text-mining protein-protein interaction corpus using concept clustering to identify intermittency. , 2008, , .		1
1644	ClustScan : an integrated program package for the semi-automatic annotation of modular biosynthetic gene clusters and in silico prediction of novel chemical structures. <i>Nucleic Acids Research</i> , 2008, 36, 6882-6892.	14.5	181
1645	A functional proteomics approach links the ubiquitin-related modifier Urm1 to a tRNA modification pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18255-18260.	7.1	97
1646	Sequence analysis of GerM and SpoVS, uncharacterized bacterial σ -sporulation™ proteins with widespread phylogenetic distribution. <i>Bioinformatics</i> , 2008, 24, 1793-1797.	4.1	30
1647	Nucleus-Specific Importin Alpha Proteins and Nucleoporins Regulate Protein Import and Nuclear Division in the Binucleate <i>Tetrahymena thermophila</i> . <i>Eukaryotic Cell</i> , 2008, 7, 1487-1499.	3.4	68
1648	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. <i>PLoS Computational Biology</i> , 2008, 4, e1000176.	3.2	493
1649	Modularity of cellular networks shows general center-periphery polarization. <i>Bioinformatics</i> , 2008, 24, 2814-2817.	4.1	12
1650	Connect the dots: exposing hidden protein family connections from the entire sequence tree. <i>Bioinformatics</i> , 2008, 24, i193-i199.	4.1	6
1652	Profiling of <i>WDR36</i> Missense Variants in German Patients with Glaucoma. , 2008, 49, 270.		55
1653	Functions of Flavin Reductase and Quinone Reductase in 2,4,6-Trichlorophenol Degradation by <i>Cupriavidus necator</i> JMP134. <i>Journal of Bacteriology</i> , 2008, 190, 1615-1619.	2.2	33
1654	Suppression of \hat{P}^{bipA} Phenotypes in <i>Escherichia coli</i> by Abolishment of Pseudouridylation at Specific Sites on the 23S rRNA. <i>Journal of Bacteriology</i> , 2008, 190, 7675-7683.	2.2	35
1655	C2 Domain Protein MIN1 Promotes Eyespot Organization in <i>Chlamydomonas reinhardtii</i> . <i>Eukaryotic Cell</i> , 2008, 7, 2100-2112.	3.4	17
1656	Evolutionary Radiation Pattern of Novel Protein Phosphatases Revealed by Analysis of Protein Data from the Completely Sequenced Genomes of Humans, Green Algae, and Higher Plants. <i>Plant Physiology</i> , 2008, 146, 323-324.	4.8	162
1657	Human ATP-binding cassette (ABC) transporter family. <i>Human Genomics</i> , 2008, 3, 281.	2.9	576
1658	Protein homology detection with biologically inspired features and interpretable statistical models. <i>International Journal of Data Mining and Bioinformatics</i> , 2008, 2, 157.	0.1	6
1659	A new approach to predict interactions between integral membrane proteins in yeast. , 2008, , .		0
1660	Molecular profiling in the age of cancer genomics. <i>Expert Review of Molecular Diagnostics</i> , 2008, 8, 263-276.	3.1	8

#	ARTICLE	IF	CITATIONS
1661	A unique cell division machinery in the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18942-18946.	7.1	308
1662	The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772.	4.1	19
1663	Genome Sequence of <i>Thermophilum pendens</i> Reveals an Exceptional Loss of Biosynthetic Pathways without Genome Reduction. Journal of Bacteriology, 2008, 190, 2957-2965.	2.2	53
1664	Evolutionary Diversification of Plant Shikimate Kinase Gene Duplicates. PLoS Genetics, 2008, 4, e1000292.	3.5	52
1665	Modifier Effects between Regulatory and Protein-Coding Variation. PLoS Genetics, 2008, 4, e1000244.	3.5	33
1666	Structure-Guided Comparative Analysis of Proteins: Principles, Tools, and Applications for Predicting Function. PLoS Computational Biology, 2008, 4, e1000151.	3.2	9
1667	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2-Like Fold but Have Evolved to Inhibit NF- κ B rather than Apoptosis. PLoS Pathogens, 2008, 4, e1000128.	4.7	136
1668	Inferring Selection on Amino Acid Preference in Protein Domains. Molecular Biology and Evolution, 2008, 26, 527-536.	8.9	9
1669	GeConT 2: gene context analysis for orthologous proteins, conserved domains and metabolic pathways. Nucleic Acids Research, 2008, 36, W176-W180.	14.5	51
1670	Recent developments in the MAFFT multiple sequence alignment program. Briefings in Bioinformatics, 2008, 9, 286-298.	6.5	3,115
1671	The Small Ubiquitin-Like Modifier (SUMO) and SUMO-Conjugating System of <i>Chlamydomonas reinhardtii</i> . Genetics, 2008, 179, 177-192.	2.9	30
1672	Characterization of novel genes induced by sexual adhesion and gamete fusion and of their transcriptional regulation in <i>Chlamydomonas reinhardtii</i> . Plant and Cell Physiology, 2008, 49, 981-993.	3.1	19
1673	Prediction of Protein Interdomain Linker Regions by a Nonstationary Hidden Markov Model. Journal of the American Statistical Association, 2008, 103, 1085-1099.	3.1	3
1674	Phylogenetic mixture models for proteins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 3965-3976.	4.0	202
1675	Distribution and molecular characterization of tetracycline resistance in <i>Laribacter hongkongensis</i> . Journal of Antimicrobial Chemotherapy, 2008, 61, 488-497.	3.0	25
1676	Experience using web services for biological sequence analysis. Briefings in Bioinformatics, 2008, 9, 493-505.	6.5	24
1677	DAhunter: a web-based server that identifies homologous proteins by comparing domain architecture. Nucleic Acids Research, 2008, 36, W60-W64.	14.5	17
1678	Domain mobility in proteins: functional and evolutionary implications. Briefings in Bioinformatics, 2008, 10, 205-216.	6.5	87

#	ARTICLE	IF	CITATIONS
1679	A novel CHHC Zn-finger domain found in spliceosomal proteins and tRNA modifying enzymes. <i>Bioinformatics</i> , 2008, 24, 2277-2280.	4.1	23
1680	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 50-62.	3.8	124
1681	Integrating expression data with domain interaction networks. <i>Bioinformatics</i> , 2008, 24, 2546-2548.	4.1	9
1682	Evolution and taxonomic distribution of nonribosomal peptide and polyketide synthases. <i>Future Microbiology</i> , 2008, 3, 361-370.	2.0	39
1683	Target Selection in Structural Genomics Projects to Increase Knowledge of Protein Structure and Function Space. <i>Advances in Protein Chemistry and Structural Biology</i> , 2008, 75, 1-52.	2.3	1
1684	Identifying Protein Domains with the Pfam Database. <i>Current Protocols in Bioinformatics</i> , 2008, 23, Unit 2.5.	25.8	61
1685	An integrated database for complex protein structure modeling. , 2008, 2008, 33-40.		0
1686	Detecting DNA-binding domain from sequence and secondary structure Information Using Kernel-based Technique. , 2008, , .		0
1687	Detection of Sequential Outliers Using a Variable Length Markov Model. , 2008, , .		3
1688	Predicting the protein family of Methyl Parathion Hydrolase. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 201.	0.2	2
1689	Large-scale Protein-Protein Interaction prediction using novel kernel methods. <i>International Journal of Data Mining and Bioinformatics</i> , 2008, 2, 145.	0.1	12
1690	Scoring and summarising gene product clusters using the Gene Ontology. <i>International Journal of Data Mining and Bioinformatics</i> , 2008, 2, 216.	0.1	4
1691	BIOFILTER: A KNOWLEDGE-INTEGRATION SYSTEM FOR THE MULTI-LOCUS ANALYSIS OF GENOME-WIDE ASSOCIATION STUDIES. , 2008, , .		53
1692	Fusion and Fission of Genes Define a Metric between Fungal Genomes. <i>PLoS Computational Biology</i> , 2008, 4, e1000200.	3.2	22
1693	Organization of Physical Interactomes as Uncovered by Network Schemas. <i>PLoS Computational Biology</i> , 2008, 4, e1000203.	3.2	16
1694	Conservation and Variability of Dengue Virus Proteins: Implications for Vaccine Design. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e272.	3.0	79
1695	Computational Analysis of Constraints on Noncoding Regions, Coding Regions and Gene Expression in Relation to Plasmodium Phenotypic Diversity. <i>PLoS ONE</i> , 2008, 3, e3122.	2.5	8
1696	Structural conservation of a short, functional, peptide-sequence motif. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 1143.	3.0	2

#	ARTICLE	IF	CITATIONS
1697	Article Commentary: Microarray Data Analysis of Gene Expression Evolution. <i>Gene Regulation and Systems Biology</i> , 2009, 3, GRSB.S2997.	2.3	0
1698	AJAX Interface: A Breakthrough in Bioinformatics Web Applications. <i>Proteomics Insights</i> , 2009, 2, PRI.S2261.	2.0	1
1699	The Analysis of Multiple Genome Comparisons in Genus <i>Escherichia</i> and Its Application to the Discovery of Uncharacterised Metabolic Genes in Uropathogenic <i>Escherichia coli</i> CFT073. <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-8.	2.0	3
1700	Overexpression of truncated ERG from TMPRSS2-ERG fusion and prostate cancer development. <i>Pathology and Laboratory Medicine International</i> , 2009, , 13.	0.2	0
1701	Fido, a Novel AMPylation Domain Common to Fic, Doc, and AvrB. <i>PLoS ONE</i> , 2009, 4, e5818.	2.5	116
1702	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	3.5	39
1703	A Comparative Chemogenomics Strategy to Predict Potential Drug Targets in the Metazoan Pathogen, <i>Schistosoma mansoni</i> . <i>PLoS ONE</i> , 2009, 4, e4413.	2.5	94
1704	Identification of Coevolving Residues and Coevolution Potentials Emphasizing Structure, Bond Formation and Catalytic Coordination in Protein Evolution. <i>PLoS ONE</i> , 2009, 4, e4762.	2.5	42
1705	The Action of Key Factors in Protein Evolution at High Temporal Resolution. <i>PLoS ONE</i> , 2009, 4, e4821.	2.5	0
1706	dndDB: A Database Focused on Phosphorothioation of the DNA Backbone. <i>PLoS ONE</i> , 2009, 4, e5132.	2.5	46
1707	Structure-Based Phylogeny as a Diagnostic for Functional Characterization of Proteins with a Cupin Fold. <i>PLoS ONE</i> , 2009, 4, e5736.	2.5	54
1708	AllerHunter: A SVM-Pairwise System for Assessment of Allergenicity and Allergic Cross-Reactivity in Proteins. <i>PLoS ONE</i> , 2009, 4, e5861.	2.5	99
1709	Something Old, Something New, Something Borrowed; How the Thermoacidophilic Archaeon <i>Sulfolobus solfataricus</i> Responds to Oxidative Stress. <i>PLoS ONE</i> , 2009, 4, e6964.	2.5	70
1710	Bioinformatics and Structural Characterization of a Hypothetical Protein from <i>Streptococcus mutans</i> : Implication of Antibiotic Resistance. <i>PLoS ONE</i> , 2009, 4, e7245.	2.5	16
1711	Comparative Analysis of the Global Transcriptome of <i>Anopheles funestus</i> from Mali, West Africa. <i>PLoS ONE</i> , 2009, 4, e7976.	2.5	13
1712	Molecular phylogenies and evolutionary behavior of AhR (aryl hydrocarbon receptor) pathway genes in aquatic animals. <i>Nature Precedings</i> , 2009, , .	0.1	0
1713	M148R and M149R are two virulence factors for myxoma virus pathogenesis in the European rabbit. <i>Veterinary Research</i> , 2009, 40, 11.	3.0	28
1714	Meta-analysis of cancer microarray data reveals signaling pathway hotspots. , 2009, , .		0

#	ARTICLE	IF	CITATIONS
1715	GO Semantic Similarity-Based False Positive Reduction of Protein-Protein Interactions. , 2009, , .		1
1718	Comprehensive classification of nucleotidyltransferase fold proteins: identification of novel families and their representatives in human. Nucleic Acids Research, 2009, 37, 7701-7714.	14.5	147
1719	spr1630 Is Responsible for the Lethality of <i>clpX</i> Mutations in <i>Streptococcus pneumoniae</i> . Journal of Bacteriology, 2009, 191, 4888-4895.	2.2	12
1720	Structural plasticity and catalysis regulation of a thermosensor histidine kinase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16185-16190.	7.1	155
1721	The Polysialic Acid-specific O-Acetyltransferase OatC from <i>Neisseria meningitidis</i> Serogroup C Evolved Apart from Other Bacterial Sialate O-Acetyltransferases. Journal of Biological Chemistry, 2009, 284, 6-16.	3.4	27
1722	Local combinational variables: an approach used in DNA-binding helix-turn-helix motif prediction with sequence information. Nucleic Acids Research, 2009, 37, 5632-5640.	14.5	22
1723	Function of the N-terminal region of the phosphate-sensing histidine kinase, SphS, in <i>Synechocystis</i> sp. PCC 6803. Microbiology (United Kingdom), 2009, 155, 2256-2264.	1.8	11
1724	IMG ER: a system for microbial genome annotation expert review and curation. Bioinformatics, 2009, 25, 2271-2278.	4.1	804
1725	Self-Enhanced Accumulation of FtsN at Division Sites and Roles for Other Proteins with a SPOR Domain (DamX, DedD, and RlpA) in <i>Escherichia coli</i> Cell Constriction. Journal of Bacteriology, 2009, 191, 7383-7401.	2.2	187
1726	Reconstitution of Human Claspin-mediated Phosphorylation of Chk1 by the ATR (Ataxia) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 503 284, 33107-33114.	3.4	48
1727	Complete Genome Sequence of the Ethanol Producer <i>Zymomonas mobilis</i> NCIMB 11163. Journal of Bacteriology, 2009, 191, 7140-7141.	2.2	39
1728	MucR, a Novel Membrane-Associated Regulator of Alginate Biosynthesis in <i>Pseudomonas aeruginosa</i> . Applied and Environmental Microbiology, 2009, 75, 1110-1120.	3.1	129
1729	ExDom: an integrated database for comparative analysis of the exonâ€“intron structures of protein domains in eukaryotes. Nucleic Acids Research, 2009, 37, D703-D711.	14.5	11
1730	Universal architecture of bacterial chemoreceptor arrays. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17181-17186.	7.1	320
1731	PLecDom: a program for identification and analysis of plant lectin domains. Nucleic Acids Research, 2009, 37, W452-W458.	14.5	8
1732	Bioinformatic identification of novel methyltransferases. Epigenomics, 2009, 1, 163-175.	2.1	47
1733	Rational stabilization of enzymes by computational redesign of surface chargeâ€“charge interactions. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2601-2606.	7.1	201
1734	Jalview Version 2â€“a multiple sequence alignment editor and analysis workbench. Bioinformatics, 2009, 25, 1189-1191.	4.1	8,091

#	ARTICLE	IF	CITATIONS
1735	Bionemo: molecular information on biodegradation metabolism. <i>Nucleic Acids Research</i> , 2009, 37, D598-D602.	14.5	52
1736	Short paths in protein structure space originate in graph structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, E137; author reply E138.	7.1	3
1737	Overlapping Genes Produce Proteins with Unusual Sequence Properties and Offer Insight into De Novo Protein Creation. <i>Journal of Virology</i> , 2009, 83, 10719-10736.	3.4	161
1738	High-resolution protein complexes from integrating genomic information with molecular simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22124-22129.	7.1	174
1739	Regulation of Quinone Oxidoreductase by the Redox-sensing Transcriptional Regulator QorR in <i>Corynebacterium glutamicum</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 16736-16742.	3.4	37
1740	A Eukaryote-like Cardiolipin Synthase Is Present in <i>Streptomyces coelicolor</i> and in Most Actinobacteria. <i>Journal of Biological Chemistry</i> , 2009, 284, 17383-17390.	3.4	45
1741	A Novel Bipartite Double-Stranded RNA Mycovirus from the White Root Rot Fungus <i>Rosellinia necatrix</i> : Molecular and Biological Characterization, Taxonomic Considerations, and Potential for Biological Control. <i>Journal of Virology</i> , 2009, 83, 12801-12812.	3.4	264
1742	In Planta Mutagenesis Determines the Functional Regions of the Wheat Puroindoline Proteins. <i>Genetics</i> , 2009, 183, 853-860.	2.9	36
1743	Evolutionary History and Stress Regulation of Plant Receptor-Like Kinase/Pelle Genes. <i>Plant Physiology</i> , 2009, 150, 12-26.	4.8	340
1744	Transcriptional Wiring of Cell Wall-Related Genes in Arabidopsis. <i>Molecular Plant</i> , 2009, 2, 1015-1024.	8.3	60
1745	Gene Mapping and Phylogenetic Analysis of the Complete Genome from 30 Single-Stranded RNA Male-Specific Coliphages (Family <i>Leviviridae</i>). <i>Journal of Virology</i> , 2009, 83, 11233-11243.	3.4	32
1746	LytM-Domain Factors Are Required for Daughter Cell Separation and Rapid Ampicillin-Induced Lysis in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2009, 191, 5094-5107.	2.2	205
1747	Molecular and Structural Basis of Drift in the Functions of Closely-Related Homologous Enzyme Domains: Implications for Function Annotation Based on Homology Searches and Structural Genomics. <i>In Silico Biology</i> , 2009, 9, S41-S55.	0.9	6
1748	Significant speedup of database searches with HMMs by search space reduction with PSSM family models. <i>Bioinformatics</i> , 2009, 25, 3251-3258.	4.1	8
1749	Dr. Zompo: an online data repository for <i>Zostera marina</i> and <i>Posidonia oceanica</i> ESTs. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap009-bap009.	3.0	38
1750	Cyclic-di-GMP-Binding CRP-Like Protein: a Spectacular New Role for a Veteran Signal Transduction Actor. <i>Journal of Bacteriology</i> , 2009, 191, 6785-6787.	2.2	9
1751	Deterministic protein inference for shotgun proteomics data provides new insights into Arabidopsis pollen development and function. <i>Genome Research</i> , 2009, 19, 1786-1800.	5.5	151
1752	Human C21orf63 is a Heparin-binding Protein. <i>Journal of Biochemistry</i> , 2009, 146, 369-373.	1.7	13

#	ARTICLE	IF	CITATIONS
1753	Understanding phototropism: from Darwin to today. <i>Journal of Experimental Botany</i> , 2009, 60, 1969-1978.	4.8	79
1754	The National Center for Biotechnology Information's Protein Clusters Database. <i>Nucleic Acids Research</i> , 2009, 37, D216-D223.	14.5	241
1755	CentrosomeDB: a human centrosomal proteins database. <i>Nucleic Acids Research</i> , 2009, 37, D175-D180.	14.5	68
1756	CDD: specific functional annotation with the Conserved Domain Database. <i>Nucleic Acids Research</i> , 2009, 37, D205-D210.	14.5	935
1757	<i>Pseudomonas</i> Genome Database: facilitating user-friendly, comprehensive comparisons of microbial genomes. <i>Nucleic Acids Research</i> , 2009, 37, D483-D488.	14.5	220
1758	NMR structural analysis of DNA recognition by a novel Myb1 DNA-binding domain in the protozoan parasite <i>Trichomonas vaginalis</i> . <i>Nucleic Acids Research</i> , 2009, 37, 2381-2394.	14.5	23
1759	TARGeT: a web-based pipeline for retrieving and characterizing gene and transposable element families from genomic sequences. <i>Nucleic Acids Research</i> , 2009, 37, e78-e78.	14.5	33
1760	HMMConverter 1.0: a toolbox for hidden Markov models. <i>Nucleic Acids Research</i> , 2009, 37, e139-e139.	14.5	6
1761	The Three Fungal Transmembrane Nuclear Pore Complex Proteins of <i>Aspergillus nidulans</i> Are Dispensable in the Presence of an Intact An-Nup84-120 Complex. <i>Molecular Biology of the Cell</i> , 2009, 20, 616-630.	2.1	86
1762	DASMI: exchanging, annotating and assessing molecular interaction data. <i>Bioinformatics</i> , 2009, 25, 1321-1328.	4.1	15
1763	QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap010.	3.0	42
1764	No Nogo66- and NgR-Mediated Inhibition of Regenerating Axons in the Zebrafish Optic Nerve. <i>Journal of Neuroscience</i> , 2009, 29, 15489-15498.	3.6	41
1765	SUT-2 potentiates tau-induced neurotoxicity in <i>Caenorhabditis elegans</i> . <i>Human Molecular Genetics</i> , 2009, 18, 1825-1838.	2.9	86
1766	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2009, 28, Unit1.4.	25.8	149
1767	Benchmarking homology detection procedures with low complexity filters. <i>Bioinformatics</i> , 2009, 25, 2500-2505.	4.1	11
1768	Legume Transcription Factor Genes: What Makes Legumes So Special? <i>Plant Physiology</i> , 2009, 151, 991-1001.	4.8	87
1769	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. <i>Nucleic Acids Research</i> , 2009, 37, 5151-5166.	14.5	67
1770	Conserved principles of mammalian transcriptional regulation revealed by RNA half-life. <i>Nucleic Acids Research</i> , 2009, 37, e115-e115.	14.5	196

#	ARTICLE	IF	CITATIONS
1771	Temporal Global Expression Data Reveal Known and Novel Salicylate-Impacted Processes and Regulators Mediating Powdery Mildew Growth and Reproduction on Arabidopsis. Plant Physiology, 2009, 149, 1435-1451.	4.8	64
1772	Physical and genetic interactions of yeast Cwc21p, an ortholog of human SRm300/SRRM2, suggest a role at the catalytic center of the spliceosome. Rna, 2009, 15, 2161-2173.	3.5	51
1773	Rapid Evolution of Functional Complexity in a Domain Family. Science Signaling, 2009, 2, ra50.	3.6	57
1774	A CAAX motif can compensate for the PH domain of Num1 for cortical dynein attachment. Cell Cycle, 2009, 8, 3182-3190.	2.6	47
1775	Chapter 11 Energetic Profiling of Protein Folds. Methods in Enzymology, 2009, 455, 299-327.	1.0	11
1776	Structural Bioinformatics: From the Sequence to Structure and Function. Current Bioinformatics, 2009, 4, 54-87.	1.5	11
1777	FancyGene: dynamic visualization of gene structures and protein domain architectures on genomic loci. Bioinformatics, 2009, 25, 2281-2282.	4.1	100
1778	Pseudofam: the pseudogene families database. Nucleic Acids Research, 2009, 37, D738-D743.	14.5	41
1779	ModLink+: improving fold recognition by using protein-protein interactions. Bioinformatics, 2009, 25, 1506-1512.	4.1	14
1780	Aspartate-Derived Amino Acid Biosynthesis in Arabidopsis thaliana. The Arabidopsis Book, 2009, 7, e0121.	0.5	82
1781	KIAft, the Kluyveromyces lactis Ortholog of Aft1 and Aft2, Mediates Activation of Iron-Responsive Transcription Through the PuCACC Aft-Type Sequence. Genetics, 2009, 183, 93-106.	2.9	32
1782	Comparative genomic analyses of the human fungal pathogens Coccidioides and their relatives. Genome Research, 2009, 19, 1722-1731.	5.5	295
1783	Plant MetGenMAP: An Integrative Analysis System for Plant Systems Biology. Plant Physiology, 2009, 151, 1758-1768.	4.8	156
1784	Benefits of Structural Genomics for Drug Discovery Research. Infectious Disorders - Drug Targets, 2009, 9, 459-474.	0.8	26
1785	Nitrogen recycling and nutritional provisioning by Blattabacterium, the cockroach endosymbiont. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19521-19526.	7.1	243
1786	GabiPD: the GABI primary database—a plant integrative 'omics' database. Nucleic Acids Research, 2009, 37, D954-D959.	14.5	40
1787	HHsvm: fast and accurate classification of profile-profile matches identified by HHsearch. Bioinformatics, 2009, 25, 3071-3076.	4.1	9
1788	A Threading-Based Method for the Prediction of DNA-Binding Proteins with Application to the Human Genome. PLoS Computational Biology, 2009, 5, e1000567.	3.2	74

#	ARTICLE	IF	CITATIONS
1789	ProGMap: an integrated annotation resource for protein orthology. <i>Nucleic Acids Research</i> , 2009, 37, W428-W434.	14.5	12
1790	Identification and Functional Characterization of N-Terminally Acetylated Proteins in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2009, 7, e1000236.	5.6	149
1791	Pushing Structural Information into the Yeast Interactome by High-Throughput Protein Docking Experiments. <i>PLoS Computational Biology</i> , 2009, 5, e1000490.	3.2	67
1792	Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2009, 5, e1000605.	3.2	587
1793	HHP1 is involved in osmotic stress sensitivity in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 1589-1604.	4.8	17
1794	CC+: a relational database of coiled-coil structures. <i>Nucleic Acids Research</i> , 2009, 37, D315-D322.	14.5	149
1795	DETORQUEO, QUIRKY, and ZERZAUST Represent Novel Components Involved in Organ Development Mediated by the Receptor-Like Kinase STRUBBELIG in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2009, 5, e1000355.	3.5	78
1796	MoKCa database—mutations of kinases in cancer. <i>Nucleic Acids Research</i> , 2009, 37, D824-D831.	14.5	51
1797	Identification of the <i>Schistosoma mansoni</i> TNF-Alpha Receptor Gene and the Effect of Human TNF-Alpha on the Parasite Gene Expression Profile. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e556.	3.0	33
1798	Reproducing the manual annotation of multiple sequence alignments using a SVM classifier. <i>Bioinformatics</i> , 2009, 25, 3093-3098.	4.1	8
1799	Prediction of Proteins Putatively Involved in the Thiol: Disulfide Redox Metabolism of a Bacterium (<i>Listeria</i>): The CXXC Motif as Query Sequence. <i>In Silico Biology</i> , 2009, 9, 407-414.	0.9	17
1800	Detection of new protein domains using co-occurrence: application to <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2009, 25, 3077-3083.	4.1	37
1801	Transcriptome profiling defines a novel regulon modulated by the LysR-type transcriptional regulator MexT in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2009, 37, 7546-7559.	14.5	85
1802	webPRC: the Profile Comparer for alignment-based searching of public domain databases. <i>Nucleic Acids Research</i> , 2009, 37, W48-W52.	14.5	17
1803	Phospholipid scramblases and Tubby-like proteins belong to a new superfamily of membrane tethered transcription factors. <i>Bioinformatics</i> , 2009, 25, 159-162.	4.1	59
1804	DASher: a stand-alone protein sequence client for DAS, the Distributed Annotation System. <i>Bioinformatics</i> , 2009, 25, 1333-1334.	4.1	8
1805	LOCP—locating pilus operons in Gram-positive bacteria. <i>Bioinformatics</i> , 2009, 25, 1187-1188.	4.1	8
1806	Diversity and dispersal of a ubiquitous protein family: acyl-CoA dehydrogenases. <i>Nucleic Acids Research</i> , 2009, 37, 5619-5631.	14.5	26

#	ARTICLE	IF	CITATIONS
1807	PhyloPars: estimation of missing parameter values using phylogeny. <i>Nucleic Acids Research</i> , 2009, 37, W179-W184.	14.5	97
1808	Anti-schistosomal Intervention Targets Identified by Lifecycle Transcriptomic Analyses. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e543.	3.0	116
1809	Modèle topologique de la structure d'un antiport vacuolaire de type NHX chez la vigne cultivée (<i>Vitis vinifera</i>). <i>Botany</i> , 2009, 87, 339-347.	1.0	1
1810	Exploration of Uncharted Regions of the Protein Universe. <i>PLoS Biology</i> , 2009, 7, e1000205.	5.6	123
1811	Drug Discovery Using Chemical Systems Biology: Identification of the Protein-Ligand Binding Network To Explain the Side Effects of CETP Inhibitors. <i>PLoS Computational Biology</i> , 2009, 5, e1000387.	3.2	232
1812	The ArsR Repressor Mediates Arsenite-Dependent Regulation of Arsenate Respiration and Detoxification Operons of <i>Shewanella</i> sp. Strain ANA-3. <i>Journal of Bacteriology</i> , 2009, 191, 6722-6731.	2.2	74
1813	SysZNF: the C2H2 zinc finger gene database. <i>Nucleic Acids Research</i> , 2009, 37, D267-D273.	14.5	33
1814	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , 2009, 37, D229-D232.	14.5	882
1815	Domain-oriented edge-based alignment of protein interaction networks. <i>Bioinformatics</i> , 2009, 25, i240-1246.	4.1	28
1816	ProtVirDB: a database of protozoan virulent proteins. <i>Bioinformatics</i> , 2009, 25, 1568-1569.	4.1	12
1817	The Genome of <i>Burkholderia cenocepacia</i> J2315, an Epidemic Pathogen of Cystic Fibrosis Patients. <i>Journal of Bacteriology</i> , 2009, 191, 261-277.	2.2	329
1818	Fine-grained annotation and classification of de novo predicted LTR retrotransposons. <i>Nucleic Acids Research</i> , 2009, 37, 7002-7013.	14.5	276
1819	Crystal Structure of a Mucus-binding Protein Repeat Reveals an Unexpected Functional Immunoglobulin Binding Activity. <i>Journal of Biological Chemistry</i> , 2009, 284, 32444-32453.	3.4	70
1820	Rapid detection, classification and accurate alignment of up to a million or more related protein sequences. <i>Bioinformatics</i> , 2009, 25, 1869-1875.	4.1	62
1821	An <i>Ehrlichia chaffeensis</i> Tandem Repeat Protein Interacts with Multiple Host Targets Involved in Cell Signaling, Transcriptional Regulation, and Vesicle Trafficking. <i>Infection and Immunity</i> , 2009, 77, 1734-1745.	2.2	73
1822	Identification of direct residue contacts in protein-protein interaction by message passing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 67-72.	7.1	902
1823	Extensive DNA mimicry by the ArdA anti-restriction protein and its role in the spread of antibiotic resistance. <i>Nucleic Acids Research</i> , 2009, 37, 4887-4897.	14.5	117
1824	seeMotif: exploring and visualizing sequence motifs in 3D structures. <i>Nucleic Acids Research</i> , 2009, 37, W552-W558.	14.5	4

#	ARTICLE	IF	CITATIONS
1825	PPISearch: a web server for searching homologous proteinâ€“protein interactions across multiple species. <i>Nucleic Acids Research</i> , 2009, 37, W369-W375.	14.5	34
1826	Cloning, Expression, and Characterization of a Peculiar Choline-Binding Î²-Galactosidase from <i>Streptococcus mitis</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 5972-5980.	3.1	10
1827	Nematode.net update 2008: improvements enabling more efficient data mining and comparative nematode genomics. <i>Nucleic Acids Research</i> , 2009, 37, D571-D578.	14.5	33
1828	The impact of long-distance horizontal gene transfer on prokaryotic genome size. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21748-21753.	7.1	58
1829	Crystal Structures of YkuL and Its Complex with Second Messenger Cyclic Di-GMP Suggest Catalytic Mechanism of Phosphodiester Bond Cleavage by EAL Domains. <i>Journal of Biological Chemistry</i> , 2009, 284, 13174-13184.	3.4	96
1830	JAIL: a structure-based interface library for macromolecules. <i>Nucleic Acids Research</i> , 2009, 37, D338-D341.	14.5	7
1831	The <i>Thermotoga maritima</i> Trk Potassium Transporterâ€“from Frameshift to Function. <i>Journal of Bacteriology</i> , 2009, 191, 2276-2284.	2.2	13
1832	A Novel WRKY-like Protein Involved in Transcriptional Activation of Cyst Wall Protein Genes in <i>Giardia lamblia</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 17975-17988.	3.4	67
1833	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	14.5	1,712
1834	Bioinformatics construction of the human cell surfaceome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16752-16757.	7.1	119
1835	RHYTHMâ€“a server to predict the orientation of transmembrane helices in channels and membrane-coils. <i>Nucleic Acids Research</i> , 2009, 37, W575-W580.	14.5	29
1836	INTS3 controls the hSSB1-mediated DNA damage response. <i>Journal of Cell Biology</i> , 2009, 187, 25-32.	5.2	80
1837	Early-Arriving Syp1p and Ede1p Function in Endocytic Site Placement and Formation in Budding Yeast. <i>Molecular Biology of the Cell</i> , 2009, 20, 4640-4651.	2.1	110
1838	Genome Sequence of <i>Azotobacter vinelandii</i> , an Obligate Aerobe Specialized To Support Diverse Anaerobic Metabolic Processes. <i>Journal of Bacteriology</i> , 2009, 191, 4534-4545.	2.2	265
1839	The Paralogous Genes <i>RADICAL-INDUCED CELL DEATH1</i> and <i>SIMILAR TO RCD ONE1</i> Have Partially Redundant Functions during Arabidopsis Development. <i>Plant Physiology</i> , 2009, 151, 180-198.	4.8	75
1840	DASMIweb: online integration, analysis and assessment of distributed protein interaction data. <i>Nucleic Acids Research</i> , 2009, 37, W122-W128.	14.5	2
1841	COMPASS server for homology detection: improved statistical accuracy, speed and functionality. <i>Nucleic Acids Research</i> , 2009, 37, W90-W94.	14.5	27
1842	Knowledge-guided inference of domainâ€“domain interactions from incomplete proteinâ€“protein interaction networks. <i>Bioinformatics</i> , 2009, 25, 2492-2499.	4.1	24

#	ARTICLE	IF	CITATIONS
1843	Diversity of Serine Hydrolase Activities of Unchallenged and Botrytis-infected Arabidopsis thaliana. Molecular and Cellular Proteomics, 2009, 8, 1082-1093.	3.8	93
1844	Proteome-wide Prediction of Signal Flow Direction in Protein Interaction Networks Based on Interacting Domains. Molecular and Cellular Proteomics, 2009, 8, 2063-2070.	3.8	28
1845	Automated inference of molecular mechanisms of disease from amino acid substitutions. Bioinformatics, 2009, 25, 2744-2750.	4.1	691
1846	3did Update: domain-domain and peptide-mediated interactions of known 3D structure. Nucleic Acids Research, 2009, 37, D300-D304.	14.5	67
1847	BB0323 Function Is Essential for <i>Borrelia burgdorferi</i> Virulence and Persistence through Tick-Rodent Transmission Cycle. Journal of Infectious Diseases, 2009, 200, 1318-1330.	4.0	55
1848	Role of Importin Alpha8, a New Member of the Importin Alpha Family of Nuclear Transport Proteins, in Early Embryonic Development in Cattle. Biology of Reproduction, 2009, 81, 333-342.	2.7	82
1849	The GTOPI database in 2009: updated content and novel features to expand and deepen insights into protein structures and functions. Nucleic Acids Research, 2009, 37, D333-D337.	14.5	30
1850	GtRNAdb: a database of transfer RNA genes detected in genomic sequence. Nucleic Acids Research, 2009, 37, D93-D97.	14.5	782
1851	Characterization and binding affinities of SmLANP: A new Schistosoma mansoni member of the ANP32 family of regulatory proteins. Molecular and Biochemical Parasitology, 2009, 165, 95-102.	1.1	1
1852	varDB: common ground for a shifting landscape. Trends in Parasitology, 2009, 25, 249-252.	3.3	4
1853	Exploiting structural classifications for function prediction: towards a domain grammar for protein function. Current Opinion in Structural Biology, 2009, 19, 349-356.	5.7	33
1854	Rhomboid Protease Dynamics and Lipid Interactions. Structure, 2009, 17, 395-405.	3.3	101
1855	PSI-2: Structural Genomics to Cover Protein Domain Family Space. Structure, 2009, 17, 869-881.	3.3	120
1856	Protein function prediction – the power of multiplicity. Trends in Biotechnology, 2009, 27, 210-219.	9.3	106
1857	Scaling laws in functional genome content across prokaryotic clades and lifestyles. Trends in Genetics, 2009, 25, 243-247.	6.7	52
1858	Different gene regulation strategies revealed by analysis of binding motifs. Trends in Genetics, 2009, 25, 434-440.	6.7	231
1859	The High Throughput Sequence Annotation Service (HT-SAS) – the shortcut from sequence to true Medline words. BMC Bioinformatics, 2009, 10, 148.	2.6	4
1860	Computational analysis of the interaction between transcription factors and the predicted secreted proteome of the yeast Kluyveromyces lactis. BMC Bioinformatics, 2009, 10, 194.	2.6	6

#	ARTICLE	IF	CITATIONS
1861	NLStradamus: a simple Hidden Markov Model for nuclear localization signal prediction. BMC Bioinformatics, 2009, 10, 202.	2.6	526
1862	Multi-level learning: improving the prediction of protein, domain and residue interactions by allowing information flow between levels. BMC Bioinformatics, 2009, 10, 241.	2.6	9
1863	Inferring protein function by domain context similarities in protein-protein interaction networks. BMC Bioinformatics, 2009, 10, 395.	2.6	22
1864	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. BMC Bioinformatics, 2009, 10, 430.	2.6	78
1865	TACOA – Taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. BMC Bioinformatics, 2009, 10, 56.	2.6	160
1866	The PHA Depolymerase Engineering Database: A systematic analysis tool for the diverse family of polyhydroxyalkanoate (PHA) depolymerases. BMC Bioinformatics, 2009, 10, 89.	2.6	116
1867	GAIA: a gram-based interaction analysis tool – an approach for identifying interacting domains in yeast. BMC Bioinformatics, 2009, 10, S60.	2.6	5
1868	XML-based approaches for the integration of heterogeneous bio-molecular data. BMC Bioinformatics, 2009, 10, S7.	2.6	21
1869	Protein comparison at the domain architecture level. BMC Bioinformatics, 2009, 10, S5.	2.6	26
1870	TGF-beta signaling proteins and the Protein Ontology. BMC Bioinformatics, 2009, 10, S3.	2.6	9
1871	Visualising biological data: a semantic approach to tool and database integration. BMC Bioinformatics, 2009, 10, S19.	2.6	32
1872	Extraction of human kinase mutations from literature, databases and genotyping studies. BMC Bioinformatics, 2009, 10, S1.	2.6	32
1873	The evolution of nuclear auxin signalling. BMC Evolutionary Biology, 2009, 9, 126.	3.2	115
1874	Evolutionary dynamics of the LTR retrotransposons roo and rooA inferred from twelve complete Drosophila genomes. BMC Evolutionary Biology, 2009, 9, 205.	3.2	15
1875	Origin and evolution of the Notch signalling pathway: an overview from eukaryotic genomes. BMC Evolutionary Biology, 2009, 9, 249.	3.2	191
1876	Emergence, development and diversification of the TGF- β signalling pathway within the animal kingdom. BMC Evolutionary Biology, 2009, 9, 28.	3.2	137
1877	Evolution of C2H2-zinc finger genes revisited. BMC Evolutionary Biology, 2009, 9, 51.	3.2	28
1878	Insights into the evolution of the snail superfamily from metazoan wide molecular phylogenies and expression data in annelids. BMC Evolutionary Biology, 2009, 9, 94.	3.2	18

#	ARTICLE	IF	CITATIONS
1879	ChlamyCyc: an integrative systems biology database and web-portal for <i>Chlamydomonas reinhardtii</i> . BMC Genomics, 2009, 10, 209.	2.8	73
1880	Biases in <i>Drosophila melanogaster</i> protein trap screens. BMC Genomics, 2009, 10, 249.	2.8	16
1881	The repertoire of G-protein-coupled receptors in <i>Xenopus tropicalis</i> . BMC Genomics, 2009, 10, 263.	2.8	34
1882	7TMRmine: a Web server for hierarchical mining of 7TMR proteins. BMC Genomics, 2009, 10, 275.	2.8	20
1883	Hmrbase: a database of hormones and their receptors. BMC Genomics, 2009, 10, 307.	2.8	31
1884	A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of <i>Pseudomonas syringae</i> pathovar tabaci 11528. BMC Genomics, 2009, 10, 395.	2.8	81
1885	UFO: a web server for ultra-fast functional profiling of whole genome protein sequences. BMC Genomics, 2009, 10, 409.	2.8	15
1886	Generation and analysis of expressed sequence tags from six developing xylem libraries in <i>Pinus radiata</i> D. Don. BMC Genomics, 2009, 10, 41.	2.8	71
1887	Complete genome sequence of the sugarcane nitrogen-fixing endophyte <i>Gluconacetobacter diazotrophicus</i> Pal5. BMC Genomics, 2009, 10, 450.	2.8	207
1888	Tardigrade workbench: comparing stress-related proteins, sequence-similar and functional protein clusters as well as RNA elements in tardigrades. BMC Genomics, 2009, 10, 469.	2.8	59
1889	The mitochondrial genomes of the ciliates <i>Euplotes minuta</i> and <i>Euplotes crassus</i> . BMC Genomics, 2009, 10, 514.	2.8	36
1890	GExplore: a web server for integrated queries of protein domains, gene expression and mutant phenotypes. BMC Genomics, 2009, 10, 529.	2.8	23
1891	Horizontal gene transfer and diverse functional constraints within a common replication-partitioning system in Alphaproteobacteria: the repABC operon. BMC Genomics, 2009, 10, 536.	2.8	54
1892	Evidence for niche adaptation in the genome of the bovine pathogen <i>Streptococcus uberis</i> . BMC Genomics, 2009, 10, 54.	2.8	101
1893	Unique sequence features of the Human Adenovirus 31 complete genomic sequence are conserved in clinical isolates. BMC Genomics, 2009, 10, 557.	2.8	18
1894	Genome-wide analysis of chimpanzee genes with premature termination codons. BMC Genomics, 2009, 10, 56.	2.8	12
1895	RNRdb, a curated database of the universal enzyme family ribonucleotide reductase, reveals a high level of misannotation in sequences deposited to Genbank. BMC Genomics, 2009, 10, 589.	2.8	109
1896	Identification of novel aspartic proteases from <i>Strongyloides ratti</i> and characterisation of their evolutionary relationships, stage-specific expression and molecular structure. BMC Genomics, 2009, 10, 611.	2.8	20

#	ARTICLE	IF	CITATIONS
1897	Large-scale identification of odorant-binding proteins and chemosensory proteins from expressed sequence tags in insects. <i>BMC Genomics</i> , 2009, 10, 632.	2.8	213
1898	Molecular evolution of the hyperthermophilic archaea of the <i>Pyrococcus</i> genus: analysis of adaptation to different environmental conditions. <i>BMC Genomics</i> , 2009, 10, 639.	2.8	28
1899	Deep RNA sequencing of <i>L. monocytogenes</i> reveals overlapping and extensive stationary phase and sigma B-dependent transcriptomes, including multiple highly transcribed noncoding RNAs. <i>BMC Genomics</i> , 2009, 10, 641.	2.8	160
1900	Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. <i>BMC Genomics</i> , 2009, 10, S11.	2.8	31
1901	Comparative study of protein-protein interaction observed in PolyGalacturonase-Inhibiting Proteins from <i>Phaseolus vulgaris</i> and <i>Glycine max</i> and PolyGalacturonase from <i>Fusarium moniliforme</i> . <i>BMC Genomics</i> , 2009, 10, S19.	2.8	24
1902	DNA-binding residues and binding mode prediction with binding-mechanism concerned models. <i>BMC Genomics</i> , 2009, 10, S23.	2.8	9
1903	Cytosolic phospholipase A2: a member of the signalling pathway of a new G protein $\hat{\pm}$ subunit in <i>Sporothrix schenckii</i> . <i>BMC Microbiology</i> , 2009, 9, 100.	3.3	28
1904	New genes of <i>Xanthomonas citri</i> subsp. <i>citri</i> involved in pathogenesis and adaptation revealed by a transposon-based mutant library. <i>BMC Microbiology</i> , 2009, 9, 12.	3.3	67
1905	Topological analysis of a haloacid permease of a <i>Burkholderia</i> sp. bacterium with a PhoA-LacZ reporter. <i>BMC Microbiology</i> , 2009, 9, 233.	3.3	13
1906	Genetic tools for the investigation of <i>Roseobacter</i> clade bacteria. <i>BMC Microbiology</i> , 2009, 9, 265.	3.3	47
1907	Identification of Archaea-specific chemotaxis proteins which interact with the flagellar apparatus. <i>BMC Microbiology</i> , 2009, 9, 56.	3.3	76
1908	Transcript and proteomic analysis of developing white lupin (<i>Lupinus albus</i> L.) roots. <i>BMC Plant Biology</i> , 2009, 9, 1.	3.6	182
1909	Microcollinearity in an ethylene receptor coding gene region of the <i>Coffea canephora</i> genome is extensively conserved with <i>Vitis vinifera</i> and other distant dicotyledonous sequenced genomes. <i>BMC Plant Biology</i> , 2009, 9, 22.	3.6	21
1910	A new genomic resource dedicated to wood formation in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2009, 9, 36.	3.6	54
1911	Phylogenetic analysis, subcellular localization, and expression patterns of RPD3/HDA1 family histone deacetylases in plants. <i>BMC Plant Biology</i> , 2009, 9, 37.	3.6	117
1912	A membrane-bound matrix metalloproteinase from <i>Nicotiana tabacum</i> cv. BY-2 is induced by bacterial pathogens. <i>BMC Plant Biology</i> , 2009, 9, 83.	3.6	31
1913	Evolution of multiple phosphodiesterase isoforms in stickleback involved in cAMP signal transduction pathway. <i>BMC Systems Biology</i> , 2009, 3, 23.	3.0	9
1914	Genome-wide detection of hybrid genes with multiple components in human. <i>BMC Research Notes</i> , 2009, 2, 75.	1.4	1

#	ARTICLE	IF	CITATIONS
1915	High Speed Biological Sequence Analysis With Hidden Markov Models on Reconfigurable Platforms. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 740-746.	3.2	15
1916	Further complexity of the genus Crinivirus revealed by the complete genome sequence of Lettuce chlorosis virus (LCV) and the similar temporal accumulation of LCV genomic RNAs 1 and 2. Virology, 2009, 390, 45-55.	2.4	29
1917	Cbf11 and Cbf12, the fission yeast CSL proteins, play opposing roles in cell adhesion and coordination of cell and nuclear division. Experimental Cell Research, 2009, 315, 1533-1547.	2.6	27
1918	Electric dipole reorientation in the interaction of botulinum neurotoxins with neuronal membranes. FEBS Letters, 2009, 583, 2321-2325.	2.8	17
1919	A kinome of 2600 in the ciliate <i>Paramecium tetraurelia</i> . FEBS Letters, 2009, 583, 3589-3592.	2.8	15
1920	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. Chemico-Biological Interactions, 2009, 178, 94-98.	4.0	329
1921	The human short-chain dehydrogenase/reductase (SDR) superfamily: A bioinformatics summary. Chemico-Biological Interactions, 2009, 178, 99-109.	4.0	92
1922	Phylogeny of the CDC25 homology domain reveals rapid differentiation of Ras pathways between early animals and fungi. Cellular Signalling, 2009, 21, 1579-1585.	3.6	21
1923	Pathogenic or not? And if so, then how? Studying the effects of missense mutations using bioinformatics methods. Human Mutation, 2009, 30, 703-714.	2.5	211
1924	B7 α is a potent inhibitor of human T α cell activation: No evidence for B7 α and TREML2 interaction. European Journal of Immunology, 2009, 39, 1754-1764.	2.9	231
1925	Domain α ligand mapping for enzymes. Journal of Molecular Recognition, 2010, 23, 194-208.	2.1	6
1926	Genome-wide analysis of <i>Carica papaya</i> reveals a small NBS resistance gene family. Molecular Genetics and Genomics, 2009, 281, 609-626.	2.1	142
1927	Plant lectins: the ties that bind in root symbiosis and plant defense. Molecular Genetics and Genomics, 2009, 282, 1-15.	2.1	175
1928	Genome-wide identification of NBS-encoding resistance genes in <i>Brassica rapa</i> . Molecular Genetics and Genomics, 2009, 282, 617-31.	2.1	139
1929	Evolutionarily evolved discriminators in the 3-TPR domain of the Toc64 family involved in protein translocation at the outer membrane of chloroplasts and mitochondria. Journal of Molecular Modeling, 2009, 15, 971-982.	1.8	29
1930	The Protein Model Portal. Journal of Structural and Functional Genomics, 2009, 10, 1-8.	1.2	130
1931	Structural analysis reveals DNA binding properties of Rv2827c, a hypothetical protein from <i>Mycobacterium tuberculosis</i> . Journal of Structural and Functional Genomics, 2009, 10, 137-150.	1.2	13
1932	Structural genomics target selection for the New York consortium on membrane protein structure. Journal of Structural and Functional Genomics, 2009, 10, 255-268.	1.2	46

#	ARTICLE	IF	CITATIONS
1933	Insights into corn genes derived from large-scale cDNA sequencing. <i>Plant Molecular Biology</i> , 2009, 69, 179-194.	3.9	212
1934	Improved prediction of malaria degradomes by supervised learning with SVM and profile kernel. <i>Genetica</i> , 2009, 136, 189-209.	1.1	31
1935	DyP-type peroxidases comprise a novel heme peroxidase family. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 1387-1403.	5.4	230
1936	To Investigate Protein Evolution by Detecting Suppressed Epitope Structures. <i>Journal of Molecular Evolution</i> , 2009, 68, 448-460.	1.8	42
1937	Phylogenetic Analysis of the NEEP21/Calcyon/P19 Family of Endocytic Proteins: Evidence for Functional Evolution in the Vertebrate CNS. <i>Journal of Molecular Evolution</i> , 2009, 69, 319-332.	1.8	16
1938	The Evolution of RecD Outside of the RecBCD Complex. <i>Journal of Molecular Evolution</i> , 2009, 69, 360-371.	1.8	18
1939	New proteins orthologous to cerato-platanin in various <i>Ceratozystis</i> species and the purification and characterization of cerato-populin from <i>Ceratozystis populicola</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 309-322.	3.6	28
1940	Molecular and biochemical characterization of a novel xylanase from the symbiotic <i>Sphingobacterium</i> sp. TN19. <i>Applied Microbiology and Biotechnology</i> , 2009, 85, 323-333.	3.6	57
1941	Prediction of helix-helix contacts and interacting helices in polytopic membrane proteins using neural networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 857-871.	2.6	61
1942	Systematic structural studies of iron superoxide dismutases from human parasites and a statistical coupling analysis of metal binding specificity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 26-37.	2.6	35
1943	Computational protein design as a tool for fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 139-158.	2.6	25
1944	The Rho GTPase inactivation domain in <i>Vibrio cholerae</i> MARTX toxin has a circularly permuted papain-like thiol protease fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 413-419.	2.6	31
1945	Solution structure of the AT-rich interaction domain of Jumonji/JARID2. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 1023-1028.	2.6	9
1946	Template-based and free modeling by RAPTOR++ in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 133-137.	2.6	19
1947	Charting online OMICS resources: A navigational chart for clinical researchers. <i>Proteomics - Clinical Applications</i> , 2009, 3, 18-29.	1.6	12
1948	CPDadh: A new peptidase family homologous to the cysteine protease domain in bacterial MARTX toxins. <i>Protein Science</i> , 2009, 18, 856-862.	7.6	5
1949	Aegerolysins: Structure, function, and putative biological role. <i>Protein Science</i> , 2009, 18, 694-706.	7.6	70
1950	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 356-365.	2.5	31

#	ARTICLE	IF	CITATIONS
1951	Crystallization and preliminary X-ray crystallographic analysis of $\hat{1}^3$ -carboxymucolactone decarboxylase from <i>Sulfolobus solfataricus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1197-1199.	0.7	2
1952	A mouse chromosome 4 balancer ENU-mutagenesis screen isolates eleven lethal lines. BMC Genetics, 2009, 10, 12.	2.7	12
1953	Mesothelin, Stereocilin, and Otoancorin are predicted to have superhelical structures with ARM-type repeats. BMC Structural Biology, 2009, 9, 1.	2.3	64
1954	Development of an accurate classification system of proteins into structured and unstructured regions that uncovers novel structural domains: its application to human transcription factors. BMC Structural Biology, 2009, 9, 26.	2.3	36
1955	Exon 6 of human JAG1 encodes a conserved structural unit. BMC Structural Biology, 2009, 9, 43.	2.3	9
1956	Prediction of calcium-binding sites by combining loop-modeling with machine learning. BMC Structural Biology, 2009, 9, 72.	2.3	23
1957	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from <i>Streptococcus pyogenes</i> . BMC Structural Biology, 2009, 9, 75.	2.3	6
1958	Mapping the human membrane proteome: a majority of the human membrane proteins can be classified according to function and evolutionary origin. BMC Biology, 2009, 7, 50.	3.8	497
1959	TonB-dependent transporters and their occurrence in cyanobacteria. BMC Biology, 2009, 7, 68.	3.8	61
1960	Conservation of core gene expression in vertebrate tissues. Journal of Biology, 2009, 8, 33.	2.7	165
1961	Arabidopsis dynamin-related proteins DRP3A and DRP3B are functionally redundant in mitochondrial fission, but have distinct roles in peroxisomal fission. Plant Journal, 2009, 58, 388-400.	5.7	115
1962	DOG 1.0: illustrator of protein domain structures. Cell Research, 2009, 19, 271-273.	12.0	505
1963	Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. ISME Journal, 2009, 3, 1335-1348.	9.8	80
1964	Abundant transposases encoded by the metagenome of a hydrothermal chimney biofilm. ISME Journal, 2009, 3, 1420-1424.	9.8	112
1965	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. Nature, 2009, 460, 345-351.	27.8	635
1966	The genome of the blood fluke <i>Schistosoma mansoni</i> . Nature, 2009, 460, 352-358.	27.8	945
1967	Transport mechanism of a bacterial homologue of glutamate transporters. Nature, 2009, 462, 880-885.	27.8	407
1968	Genome sequence of the recombinant protein production host <i>Pichia pastoris</i> . Nature Biotechnology, 2009, 27, 561-566.	17.5	422

#	ARTICLE	IF	CITATIONS
1969	Protein structure homology modeling using SWISS-MODEL workspace. <i>Nature Protocols</i> , 2009, 4, 1-13.	12.0	1,092
1970	Protein structure prediction on the Web: a case study using the Phyre server. <i>Nature Protocols</i> , 2009, 4, 363-371.	12.0	3,815
1971	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	12.0	769
1972	PSI protein classifier: A new program automating PSI-BLAST search results. <i>Molecular Biology</i> , 2009, 43, 652-664.	1.3	14
1973	Arrestin-mediated Endocytosis of Yeast Plasma Membrane Transporters. <i>Traffic</i> , 2009, 10, 1856-1867.	2.7	212
1974	A novel ATP-binding cassette transporter is responsible for resistance to viologen herbicides in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>FEBS Journal</i> , 2009, 276, 4001-4011.	4.7	20
1975	Distribution and Expression of Elicitin-like Protein Genes of the Biocontrol Agent <i>Pythium oligandrum</i> . <i>Journal of Phytopathology</i> , 2010, 158, 417-426.	1.0	26
1976	Thalidomide attenuates nitric oxide-driven angiogenesis by interacting with soluble guanylyl cyclase. <i>British Journal of Pharmacology</i> , 2009, 158, 1720-1734.	5.4	53
1977	Phylogenetic relationships among iguanian lizards using alternative partitioning methods and TSHZ1: A new phylogenetic marker for reptiles. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 391-396.	2.7	16
1978	Apicortin, a unique protein, with a putative cytoskeletal role, shared only by apicomplexan parasites and the placozoan <i>Trichoplax adhaerens</i> . <i>Infection, Genetics and Evolution</i> , 2009, 9, 1275-1286.	2.3	28
1979	LysR family transcriptional regulator PqsR as repressor of pyoluteorin biosynthesis and activator of phenazine-1-carboxylic acid biosynthesis in <i>Pseudomonas</i> sp. M18. <i>Journal of Biotechnology</i> , 2009, 143, 1-9.	3.8	26
1980	<i>Arabidopsis thaliana</i> GPAT8 and GPAT9 are localized to the ER and possess distinct ER retrieval signals: Functional divergence of the dilysine ER retrieval motif in plant cells. <i>Plant Physiology and Biochemistry</i> , 2009, 47, 867-879.	5.8	128
1981	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. <i>Journal of Proteomics</i> , 2009, 72, 567-573.	2.4	80
1982	A scheme for multiple sequence alignment optimization—an improvement based on family representative mechanics features. <i>Journal of Theoretical Biology</i> , 2009, 261, 593-597.	1.7	4
1983	The first peptides: The evolutionary transition between prebiotic amino acids and early proteins. <i>Journal of Theoretical Biology</i> , 2009, 261, 531-539.	1.7	74
1984	The Dual Function of the <i>Mycobacterium tuberculosis</i> FadD32 Required for Mycolic Acid Biosynthesis. <i>Chemistry and Biology</i> , 2009, 16, 510-519.	6.0	76
1985	Structural characterization of the protein cce_0567 from <i>Cyanothece</i> 51142, a metalloprotein associated with nitrogen fixation in the DUF683 family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 627-633.	2.3	4
1986	The O-specific polysaccharide structure and biosynthetic gene cluster of <i>Yersinia pseudotuberculosis</i> serotype O:11. <i>Carbohydrate Research</i> , 2009, 344, 1533-1540.	2.3	17

#	ARTICLE	IF	CITATIONS
1987	Biochemical characterization of Alr1529, a novel SGNH hydrolase variant from <i>Anabaena</i> sp. PCC 7120. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 324-334.	2.3	9
1988	Generation de marqueurs de séquences exprimées et développement de marqueurs microsatellites pour <i>Castanopsis sieboldii</i> var. <i>sieboldii</i> (Fagaceae). <i>Annals of Forest Science</i> , 2009, 66, 509-509.	2.0	20
1989	Biological Insights from Structures of Two-Component Proteins. <i>Annual Review of Microbiology</i> , 2009, 63, 133-154.	7.3	675
1990	Prediction of novel archaeal enzymes from sequence-derived features. <i>Protein Science</i> , 2009, 11, 2894-2898.	7.6	33
1991	A novel member of the YchN-like fold: Solution structure of the hypothetical protein Tm0979 from <i>Thermotoga maritima</i> . <i>Protein Science</i> , 2009, 14, 216-223.	7.6	8
1992	The solution structure of the oxidative stress-related protein YggX from <i>Escherichia coli</i> . <i>Protein Science</i> , 2009, 14, 1673-1678.	7.6	12
1993	Structural model of the amino propeptide of collagen XI ± 1 chain with similarity to the LNS domains. <i>Protein Science</i> , 2005, 14, 1526-1537.	7.6	28
1994	The C-Ala Domain Brings Together Editing and Aminoacylation Functions on One tRNA. <i>Science</i> , 2009, 325, 744-747.	12.6	71
1995	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	12.6	3,883
1996	Directed evolution of a <i>Bacillus</i> chitinase. <i>Biotechnology Journal</i> , 2009, 4, 501-509.	3.5	25
1997	Bioinformatic search of plant protein kinases involved in the phosphorylation of microtubular proteins and the regulation of the cell cycle. <i>Cytology and Genetics</i> , 2009, 43, 201-215.	0.5	1
1998	NOPdb: Nucleolar Proteome Database–2008 update. <i>Nucleic Acids Research</i> , 2009, 37, D181-D184.	14.5	243
1999	Structure and Function of <i>Bacillus subtilis</i> YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. <i>Biochemistry</i> , 2009, 48, 8664-8671.	2.5	37
2000	A mathematical model for generating bipartite graphs and its application to protein networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009, 42, 485005.	2.1	7
2001	Top-Down Identification of Protein Biomarkers in Bacteria with Unsequenced Genomes. <i>Analytical Chemistry</i> , 2009, 81, 9633-9642.	6.5	69
2002	Biochemical Analysis of the Biosynthetic Pathway of an Anticancer Tetracycline SF2575. <i>Journal of the American Chemical Society</i> , 2009, 131, 17677-17689.	13.7	88
2003	Characterization and Structure of the Manganese-Responsive Transcriptional Regulator ScaR ⁺ . <i>Biochemistry</i> , 2009, 48, 10308-10320.	2.5	47
2004	Plasmid-Mediated Quinolone Resistance: a Multifaceted Threat. <i>Clinical Microbiology Reviews</i> , 2009, 22, 664-689.	13.6	786

#	ARTICLE	IF	CITATIONS
2005	The SWISS-MODEL Repository and associated resources. <i>Nucleic Acids Research</i> , 2009, 37, D387-D392.	14.5	1,789
2006	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	2.1	99
2007	Functional characterization of a C-4 sterol methyl oxidase from the endomycorrhizal fungus <i>Glomus intraradices</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, 486-495.	2.1	17
2008	The Amoebal MAP Kinase Response to <i>Legionella pneumophila</i> Is Regulated by DupA. <i>Cell Host and Microbe</i> , 2009, 6, 253-267.	11.0	35
2009	A major mutation of KIF21A associated with congenital fibrosis of the extraocular muscles type 1 (CFEOM1) enhances translocation of Kank1 to the membrane. <i>Biochemical and Biophysical Research Communications</i> , 2009, 386, 639-644.	2.1	36
2010	CpcF-dependent regulation of pigmentation and development in <i>Fremyella diplosiphon</i> . <i>Biochemical and Biophysical Research Communications</i> , 2009, 389, 602-606.	2.1	20
2011	Interleukin-17D in Atlantic salmon (<i>Salmo salar</i>): Molecular characterization, 3D modelling and promoter analysis. <i>Fish and Shellfish Immunology</i> , 2009, 27, 647-659.	3.6	61
2012	Differentially conserved staphylococcal SH3b_5 cell wall binding domains confer increased staphylococcal and streptococcal activity to a streptococcal prophage endolysin domain. <i>Gene</i> , 2009, 443, 32-41.	2.2	102
2013	Fungal LysM effectors: extinguishers of host immunity?. <i>Trends in Microbiology</i> , 2009, 17, 151-157.	7.7	243
2014	Purification, cloning and characterization of fragaceatoxin C, a novel actinoporin from the sea anemone <i>Actinia fragacea</i> . <i>Toxicon</i> , 2009, 54, 869-880.	1.6	63
2015	A novel human protein is able to interact with hepatitis B virus core deletion mutant but not with the wild-type protein. <i>Virus Research</i> , 2009, 146, 130-134.	2.2	1
2016	Short ultraconserved promoter regions delineate a class of preferentially expressed alternatively spliced transcripts. <i>Genomics</i> , 2009, 94, 308-316.	2.9	11
2017	Investigating transcriptional regulation: From analysis of complex networks to discovery of cis-regulatory elements. <i>Methods</i> , 2009, 48, 277-286.	3.8	4
2018	The 2.5 Å resolution crystal structure of HetL, a pentapeptide repeat protein involved in regulation of heterocyst differentiation in the cyanobacterium <i>Nostoc</i> sp. strain PCC 7120. <i>Journal of Structural Biology</i> , 2009, 165, 47-52.	2.8	28
2019	Crystal structure of MqnD (TTHA1568), a menaquinone biosynthetic enzyme from <i>Thermus thermophilus</i> HB8. <i>Journal of Structural Biology</i> , 2009, 168, 575-581.	2.8	13
2020	Comparative and functional genomics of lipases in holometabolous insects. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 547-567.	2.7	101
2021	Crystal Structure of the Resuscitation-Promoting Factor γ DUFpB from <i>M. tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2009, 385, 153-162.	4.2	72
2022	Structure and Mechanism of a Eukaryotic FMN Adenylyltransferase. <i>Journal of Molecular Biology</i> , 2009, 389, 388-400.	4.2	45

#	ARTICLE	IF	CITATIONS
2023	Remote Homology between Munc13 MUN Domain and Vesicle Tethering Complexes. Journal of Molecular Biology, 2009, 391, 509-517.	4.2	68
2024	Characterization of Two Novel Aldo-Keto Reductases from Arabidopsis: Expression Patterns, Broad Substrate Specificity, and an Open Active-Site Structure Suggest a Role in Toxicant Metabolism Following Stress. Journal of Molecular Biology, 2009, 392, 465-480.	4.2	123
2025	Molecular Geometry of CsrA (RsmA) Binding to RNA and Its Implications for Regulated Expression. Journal of Molecular Biology, 2009, 392, 511-528.	4.2	103
2026	PILZ Protein Structure and Interactions with PILB and the FIMX EAL Domain: Implications for Control of Type IV Pilus Biogenesis. Journal of Molecular Biology, 2009, 393, 848-866.	4.2	100
2027	Alternative to Homo-oligomerisation: The Creation of Local Symmetry in Proteins by Internal Amplification. Journal of Molecular Biology, 2009, 394, 522-534.	4.2	19
2028	Structural genomics approach to drug discovery for Mycobacterium tuberculosis. Current Opinion in Microbiology, 2009, 12, 318-325.	5.1	31
2029	The Otubain YOD1 Is a Deubiquitinating Enzyme that Associates with p97 to Facilitate Protein Dislocation from the ER. Molecular Cell, 2009, 36, 28-38.	9.7	177
2030	Transcription factor GATA-3 in Atlantic salmon (<i>Salmo salar</i>): Molecular characterization, promoter activity and expression analysis. Molecular Immunology, 2009, 46, 3099-3107.	2.2	40
2031	Large-Scale Structural Biology of the Human Proteome. Annual Review of Biochemistry, 2009, 78, 541-568.	11.1	49
2032	Large-Scale Phosphoprotein Analysis in <i>Medicago truncatula</i> Roots Provides Insight into in Vivo Kinase Activity in Legumes. Plant Physiology, 2009, 152, 19-28.	4.8	133
2033	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16428-16433.	7.1	774
2034	Computational Fragment-Based Approach at PDB Scale by Protein Local Similarity. Journal of Chemical Information and Modeling, 2009, 49, 280-294.	5.4	42
2035	Single-Molecule Fluorescence Studies of a PH Domain: New Insights into the Membrane Docking Reaction. Biophysical Journal, 2009, 96, 566-582.	0.5	99
2036	An Energetic Representation of Protein Architecture that Is Independent of Primary and Secondary Structure. Biophysical Journal, 2009, 97, 1461-1470.	0.5	5
2037	Protein Structure Modeling. NATO Science for Peace and Security Series A: Chemistry and Biology, 2009, , 139-151.	0.5	5
2038	Genomic Analyses of the Microsporidian <i>Nosema ceranae</i> , an Emergent Pathogen of Honey Bees. PLoS Pathogens, 2009, 5, e1000466.	4.7	194
2039	Chapter 41 Parallel Methods for Expression and Purification. Methods in Enzymology, 2009, 463, 767-785.	1.0	13
2040	Mining cyanobacterial genomes for genes encoding complex biosynthetic pathways. Natural Product Reports, 2009, 26, 1447.	10.3	60

#	ARTICLE	IF	CITATIONS
2041	Finding Homologs in Amino Acid Sequences Using Network BLAST Searches. Current Protocols in Bioinformatics, 2009, 25, Unit 3.4.	25.8	14
2042	Structural and functional constraints in the evolution of protein families. Nature Reviews Molecular Cell Biology, 2009, 10, 709-720.	37.0	179
2043	The Basic Concepts of Molecular Modeling. Methods in Enzymology, 2009, 467, 307-334.	1.0	23
2044	FACS-Assisted Microarray Profiling Implicates Novel Genes and Pathways in Zebrafish Gastrointestinal Tract Development. Gastroenterology, 2009, 137, 1321-1332.	1.3	51
2045	A Novel Class of Modular Transporters for Vitamins in Prokaryotes. Journal of Bacteriology, 2009, 191, 42-51.	2.2	280
2046	Thoroughly sampling sequence space: Large-scale protein design of structural ensembles. Protein Science, 2009, 11, 2804-2813.	7.6	101
2047	Rapid protein domain assignment from amino acid sequence using predicted secondary structure. Protein Science, 2009, 11, 2814-2824.	7.6	122
2048	Metal ions and phosphate binding in the H-N-H motif: Crystal structures of the nuclease domain of ColE7/Im7 in complex with a phosphate ion and different divalent metal ions. Protein Science, 2009, 11, 2947-2957.	7.6	51
2049	Engineering Bacterial Signals and Sensors. Contributions To Microbiology, 2009, 16, 194-225.	2.1	47
2050	Profile-profile comparisons by COMPASS predict intricate homologies between protein families. Protein Science, 2009, 12, 2262-2272.	7.6	44
2051	Solution structure of the rhodanese homology domain At4g01050(175-295) from Arabidopsis thaliana. Protein Science, 2009, 14, 224-230.	7.6	24
2052	On the use of DXMS to produce more crystallizable proteins: Structures of the T. maritima proteins TM0160 and TM1171. Protein Science, 2009, 13, 3187-3199.	7.6	55
2053	Generation and analysis of transcriptomic resources for a model system on the rise: the sea anemone Aiptasia pallida and its dinoflagellate endosymbiont. BMC Genomics, 2009, 10, 258.	2.8	169
2054	Proteins recruited by SH3 domains of Ruk/CIN85 adaptor identified by LC-MS/MS. Proteome Science, 2009, 7, 21.	1.7	41
2055	In vitro nuclear interactome of the HIV-1 Tat protein. Retrovirology, 2009, 6, 47.	2.0	86
2056	A potentially novel overlapping gene in the genomes of Israeli acute paralysis virus and its relatives. Virology Journal, 2009, 6, 144.	3.4	25
2057	The Anabaena sensory rhodopsin transducer defines a novel superfamily of prokaryotic small-molecule binding domains. Biology Direct, 2009, 4, 25.	4.6	7
2058	Role of a Conserved Active Site Cation π Interaction in <i>Escherichia coli</i> Serine Hydroxymethyltransferase. Biochemistry, 2009, 48, 12034-12046.	2.5	35

#	ARTICLE	IF	CITATIONS
2059	Finding Similar Nucleotide Sequences Using Network BLAST Searches. Current Protocols in Bioinformatics, 2009, 26, Unit 3.3.	25.8	16
2060	Genome and proteome annotation: organization, interpretation and integration. Journal of the Royal Society Interface, 2009, 6, 129-147.	3.4	45
2061	Chapter 1 Variation in Form and Function. Advances in Applied Microbiology, 2009, 69, 1-22.	2.4	123
2062	Structural interactomics: informatics approaches to aid the interpretation of genetic variation and the development of novel therapeutics. Molecular BioSystems, 2009, 5, 1456.	2.9	8
2064	Genome-wide comparative analysis of the Brassica rapa gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. Genome Biology, 2009, 10, R111.	9.6	183
2065	Draft genome sequence of the Daphnia pathogen Octospora bayeri: insights into the gene content of a large microsporidian genome and a model for host-parasite interactions. Genome Biology, 2009, 10, R106.	9.6	67
2066	The origin recognition complex protein family. Genome Biology, 2009, 10, 214.	9.6	119
2067	Protein function annotation by homology-based inference. Genome Biology, 2009, 10, 207.	9.6	182
2068	Sequence-based feature prediction and annotation of proteins. Genome Biology, 2009, 10, 206.	9.6	53
2069	Poly(ADP-ribose) polymerase inhibition in cancer therapy: are we close to maturity?. Expert Opinion on Therapeutic Patents, 2009, 19, 1377-1400.	5.0	36
2070	Genome Sequence Databases: Types of Data and Bioinformatic Tools. , 2009, , 211-236.		1
2071	Domain content based protein function prediction using incomplete GO annotation information. , 2009, , .		0
2072	A Protein-Protein Interaction Prediction Method Embracing Intra-protein Domain Cohesion Information. , 2009, , .		0
2073	The Thermoplasma acidophilum LplA-LplB Complex Defines a New Class of Bipartite Lipoate-protein Ligases. Journal of Biological Chemistry, 2009, 284, 21317-21326.	3.4	31
2074	How effective is the data on co-occurrence of domains in multi-domain proteins in prediction of protein-protein interactions?. , 2009, , .		1
2075	Experimental Study of Different FSAs in Classifying Protein Function. , 2009, , .		3
2076	Predicting Yeast Synthetic Lethal Genetic Interactions Using Protein Domains. , 2009, , .		0
2077	Chapter 11 Unexpected Turns and Twists in Structure/Function of PR-Proteins that Connect Energy Metabolism and Immunity. Advances in Botanical Research, 2009, 51, 439-489.	1.1	18

#	ARTICLE	IF	CITATIONS
2078	Identifying structural repeats in proteins using graph centrality measures. , 2009, , .		1
2079	Analysis of the Bipartite Networks of Domain Compositions and Metabolic Reactions. , 2009, , .		0
2080	Diverse circovirus-like genome architectures revealed by environmental metagenomics. Journal of General Virology, 2009, 90, 2418-2424.	2.9	145
2081	Genetic makeup of the <i>Corynebacterium glutamicum</i> LexA regulon deduced from comparative transcriptomics and in vitro DNA band shift assays. Microbiology (United Kingdom), 2009, 155, 1459-1477.	1.8	41
2082	Evolution, ecology and the engineered organism: lessons for synthetic biology. Genome Biology, 2009, 10, 114.	9.6	7
2083	The WUS homeobox-containing (WOX) protein family. Genome Biology, 2009, 10, 248.	9.6	354
2084	Rational design of peptide-based building blocks for nanoscience and synthetic biology. Faraday Discussions, 2009, 143, 305.	3.2	30
2085	Bioinformatic analysis of microRNA biogenesis and function related proteins in eleven animal genomes. Journal of Genetics and Genomics, 2009, 36, 591-601.	3.9	16
2086	Biochemical Characterization of the RNase II Family of Exoribonucleases from the Human Pathogens <i>Salmonella typhimurium</i> and <i>Streptococcus pneumoniae</i> . Biochemistry, 2009, 48, 11848-11857.	2.5	21
2087	Molecular Basis and Regulation of Ammonium Transporter in Rice. Rice Science, 2009, 16, 314-322.	3.9	58
2088	Testing temperature-induced proteomic changes in the plant-associated bacterium <i>Pseudomonas fluorescens</i> SBW25. Environmental Microbiology Reports, 2010, 2, 396-402.	2.4	5
2089	Comparative Analysis of Complete Genome Sequences of Three Avian Coronaviruses Reveals a Novel Group 3c Coronavirus. Journal of Virology, 2009, 83, 908-917.	3.4	196
2090	Structural Mechanism of Absciscic Acid Binding and Signaling by Dimeric PYR1. Science, 2009, 326, 1373-1379.	12.6	457
2091	Human aldehyde dehydrogenase genes: alternatively spliced transcriptional variants and their suggested nomenclature. Pharmacogenetics and Genomics, 2009, 19, 893-902.	1.5	55
2092	Comparative Genome Analysis. , 2009, , 33-58.		0
2093	A novel motif at the C-terminus of palmitoyltransferases is essential for Swf1 and Pfa3 function <i>in vivo</i> . Biochemical Journal, 2009, 419, 301-308.	3.7	39
2094	The evolution of protein functions and networks: a family-centric approach. Biochemical Society Transactions, 2009, 37, 745-750.	3.4	3
2095	Three dimensional structure of the closed conformation (active) of human merlin reveals masking of actin binding site in the FERM domain. International Journal of Bioinformatics Research and Applications, 2009, 5, 516.	0.2	4

#	ARTICLE	IF	CITATIONS
2096	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.	2.0	32
2097	Sequence Analysis of the Full-length cDNA and Protein Structure Homology Modeling of FABP2 from <i>Paralichthys Olivaceus</i> . <i>Bioinformatics and Biology Insights</i> , 2009, 3, BBI.S2287.	2.0	7
2099	Protein-protein interaction databases: keeping up with growing interactomes. <i>Human Genomics</i> , 2009, 3, 291-7.	2.9	128
2100	Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009, 1, 189-196.	1.5	34
2101	The Importance of Being Flexible: The Case of Basic Region Leucine Zipper Transcriptional Regulators. <i>Current Protein and Peptide Science</i> , 2009, 10, 244-269.	1.4	91
2102	Signal Processing for Metagenomics: Extracting Information from the Soup. <i>Current Genomics</i> , 2009, 10, 493-510.	1.6	26
2103	The DOE-JGI Standard Operating Procedure for the Annotations of Microbial Genomes. <i>Standards in Genomic Sciences</i> , 2009, 1, 63-67.	1.5	218
2104	Comparative Analyses of Plant Transcription Factor Databases. <i>Current Genomics</i> , 2009, 10, 10-17.	1.6	24
2105	Modulating Proteostasis: Peptidomimetic Inhibitors and Activators of Protein Folding. <i>Current Pharmaceutical Design</i> , 2009, 15, 2488-2507.	1.9	13
2106	Hidden Markov Models and their Applications in Biological Sequence Analysis. <i>Current Genomics</i> , 2009, 10, 402-415.	1.6	252
2107	Biochemical characterization, membrane association and identification of amino acids essential for the function of Alg11 from <i>Saccharomyces cerevisiae</i> , an α 1,2-mannosyltransferase catalysing two sequential glycosylation steps in the formation of the lipid-linked core oligosaccharide. <i>Biochemical Journal</i> , 2010, 426, 205-217.	3.7	34
2108	Fast Revelation of the Motif Mode for a Yeast Protein Interaction Network Through Intelligent Agent-Based Distributed Computing. <i>Protein and Peptide Letters</i> , 2010, 17, 1091-1101.	0.9	1
2109	Detecting Atypical Examples of Known Domain Types by Sequence Similarity Searching: The SBASE Domain Library Approach. <i>Current Protein and Peptide Science</i> , 2010, 11, 538-549.	1.4	6
2110	Proteins: Sequence to Structure and Function – Current Status. <i>Current Protein and Peptide Science</i> , 2010, 11, 498-514.	1.4	55
2111	Inferring Protein-Protein Interactions Using a Hybrid Genetic Algorithm/Support Vector Machine Method. <i>Protein and Peptide Letters</i> , 2010, 17, 1079-1084.	0.9	9
2112	Genome-Wide Phylogenetic Comparative Analysis of Plant Transcriptional Regulation: A Timeline of Loss, Gain, Expansion, and Correlation with Complexity. <i>Genome Biology and Evolution</i> , 2010, 2, 488-503.	2.5	174
2113	Identification and characterization of a surface-associated, subtilisin-like serine protease in <i>Trichomonas vaginalis</i> . <i>Parasitology</i> , 2010, 137, 1621-1635.	1.5	14
2114	The diversity and molecular modelling analysis of B ₁₂ -dependent and B ₁₂ -independent glycerol dehydratases. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 484.	0.2	13

#	ARTICLE	IF	CITATIONS
2115	Detecting distant homologies on protozoans metabolic pathways using scientific workflows. International Journal of Data Mining and Bioinformatics, 2010, 4, 256.	0.1	5
2116	Fuzzy Clustering of Large Relational Bioinformatics Datasets. , 0, , 379-399.		0
2117	Marine Metagenomics: New Tools for the Study and Exploitation of Marine Microbial Metabolism. Marine Drugs, 2010, 8, 608-628.	4.6	152
2119	Expression of Usherin in the Anthozoan <i>Nematostella vectensis</i> . Biological Bulletin, 2010, 218, 105-112.	1.8	7
2120	Mining Cytochrome b561 proteins from plant genomes. International Journal of Bioinformatics Research and Applications, 2010, 6, 209.	0.2	5
2121	Prediction of protein protein interactions from primary sequences. International Journal of Data Mining and Bioinformatics, 2010, 4, 211.	0.1	12
2122	<i>ACTTS3</i> Encoding a Polyketide Synthase Is Essential for the Biosynthesis of ACT-Toxin and Pathogenicity in the Tangerine Pathotype of <i>Alternaria alternata</i> . Molecular Plant-Microbe Interactions, 2010, 23, 406-414.	2.6	47
2123	Six New Genes Required for Production of T-Toxin, a Polyketide Determinant of High Virulence of <i>Cochliobolus heterostrophus</i> to Maize. Molecular Plant-Microbe Interactions, 2010, 23, 458-472.	2.6	64
2124	Role of the Host-Selective ACT-Toxin Synthesis Gene <i>ACTTS2</i> Encoding an Enoyl-Reductase in Pathogenicity of the Tangerine Pathotype of <i>Alternaria alternata</i> . Phytopathology, 2010, 100, 120-126.	2.2	49
2125	An Allergen Portrait Gallery: Representative Structures and an Overview of IgE Binding Surfaces. Bioinformatics and Biology Insights, 2010, 4, BBI.S5737.	2.0	19
2126	Basic characterization of 90 kDa heat shock protein genes <i>HSP90AA1</i> , <i>HSP90AB1</i> , <i>HSP90B1</i> and <i>TRAP1</i> expressed in Japanese quail (<i>Coturnix japonica</i>). Animal Science Journal, 2010, 81, 513-518.	1.4	8
2127	Characterization of a Nitric Oxide Synthase from the Plant Kingdom: NO Generation from the Green Alga <i>Ostreococcus tauri</i> Is Light Irradiance and Growth Phase Dependent. Plant Cell, 2010, 22, 3816-3830.	6.6	313
2128	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen <i>Enterococcus faecium</i> and identification of a large transferable pathogenicity island. BMC Genomics, 2010, 11, 239.	2.8	190
2129	The Complete Genome Sequence of <i>Cupriavidus metallidurans</i> Strain CH34, a Master Survivalist in Harsh and Anthropogenic Environments. PLoS ONE, 2010, 5, e10433.	2.5	275
2130	The pheV Phenylalanine tRNA Gene in <i>Klebsiella pneumoniae</i> Clinical Isolates Is an Integration Hotspot for Possible Niche-Adaptation Genomic Islands. Current Microbiology, 2010, 60, 210-216.	2.2	11
2131	Mutations in the <i>Cc.rmt1</i> gene encoding a putative protein arginine methyltransferase alter developmental programs in the basidiomycete <i>Coprinopsis cinerea</i> . Current Genetics, 2010, 56, 361-367.	1.7	26
2132	From protein sequences to 3D-structures and beyond: the example of the UniProt Knowledgebase. Cellular and Molecular Life Sciences, 2010, 67, 1049-1064.	5.4	33
2133	Repeated two-hybrid screening detects transient protein-protein interactions. Theoretical Chemistry Accounts, 2010, 125, 613-619.	1.4	16

#	ARTICLE	IF	CITATIONS
2134	Evolutionary Bases of Carbohydrate Recognition and Substrate Discrimination in the ROK Protein Family. <i>Journal of Molecular Evolution</i> , 2010, 70, 545-556.	1.8	40
2135	A robust and extracellular heme-containing peroxidase from <i>Thermobifida fusca</i> as prototype of a bacterial peroxidase superfamily. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 1419-1430.	3.6	168
2136	The tetratricopeptide repeats (TPR)-like superfamily of proteins in <i>Leishmania</i> spp., as revealed by multi-relational data mining. <i>Pattern Recognition Letters</i> , 2010, 31, 2178-2189.	4.2	5
2137	Role of a novel disulfide bridge within the all-beta fold of soluble Rieske proteins. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 271-281.	2.6	7
2138	The manganese/iron-carboxylate proteins: what is what, where are they, and what can the sequences tell us?. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 339-349.	2.6	34
2139	A systematic investigation of multiheme c-type cytochromes in prokaryotes. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 559-571.	2.6	76
2140	TollML: a database of toll-like receptor structural motifs. <i>Journal of Molecular Modeling</i> , 2010, 16, 1283-1289.	1.8	17
2141	Molecular Characterization of a Novel Bacterial Aryl Acylamidase Belonging to the Amidase Signature Enzyme Family. <i>Molecules and Cells</i> , 2010, 29, 485-492.	2.6	23
2142	Germin-like proteins (GLPs) in cereal genomes: gene clustering and dynamic roles in plant defence. <i>Functional and Integrative Genomics</i> , 2010, 10, 463-476.	3.5	70
2143	A TonB-dependent transducer is responsible for regulation of pathogenicity-related genes in <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Journal of General Plant Pathology</i> , 2010, 76, 132-142.	1.0	7
2144	A novel monopartite dsRNA virus from rhododendron. <i>Archives of Virology</i> , 2010, 155, 1859-1863.	2.1	35
2145	Computational Challenges in Deciphering Genomic Structures of Bacteria. <i>Journal of Computer Science and Technology</i> , 2010, 25, 53-70.	1.5	1
2146	Prediction of multiple drug resistance phenotype in cancer cell lines using gene expression profiles and phylogenetic trees. <i>Science Bulletin</i> , 2010, 55, 3778-3786.	1.7	1
2147	Comparative study of network-based prioritization of protein domains associated with human complex diseases. <i>Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities</i> , 2010, 5, 107-118.	0.6	4
2148	Cloning of a New Xylanase Gene from <i>Streptomyces</i> sp. TN119 Using a Modified Thermal Asymmetric Interlaced-PCR Specific for GC-Rich Genes and Biochemical Characterization. <i>Applied Biochemistry and Biotechnology</i> , 2010, 160, 1277-1292.	2.9	31
2149	Lysozymes in the animal kingdom. <i>Journal of Biosciences</i> , 2010, 35, 127-160.	1.1	580
2150	The Role of Lipid Transfer Proteins in Allergic Diseases. <i>Current Allergy and Asthma Reports</i> , 2010, 10, 326-335.	5.3	136
2151	Cloning, Overexpression, Purification and Preliminary Characterization of Human Septin 8. <i>Protein Journal</i> , 2010, 29, 328-335.	1.6	2

#	ARTICLE	IF	CITATIONS
2152	Characterization of proteins with wide-angle X-ray solution scattering (WAXS). Journal of Structural and Functional Genomics, 2010, 11, 9-19.	1.2	47
2153	High-throughput computational structure-based characterization of protein families: START domains and implications for structural genomics. Journal of Structural and Functional Genomics, 2010, 11, 51-59.	1.2	10
2154	Basal expression studies of cystatins during specific growth stages of wheat spikes for defining their possible role in differential and stage dependent immunity against Karnal bunt (<i>Tilletia indica</i>). Molecular Biology Reports, 2010, 37, 1377-1389.	2.3	8
2155	Molecular cloning and characterization of five genes encoding pentatricopeptide repeat proteins from Upland cotton (<i>Gossypium hirsutum</i> L.). Molecular Biology Reports, 2010, 37, 801-808.	2.3	12
2156	5â€² and 3â€² end modifications of spliceosomal RNAs in <i>Plasmodium falciparum</i> . Molecular Biology Reports, 2010, 37, 2125-2133.	2.3	12
2157	Generation and analysis of expressed sequence tags from leaf and root of <i>Withania somnifera</i> (Ashwgandha). Molecular Biology Reports, 2010, 37, 893-902.	2.3	33
2158	Genome-wide analysis of primary auxin-responsive Aux/IAA gene family in maize (<i>Zea mays</i> . L.). Molecular Biology Reports, 2010, 37, 3991-4001.	2.3	108
2159	Genome-wide analysis of helicase gene family from rice and <i>Arabidopsis</i> : a comparison with yeast and human. Plant Molecular Biology, 2010, 73, 449-465.	3.9	86
2160	Belief Propagation Estimation of Protein and Domain Interactions Using the Sumâ€“Product Algorithm. IEEE Transactions on Information Theory, 2010, 56, 742-755.	2.4	6
2161	A novel thermostable cellulase from <i>Fervidobacterium nodosum</i> . Journal of Molecular Catalysis B: Enzymatic, 2010, 66, 294-301.	1.8	58
2162	Integration of heterogeneous data sources for gene function prediction using decision templates and ensembles of learning machines. Neurocomputing, 2010, 73, 1533-1537.	5.9	20
2163	Evolution of domain combinations in protein kinases and its implications for functional diversity. Progress in Biophysics and Molecular Biology, 2010, 102, 1-15.	2.9	36
2164	Protein annotation in the era of personal genomics. Current Opinion in Structural Biology, 2010, 20, 335-341.	5.7	1
2165	Dynamics of SecY Translocons with Translocation-Defective Mutations. Structure, 2010, 18, 847-857.	3.3	47
2166	MoDEL (Molecular Dynamics Extended Library): AÂDatabase of Atomistic Molecular Dynamics Trajectories. Structure, 2010, 18, 1399-1409.	3.3	123
2167	Finding scaffold proteins in interactomes. Trends in Cell Biology, 2010, 20, 2-4.	7.9	13
2168	Increased sequence conservation of domain repeats in prokaryotic proteins. Trends in Genetics, 2010, 26, 383-387.	6.7	8
2169	Missing genes in the annotation of prokaryotic genomes. BMC Bioinformatics, 2010, 11, 131.	2.6	94

#	ARTICLE	IF	CITATIONS
2170	Protein sequences classification by means of feature extraction with substitution matrices. BMC Bioinformatics, 2010, 11, 175.	2.6	50
2171	Structural fragment clustering reveals novel structural and functional motifs in α -helical transmembrane proteins. BMC Bioinformatics, 2010, 11, 204.	2.6	13
2172	Analysis of substructural variation in families of enzymatic proteins with applications to protein function prediction. BMC Bioinformatics, 2010, 11, 242.	2.6	15
2173	PhenoFam-gene set enrichment analysis through protein structural information. BMC Bioinformatics, 2010, 11, 254.	2.6	6
2174	Modular composition predicts kinase/substrate interactions. BMC Bioinformatics, 2010, 11, 349.	2.6	7
2175	FACT: Functional annotation transfer between proteins with similar feature architectures. BMC Bioinformatics, 2010, 11, 417.	2.6	26
2176	TOPSAN: a collaborative annotation environment for structural genomics. BMC Bioinformatics, 2010, 11, 426.	2.6	19
2177	Hidden Markov model speed heuristic and iterative HMM search procedure. BMC Bioinformatics, 2010, 11, 431.	2.6	966
2178	CMASA: an accurate algorithm for detecting local protein structural similarity and its application to enzyme catalytic site annotation. BMC Bioinformatics, 2010, 11, 439.	2.6	16
2179	Sites Inferred by Metabolic Background Assertion Labeling (SIMBAL): adapting the Partial Phylogenetic Profiling algorithm to scan sequences for signatures that predict protein function. BMC Bioinformatics, 2010, 11, 52.	2.6	12
2180	DODO: an efficient orthologous genes assignment tool based on domain architectures. Domain based ortholog detection. BMC Bioinformatics, 2010, 11, S6.	2.6	13
2181	Patterns of kinesin evolution reveal a complex ancestral eukaryote with a multifunctional cytoskeleton. BMC Evolutionary Biology, 2010, 10, 110.	3.2	138
2182	Gene duplication and the origins of morphological complexity in pancrustacean eyes, a genomic approach. BMC Evolutionary Biology, 2010, 10, 123.	3.2	52
2183	The molecular evolution of PL10 homologs. BMC Evolutionary Biology, 2010, 10, 127.	3.2	26
2184	A phylogenetic survey of myotubularin genes of eukaryotes: distribution, protein structure, evolution, and gene expression. BMC Evolutionary Biology, 2010, 10, 196.	3.2	24
2185	Evolutionary history of the poly(ADP-ribose) polymerase gene family in eukaryotes. BMC Evolutionary Biology, 2010, 10, 308.	3.2	108
2186	Ancient origin of animal U-box ubiquitin ligases. BMC Evolutionary Biology, 2010, 10, 331.	3.2	23
2187	Structural classification by the Lipase Engineering Database: a case study of Candida antarctica lipase A. BMC Genomics, 2010, 11, 123.	2.8	78

#	ARTICLE	IF	CITATIONS
2188	Comparative analysis of fungal protein kinases and associated domains. BMC Genomics, 2010, 11, 133.	2.8	43
2189	Conservation and divergence of known apicomplexan transcriptional regulons. BMC Genomics, 2010, 11, 147.	2.8	14
2190	Transcriptome analysis of reproductive tissue and intrauterine developmental stages of the tsetse fly (<i>Glossina morsitans morsitans</i>). BMC Genomics, 2010, 11, 160.	2.8	23
2191	Comparative genomics and proteomics of <i>Helicobacter mustelae</i> , an ulcerogenic and carcinogenic gastric pathogen. BMC Genomics, 2010, 11, 164.	2.8	40
2192	Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of <i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> . BMC Genomics, 2010, 11, 238.	2.8	102
2193	Origin and fate of pseudogenes in Hemiascomycetes: a comparative analysis. BMC Genomics, 2010, 11, 260.	2.8	27
2194	A comparison of massively parallel nucleotide sequencing with oligonucleotide microarrays for global transcription profiling. BMC Genomics, 2010, 11, 282.	2.8	124
2195	Genome-wide in silico screen for CCCH-type zinc finger proteins of <i>Trypanosoma brucei</i> , <i>Trypanosoma cruzi</i> and <i>Leishmania major</i> . BMC Genomics, 2010, 11, 283.	2.8	78
2196	Computational prediction of the osmoregulation network in <i>Synechococcus</i> sp. WH8102. BMC Genomics, 2010, 11, 291.	2.8	14
2197	The proteolytic system of lactic acid bacteria revisited: a genomic comparison. BMC Genomics, 2010, 11, 36.	2.8	311
2198	The <i>Giardia lamblia</i> vsp gene repertoire: characteristics, genomic organization, and evolution. BMC Genomics, 2010, 11, 424.	2.8	70
2199	A versatile palindromic amphipathic repeat coding sequence horizontally distributed among diverse bacterial and eucaryotic microbes. BMC Genomics, 2010, 11, 430.	2.8	15
2200	Genomic survey of the ectoparasitic mite <i>Varroa destructor</i> , a major pest of the honey bee <i>Apis mellifera</i> . BMC Genomics, 2010, 11, 602.	2.8	118
2201	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.	2.8	82
2202	Genome sequence of the pattern forming <i>Paenibacillus vortex</i> bacterium reveals potential for thriving in complex environments. BMC Genomics, 2010, 11, 710.	2.8	40
2203	Comparative genomics reveals selective distribution and domain organization of FYVE and PX domain proteins across eukaryotic lineages. BMC Genomics, 2010, 11, 83.	2.8	17
2204	Bioinformatic search of plant microtubule-and cell cycle related serine-threonine protein kinases. BMC Genomics, 2010, 11, S14.	2.8	23
2205	Unraveling the molecular mechanisms of nitrogenase conformational protection against oxygen in diazotrophic bacteria. BMC Genomics, 2010, 11, S7.	2.8	19

#	ARTICLE	IF	CITATIONS
2206	Genes and pathways for CO ₂ fixation in the obligate, chemolithoautotrophic acidophile, <i>Acidithiobacillus ferrooxidans</i> , Carbon fixation in <i>A. ferrooxidans</i> . BMC Microbiology, 2010, 10, 229.	3.3	65
2207	<i>Pseudomonas aeruginosa</i> β -lactamase induction requires two permeases, AmpG and AmpP. BMC Microbiology, 2010, 10, 328.	3.3	41
2208	GASdb: a large-scale and comparative exploration database of glycosyl hydrolysis systems. BMC Microbiology, 2010, 10, 69.	3.3	10
2209	Analysis of promoter activity of members of the PECTATE LYASE-LIKE (PLL) gene family in cell separation in <i>Arabidopsis</i> . BMC Plant Biology, 2010, 10, 152.	3.6	80
2210	Molecular and phylogenetic characterization of the sieve element occlusion gene family in Fabaceae and non-Fabaceae plants. BMC Plant Biology, 2010, 10, 219.	3.6	61
2211	The aconitate hydratase family from <i>Citrus</i> . BMC Plant Biology, 2010, 10, 222.	3.6	60
2212	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. BMC Plant Biology, 2010, 10, 98.	3.6	16
2213	Wheat beta-expansin (EXPB11) genes: Identification of the expressed gene on chromosome 3BS carrying a pollen allergen domain. BMC Plant Biology, 2010, 10, 99.	3.6	17
2214	Screening and sequence analysis of the hemolysin gene of <i>Fusobacterium necrophorum</i> . Anaerobe, 2010, 16, 402-404.	2.1	8
2215	Genetic analysis of mobile tetQ elements in oral <i>Prevotella</i> species. Anaerobe, 2010, 16, 604-609.	2.1	14
2216	Practical application of bioinformatics by the multidisciplinary VIZIER consortium. Antiviral Research, 2010, 87, 95-110.	4.1	39
2217	The evolution of protein targeting and translocation systems. Biochimica Et Biophysica Acta - Molecular Cell Research, 2010, 1803, 1115-1130.	4.1	38
2218	Prediction of pathogenicity islands in Enterohemorrhagic <i>Escherichia coli</i> O157:H7 using genomic barcodes. FEBS Letters, 2010, 584, 194-198.	2.8	19
2219	Mining metagenomic data for novel domains: BACON, a new carbohydrate-binding module. FEBS Letters, 2010, 584, 2421-2426.	2.8	41
2220	<i>Drosophila</i> SMN complex proteins Gemin2, Gemin3, and Gemin5 are components of U bodies. Experimental Cell Research, 2010, 316, 2354-2364.	2.6	36
2221	Characterization of the Apical Membrane Antigen-1 in Italian Strains of <i>Babesia bigemina</i> . Transboundary and Emerging Diseases, 2010, 57, 52-56.	3.0	18
2222	Myosin diversity in the diatom <i>Phaeodactylum tricornutum</i> . Cytoskeleton, 2010, 67, 142-151.	2.0	4
2223	Fatgraph models of proteins. Communications on Pure and Applied Mathematics, 2010, 63, 1249-1297.	3.1	37

#	ARTICLE	IF	CITATIONS
2224	The Roche Cancer Genome Database (RCGDB). <i>Human Mutation</i> , 2010, 31, 407-413.	2.5	12
2226	Pacidamycin Biosynthesis: Identification and Heterologous Expression of the First Uridyl Peptide Antibiotic Gene Cluster. <i>ChemBioChem</i> , 2010, 11, 1700-1709.	2.6	68
2227	Eukaryotic cold shock domain proteins: highly versatile regulators of gene expression. <i>BioEssays</i> , 2010, 32, 109-118.	2.5	141
2228	Enhanced expression and activity yields of <i>Clostridium thermocellum</i> xylanases without non-catalytic domains. <i>Journal of Biotechnology</i> , 2010, 145, 38-42.	3.8	27
2229	Influence of transposition and insertion of additional binding domain on expression and characteristics of xylanase C of <i>Clostridium thermocellum</i> . <i>Journal of Biotechnology</i> , 2010, 150, 1-5.	3.8	6
2230	Characterization of potential allergens in fenugreek (<i>Trigonella foenum-graecum</i>) using patient sera and MS-based proteomic analysis. <i>Journal of Proteomics</i> , 2010, 73, 1321-1333.	2.4	38
2231	The immunoregulatory properties of oncolytic myxoma virus and their implications in therapeutics. <i>Microbes and Infection</i> , 2010, 12, 1144-1152.	1.9	30
2232	Assessment of protein domain fusions in human protein interaction networks prediction: Application to the human kinetochore model. <i>New Biotechnology</i> , 2010, 27, 755-765.	4.4	9
2233	Application of Chemoproteomics to Drug Discovery: Identification of a Clinical Candidate Targeting Hsp90. <i>Chemistry and Biology</i> , 2010, 17, 686-694.	6.0	79
2234	Systematic analysis of an amidase domain CHAP in 12 <i>Staphylococcus aureus</i> genomes and 44 staphylococcal phage genomes. <i>Computational Biology and Chemistry</i> , 2010, 34, 251-257.	2.3	25
2235	The role of internal duplication in the evolution of multi-domain proteins. <i>BioSystems</i> , 2010, 101, 127-135.	2.0	16
2236	Cell surface display of chimeric glycoproteins via the S-layer of <i>Paenibacillus alvei</i> . <i>Carbohydrate Research</i> , 2010, 345, 1422-1431.	2.3	21
2237	Structural and genetic characterization of the O-antigen of <i>Salmonella enterica</i> O56 containing a novel derivative of 4-amino-4,6-dideoxy-d-glucose. <i>Carbohydrate Research</i> , 2010, 345, 1891-1895.	2.3	8
2238	Incorporating multiple genomic features with the utilization of interacting domain patterns to improve the prediction of protein-protein interactions. <i>Information Sciences</i> , 2010, 180, 3955-3973.	6.9	6
2239	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1174-1181.	0.7	8
2240	Structure of LP2179, the first representative of Pfam family PF08866, suggests a new fold with a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1205-1210.	0.7	3
2241	The structure of Jann_2411 (DUF1470) from <i>Jannaschia</i> sp. at 1.45 Å resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1198-1204.	0.7	9
2242	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1245-1253.	0.7	8

#	ARTICLE	IF	CITATIONS
2243	The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1265-1273.	0.7	8
2244	The structure of DinB from <i>Geobacillus stearothermophilus</i> : a representative of a unique four-helix-bundle superfamily. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 219-224.	0.7	14
2245	DUFs: families in search of function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1148-1152.	0.7	203
2246	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1167-1173.	0.7	3
2247	Ligands in PSI structures. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1309-1316.	0.7	14
2248	Crystallization and preliminary crystallographic analysis of the central domain of <i>Drosophila</i> Dribble, a protein that is essential for ribosome biogenesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 546-548.	0.7	0
2249	Crystallization and preliminary crystallographic analysis of nosiheptide-resistance methyltransferase from <i>Streptomyces actuosus</i> in complex with SAM. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 579-582.	0.7	0
2250	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved $\alpha\pm\alpha^2$ core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1335-1346.	0.7	8
2251	Structure of the β^3 - α -D-glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with α -L-Ala- β^3 -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364.	0.7	64
2252	Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1297-1305.	0.7	30
2254	Assessing the structural conservation of protein pockets to study functional and allosteric sites: implications for drug discovery. <i>BMC Structural Biology</i> , 2010, 10, 9.	2.3	34
2255	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010, 5, 31.	4.6	119
2256	The ancient function of RB-E2F Pathway: insights from its evolutionary history. <i>Biology Direct</i> , 2010, 5, 55.	4.6	45
2257	Cooperativity within proximal phosphorylation sites is revealed from large-scale proteomics data. <i>Biology Direct</i> , 2010, 5, 6.	4.6	95
2258	Computer aided selection of candidate vaccine antigens. <i>Immunome Research</i> , 2010, 6, S1.	0.1	93
2259	Archaic chaos: intrinsically disordered proteins in Archaea. <i>BMC Systems Biology</i> , 2010, 4, S1.	3.0	111
2260	ATHENA: A knowledge-based hybrid backpropagation-grammatical evolution neural network algorithm for discovering epistasis among quantitative trait Loci. <i>BioData Mining</i> , 2010, 3, 5.	4.0	43
2261	Domain distribution and intrinsic disorder in hubs in the human protein-protein interaction network. <i>Protein Science</i> , 2010, 19, 1461-1468.	7.6	62

#	ARTICLE	IF	CITATIONS
2262	The crystal structure of <i>Escherichia coli</i> SpoV. Protein Science, 2010, 19, 2252-2259.	7.6	31
2263	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the C-terminal domain of human Sufu. Protein Science, 2010, 19, 2131-2140.	7.6	12
2264	Differential proteomic analysis using iTRAQ reveals changes in thylakoids associated with Photosystem II-acquired thermotolerance in <i>Synechocystis</i> sp. PCC 6803. Proteomics, 2010, 10, 1917-1929.	2.2	30
2265	From proteome lists to biological impact: tools and strategies for the analysis of large MS data sets. Proteomics, 2010, 10, 1270-1283.	2.2	54
2266	Identifying secreted proteins of <i>Marssonina brunnea</i> by degenerate PCR. Proteomics, 2010, 10, 2406-2417.	2.2	33
2267	A proteomic approach towards the identification of the matrix protein content of the two types of microbodies in <i>Neurospora crassa</i> . Proteomics, 2010, 10, 3222-3234.	2.2	25
2268	Optimal protein-RNA area, OPRA: A propensity-based method to identify RNA-binding sites on proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 25-35.	2.6	83
2269	Structural domain-domain interactions: Assessment and comparison with protein-protein interaction data to improve the interactome. Proteins: Structure, Function and Bioinformatics, 2010, 78, 109-117.	2.6	21
2270	Crystal structure of an eIF4G-like protein from <i>Danio rerio</i> . Proteins: Structure, Function and Bioinformatics, 2010, 78, 1803-1806.	2.6	2
2271	Solution structure and function of YndB, an AHS1 protein from <i>Bacillus subtilis</i> . Proteins: Structure, Function and Bioinformatics, 2010, 78, 3328-3340.	2.6	13
2272	Characterization of <i>drCol 15a1b</i> : A Novel Component of the Stem Cell Niche in the Zebrafish Retina. Stem Cells, 2010, 28, 1399-1411.	3.2	16
2273	Origin of animal epithelia: insights from the sponge genome. Evolution & Development, 2010, 12, 601-617.	2.0	94
2274	INTRACELLULAR LOCALIZATION OF AN ENDOGENOUS CELLULOSE SYNTHASE OF MICRASTERIAS DENTICULATA (DESMIDIALES, CHLOROPHYTA) BY MEANS OF TRANSIENT GENETIC TRANSFORMATION1. Journal of Phycology, 2010, 46, 839-845.	2.3	18
2275	Archaeal transformation of metals in the environment. FEMS Microbiology Ecology, 2010, 73, 1-16.	2.7	81
2276	Evidence for bacteriophage activity causing community and performance changes in a phosphorus-removal activated sludge. FEMS Microbiology Ecology, 2010, 74, 631-642.	2.7	59
2277	New plasmids and putative virulence factors from the draft genome of an Australian clinical isolate of <i>Photobacterium</i> <i>asymbiotica</i> . FEMS Microbiology Letters, 2010, 309, no-no.	1.8	22
2278	Targeting mechanism of the retinoblastoma tumor suppressor by a prototypical viral oncoprotein. FEBS Journal, 2010, 277, 973-988.	4.7	52
2279	Brittle-Culm12, a dual-targeting kinesin-4 protein, controls cell cycle progression and wall properties in rice. Plant Journal, 2010, 63, 312-328.	5.7	114

#	ARTICLE	IF	CITATIONS
2280	Expansion of genes encoding a novel type of dynamin in the genome of the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Insect Molecular Biology</i> , 2010, 19, 165-173.	2.0	8
2281	Chitinase-like proteins encoded in the genome of the pea aphid, <i>Acyrtosiphon pisum</i> . <i>Insect Molecular Biology</i> , 2010, 19, 175-185.	2.0	64
2282	Asymmetric cross-regulation between the nitrate-responsive NarX-NarL and NarX-NarP two-component regulatory systems from <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2010, 75, 394-412.	2.5	88
2283	Structure determination and analysis of a haemolytic gingipain adhesin domain from <i>Porphyromonas gingivalis</i> . <i>Molecular Microbiology</i> , 2010, 76, 861-873.	2.5	30
2284	A post-translational, c-di-GMP-dependent mechanism regulating flagellar motility. <i>Molecular Microbiology</i> , 2010, 76, 1295-1305.	2.5	206
2285	THAP proteins target specific DNA sites through bipartite recognition of adjacent major and minor grooves. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 117-123.	8.2	67
2286	Bactofilins, a ubiquitous class of cytoskeletal proteins mediating polar localization of a cell wall synthase in <i>Caulobacter crescentus</i> . <i>EMBO Journal</i> , 2010, 29, 327-339.	7.8	143
2287	Gene-targeted-metagenomics reveals extensive diversity of aromatic dioxygenase genes in the environment. <i>ISME Journal</i> , 2010, 4, 279-285.	9.8	121
2288	Viruses in the faecal microbiota of monozygotic twins and their mothers. <i>Nature</i> , 2010, 466, 334-338.	27.8	1,054
2289	Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , 2010, 468, 60-66.	27.8	280
2290	GORDITA (AGL63) is a young paralog of the Arabidopsis thaliana Bister MADS box gene ABS (TT16) that has undergone neofunctionalization. <i>Plant Journal</i> , 2010, 63, 914-924.	5.7	49
2291	The S1 ribosomal protein family contains a unique conservative domain. <i>Molecular Biology</i> , 2010, 44, 642-647.	1.3	9
2292	Visualization of multiple alignments, phylogenies and gene family evolution. <i>Nature Methods</i> , 2010, 7, S16-S25.	19.0	73
2293	Bacterial nucleoid-associated proteins, nucleoid structure and gene expression. <i>Nature Reviews Microbiology</i> , 2010, 8, 185-195.	28.6	755
2294	Detecting genomic islands using bioinformatics approaches. <i>Nature Reviews Microbiology</i> , 2010, 8, 373-382.	28.6	257
2295	Antifreeze proteins in polar sea ice diatoms: diversity and gene expression in the genus <i>Fragilariopsis</i> . <i>Environmental Microbiology</i> , 2010, 12, 1041-1052.	3.8	81
2296	Structure and putative function of NFX1-like proteins in plants. <i>Plant Biology</i> , 2010, 12, 381-394.	3.8	20
2297	The plant PRAT proteins are preprotein and amino acid transport in mitochondria and chloroplasts*. <i>Plant Biology</i> , 2010, 12, 42-55.	3.8	24

#	ARTICLE	IF	CITATIONS
2298	AMPylation: something old is new again. <i>Frontiers in Microbiology</i> , 2010, 1, 113.	3.5	60
2299	Complete Genome Sequence of <i>Rothia mucilaginosa</i> DY-18: A Clinical Isolate with Dense Meshwork-Like Structures from a Persistent Apical Periodontitis Lesion. <i>Sequencing</i> , 2010, 2010, 1-6.	0.5	22
2300	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	3.5	213
2301	Sequence Alignment Reveals Possible MAPK Docking Motifs on HIV Proteins. <i>PLoS ONE</i> , 2010, 5, e8942.	2.5	10
2302	Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. <i>PLoS ONE</i> , 2010, 5, e9083.	2.5	76
2303	The Porcelain Crab Transcriptome and PCAD, the Porcelain Crab Microarray and Sequence Database. <i>PLoS ONE</i> , 2010, 5, e9327.	2.5	21
2304	The Complete Genome Sequence of <i>Haloferax volcanii</i> DS2, a Model Archaeon. <i>PLoS ONE</i> , 2010, 5, e9605.	2.5	234
2305	Transcriptome Profiling of a Toxic Dinoflagellate Reveals a Gene-Rich Protist and a Potential Impact on Gene Expression Due to Bacterial Presence. <i>PLoS ONE</i> , 2010, 5, e9688.	2.5	134
2306	Metagenomes from High-Temperature Chemotrophic Systems Reveal Geochemical Controls on Microbial Community Structure and Function. <i>PLoS ONE</i> , 2010, 5, e9773.	2.5	186
2307	Validation of Coevolving Residue Algorithms via Pipeline Sensitivity Analysis: ELSC and OMES and ZNMI, Oh My!. <i>PLoS ONE</i> , 2010, 5, e10779.	2.5	31
2308	CODA: Accurate Detection of Functional Associations between Proteins in Eukaryotic Genomes Using Domain Fusion. <i>PLoS ONE</i> , 2010, 5, e10908.	2.5	10
2309	Slip-Sliding Away: Serial Changes and Homoplasmy in Repeat Number in the <i>Drosophila yakuba</i> Homolog of Human Cancer Susceptibility Gene BRCA2. <i>PLoS ONE</i> , 2010, 5, e11006.	2.5	4
2310	The Phosphatomes of the Multicellular Myxobacteria <i>Myxococcus xanthus</i> and <i>Sorangium cellulosum</i> in Comparison with Other Prokaryotic Genomes. <i>PLoS ONE</i> , 2010, 5, e11164.	2.5	6
2311	Combining Next-Generation Sequencing Strategies for Rapid Molecular Resource Development from an Invasive Aphid Species, <i>Aphis glycines</i> . <i>PLoS ONE</i> , 2010, 5, e11370.	2.5	77
2312	Genomic Characterization of <i>Campylobacter jejuni</i> Strain M1. <i>PLoS ONE</i> , 2010, 5, e12253.	2.5	86
2313	Comparative Genome Analysis Reveals an Absence of Leucine-Rich Repeat Pattern-Recognition Receptor Proteins in the Kingdom Fungi. <i>PLoS ONE</i> , 2010, 5, e12725.	2.5	31
2314	Comparative Genomic Evidence for a Complete Nuclear Pore Complex in the Last Eukaryotic Common Ancestor. <i>PLoS ONE</i> , 2010, 5, e13241.	2.5	132
2315	Evolutionary Mode and Functional Divergence of Vertebrate NMDA Receptor Subunit 2 Genes. <i>PLoS ONE</i> , 2010, 5, e13342.	2.5	18

2317 Tissue-Specific Transcriptomics of the Exotic Invasive Insect Pest Emerald Ash Borer (*Agrilus*) Tj ETQq1 1 0.784314 rgBT /Overlock 10

#	ARTICLE	IF	CITATIONS
2334	Predicting Meiotic Pathways in Human Fetal Oogenesis1. <i>Biology of Reproduction</i> , 2010, 82, 543-551.	2.7	11
2335	Rodent and nonrodent malaria parasites differ in their phospholipid metabolic pathways. <i>Journal of Lipid Research</i> , 2010, 51, 81-96.	4.2	51
2336	Dual coding in alternative reading frames correlates with intrinsic protein disorder. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5429-5434.	7.1	92
2337	MicrobesOnline: an integrated portal for comparative and functional genomics. <i>Nucleic Acids Research</i> , 2010, 38, D396-D400.	14.5	408
2338	A highly coordinated cell wall degradation machine governs spore morphogenesis in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , 2010, 24, 411-422.	5.9	91
2339	A Thiolase of <i>Mycobacterium tuberculosis</i> Is Required for Virulence and Production of Androstenedione and Androstadienedione from Cholesterol. <i>Infection and Immunity</i> , 2010, 78, 275-282.	2.2	178
2340	DMDM: domain mapping of disease mutations. <i>Bioinformatics</i> , 2010, 26, 2458-2459.	4.1	53
2341	MidA is a putative methyltransferase that is required for mitochondrial complex I function. <i>Journal of Cell Science</i> , 2010, 123, 1674-1683.	2.0	49
2342	REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. <i>Nucleic Acids Research</i> , 2010, 38, D234-D236.	14.5	736
2343	Genome Sequence of the Polysaccharide-Degrading, Thermophilic Anaerobe <i>Spirochaeta thermophila</i> DSM 6192. <i>Journal of Bacteriology</i> , 2010, 192, 6492-6493.	2.2	19
2344	Ancestral centriole and flagella proteins identified by analysis of <i>Naegleria</i> differentiation. <i>Journal of Cell Science</i> , 2010, 123, 4024-4031.	2.0	29
2345	POLYVIEW-MM: web-based platform for animation and analysis of molecular simulations. <i>Nucleic Acids Research</i> , 2010, 38, W662-W666.	14.5	25
2346	RosR (Cg1324), a Hydrogen Peroxide-sensitive MarR-type Transcriptional Regulator of <i>Corynebacterium glutamicum</i> *. <i>Journal of Biological Chemistry</i> , 2010, 285, 29305-29318.	3.4	56
2347	A Novel Pax-like Protein Involved in Transcriptional Activation of Cyst Wall Protein Genes in <i>Giardia lamblia</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 32213-32226.	3.4	22
2348	Semantic integration of data on transcriptional regulation. <i>Bioinformatics</i> , 2010, 26, 1651-1661.	4.1	15
2349	A Conformational Switch in the Scaffolding Protein NHERF1 Controls Autoinhibition and Complex Formation. <i>Journal of Biological Chemistry</i> , 2010, 285, 9981-9994.	3.4	54
2350	GTP-dependent structural rearrangement of the eRF1:eRF3 complex and eRF3 sequence motifs essential for PABP binding. <i>Nucleic Acids Research</i> , 2010, 38, 548-558.	14.5	30
2351	Transposases are the most abundant, most ubiquitous genes in nature. <i>Nucleic Acids Research</i> , 2010, 38, 4207-4217.	14.5	270

#	ARTICLE	IF	CITATIONS
2352	PROFESS: a PROtein Function, Evolution, Structure and Sequence database. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq011-baq011.	3.0	6
2353	Effects of cadmium exposure and intermittent anoxia on nitric oxide metabolism in eastern oysters, <i>Crassostrea virginica</i> . Journal of Experimental Biology, 2010, 213, 433-444.	1.7	27
2354	Comparative Proteomic Analysis of Extracellular Proteins of <i>Clostridium perfringens</i> Type A and Type C Strains. Infection and Immunity, 2010, 78, 3957-3968.	2.2	42
2355	Cascleave: towards more accurate prediction of caspase substrate cleavage sites. Bioinformatics, 2010, 26, 752-760.	4.1	148
2356	The Abi Proteins and Their Involvement in Bacteriocin Self-Immunity. Journal of Bacteriology, 2010, 192, 2068-2076.	2.2	108
2357	3D-footprint: a database for the structural analysis of protein-DNA complexes. Nucleic Acids Research, 2010, 38, D91-D97.	14.5	66
2358	Discovery of a minimal form of RNase P in <i>Pyrobaculum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22493-22498.	7.1	41
2359	Identification of the gene encoding alkylglycerol monooxygenase defines a third class of tetrahydrobiopterin-dependent enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13672-13677.	7.1	74
2360	CdnL, a member of the large CarD-like family of bacterial proteins, is vital for <i>Myxococcus xanthus</i> and differs functionally from the global transcriptional regulator CarD. Nucleic Acids Research, 2010, 38, 4586-4598.	14.5	44
2361	Gene3D: merging structure and function for a Thousand genomes. Nucleic Acids Research, 2010, 38, D296-D300.	14.5	50
2362	Homologous over-extension: a challenge for iterative similarity searches. Nucleic Acids Research, 2010, 38, 2177-2189.	14.5	50
2363	Structure and function of polarity-inducing kinase family MARK/ParA within the branch of AMPK/Snf1-related kinases. FASEB Journal, 2010, 24, 1637-1648.	0.5	108
2364	The C-terminal Repeat Domain of Spt5 Plays an Important Role in Suppression of Rad26-independent Transcription Coupled Repair. Journal of Biological Chemistry, 2010, 285, 5317-5326.	3.4	48
2365	Extensive Divergence in Alternative Splicing Patterns after Gene and Genome Duplication During the Evolutionary History of Arabidopsis. Molecular Biology and Evolution, 2010, 27, 1686-1697.	8.9	53
2366	Bioinformatical approaches to characterize intrinsically disordered/unstructured proteins. Briefings in Bioinformatics, 2010, 11, 225-243.	6.5	107
2367	The comprehensive microbial resource. Nucleic Acids Research, 2010, 38, D340-D345.	14.5	241
2368	Expansion of the miRNA Pathway in the Hemipteran Insect <i>Acyrtosiphon pisum</i> . Molecular Biology and Evolution, 2010, 27, 979-987.	8.9	56
2369	Selective modification of rice (<i>Oryza sativa</i>) gene expression by rice stripe virus infection. Journal of General Virology, 2010, 91, 294-305.	2.9	97

#	ARTICLE	IF	CITATIONS
2370	PCFamily: a web server for searching homologous protein complexes. <i>Nucleic Acids Research</i> , 2010, 38, W516-W522.	14.5	12
2371	Expression and Physiological Role of Three <i>Myxococcus xanthus</i> Copper-Dependent P _{1B} -Type ATPases during Bacterial Growth and Development. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6077-6084.	3.1	19
2372	Identification of DIM-7, a protein required to target the DIM-5 H3 methyltransferase to chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8310-8315.	7.1	41
2373	Changes in reflectin protein phosphorylation are associated with dynamic iridescence in squid. <i>Journal of the Royal Society Interface</i> , 2010, 7, 549-560.	3.4	66
2374	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2010, 38, D308-D317.	14.5	108
2375	A recombination hotspot leads to sequence variability within a novel gene (AK005651) and contributes to type 1 diabetes susceptibility. <i>Genome Research</i> , 2010, 20, 1629-1638.	5.5	14
2376	PepX: a structural database of non-redundant protein-peptide complexes. <i>Nucleic Acids Research</i> , 2010, 38, D545-D551.	14.5	102
2377	ProPhyLER: A curated online resource for protein function and structure based on evolutionary constraint analyses. <i>Genome Research</i> , 2010, 20, 142-154.	5.5	28
2378	The S Helix Mediates Signal Transmission as a HAMP Domain Coiled-Coil Extension in the NarX Nitrate Sensor from <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 2010, 192, 734-745.	2.2	46
2379	<i>Legionella pneumophila</i> Strain 130b Possesses a Unique Combination of Type IV Secretion Systems and Novel Dot/Icm Secretion System Effector Proteins. <i>Journal of Bacteriology</i> , 2010, 192, 6001-6016.	2.2	104
2380	A Genetic Determinant in <i>Streptococcus gordonii</i> Challis Encodes a Peptide with Activity Similar to That of Enterococcal Sex Pheromone cAM373, Which Facilitates Intergeneric DNA Transfer. <i>Journal of Bacteriology</i> , 2010, 192, 2535-2545.	2.2	26
2381	Protein Kinase A Phosphorylation Activates Vpr-Induced Cell Cycle Arrest during Human Immunodeficiency Virus Type 1 Infection. <i>Journal of Virology</i> , 2010, 84, 6410-6424.	3.4	35
2382	Amot Recognizes a Juxtanuclear Endocytic Recycling Compartment via a Novel Lipid Binding Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 12308-12320.	3.4	50
2383	Novel Zn ²⁺ -binding Sites in Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2010, 285, 31731-31741.	3.4	42
2384	The Role of cis Dimerization of Signal Regulatory Protein Î± (SIRPÎ±) in Binding to CD47. <i>Journal of Biological Chemistry</i> , 2010, 285, 37953-37963.	3.4	22
2385	The integrated microbial genomes system: an expanding comparative analysis resource. <i>Nucleic Acids Research</i> , 2010, 38, D382-D390.	14.5	237
2386	Threshold Average Precision (TAP-k): a measure of retrieval designed for bioinformatics. <i>Bioinformatics</i> , 2010, 26, 1708-1713.	4.1	25
2387	Search and clustering orders of magnitude faster than BLAST. <i>Bioinformatics</i> , 2010, 26, 2460-2461.	4.1	18,572

#	ARTICLE	IF	CITATIONS
2388	GeMMA: functional subfamily classification within superfamilies of predicted protein structural domains. <i>Nucleic Acids Research</i> , 2010, 38, 720-737.	14.5	65
2389	When simple sequence comparison fails: the cryptic case of the shared domains of the bacterial replication initiation proteins DnaB and DnaD. <i>Nucleic Acids Research</i> , 2010, 38, 6930-6942.	14.5	26
2390	PANDITplus: toward better integration of evolutionary view on molecular sequences with supplementary bioinformatics resources. <i>Trends in Evolutionary Biology</i> , 2010, 2, 1.	0.4	6
2391	Biological Functions of the Genes in the Mammaprint Breast Cancer Profile Reflect the Hallmarks of Cancer. <i>Biomarker Insights</i> , 2010, 5, BML.S6184.	2.5	103
2392	Preferential use of protein domain pairs as interaction mediators: order and transitivity. <i>Bioinformatics</i> , 2010, 26, 2564-2570.	4.1	11
2393	Genomics and Bioinformatics Resources for Crop Improvement. <i>Plant and Cell Physiology</i> , 2010, 51, 497-523.	3.1	177
2394	Identification of subfamily-specific sites based on active sites modeling and clustering. <i>Bioinformatics</i> , 2010, 26, 3075-3082.	4.1	35
2395	Genomic Analysis of Two-Component Signal Transduction Proteins in Basidiomycetes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 18, 63-73.	1.0	14
2396	MeMotif: a database of linear motifs in α -helical transmembrane proteins. <i>Nucleic Acids Research</i> , 2010, 38, D181-D189.	14.5	18
2397	Structure of a Eukaryotic Nonribosomal Peptide Synthetase Adenylation Domain That Activates a Large Hydroxamate Amino Acid in Siderophore Biosynthesis. <i>Journal of Biological Chemistry</i> , 2010, 285, 2415-2427.	3.4	57
2398	Fission Yeast Iec1-Iso80-Mediated Nucleosome Eviction Regulates Nucleotide and Phosphate Metabolism. <i>Molecular and Cellular Biology</i> , 2010, 30, 657-674.	2.3	45
2399	Use of the Plant Defense Protein Osmotin To Identify <i>Fusarium oxysporum</i> Genes That Control Cell Wall Properties. <i>Eukaryotic Cell</i> , 2010, 9, 558-568.	3.4	19
2400	Defective nucleolar localization and dominant interfering properties of a parafibromin L95P missense mutant causing the hyperparathyroidism-“jaw tumor syndrome. <i>Endocrine-Related Cancer</i> , 2010, 17, 513-524.	3.1	36
2401	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. <i>Nucleic Acids Research</i> , 2010, 38, D190-D195.	14.5	202
2402	Effective Gene Silencing in a Microsporidian Parasite Associated with Honeybee (<i>Apis mellifera</i>) Colony Declines. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5960-5964.	3.1	100
2403	MEROPS: the peptidase database. <i>Nucleic Acids Research</i> , 2010, 38, D227-D233.	14.5	786
2404	PROSITE, a protein domain database for functional characterization and annotation. <i>Nucleic Acids Research</i> , 2010, 38, D161-D166.	14.5	744
2405	Genome-wide computational identification of WG/GW Argonaute-binding proteins in Arabidopsis. <i>Nucleic Acids Research</i> , 2010, 38, 4231-4245.	14.5	47

#	ARTICLE	IF	CITATIONS
2406	The Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter ruminantium</i> Reveals New Possibilities for Controlling Ruminant Methane Emissions. <i>PLoS ONE</i> , 2010, 5, e8926.	2.5	256
2407	Discovery and Characterization of Three New <i>Escherichia coli</i> Septal Ring Proteins That Contain a SPOR Domain: DamX, DedD, and RlpA. <i>Journal of Bacteriology</i> , 2010, 192, 242-255.	2.2	78
2408	Expansion of the target of rapamycin (TOR) kinase family and function in <i>Leishmania</i> shows that TOR3 is required for acidocalcisome biogenesis and animal infectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 11965-11970.	7.1	78
2409	Isolation and Properties of Malic Enzyme and Its Gene in <i>Rhodopseudomonas palustris</i> No. 7. <i>Bioscience, Biotechnology and Biochemistry</i> , 2010, 74, 75-81.	1.3	6
2410	An Arthropod Enzyme, Dfurin 1, and a Vertebrate Furin Homolog Display Distinct Cleavage Site Sequence Preferences for a Shared Viral Proprotein Substrate. <i>Journal of Insect Science</i> , 2010, 10, 1-16.	1.5	8
2411	A Scalable Parallel Algorithm for Large-Scale Protein Sequence Homology Detection. , 2010, , .		2
2412	Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2010, 17, 443-457.	1.6	12
2413	Lethal protein produced in response to competition between sibling bacterial colonies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6258-6263.	7.1	52
2414	Decision support based on genomics: integration of data- and knowledge-driven reasoning. <i>International Journal of Biomedical Engineering and Technology</i> , 2010, 3, 287.	0.2	3
2415	Outer membrane pore protein prediction in mycobacteria using genomic comparison. <i>Microbiology (United Kingdom)</i> , 2010, 156, 2506-2515.	1.8	20
2416	Bacterial Lifestyle in a Deep-sea Hydrothermal Vent Chimney Revealed by the Genome Sequence of the Thermophilic Bacterium <i>Deferribacter desulfuricans</i> SSM1. <i>DNA Research</i> , 2010, 17, 123-137.	3.4	41
2417	Differential Regulation of Six Heavy Metal Efflux Systems in the Response of <i>Myxococcus xanthus</i> to Copper. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6069-6076.	3.1	31
2418	Independent evolution of the core domain and its flanking sequences in small heat shock proteins. <i>FASEB Journal</i> , 2010, 24, 3633-3642.	0.5	219
2419	Tryptophanyl-tRNA Synthetase Urzyme. <i>Journal of Biological Chemistry</i> , 2010, 285, 38590-38601.	3.4	58
2420	A Novel L-Amino Acid Ligase from <i>Bacillus subtilis</i> NBRC3134 Catalyzed Oligopeptide Synthesis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2010, 74, 129-134.	1.3	20
2421	Arabidopsis AtSerp1, Crystal Structure and in Vivo Interaction with Its Target Protease RESPONSIVE TO DESICCATION-21 (RD21). <i>Journal of Biological Chemistry</i> , 2010, 285, 13550-13560.	3.4	73
2422	Structural and Enzymatic Insights into the ATP Binding and Autophosphorylation Mechanism of a Sensor Histidine Kinase. <i>Journal of Biological Chemistry</i> , 2010, 285, 24892-24903.	3.4	46
2423	Identification and Characterization of a Novel Deoxyhypusine Synthase in <i>Leishmania donovani</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 453-463.	3.4	47

#	ARTICLE	IF	CITATIONS
2424	Discovery and Characterization of Cadherin Domains in <i>Saccharophagus degradans</i> 2-40. Journal of Bacteriology, 2010, 192, 1066-1074.	2.2	46
2425	Characterization of the two-protein complex in <i>Escherichia coli</i> responsible for lipopolysaccharide assembly at the outer membrane. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5363-5368.	7.1	184
2426	Siderophores Are Not Involved in Fe(III) Solubilization during Anaerobic Fe(III) Respiration by <i>Shewanella oneidensis</i> MR-1. Applied and Environmental Microbiology, 2010, 76, 2425-2432.	3.1	39
2427	SpoIID-Mediated Peptidoglycan Degradation Is Required throughout Engulfment during <i>Bacillus subtilis</i> Sporulation. Journal of Bacteriology, 2010, 192, 3174-3186.	2.2	43
2428	Human Carboxymethylenebutenolidase as a Bioactivating Hydrolase of Olmesartan Medoxomil in Liver and Intestine. Journal of Biological Chemistry, 2010, 285, 11892-11902.	3.4	46
2429	A fast and automated solution for accurately resolving protein domain architectures. Bioinformatics, 2010, 26, 745-751.	4.1	47
2430	SALAD database: a motif-based database of protein annotations for plant comparative genomics. Nucleic Acids Research, 2010, 38, D835-D842.	14.5	64
2431	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq019-baq019.	3.0	22
2432	Characterization of a putative 3-deoxy-D-manno-2-octulosonic acid (Kdo) transferase gene from <i>Arabidopsis thaliana</i> . Glycobiology, 2010, 20, 617-628.	2.5	23
2433	Towards Viral Genome Annotation Standards, Report from the 2010 NCBI Annotation Workshop. Viruses, 2010, 2, 2258-2268.	3.3	27
2434	Orthopoxvirus Genome Evolution: The Role of Gene Loss. Viruses, 2010, 2, 1933-1967.	3.3	160
2435	Allosteric Modulation of G Protein Coupled Receptors by Cytoplasmic, Transmembrane and Extracellular Ligands. Pharmaceuticals, 2010, 3, 3324-3342.	3.8	15
2436	The Construction and Use of Log-Odds Substitution Scores for Multiple Sequence Alignment. PLoS Computational Biology, 2010, 6, e1000852.	3.2	58
2437	Networks of High Mutual Information Define the Structural Proximity of Catalytic Sites: Implications for Catalytic Residue Identification. PLoS Computational Biology, 2010, 6, e1000978.	3.2	74
2438	Cholera- and Anthrax-Like Toxins Are among Several New ADP-Ribosyltransferases. PLoS Computational Biology, 2010, 6, e1001029.	3.2	53
2439	Identification and Genome-Wide Prediction of DNA Binding Specificities for the ApiAP2 Family of Regulators from the Malaria Parasite. PLoS Pathogens, 2010, 6, e1001165.	4.7	226
2440	The MiST2 database: a comprehensive genomics resource on microbial signal transduction. Nucleic Acids Research, 2010, 38, D401-D407.	14.5	235
2441	Pathema: a clade-specific bioinformatics resource center for pathogen research. Nucleic Acids Research, 2010, 38, D408-D414.	14.5	18

#	ARTICLE	IF	CITATIONS
2442	Highly Divergent Mitochondrial ATP Synthase Complexes in <i>Tetrahymena thermophila</i> . PLoS Biology, 2010, 8, e1000418.	5.6	72
2443	Functional Characterization of Transcription Factor Motifs Using Cross-species Comparison across Large Evolutionary Distances. PLoS Computational Biology, 2010, 6, e1000652.	3.2	28
2444	Getting Started in Gene Orthology and Functional Analysis. PLoS Computational Biology, 2010, 6, e1000703.	3.2	100
2445	Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. PLoS Computational Biology, 2010, 6, e1000798.	3.2	52
2446	<i>Plasmodium falciparum</i> Erythrocyte Membrane Protein 1 Diversity in Seven Genomes “Divide and Conquer. PLoS Computational Biology, 2010, 6, e1000933.	3.2	302
2447	Phylogenomics of Ligand-Gated Ion Channels Predicts Monepantel Effect. PLoS Pathogens, 2010, 6, e1001091.	4.7	59
2448	Evolution of Characterized Phosphorylation Sites in Budding Yeast. Molecular Biology and Evolution, 2010, 27, 2027-2037.	8.9	62
2449	Low-homology protein threading. Bioinformatics, 2010, 26, i294-i300.	4.1	74
2450	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. Nucleic Acids Research, 2010, 38, W755-W762.	14.5	310
2451	Detecting subtle functional differences in ketopantoate reductase and related enzymes using a rule-based approach with sequence-structure homology recognition scores. Protein Engineering, Design and Selection, 2010, 23, 859-869.	2.1	1
2452	The Essentials of Protein Import in the Degenerate Mitochondrion of <i>Entamoeba histolytica</i> . PLoS Pathogens, 2010, 6, e1000812.	4.7	64
2453	Computing biological functions using Bio π , a formal description of biological processes based on elementary bricks of actions. Bioinformatics, 2010, 26, 1542-1547.	4.1	3
2454	Immunology and Cell Biology of Parasitic Diseases. Journal of Biomedicine and Biotechnology, 2010, 1-5.	3.0	4
2455	Novel Peptide-Mediated Interactions Derived from High-Resolution 3-Dimensional Structures. PLoS Computational Biology, 2010, 6, e1000789.	3.2	56
2456	De novo Assembly of a 40 Mb Eukaryotic Genome from Short Sequence Reads: <i>Sordaria macrospora</i> , a Model Organism for Fungal Morphogenesis. PLoS Genetics, 2010, 6, e1000891.	3.5	169
2457	Finding the “Dark Matter” in Human and Yeast Protein Network Prediction and Modelling. PLoS Computational Biology, 2010, 6, e1000945.	3.2	21
2458	Ancient Protostome Origin of Chemosensory Ionotropic Glutamate Receptors and the Evolution of Insect Taste and Olfaction. PLoS Genetics, 2010, 6, e1001064.	3.5	680
2459	Hub Promiscuity in Protein-Protein Interaction Networks. International Journal of Molecular Sciences, 2010, 11, 1930-1943.	4.1	148

#	ARTICLE	IF	CITATIONS
2460	Mitochondria-specific transgenic overexpression of connexin-43 simulates preconditioning-induced cytoprotection of stem cells. Cardiovascular Research, 2010, 88, 277-286.	3.8	73
2461	Comparative genomics of the mesophilic cellulosome-producing <i>Clostridium cellulovorans</i> and its application to biofuel production via consolidated bioprocessing. Environmental Technology (United Kingdom), 2010, 31, 889-903.	2.2	67
2462	Expression of BfrH, a Putative Siderophore Receptor of <i>Bordetella bronchiseptica</i> , Is Regulated by Iron, Fur1, and the Extracellular Function Sigma Factor EcfI. Infection and Immunity, 2010, 78, 1147-1162.	2.2	4
2463	Meeting report: a workshop on Best Practices in Genome Annotation. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq001-baq001.	3.0	18
2464	A Primer on Metagenomics. PLoS Computational Biology, 2010, 6, e1000667.	3.2	523
2465	Mitigating Allergenicity of Crops. Advances in Agronomy, 2010, 107, 93-121.	5.2	1
2466	The ABC Transporter HrtAB Confers Resistance to Hemin Toxicity and Is Regulated in a Hemin-Dependent Manner by the ChrAS Two-Component System in <i>Corynebacterium diphtheriae</i> . Journal of Bacteriology, 2010, 192, 4606-4617.	2.2	49
2467	Laser microsurgery provides evidence for merotelic kinetochore attachments in fission yeast cells lacking Pcs1 or Clr4. Cell Cycle, 2010, 9, 3997-4004.	2.6	52
2468	Representative sequence selection in unsupervised anomaly detection using spectrum kernel with theoretical parameter setting. , 2010, , .		1
2469	Tandem BRCT Domains: DNA's Praetorian Guard. Genes and Cancer, 2010, 1, 1140-1146.	1.9	15
2470	Apicomplexan perforin-like proteins. Communicative and Integrative Biology, 2010, 3, 18-23.	1.4	38
2471	The Genome of the Amoeba Symbiont <i>Candidatus</i> <i>Amoebophilus asiaticus</i> Reveals Common Mechanisms for Host Cell Interaction among Amoeba-Associated Bacteria. Journal of Bacteriology, 2010, 192, 1045-1057.	2.2	138
2472	Rice DENSE AND ERECT PANICLE 2 is essential for determining panicle outgrowth and elongation. Cell Research, 2010, 20, 838-849.	12.0	138
2473	Mendel. , 2010, , .		8
2474	The DamX protein of <i>Escherichia coli</i> and <i>Salmonella enterica</i> . Gut Microbes, 2010, 1, 285-288.	9.8	10
2475	The Mixed Lineage Nature of Nitrogen Transport and Assimilation in Marine Eukaryotic Phytoplankton: A Case Study of Micromonas. Molecular Biology and Evolution, 2010, 27, 2268-2283.	8.9	66
2476	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. Genome Research, 2010, 20, 1010-1019.	5.5	102
2477	Inference of Direct Residue Contacts in Two-Component Signaling. Methods in Enzymology, 2010, 471, 17-41.	1.0	40

#	ARTICLE	IF	CITATIONS
2478	Marsupial Sequencing Projects and Bioinformatics Challenges. , 2010, , 121-132.		1
2479	BLAST Tree: Fast Filtering for Genomic Sequence Classification. , 2010, , .		1
2480	Outer Membrane-Associated Serine Protease Involved in Adhesion of <i>Shewanella oneidensis</i> to Fe(III) Oxides. Environmental Science & Technology, 2010, 44, 68-73.	10.0	41
2481	The Noncanonical Disulfide Bond as the Important Stabilizing Element of the Immunoglobulin Fold of the Dr Fimbrial DraE Subunit. Biochemistry, 2010, 49, 1460-1468.	2.5	22
2482	Genome-wide analysis of eukaryotic twin CX9C proteins. Molecular BioSystems, 2010, 6, 2459.	2.9	91
2484	Liverbase: A Comprehensive View of Human Liver Biology. Journal of Proteome Research, 2010, 9, 50-58.	3.7	41
2485	Identifying wood-inhabiting fungi with 454 sequencing – what is the probability that BLAST gives the correct species?. Fungal Ecology, 2010, 3, 274-283.	1.6	97
2486	The structure of the dust mite allergen Der p 7 reveals similarities to innate immune proteins. Journal of Allergy and Clinical Immunology, 2010, 125, 909-917.e4.	2.9	99
2487	Identification of a Tc1-like transposon integration site in the genome of the flounder (<i>Platichthys</i>) Tj ETQq0 0 0 rgBTJ/Overlock 10 Tf 50	1.1	2
2488	Role of Hsp70 ATPase Domain Intrinsic Dynamics and Sequence Evolution in Enabling its Functional Interactions with NEFs. PLoS Computational Biology, 2010, 6, e1000931.	3.2	60
2489	Prediction of prognostic biomarkers for Interferon-based therapy to Hepatitis C Virus patients: a metaanalysis of the NS5A protein in subtypes 1a, 1b, and 3a. Virology Journal, 2010, 7, 130.	3.4	22
2490	A poxvirus Bcl-2-like gene family involved in regulation of host immune response: sequence similarity and evolutionary history. Virology Journal, 2010, 7, 59.	3.4	62
2491	Crystal Structure of a Putative Histidine-containing Phosphotransfer Protein from <i>Oryza sativa</i> . Journal of the Korean Society for Applied Biological Chemistry, 2010, 53, 852-856.	0.9	4
2492	Contribution of oxygen-limiting conditions to persistent infection of <i>Pseudomonas aeruginosa</i> . Future Microbiology, 2010, 5, 603-621.	2.0	58
2493	Novel Candidate Cancer Genes Identified by a Large-Scale Cross-Species Comparative Oncogenomics Approach. Cancer Research, 2010, 70, 883-895.	0.9	40
2494	Variations at the Semiconserved Glycine in the IQ Domain Consensus Sequence Have a Major Impact on Ca ²⁺ -Dependent Switching in Calmodulin~IQ Domain Complexes. Biochemistry, 2010, 49, 78-83.	2.5	7
2495	CAZymes Analysis Toolkit (CAT): Web service for searching and analyzing carbohydrate-active enzymes in a newly sequenced organism using CAZy database. Glycobiology, 2010, 20, 1574-1584.	2.5	335
2496	Comparative genomics of cyclic-di-GMP signalling in bacteria: post-translational regulation and catalytic activity. Nucleic Acids Research, 2010, 38, 5970-5981.	14.5	117

#	ARTICLE	IF	CITATIONS
2497	Proteins Required for Lipopolysaccharide Assembly in <i>Escherichia coli</i> Form a Transenvelope Complex. <i>Biochemistry</i> , 2010, 49, 4565-4567.	2.5	140
2498	PlnTFDB: updated content and new features of the plant transcription factor database. <i>Nucleic Acids Research</i> , 2010, 38, D822-D827.	14.5	635
2499	New γ -Amino Acid Ligases Catalyzing Oligopeptide Synthesis from Various Microorganisms. <i>Bioscience, Biotechnology and Biochemistry</i> , 2010, 74, 1572-1577.	1.3	18
2500	Human Genome Sequence and Variation. , 2010, , 31-53.		3
2501	Diversity of structure and function of response regulator output domains. <i>Current Opinion in Microbiology</i> , 2010, 13, 150-159.	5.1	308
2502	Isolation and immunological characterization of a novel <i>Cladosporium herbarum</i> allergen structurally homologous to the β hydrolase fold superfamily. <i>Molecular Immunology</i> , 2010, 47, 1366-1377.	2.2	5
2503	What the loss of the hormone neuroparsin in the melanogaster subgroup of <i>Drosophila</i> can tell us about its function. <i>Insect Biochemistry and Molecular Biology</i> , 2010, 40, 354-361.	2.7	39
2504	Identification of prophage gene z2389 in <i>Escherichia coli</i> EDL933 encoding a DNA cytosine methyltransferase for full protection of NotI sites. <i>International Journal of Medical Microbiology</i> , 2010, 300, 296-303.	3.6	3
2505	A novel coiled-coil repeat variant in a class of bacterial cytoskeletal proteins. <i>Journal of Structural Biology</i> , 2010, 170, 202-215.	2.8	30
2506	High-throughput production of human proteins for crystallization: The SGC experience. <i>Journal of Structural Biology</i> , 2010, 172, 3-13.	2.8	281
2507	The Crystal Structure of the Novobiocin Biosynthetic Enzyme NovP: The First Representative Structure for the TylF O-Methyltransferase Superfamily. <i>Journal of Molecular Biology</i> , 2010, 395, 390-407.	4.2	29
2508	Structural Determinants of DNA Binding by a <i>P. falciparum</i> ApiAP2 Transcriptional Regulator. <i>Journal of Molecular Biology</i> , 2010, 395, 558-567.	4.2	59
2509	Model-Guided Mutagenesis Drives Functional Studies of Human NHA2, Implicated in Hypertension. <i>Journal of Molecular Biology</i> , 2010, 396, 1181-1196.	4.2	53
2510	The Crystal Structure and Activity of a Putative Trypanosomal Nucleoside Phosphorylase Reveal It to be a Homodimeric Uridine Phosphorylase. <i>Journal of Molecular Biology</i> , 2010, 396, 1244-1259.	4.2	16
2511	Crystal Structure of the First Eubacterial Mre11 Nuclease Reveals Novel Features that May Discriminate Substrates During DNA Repair. <i>Journal of Molecular Biology</i> , 2010, 397, 647-663.	4.2	41
2512	Crystal Structures of the CBS and DRTGG Domains of the Regulatory Region of <i>Clostridium perfringens</i> Pyrophosphatase Complexed with the Inhibitor, AMP, and Activator, Diadenosine Tetraphosphate. <i>Journal of Molecular Biology</i> , 2010, 398, 400-413.	4.2	35
2513	T-RMSD: A Fine-grained, Structure-based Classification Method and its Application to the Functional Characterization of TNF Receptors. <i>Journal of Molecular Biology</i> , 2010, 400, 605-617.	4.2	5
2514	The expression of ELK transcription factors in adult DRG: Novel isoforms, antisense transcripts and upregulation by nerve damage. <i>Molecular and Cellular Neurosciences</i> , 2010, 44, 165-177.	2.2	20

#	ARTICLE	IF	CITATIONS
2515	A vacuolar-type proton (H ⁺) translocating ATPase $\hat{1}\pm$ subunit encoded by the Hc-vha-6 gene of <i>Haemonchus contortus</i> . <i>Molecular and Cellular Probes</i> , 2010, 24, 196-203.	2.1	3
2516	Molecular cloning and immune responsive expression of MDA5 gene, a pivotal member of the RLR gene family from grass carp <i>Ctenopharyngodon idella</i> . <i>Fish and Shellfish Immunology</i> , 2010, 28, 712-718.	3.6	94
2517	Identification and expression profiling analysis of grass carp <i>Ctenopharyngodon idella</i> LGP2 cDNA. <i>Fish and Shellfish Immunology</i> , 2010, 29, 349-355.	3.6	60
2518	In silico analysis of Ardmore, a novel mycobacteriophage isolated from soil. <i>Gene</i> , 2010, 453, 9-23.	2.2	22
2519	Evidence of alternative splicing of the chi2 chitinase gene from <i>Metarhizium anisopliae</i> . <i>Gene</i> , 2010, 462, 1-7.	2.2	15
2520	Differential behaviour of <i>Pseudomonas</i> sp. 42A2 LipC, a lipase showing greater versatility than its counterpart LipA. <i>Biochimie</i> , 2010, 92, 307-316.	2.6	35
2521	In search of the origin of FREPs: Characterization of <i>Aplysia californica</i> fibrinogen-related proteins. <i>Developmental and Comparative Immunology</i> , 2010, 34, 465-473.	2.3	38
2522	MgC1q, a novel C1q-domain-containing protein involved in the immune response of <i>Mytilus galloprovincialis</i> . <i>Developmental and Comparative Immunology</i> , 2010, 34, 926-934.	2.3	91
2523	Global regulator H-NS and lipoprotein NlpI influence production of extracellular DNA in <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 401, 197-202.	2.1	26
2524	The dst2 gene essential for photomorphogenesis of <i>Coprinopsis cinerea</i> encodes a protein with a putative FAD-binding-4 domain. <i>Fungal Genetics and Biology</i> , 2010, 47, 152-158.	2.1	58
2525	Fungal PDR transporters: Phylogeny, topology, motifs and function. <i>Fungal Genetics and Biology</i> , 2010, 47, 127-142.	2.1	141
2526	Identification and characterization of genes responsible for biosynthesis of kojic acid, an industrially important compound from <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2010, 47, 953-961.	2.1	145
2527	Engineering Signal Transduction Pathways. <i>Cell</i> , 2010, 140, 33-47.	28.9	112
2528	The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.	28.9	399
2529	Peptidoglycan Crosslinking Relaxation Promotes <i>Helicobacter pylori</i> 's Helical Shape and Stomach Colonization. <i>Cell</i> , 2010, 141, 822-833.	28.9	240
2530	The Protein Composition of Mitotic Chromosomes Determined Using Multiclassifier Combinatorial Proteomics. <i>Cell</i> , 2010, 142, 810-821.	28.9	266
2531	Lipoprotein Cofactors Located in the Outer Membrane Activate Bacterial Cell Wall Polymerases. <i>Cell</i> , 2010, 143, 1110-1120.	28.9	286
2532	Molecular phylogenies and evolutionary behavior of AhR (aryl hydrocarbon receptor) pathway genes in aquatic animals: Implications for the toxicology mechanism of some persistent organic pollutants (POPs). <i>Chemosphere</i> , 2010, 78, 193-205.	8.2	27

#	ARTICLE	IF	CITATIONS
2533	The Systematic Functional Analysis of Plasmodium Protein Kinases Identifies Essential Regulators of Mosquito Transmission. <i>Cell Host and Microbe</i> , 2010, 8, 377-387.	11.0	267
2534	Insulin-like Signaling Determines Survival during Stress via Posttranscriptional Mechanisms in <i>C. elegans</i> . <i>Cell Metabolism</i> , 2010, 12, 260-272.	16.2	113
2535	Formateâ€“nitrite transporters: Optimisation of expression, purification and analysis of prokaryotic and eukaryotic representatives. <i>Protein Expression and Purification</i> , 2010, 71, 184-189.	1.3	7
2536	Bioinformatic mapping and production of recombinant N-terminal domains of human cardiac ryanodine receptor 2. <i>Protein Expression and Purification</i> , 2010, 71, 33-41.	1.3	6
2537	A software tool to accelerate design of protein constructs for recombinant expression. <i>Protein Expression and Purification</i> , 2010, 72, 175-178.	1.3	15
2538	Expression analyses indicate the involvement of sunflower WRKY transcription factors in stress responses, and phylogenetic reconstructions reveal the existence of a novel clade in the Asteraceae. <i>Plant Science</i> , 2010, 178, 398-410.	3.6	32
2539	Identification and mapping of genes related to caffeoylquinic acid synthesis in <i>Cynara cardunculus</i> L.. <i>Plant Science</i> , 2010, 179, 338-347.	3.6	54
2540	Functional diversity of ankyrin repeats in microbial proteins. <i>Trends in Microbiology</i> , 2010, 18, 132-139.	7.7	178
2541	Mago Nashi, Tsunagi/Y14, and Ranshi form a complex that influences oocyte differentiation in <i>Drosophila melanogaster</i> . <i>Developmental Biology</i> , 2010, 339, 307-319.	2.0	18
2542	A strawberry notch homolog, <i>let-765/nsh-1</i> , positively regulates <i>lin-3/egf</i> expression to promote RAS-dependent vulval induction in <i>C. elegans</i> . <i>Developmental Biology</i> , 2010, 341, 472-485.	2.0	9
2543	Analysis of floral transcription factors from <i>Lycoris longituba</i> . <i>Genomics</i> , 2010, 96, 119-127.	2.9	11
2544	Expanding Small-Molecule Functional Metagenomics through Parallel Screening of Broad-Host-Range Cosmid Environmental DNA Libraries in Diverse <i>Proteobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 1633-1641.	3.1	188
2545	Role of the 207â€“218 peptide region of Moloney murine leukemia virus integrase in enzyme catalysis. <i>Archives of Biochemistry and Biophysics</i> , 2010, 495, 28-34.	3.0	5
2546	Deletion of competenceâ€“induced genes overâ€“expressed in biofilms caused transformation deficiencies in <i>Streptococcus mutans</i> . <i>Molecular Oral Microbiology</i> , 2010, 25, 406-417.	2.7	7
2547	A systematic screen for proteinâ€“lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	7.2	146
2548	Bioinformatics in bioinorganic chemistry. <i>Metallomics</i> , 2010, 2, 39-51.	2.4	17
2549	A subtilisin-like protein from soybean contains an embedded, cryptic signal that activates defense-related genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14921-14925.	7.1	115
2550	The LabelHash algorithm for substructure matching. <i>BMC Bioinformatics</i> , 2010, 11, 555.	2.6	33

#	ARTICLE	IF	CITATIONS
2551	A gene family-based method for interspecies comparisons of sequencing-based transcriptomes and its use in environmental adaptation analysis. <i>Journal of Genetics and Genomics</i> , 2010, 37, 205-218.	3.9	3
2552	Biochemical networks: The evolution of gene annotation. <i>Nature Chemical Biology</i> , 2010, 6, 4-5.	8.0	9
2553	Detection and Architecture of Small Heat Shock Protein Monomers. <i>PLoS ONE</i> , 2010, 5, e9990.	2.5	83
2554	Databases and Genome Browsers. , 2010, , 905-921.		0
2555	Genovo: De Novo Assembly for Metagenomes. <i>Lecture Notes in Computer Science</i> , 2010, , 341-356.	1.3	8
2557	Efficient algorithms for training the parameters of hidden Markov models using stochastic expectation maximization (EM) training and Viterbi training. <i>Algorithms for Molecular Biology</i> , 2010, 5, 38.	1.2	6
2558	Novel genes exhibit distinct patterns of function acquisition and network integration. <i>Genome Biology</i> , 2010, 11, R127.	9.6	71
2559	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010, 11, R94.	9.6	66
2560	Quantifying the mechanisms of domain gain in animal proteins. <i>Genome Biology</i> , 2010, 11, R74.	9.6	93
2561	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.	9.6	391
2562	Immunity and other defenses in pea aphids, <i>Acyrtosiphon pisum</i> . <i>Genome Biology</i> , 2010, 11, R21.	9.6	389
2563	Interplay of heritage and habitat in the distribution of bacterial signal transduction systems. <i>Molecular BioSystems</i> , 2010, 6, 721.	2.9	87
2564	<i>Streptomyces scabies</i> 87-22 Contains a Coronafacic Acid-Like Biosynthetic Cluster That Contributes to Plant-Microbe Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 161-175.	2.6	101
2565	In Silico Screening for Pathogenesis Related-2 Gene Candidates in <i>Vigna Unguiculata</i> Transcriptome. <i>Lecture Notes in Computer Science</i> , 2010, , 70-81.	1.3	27
2566	A Sequence Data Mining Protocol to Identify Best Representative Sequence for Protein Domain Families. , 2010, , .		1
2567	Identity and divergence of protein domain architectures after the yeast whole-genome duplication event. <i>Molecular BioSystems</i> , 2010, 6, 2305.	2.9	20
2568	Yeast protein-protein interaction binding sites: prediction from the motif-motif, motif-domain and domain-domain levels. <i>Molecular BioSystems</i> , 2010, 6, 2164.	2.9	11
2569	Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. <i>Molecular BioSystems</i> , 2010, 6, 1475.	2.9	12

#	ARTICLE	IF	CITATIONS
2570	Dicer is Required for the Normal Development of Sea Urchin, <i>Hemicentrotus pulcherrimus</i> . Zoological Science, 2010, 27, 477-486.	0.7	7
2571	EpiC: An Open Resource for Exploring Epitopes To Aid Antibody-Based Experiments. Journal of Proteome Research, 2010, 9, 3759-3763.	3.7	8
2572	Fast and efficient mining for frequent patterns on biological sequence. , 2010, , .		0
2573	Analogies between structural and systems biology and systems-of-systems engineering in dynamic environments. , 2010, , .		0
2574	Analysing the Similarity of Proteins Based on a New Approach to Empirical Mode Decomposition. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	4
2575	Multiple Biological Sequence Alignment with a Parallel Island Injection Genetic Algorithm. , 2010, , .		3
2576	Cross-species identification of hydroxylation sites for ARD and FIH interaction. , 2011, , .		0
2577	Sequence-Based Enzyme Catalytic Domain Prediction Using Clustering and Aggregated Mutual Information Content. , 2011, , .		0
2578	SCOP family fingerprints: An information theoretic approach to structural classification of protein domains. , 2011, , .		0
2579	Predicing Yeast Synthetic Lethal Genetic Interactions Using Short Polypeptide Clusters. , 2011, , .		0
2580	Discriminative random field approach to prediction of protein residue contacts. , 2011, , .		5
2581	Interactive visual comparison of multiple trees. , 2011, , .		60
2582	A ranking-based method to predict protein function in terms of gene ontology. , 2011, , .		0
2583	ASD: a comprehensive database of allosteric proteins and modulators. Nucleic Acids Research, 2011, 39, D663-D669.	14.5	157
2584	Cdc45: the missing RecJ ortholog in eukaryotes?. Bioinformatics, 2011, 27, 1885-1888.	4.1	67
2585	Large scale identification of protein-protein interaction of <i>Aspergillus terreus</i> NIH2624 using computational approaches. , 2011, , .		0
2586	ECF sigma factor-associated regulatory networks in <i>Streptomyces colicolor</i> A3(2). , 2011, , .		0
2587	The Ubiquity of the Insulin Superfamily Across the Eukaryotes Detected Using a Bioinformatics Approach. OMICS A Journal of Integrative Biology, 2011, 15, 439-447.	2.0	10

#	ARTICLE	IF	CITATIONS
2588	Discovering Drug-Protein Interactions Based on their Fingerprints. , 2011, , .		2
2589	In Calmodulinâ€‘IQ Domain Complexes, the Ca ²⁺ -Free and Ca ²⁺ -Bound Forms of the Calmodulin C-Lobe Direct the N-Lobe to Different Binding Sites. <i>Biochemistry</i> , 2011, 50, 10061-10068.	2.5	15
2590	True Path Rule Hierarchical Ensembles for Genome-Wide Gene Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 832-847.	3.0	104
2591	Basis of the Intrinsic Flexibility of the CÎµ3 Domain of IgE. <i>Biochemistry</i> , 2011, 50, 4608-4614.	2.5	19
2592	Molecular Basis of the Thermostability and Thermophilicity of Laminarinases: X-ray Structure of the Hyperthermostable Laminarinase from <i>Rhodothermus marinus</i> and Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2011, 115, 7940-7949.	2.6	26
2593	Insertion sequence-excision enhancer removes transposable elements from bacterial genomes and induces various genomic deletions. <i>Nature Communications</i> , 2011, 2, 152.	12.8	45
2594	The Laccase Engineering Database: a classification and analysis system for laccases and related multicopper oxidases. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar006.	3.0	103
2595	Exploring Metabolic Pathway Reconstruction and Genome-Wide Expression Profiling in <i>Lactobacillus reuteri</i> to Define Functional Probiotic Features. <i>PLoS ONE</i> , 2011, 6, e18783.	2.5	147
2596	Systematic computational prediction of protein interaction networks. <i>Physical Biology</i> , 2011, 8, 035008.	1.8	35
2597	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , 2011, 6, 1669-1682.	12.0	87
2598	A mass spectrometryâ€‘guided genome mining approach for natural product peptidogenomics. <i>Nature Chemical Biology</i> , 2011, 7, 794-802.	8.0	329
2601	Evolution of domain promiscuity in eukaryotic genomesâ€‘a perspective from the inferred ancestral domain architectures. <i>Molecular BioSystems</i> , 2011, 7, 784-792.	2.9	17
2602	Constructing de Novo Biosynthetic Pathways for Chemical Synthesis inside Living Cells. <i>Biochemistry</i> , 2011, 50, 5404-5418.	2.5	35
2603	<i>C. elegans</i> as a Resource for Studies on Plant Parasitic Nematodes. , 2011, , 175-220.		10
2604	D-SLIMMER: Domainâ€‘SLiM Interaction Motifs Miner for Sequence Based Proteinâ€‘Protein Interaction Data. <i>Journal of Proteome Research</i> , 2011, 10, 5285-5295.	3.7	6
2605	Functional Enrichment Analysis with Structural Variants: Pitfalls and Strategies. <i>Cytogenetic and Genome Research</i> , 2011, 135, 277-285.	1.1	24
2606	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	9.6	141
2607	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. <i>Genome Biology</i> , 2011, 12, R4.	9.6	84

#	ARTICLE	IF	CITATIONS
2609	Molecular characterization and mRNA expression of two key enzymes of hypoxia-sensing pathways in eastern oysters <i>Crassostrea virginica</i> (Gmelin): Hypoxia-inducible factor 1α (HIF- 1α) and HIF-prolyl hydroxylase (PHD). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 103-114.	1.0	44
2610	The Coding of Temperature in the <i>Drosophila</i> Brain. <i>Cell</i> , 2011, 144, 614-624.	28.9	236
2611	The STARD9/Kif16a Kinesin Associates with Mitotic Microtubules and Regulates Spindle Pole Assembly. <i>Cell</i> , 2011, 147, 1309-1323.	28.9	67
2612	The protein P23 identifies capsule-forming plasmacytes in the moth <i>Pseudaletia includens</i> . <i>Developmental and Comparative Immunology</i> , 2011, 35, 501-510.	2.3	11
2613	Cloning, expression analysis and promoter structure of TBK1 (TANK-binding kinase 1) in Atlantic cod (<i>Gadus morhua</i> L.). <i>Fish and Shellfish Immunology</i> , 2011, 30, 1055-1063.	3.6	28
2614	The role of Fras1/Frem proteins in the structure and function of basement membrane. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 487-495.	2.8	70
2615	A mutation in the <i>Cc.ubc2</i> gene affects clamp cell morphogenesis as well as nuclear migration for dikaryosis in <i>Coprinopsis cinerea</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 519-525.	2.1	18
2616	The size distribution of protein families within different types of folds. <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 218-222.	2.1	6
2617	Towards artificial metallonucleases for gene therapy: recent advances and new perspectives. <i>Future Medicinal Chemistry</i> , 2011, 3, 1935-1966.	2.3	20
2618	Prediction of protein-protein interactions between human host and a pathogen and its application to three pathogenic bacteria. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 613-619.	7.5	49
2619	The study of the E-class SEPALLATA3-like MADS-box genes in wild-type and mutant flowers of cultivated saffron crocus (<i>Crocus sativus</i> L.) and its putative progenitors. <i>Journal of Plant Physiology</i> , 2011, 168, 1675-1684.	3.5	36
2620	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011, 175, 127-134.	2.8	66
2621	Structural Features and Chaperone Activity of the NudC Protein Family. <i>Journal of Molecular Biology</i> , 2011, 409, 722-741.	4.2	38
2622	The Rate of PolyQ-Mediated Aggregation Is Dramatically Affected by the Number and Location of Surrounding Domains. <i>Journal of Molecular Biology</i> , 2011, 413, 879-887.	4.2	20
2623	The zebrafish maternal-effect gene mission impossible encodes the DEAH-box helicase Dhx16 and is essential for the expression of downstream endodermal genes. <i>Developmental Biology</i> , 2011, 353, 275-289.	2.0	16
2624	Data-mining of the <i>Meloidogyne incognita</i> degradome and comparative analysis of proteases in nematodes. <i>Genomics</i> , 2011, 97, 29-36.	2.9	23
2625	Protein folds and protein folding. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 11-19.	2.1	59
2626	Baculovirus VP80 Protein and the F-Actin Cytoskeleton Interact and Connect the Viral Replication Factory with the Nuclear Periphery. <i>Journal of Virology</i> , 2011, 85, 5350-5362.	3.4	54

#	ARTICLE	IF	CITATIONS
2627	Genovo: <i>De Novo</i> Assembly for Metagenomes. Journal of Computational Biology, 2011, 18, 429-443.	1.6	193
2628	A Fast Multiple Longest Common Subsequence (MLCS) Algorithm. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 321-334.	5.7	56
2629	Omics, Bioinformatics, and Infectious Disease Research. , 2011, , 523-539.		1
2630	Classification of human vs. non-human, and subtyping of human influenza viral strains using Profile Hidden Markov Models. , 2011, , .		1
2631	Exploring the link between MORF4L1 and risk of breast cancer. Breast Cancer Research, 2011, 13, R40.	5.0	23
2632	Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. Genome Biology, 2011, 12, R63.	8.8	35
2633	Proteome-wide evidence for enhanced positive Darwinian selection within intrinsically disordered regions in proteins. Genome Biology, 2011, 12, R65.	9.6	68
2634	InterPro Protein Classification. Methods in Molecular Biology, 2011, 694, 37-47.	0.9	63
2635	Protein Bioinformatics Databases and Resources. Methods in Molecular Biology, 2011, 694, 3-24.	0.9	27
2636	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. PLoS ONE, 2011, 6, e14519.	2.5	208
2637	Predicting Sumoylation Site by Feature Selection Method. Journal of Biomolecular Structure and Dynamics, 2011, 28, 797-804.	3.5	14
2638	Sulfur Metabolism in the Extreme Acidophile Acidithiobacillus Caldus. Frontiers in Microbiology, 2011, 2, 17.	3.5	145
2639	Selecting different protein representations and classification algorithms in hierarchical protein function prediction. Intelligent Data Analysis, 2011, 15, 979-999.	0.9	18
2640	Absciscic acid-inducible 25 kDa xylem sap protein abundant in winter poplar. Plant Root, 2011, 5, 63-68.	0.3	2
2641	Basidiomycetes Telomeres “ A Bioinformatics Approach. , 0, , .		4
2642	Allergen Bioinformatics: Recent Trends and Developments. , 0, , .		4
2643	Systematic and Phylogenetic Analysis of the Ole e 1 Pollen Protein Family Members in Plants. , 0, , .		3
2644	Modeling the Metal Binding Site in Cupin Proteins. , 2011, , .		3

#	ARTICLE	IF	CITATIONS
2645	Vector Space Information Retrieval Techniques for Bioinformatics Data Mining. , 2011, , .		2
2646	Assessing Multiple Sequence Alignments Using Visual Tools. , 0, , .		0
2647	A Pattern Search Method for Discovering Conserved Motifs in Bioactive Peptide Families. , 2011, , .		2
2648	ProDGe: investigating protein-protein interactions at the domain level. Nature Precedings, 2011, , .	0.1	0
2649	Role of Shwachman-Bodian-Diamond syndrome protein in translation machinery and cell chemotaxis: a comparative genomics approach. Advances and Applications in Bioinformatics and Chemistry, 2011, 4, 43.	2.6	1
2650	Comparative analysis of two component signal transduction systems of the Lactobacillus acidophilus group. Brazilian Journal of Microbiology, 2011, 42, 147-157.	2.0	5
2651	Partial Gene Duplication and the Formation of Novel Genes. , 2011, , .		4
2652	Mining Disease-Resistance Genes in Roses: Functional and Molecular Characterization of the Rdr1 Locus. Frontiers in Plant Science, 2011, 2, 35.	3.6	39
2653	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. Frontiers in Genetics, 2011, 2, 69.	2.3	12
2654	Is the Genetic Landscape of the Deep Subsurface Biosphere Affected by Viruses?. Frontiers in Microbiology, 2011, 2, 219.	3.5	56
2655	The Human Postsynaptic Density Shares Conserved Elements with Proteomes of Unicellular Eukaryotes and Prokaryotes. Frontiers in Neuroscience, 2011, 5, 44.	2.8	19
2656	Trimeric autotransporter adhesins in members of the Burkholderia cepacia complex: a multifunctional family of proteins implicated in virulence. Frontiers in Cellular and Infection Microbiology, 2011, 1, 13.	3.9	24
2657	Complete Genome Sequence of the Soybean Symbiont Bradyrhizobium japonicum Strain USDA6T. Genes, 2011, 2, 763-787.	2.4	108
2659	Disordered Patterns in Clustered Protein Data Bank and in Eukaryotic and Bacterial Proteomes. PLoS ONE, 2011, 6, e27142.	2.5	20
2660	Using Amino Acid Correlation and Community Detection Algorithms to Identify Functional Determinants in Protein Families. PLoS ONE, 2011, 6, e27786.	2.5	25
2661	A Computational Method for Prediction of Excretory Proteins and Application to Identification of Gastric Cancer Markers in Urine. PLoS ONE, 2011, 6, e16875.	2.5	32
2662	HMMerThread: Detecting Remote, Functional Conserved Domains in Entire Genomes by Combining Relaxed Sequence-Database Searches with Fold Recognition. PLoS ONE, 2011, 6, e17568.	2.5	2
2663	A Bioinformatics Classifier and Database for Heme-Copper Oxygen Reductases. PLoS ONE, 2011, 6, e19117.	2.5	60

#	ARTICLE	IF	CITATIONS
2664	Evolution of the Karyopherin- β Family of Nucleocytoplasmic Transport Factors; Ancient Origins and Continued Specialization. PLoS ONE, 2011, 6, e19308.	2.5	64
2665	Structure Collisions between Interacting Proteins. PLoS ONE, 2011, 6, e19581.	2.5	3
2666	Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. PLoS ONE, 2011, 6, e19586.	2.5	60
2667	Gene Coexpression Network Analysis as a Source of Functional Annotation for Rice Genes. PLoS ONE, 2011, 6, e22196.	2.5	123
2668	An Alignment-Free Approach for Eukaryotic ITS2 Annotation and Phylogenetic Inference. PLoS ONE, 2011, 6, e26638.	2.5	10
2669	Origins and Evolution of the HET-s Prion-Forming Protein: Searching for Other Amyloid-Forming Solenoids. PLoS ONE, 2011, 6, e27342.	2.5	8
2670	Identification of Anaplasma marginale Type IV Secretion System Effector Proteins. PLoS ONE, 2011, 6, e27724.	2.5	53
2671	Protein analysis tools and services at IBIVU. Journal of Integrative Bioinformatics, 2011, 8, 157-164.	1.5	3
2673	Dynamics of Gene Duplication in the Genomes of Chlorophyll d-Producing Cyanobacteria: Implications for the Ecological Niche. Genome Biology and Evolution, 2011, 3, 601-613.	2.5	48
2674	X-ray structural studies of the entire extracellular region of the serine/threonine kinase PrkC from Staphylococcus aureus. Biochemical Journal, 2011, 435, 33-41.	3.7	48
2675	PlantPls “ An Interactive Web Resource on Plant Protease Inhibitors. Current Protein and Peptide Science, 2011, 12, 448-454.	1.4	10
2676	Gene prediction in metagenomic fragments based on the SVM algorithm. , 2011, , .		2
2677	Solution structure of the Taf14 YEATS domain and its roles in cell growth of <i>Saccharomyces cerevisiae</i> . Biochemical Journal, 2011, 436, 83-90.	3.7	17
2679	Prediction of disease causing gene in Xq22.1 region of human X-chromosome. International Journal of Bioinformatics Research and Applications, 2011, 7, 130.	0.2	0
2680	METADOMAIN: A PROFILE HMM-BASED PROTEIN DOMAIN CLASSIFICATION TOOL FOR SHORT SEQUENCES. , 2011, , .		5
2681	Whole Genome Annotation: In Silico Analysis. , 0, , .		1
2682	Gingipains from <i>Porphyromonas gingivalis</i> “ complex domain structures confer diverse functions. European Journal of Microbiology and Immunology, 2011, 1, 41-58.	2.8	68
2683	INTRINSIC DISORDER WITHIN AND FLANKING THE DNA-BINDING DOMAINS OF HUMAN TRANSCRIPTION FACTORS. , 2011, , .		12

#	ARTICLE	IF	CITATIONS
2684	A Protocol for Computer-Based Protein Structure and Function Prediction. Journal of Visualized Experiments, 2011, , e3259.	0.3	54
2685	Missense SLC25A38 variations play an important role in autosomal recessive inherited sideroblastic anemia. Haematologica, 2011, 96, 808-813.	3.5	57
2686	Cyclic diguanylate turnover mediated by the sole GGDEF/EAL response regulator in <i>Pseudomonas putida</i> : its role in the rhizosphere and an analysis of its target processes. Environmental Microbiology, 2011, 13, 1745-1766.	3.8	81
2687	In search of Brucella abortus type IV secretion substrates: screening and identification of four proteins translocated into host cells through VirB system. Cellular Microbiology, 2011, 13, 1261-1274.	2.1	118
2688	Investigating heat shock proteins of tardigrades in active versus anhydrobiotic state using shotgun proteomics. Journal of Zoological Systematics and Evolutionary Research, 2011, 49, 111-119.	1.4	25
2689	<i>Ehd3</i> , encoding a plant homeodomain finger-containing protein, is a critical promoter of rice flowering. Plant Journal, 2011, 66, 603-612.	5.7	182
2690	The modular structure of haemagglutinin/adhesin regions in gingipains of <i>Porphyromonas gingivalis</i> . Molecular Microbiology, 2011, 81, 1358-1373.	2.5	20
2691	Structures of type B ribose 5-phosphate isomerase from <i>Trypanosoma cruzi</i> shed light on the determinants of sugar specificity in the structural family. FEBS Journal, 2011, 278, 793-808.	4.7	26
2692	The subcellular localization of a C-terminal processing protease in <i>Pseudomonas aeruginosa</i> . FEMS Microbiology Letters, 2011, 316, 23-30.	1.8	31
2693	The annotated complete DNA sequence of Enterococcus faecalis bacteriophage Îf11 and its comparison with all available phage and predicted prophage genomes. FEMS Microbiology Letters, 2011, 317, 9-26.	1.8	31
2694	Overproduction of YjbB reduces the level of polyphosphate in Escherichia coli: a hypothetical role of YjbB in phosphate export and polyphosphate accumulation. FEMS Microbiology Letters, 2011, 320, 25-32.	1.8	29
2695	A tetrapyrrole-regulated ubiquitin ligase controls algal nuclear DNA replication. Nature Cell Biology, 2011, 13, 483-487.	10.3	52
2696	The Contribution of Entropy, Enthalpy, and Hydrophobic Desolvation to Cooperativity in Repeat-Protein Folding. Structure, 2011, 19, 349-360.	3.3	67
2697	The MycoBrowser portal: A comprehensive and manually annotated resource for mycobacterial genomes. Tuberculosis, 2011, 91, 8-13.	1.9	355
2698	MtbSD: A comprehensive structural database for Mycobacterium tuberculosis. Tuberculosis, 2011, 91, 556-562.	1.9	5
2699	An atypical proprotein convertase in Giardia lamblia differentiation. Molecular and Biochemical Parasitology, 2011, 175, 169-180.	1.1	17
2700	The Apicomplexan AP2 family: Integral factors regulating Plasmodium development. Molecular and Biochemical Parasitology, 2011, 176, 1-7.	1.1	195
2701	A survey of schistosome protein domain types: Insights into unique biological properties. Molecular and Biochemical Parasitology, 2011, 177, 100-105.	1.1	2

#	ARTICLE	IF	CITATIONS
2702	Cloning, sequence identification and expression profile analysis of α -L-fucosidase gene from the Mediterranean fruit fly <i>Ceratitis capitata</i> . <i>Journal of Insect Physiology</i> , 2011, 57, 452-461.	2.0	4
2703	Area 51: How do <i>Acanthamoeba</i> invade the central nervous system?. <i>Trends in Parasitology</i> , 2011, 27, 185-189.	3.3	22
2704	Identification of a Mastigoneme Protein from <i>Phytophthora nicotianae</i> . <i>Protist</i> , 2011, 162, 100-114.	1.5	7
2705	Experimental annotation of post-translational features and translated coding regions in the pathogen <i>Salmonella Typhimurium</i> . <i>BMC Genomics</i> , 2011, 12, 433.	2.8	29
2706	A shortest-path graph kernel for estimating gene product semantic similarity. <i>Journal of Biomedical Semantics</i> , 2011, 2, 3.	1.6	31
2707	Isolation and partial characterization of the <i>Chlamydomonas reinhardtii</i> β -glutamyl kinase. <i>Journal of Bioscience and Bioengineering</i> , 2011, 112, 75-78.	2.2	2
2708	Differential proteomic analysis of salt stress response in <i>Sorghum bicolor</i> leaves. <i>Environmental and Experimental Botany</i> , 2011, 71, 321-328.	4.2	83
2709	Clostridial spore germination versus bacilli: Genome mining and current insights. <i>Food Microbiology</i> , 2011, 28, 266-274.	4.2	59
2710	The interplay of descriptor-based computational analysis with pharmacophore modeling builds the basis for a novel classification scheme for feruloyl esterases. <i>Biotechnology Advances</i> , 2011, 29, 94-110.	11.7	74
2711	Screening strategies for discovery of antibacterial natural products. <i>Expert Review of Anti-Infective Therapy</i> , 2011, 9, 589-613.	4.4	45
2712	Molecular Basis for Mycophenolic Acid Biosynthesis in <i>Penicillium brevicompactum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 3035-3043.	3.1	130
2713	Extracting Sets of Chemical Substructures and Protein Domains Governing Drug-Target Interactions. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 1183-1194.	5.4	71
2714	Monoamine Neurotransmitters as Substrates for Novel Tick Sulfotransferases, Homology Modeling, Molecular Docking, and Enzyme Kinetics. <i>ACS Chemical Biology</i> , 2011, 6, 176-184.	3.4	14
2715	Investigating Cancer-related Proteins Specific Domain Interactions and Differential Protein Interactions Caused by Alternative Splicing. , 2011, , .		1
2716	Detection of selection utilizing molecular phylogenetics: a possible approach. <i>Genetica</i> , 2011, 139, 639-648.	1.1	1
2717	Molecular evolution of the membrane associated progesterone receptor in the <i>Brachionus plicatilis</i> (Rotifera, Monogononta) species complex. <i>Hydrobiologia</i> , 2011, 662, 99-106.	2.0	9
2718	ARABIDILLO proteins have a novel and conserved domain structure important for the regulation of their stability. <i>Plant Molecular Biology</i> , 2011, 75, 77-92.	3.9	17
2719	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 45-54.	1.2	65

#	ARTICLE	IF	CITATIONS
2720	Bioinformatic identification of novel protein phosphatases in the dog genome. <i>Molecular and Cellular Biochemistry</i> , 2011, 351, 149-156.	3.1	1
2721	Prediction of mucin-type O-glycosylation sites by a two-staged strategy. <i>Molecular Diversity</i> , 2011, 15, 427-433.	3.9	6
2722	Genome-wide analysis of BURP domain-containing genes in Maize and Sorghum. <i>Molecular Biology Reports</i> , 2011, 38, 4553-4563.	2.3	29
2723	Crystal structure of tarocystatin-papain complex: implications for the inhibition property of group-2 phytocystatins. <i>Planta</i> , 2011, 234, 243-254.	3.2	38
2724	Molecular modeling studies of Fatty acyl-CoA synthetase (FadD13) from <i>Mycobacterium tuberculosis</i> a potential target for the development of antitubercular drugs. <i>Journal of Molecular Modeling</i> , 2011, 17, 301-313.	1.8	20
2725	Symbiotic <i>Streptomyces</i> sp. TN119 GH 11 xylanase: a new pH-stable, protease- and SDS-resistant xylanase. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2011, 38, 523-530.	3.0	34
2726	Glycoside hydrolases as components of putative carbohydrate biosensor proteins in <i>Clostridium thermocellum</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2011, 38, 825-832.	3.0	41
2727	tdd8: a TerD domain-encoding gene involved in <i>Streptomyces coelicolor</i> differentiation. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 385-398.	1.7	16
2728	The KP4 killer protein gene family. <i>Current Genetics</i> , 2011, 57, 51-62.	1.7	22
2729	Identification of a bacterial inhibitor against g-type lysozyme. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 1053-1064.	5.4	48
2730	Evolution of the TOR Pathway. <i>Journal of Molecular Evolution</i> , 2011, 73, 209-220.	1.8	118
2731	Taxonomic and Functional Metagenomic Profiling of the Microbial Community in the Anoxic Sediment of a Sub-saline Shallow Lake (Laguna de Carrizo, Central Spain). <i>Microbial Ecology</i> , 2011, 62, 824-837.	2.8	51
2732	Discovery and characterization of d-phenylserine deaminase from <i>Arthrobacter</i> sp. TKS1. <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 159-172.	3.6	1
2733	Non-linear models based on simple topological indices to identify RNase III protein members. <i>Journal of Theoretical Biology</i> , 2011, 273, 167-178.	1.7	7
2734	Meet Me Halfway: When Genomics Meets Structural Bioinformatics. <i>Journal of Cardiovascular Translational Research</i> , 2011, 4, 281-303.	2.4	13
2735	An overview of human protein databases and their application to functional proteomics in health and disease. <i>Science China Life Sciences</i> , 2011, 54, 988-998.	4.9	7
2736	1,000 structures and more from the MCSG. <i>BMC Structural Biology</i> , 2011, 11, 2.	2.3	14
2737	Comparative void-volume analysis of psychrophilic and mesophilic enzymes: Structural bioinformatics of psychrophilic enzymes reveals sources of core flexibility. <i>BMC Structural Biology</i> , 2011, 11, 42.	2.3	67

#	ARTICLE	IF	CITATIONS
2738	The origin of a derived superkingdom: how a gram-positive bacterium crossed the desert to become an archaeon. <i>Biology Direct</i> , 2011, 6, 16.	4.6	28
2739	Evolution of vacuolar proton pyrophosphatase domains and volutin granules: clues into the early evolutionary origin of the acidocalcisome. <i>Biology Direct</i> , 2011, 6, 50.	4.6	45
2740	Global network analysis of drug tolerance, mode of action and virulence in methicillin-resistant <i>S. aureus</i> . <i>BMC Systems Biology</i> , 2011, 5, 68.	3.0	36
2741	Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 4.	7.6	93
2742	Ultra-fast sequence clustering from similarity networks with SiLiX. <i>BMC Bioinformatics</i> , 2011, 12, 116.	2.6	271
2743	A user-friendly web portal for T-Coffee on supercomputers. <i>BMC Bioinformatics</i> , 2011, 12, 150.	2.6	5
2744	Comprehensive, atomic-level characterization of structurally characterized protein-protein interactions: the PICCOLO database. <i>BMC Bioinformatics</i> , 2011, 12, 313.	2.6	56
2745	CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. <i>BMC Bioinformatics</i> , 2011, 12, 356.	2.6	246
2746	GARNET – gene set analysis with exploration of annotation relations. <i>BMC Bioinformatics</i> , 2011, 12, S25.	2.6	11
2747	BEL/Pao retrotransposons in metazoan genomes. <i>BMC Evolutionary Biology</i> , 2011, 11, 154.	3.2	42
2748	Analysis of genome-wide association study data using the protein knowledge base. <i>BMC Genetics</i> , 2011, 12, 98.	2.7	10
2749	Bioinformatic evidence for a widely distributed, ribosomally produced electron carrier precursor, its maturation proteins, and its nicotinoprotein redox partners. <i>BMC Genomics</i> , 2011, 12, 21.	2.8	85
2750	Spatial analysis of biomineralization associated gene expression from the mantle organ of the pearl oyster <i>Pinctada maxima</i> . <i>BMC Genomics</i> , 2011, 12, 455.	2.8	76
2751	RNA-seq analyses of blood-induced changes in gene expression in the mosquito vector species, <i>Aedes aegypti</i> . <i>BMC Genomics</i> , 2011, 12, 82.	2.8	133
2752	Noncellulosomal cohesin from the hyperthermophilic archaeon <i>Archaeoglobus fulgidus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 50-60.	2.6	6
2753	Structural and functional analysis of the Lmo2642 cyclic nucleotide phosphodiesterase from <i>Listeria monocytogenes</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1205-1214.	2.6	11
2754	Analysis of protein function and its prediction from amino acid sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2086-2096.	2.6	124
2755	ProteoConnections: A bioinformatics platform to facilitate proteome and phosphoproteome analyses. <i>Proteomics</i> , 2011, 11, 2654-2671.	2.2	23

#	ARTICLE	IF	CITATIONS
2756	Proteome reference map of <i>Lactobacillus acidophilus</i> NCFM and quantitative proteomics towards understanding the prebiotic action of lactitol. <i>Proteomics</i> , 2011, 11, 3470-3481.	2.2	43
2757	Integrating computational protein function prediction into drug discovery initiatives. <i>Drug Development Research</i> , 2011, 72, 4-16.	2.9	7
2758	Analysis of the disintegrin-metalloproteinases family reveals ADAM29 and ADAM7 are often mutated in melanoma. <i>Human Mutation</i> , 2011, 32, E2148-E2175.	2.5	33
2759	Cancer predisposing mutations in BRCT domains. <i>IUBMB Life</i> , 2011, 63, 503-512.	3.4	16
2760	Comparative metabolic capabilities for <i>Micrococcus luteus</i> NCTC 2665, the "Fleming" strain, and actinobacteria. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2770-2775.	3.3	6
2761	Information-theoretic approaches to SVM feature selection for metagenome read classification. <i>Computational Biology and Chemistry</i> , 2011, 35, 199-209.	2.3	19
2762	EuPathDomains: The divergent domain database for eukaryotic pathogens. <i>Infection, Genetics and Evolution</i> , 2011, 11, 698-707.	2.3	8
2763	Apicomplexan apicortins possess a long disordered N-terminal extension. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1037-1044.	2.3	10
2764	Network-based function prediction and interactomics: The case for metabolic enzymes. <i>Metabolic Engineering</i> , 2011, 13, 1-10.	7.0	43
2765	Present Perspectives on the Automated Classification of the G-Protein Coupled Receptors (GPCRs) at the Protein Sequence Level. <i>Current Topics in Medicinal Chemistry</i> , 2011, 11, 1994-2009.	2.1	8
2766	Nucleotide Parasitism by <i>Simkania negevensis</i> (<i>Chlamydiae</i>). <i>Journal of Bacteriology</i> , 2011, 193, 225-235.	2.2	27
2767	Specific inhibition of bacterial RNase T2 by helix 41 of 16S ribosomal RNA. <i>Nature Communications</i> , 2011, 2, 549.	12.8	28
2768	Evolution of the Ras-like small GTPases and their regulators. <i>Small GTPases</i> , 2011, 2, 4-16.	1.6	54
2769	Genetic characterization of ebi reveals its critical role in <i>Drosophila</i> wing growth. <i>Fly</i> , 2011, 5, 291-303.	1.7	4
2770	Abundant class of non-coding RNA regulates development in the social amoeba <i>Dictyostelium discoideum</i> . <i>RNA Biology</i> , 2011, 8, 1094-1104.	3.1	15
2771	A Domain-Centric Analysis of Oomycete Plant Pathogen Genomes Reveals Unique Protein Organization. <i>Plant Physiology</i> , 2011, 155, 628-644.	4.8	79
2772	Discovery of the First Insect Nidovirus, a Missing Evolutionary Link in the Emergence of the Largest RNA Virus Genomes. <i>PLoS Pathogens</i> , 2011, 7, e1002215.	4.7	169
2773	The Proteome Folding Project: Proteome-scale prediction of structure and function. <i>Genome Research</i> , 2011, 21, 1981-1994.	5.5	40

#	ARTICLE	IF	CITATIONS
2774	Regulation of phenotypic heterogeneity permits <i>Salmonella</i> evasion of the host caspase-1 inflammatory response. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20742-20747.	7.1	93
2775	A GRAPH-BASED SEMANTIC SIMILARITY MEASURE FOR THE GENE ONTOLOGY. Journal of Bioinformatics and Computational Biology, 2011, 09, 681-695.	0.8	17
2776	Discriminative Motif Finding for Predicting Protein Subcellular Localization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 441-451.	3.0	32
2777	Inferring domain-domain interactions using an extended parsimony model. , 2011, , .		1
2778	Reconstruction of genome-scale metabolic pathway in <i>Aspergillus terreus</i> NIH2624. , 2011, , .		0
2779	Small sets of interacting proteins suggest functional linkage mechanisms via Bayesian analogical reasoning. Bioinformatics, 2011, 27, i374-i382.	4.1	0
2780	Regulation of Biofilm Components in <i>Salmonella enterica</i> Serovar Typhimurium by Lytic Transglycosylases Involved in Cell Wall Turnover. Journal of Bacteriology, 2011, 193, 6443-6451.	2.2	40
2781	Identification of family-determining residues in PHD fingers. Nucleic Acids Research, 2011, 39, 1666-1679.	14.5	12
2782	Augmented Annotation of the <i>Schizosaccharomyces pombe</i> Genome Reveals Additional Genes Required for Growth and Viability. Genetics, 2011, 187, 1207-1217.	2.9	26
2783	Conserved Meiotic Machinery in <i>Glomus</i> spp., a Putatively Ancient Asexual Fungal Lineage. Genome Biology and Evolution, 2011, 3, 950-958.	2.5	129
2784	Characterization of a porin channel in the endosymbiont of the trypanosomatid protozoan <i>Crithidia deanei</i> . Microbiology (United Kingdom), 2011, 157, 2818-2830.	1.8	7
2785	Verification of alternative splicing variants based on domain integrity, truncation length and intrinsic protein disorder. Nucleic Acids Research, 2011, 39, 1208-1219.	14.5	46
2786	Brr6 drives the <i>Schizosaccharomyces pombe</i> spindle pole body nuclear envelope insertion/extrusion cycle. Journal of Cell Biology, 2011, 195, 467-484.	5.2	54
2787	A Novel E2F-like Protein Involved in Transcriptional Activation of Cyst Wall Protein Genes in <i>Giardia lamblia</i> *. Journal of Biological Chemistry, 2011, 286, 34101-34120.	3.4	20
2788	Diversity and distribution of transcription factors: their partner domains play an important role in regulatory plasticity in bacteria. Microbiology (United Kingdom), 2011, 157, 2308-2318.	1.8	26
2789	Structural basis for the dual RNA-recognition modes of human Tra2- β RRM. Nucleic Acids Research, 2011, 39, 1538-1553.	14.5	62
2790	Complete Genome Sequence of the Commensal <i>Enterococcus faecalis</i> 62, Isolated from a Healthy Norwegian Infant. Journal of Bacteriology, 2011, 193, 2377-2378.	2.2	46
2791	Selection patterns on restorer-like genes reveal a conflict between nuclear and mitochondrial genomes throughout angiosperm evolution. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1723-1728.	7.1	236

#	ARTICLE	IF	CITATIONS
2792	Surveying the Manifold Divergence of an Entire Protein Class for Statistical Clues to Underlying Biochemical Mechanisms. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, Article 36.	0.6	16
2793	Identification of a Family of Effectors Secreted by the Type III Secretion System That Are Conserved in Pathogenic Chlamydiae. <i>Infection and Immunity</i> , 2011, 79, 571-580.	2.2	42
2794	The H/ACA RNP assembly factor SHQ1 functions as an RNA mimic. <i>Genes and Development</i> , 2011, 25, 2398-2408.	5.9	50
2795	Novel Family of Carbohydrate-Binding Modules Revealed by the Genome Sequence of <i>Spirochaeta thermophila</i> DSM 6192. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5483-5489.	3.1	12
2796	The Dca Gene Involved in Cold Adaptation in <i>Drosophila melanogaster</i> Arose by Duplication of the Ancestral regucalcin Gene. <i>Molecular Biology and Evolution</i> , 2011, 28, 2185-2195.	8.9	15
2797	Structure and evolutionary history of DISC1. <i>Human Molecular Genetics</i> , 2011, 20, R175-R181.	2.9	13
2798	SalmonDB: a bioinformatics resource for <i>Salmo salar</i> and <i>Oncorhynchus mykiss</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar050-bar050.	3.0	28
2799	Heat shock response in olive (<i>Olea europaea</i> L.) twigs: Identification and analysis of a cDNA coding a class I small heat shock protein. <i>Plant Biosystems</i> , 2011, 145, 419-425.	1.6	9
2800	Evolution of Patchily Distributed Proteins Shared between Eukaryotes and Prokaryotes: <i>Dictyostelium</i> as a Case Study. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 20, 83-95.	1.0	18
2801	Functional Annotation Analytics of <i>Rhodospseudomonas palustris</i> Genomes. <i>Bioinformatics and Biology Insights</i> , 2011, 5, BBI.S7316.	2.0	13
2802	Methods and strategies for gene structure curation in WormBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, baq039-baq039.	3.0	15
2803	Physiological and Biochemical Characterization of AnNitA, the <i>Aspergillus nidulans</i> High-Affinity Nitrite Transporter. <i>Eukaryotic Cell</i> , 2011, 10, 1724-1732.	3.4	10
2804	Feed-Forward Regulation of Microbisporicin Biosynthesis in <i>Microbispora corallina</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3064-3071.	2.2	39
2805	Genome Sequence of <i>Rheinheimera</i> sp. Strain A13L, Isolated from Pangong Lake, India. <i>Journal of Bacteriology</i> , 2011, 193, 5873-5874.	2.2	40
2806	Genome Sequence of <i>Idiomarina</i> sp. Strain A28L, Isolated from Pangong Lake, India. <i>Journal of Bacteriology</i> , 2011, 193, 5875-5876.	2.2	14
2807	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011, 21, 898-907.	5.5	41
2808	A Three-Step Validation Following Genome-Wide Data Mining for Myosin Family Members Improves Search Efficiency. , 2011,, .		1
2809	Characterization of the Deoxynucleotide Triphosphate Triphosphohydrolase (dNTPase) Activity of the EF1143 Protein from <i>Enterococcus faecalis</i> and Crystal Structure of the Activator-Substrate Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 33158-33166.	3.4	31

#	ARTICLE	IF	CITATIONS
2810	Genome Expansion and Differential Expression of Amino Acid Transporters at the Aphid/Buchnera Symbiotic Interface. <i>Molecular Biology and Evolution</i> , 2011, 28, 3113-3126.	8.9	66
2811	Infectivity Acts as <i>In Vivo</i> Selection for Maintenance of the Chlamydial Cryptic Plasmid. <i>Infection and Immunity</i> , 2011, 79, 98-107.	2.2	48
2812	A Systems Biology Approach for the Investigation of the Heparin/Heparan Sulfate Interactome. <i>Journal of Biological Chemistry</i> , 2011, 286, 19892-19904.	3.4	203
2813	Autophagy in protists. <i>Autophagy</i> , 2011, 7, 127-158.	9.1	148
2814	Comparative Modeling: The State of the Art and Protein Drug Target Structure Prediction. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2011, 14, 532-547.	1.1	42
2815	The fast Viterbi algorithm caching Profile Hidden Markov Models on graphic processing units. , 2011, , .		2
2816	Explore the domain features of co-regulation proteins, co-interaction proteins and co-regulation & Co-interaction proteins. , 2011, , .		0
2817	The Solute Carrier Families Have a Remarkably Long Evolutionary History with the Majority of the Human Families Present before Divergence of Bilaterian Species. <i>Molecular Biology and Evolution</i> , 2011, 28, 1531-1541.	8.9	182
2818	A Targeted siRNA Screen Identifies Regulators of Cdc42 Activity at the Natural Killer Cell Immunological Synapse. <i>Science Signaling</i> , 2011, 4, ra81.	3.6	46
2819	The SH2 Domain-Containing Proteins in 21 Species Establish the Provenance and Scope of Phosphotyrosine Signaling in Eukaryotes. <i>Science Signaling</i> , 2011, 4, ra83.	3.6	81
2820	A Negative Effector of Blue Light-Induced and Gravitropic Bending in Arabidopsis. <i>Plant Physiology</i> , 2011, 156, 439-447.	4.8	29
2821	Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> Lectotype Strain ATCC 10988. <i>Journal of Bacteriology</i> , 2011, 193, 5051-5052.	2.2	30
2822	Genome Sequence of the Ethanol-Producing <i>Zymomonas mobilis</i> subsp. <i>pomaceae</i> Lectotype Strain ATCC 29192. <i>Journal of Bacteriology</i> , 2011, 193, 5049-5050.	2.2	22
2823	Theoretical and Experimental Characterization of the Scope of Protein O-Glycosylation in <i>Bacteroides fragilis</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 3219-3226.	3.4	45
2824	Structural and Biochemical Characterization of the Salicyl-acyltransferase SsfX3 from a Tetracycline Biosynthetic Pathway. <i>Journal of Biological Chemistry</i> , 2011, 286, 41539-41551.	3.4	14
2825	AS160 Phosphotyrosine-binding Domain Constructs Inhibit Insulin-stimulated GLUT4 Vesicle Fusion with the Plasma Membrane. <i>Journal of Biological Chemistry</i> , 2011, 286, 16574-16582.	3.4	29
2826	Implications of the Inability of <i>Listeria monocytogenes</i> EGD-e To Grow Anaerobically Due to a Deletion in the Class III NrdD Ribonucleotide Reductase for Its Use as a Model Laboratory Strain. <i>Journal of Bacteriology</i> , 2011, 193, 2931-2940.	2.2	9
2827	BlastR-fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 6886-6895.	14.5	28

#	ARTICLE	IF	CITATIONS
2828	Strain-specific activation of the NF- κ B pathway by GRA15, a novel <i>Toxoplasma gondii</i> dense granule protein. <i>Journal of Experimental Medicine</i> , 2011, 208, 195-212.	8.5	375
2829	Comparison of the Specificities and Efficacies of Primers for Aromatic Dioxygenase Gene Analysis of Environmental Samples. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3551-3557.	3.1	64
2830	Protein Folding and Quality Control in the ER. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a007526-a007526.	5.5	290
2831	The multiple functions of plant serine protease inhibitors. <i>Plant Signaling and Behavior</i> , 2011, 6, 1009-1011.	2.4	42
2832	Draft Genome Sequencing and Comparative Analysis of <i>Aspergillus sojae</i> NBRC4239. <i>DNA Research</i> , 2011, 18, 165-176.	3.4	75
2833	Multiple congenital anomalies-hypotonia-seizures syndrome is caused by a mutation in PIGN. <i>Journal of Medical Genetics</i> , 2011, 48, 383-389.	3.2	138
2834	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2011, 39, D402-D410.	14.5	64
2835	Detecting anomalies in symbolic sequence dataset. , 2011, , .		0
2836	Molecular Characterization of <i>Cronobacter</i> Lipopolysaccharide O-Antigen Gene Clusters and Development of Serotype-Specific PCR Assays. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4017-4026.	3.1	91
2837	Insights into the Evolution of Vitamin B12 Auxotrophy from Sequenced Algal Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2921-2933.	8.9	246
2838	Evidence for Direct Electron Transfer by a Gram-Positive Bacterium Isolated from a Microbial Fuel Cell. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7633-7639.	3.1	195
2839	EXORDIUM-LIKE1 Promotes Growth during Low Carbon Availability in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2011, 156, 1620-1630.	4.8	60
2840	A Novel Cold-Adapted Lipase from <i>Sorangium cellulosum</i> Strain So0157-2: Gene Cloning, Expression, and Enzymatic Characterization. <i>International Journal of Molecular Sciences</i> , 2011, 12, 6765-6780.	4.1	17
2841	<i>Klebsiella pneumoniae</i> yggG Gene Product: A Zinc-Dependent Metalloprotease. <i>International Journal of Molecular Sciences</i> , 2011, 12, 4441-4455.	4.1	4
2842	LinkinPath: from sequence to interconnected pathway. <i>Bioinformatics</i> , 2011, 27, 2015-2017.	4.1	1
2843	Independent HHsearch, Needleman-Wunsch-Based, and Motif Analyses Reveal the Overall Hierarchy for Most of the G Protein-Coupled Receptor Families. <i>Molecular Biology and Evolution</i> , 2011, 28, 2471-2480.	8.9	145
2844	Genome-Wide Survey of Natural Selection on Functional, Structural, and Network Properties of Polymorphic Sites in <i>Saccharomyces paradoxus</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 2615-2627.	8.9	18
2845	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species. <i>Plant Cell</i> , 2011, 23, 895-910.	6.6	297

#	ARTICLE	IF	CITATIONS
2846	Biological Systems Discovery In Silico: Radical <i>S</i> -Adenosylmethionine Protein Families and Their Target Peptides for Posttranslational Modification. <i>Journal of Bacteriology</i> , 2011, 193, 2745-2755.	2.2	152
2847	Identification of genes and gene clusters involved in mycotoxin synthesis. , 2011, , 332-348.		2
2848	The <i>Lymantria dispar</i> IPLB-Ld652Y Cell Line Transcriptome Comprises Diverse Virus-Associated Transcripts. <i>Viruses</i> , 2011, 3, 2339-2350.	3.3	16
2849	Molecular Characterization and Expression Pattern of Tripartite Motif Protein 39 in <i>Gallus gallus</i> with a Complete PRY/SPRY Domain. <i>International Journal of Molecular Sciences</i> , 2011, 12, 3797-3809.	4.1	7
2850	Adding unaligned sequences into an existing alignment using MAFFT and LAST. <i>Bioinformatics</i> , 2012, 28, 3144-3146.	4.1	217
2851	Genome Reduction and Co-evolution between the Primary and Secondary Bacterial Symbionts of Psyllids. <i>Molecular Biology and Evolution</i> , 2012, 29, 3781-3792.	8.9	175
2852	Uncovering MicroRNA and Transcription Factor Mediated Regulatory Networks in Glioblastoma. <i>PLoS Computational Biology</i> , 2012, 8, e1002488.	3.2	124
2853	Co-expression of cell-wall related genes: new tools and insights. <i>Frontiers in Plant Science</i> , 2012, 3, 83.	3.6	55
2854	Deep Sequencing of <i>Porphyromonas gingivalis</i> and Comparative Transcriptome Analysis of a LuxS Mutant. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 79.	3.9	27
2855	Structural Analysis of Hypothetical Proteins from <i>Helicobacter pylori</i> : An Approach to Estimate Functions of Unknown or Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7109-7137.	4.1	17
2856	Zds1 regulates PP2Acdc55 activity and Cdc14 activation during mitotic exit via its Zds_C motif. <i>Journal of Cell Science</i> , 2012, 125, 2875-84.	2.0	13
2857	Interpretation of the Consequences of Mutations in Protein Kinases: Combined Use of Bioinformatics and Text Mining. <i>Frontiers in Physiology</i> , 2012, 3, 323.	2.8	9
2858	Molecular Characterization and Comparative Sequence Analysis of Defense-Related Gene, <i>Oryza rufipogon</i> Receptor-Like Protein Kinase 1. <i>International Journal of Molecular Sciences</i> , 2012, 13, 9343-9362.	4.1	5
2859	CombFunc: predicting protein function using heterogeneous data sources. <i>Nucleic Acids Research</i> , 2012, 40, W466-W470.	14.5	63
2860	Sequence Evolution Correlates with Structural Dynamics. <i>Molecular Biology and Evolution</i> , 2012, 29, 2253-2263.	8.9	132
2861	Novel Metagenome-Derived, Cold-Adapted Alkaline Phospholipase with Superior Lipase Activity as an Intermediate between Phospholipase and Lipase. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4959-4966.	3.1	21
2862	Comparative Analysis of the Genomes of Two Field Isolates of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2012, 8, e1002869.	3.5	167
2863	Genome-Wide Identification and in Silico Analysis of Poplar Peptide Deformylases. <i>International Journal of Molecular Sciences</i> , 2012, 13, 5112-5124.	4.1	4

#	ARTICLE	IF	CITATIONS
2864	Characterization of Erysiphe necator-Responsive Genes in Chinese Wild Vitis quinquangularis. International Journal of Molecular Sciences, 2012, 13, 11497-11519.	4.1	16
2865	Comparative Genomics Suggests an Independent Origin of Cytoplasmic Incompatibility in Cardinium hertigii. PLoS Genetics, 2012, 8, e1003012.	3.5	135
2866	State of the Art in Silico Tools for the Study of Signaling Pathways in Cancer. International Journal of Molecular Sciences, 2012, 13, 6561-6581.	4.1	4
2867	Identification of chemogenomic features from drug-target interaction networks using interpretable classifiers. Bioinformatics, 2012, 28, i487-i494.	4.1	78
2868	Computational Prediction and Molecular Characterization of an Oomycete Effector and the Cognate Arabidopsis Resistance Gene. PLoS Genetics, 2012, 8, e1002502.	3.5	68
2869	Chapter 12: Human Microbiome Analysis. PLoS Computational Biology, 2012, 8, e1002808.	3.2	408
2870	Eleven diverse nuclear-encoded phylogenetic markers for the subfamily Panicoideae (Poaceae). American Journal of Botany, 2012, 99, e443-6.	1.7	7
2871	Analysis of Two l-Galactono-1,4-Lactone-Responsive Genes with Complementary Expression During the Development of Arabidopsis thaliana. Plant and Cell Physiology, 2012, 53, 592-601.	3.1	14
2872	Origin and Evolution of Laminin Gene Family Diversity. Molecular Biology and Evolution, 2012, 29, 1823-1836.	8.9	45
2873	The Csr/Rsm system of Yersinia and related pathogens. RNA Biology, 2012, 9, 379-391.	3.1	87
2874	A Response Regulator Interfaces between the Frz Chemosensory System and the MglA/MglB GTPase/GAP Module to Regulate Polarity in Myxococcus xanthus. PLoS Genetics, 2012, 8, e1002951.	3.5	60
2875	Selecting Negative Samples for PPI Prediction Using Hierarchical Clustering Methodology. Journal of Applied Mathematics, 2012, 2012, 1-23.	0.9	1
2876	Constructing the angiome: a global angiogenesis protein interaction network. Physiological Genomics, 2012, 44, 915-924.	2.3	30
2877	Strain Variation in the Transcriptome of the Dengue Fever Vector, <i>Aedes aegypti</i> . G3: Genes, Genomes, Genetics, 2012, 2, 103-114.	1.8	36
2878	General Trends in the Utilization of Structural Factors Contributing to Biological Complexity. Molecular Biology and Evolution, 2012, 29, 1957-1968.	8.9	11
2879	SMURFLite: combining simplified Markov random fields with simulated evolution improves remote homology detection for beta-structural proteins into the twilight zone. Bioinformatics, 2012, 28, 1216-1222.	4.1	25
2880	Genome Sequence of Reyranelia massiliensis, a Bacterium Associated with Amoebae. Journal of Bacteriology, 2012, 194, 5698-5698.	2.2	6
2881	Comparative Analysis of Benzoxazinoid Biosynthesis in Monocots and Dicots: Independent Recruitment of Stabilization and Activation Functions. Plant Cell, 2012, 24, 915-928.	6.6	58

#	ARTICLE	IF	CITATIONS
2882	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	3.0	38
2883	The Armadillo Repeat Gene <i>ZAK IXIK</i> Promotes <i>Arabidopsis</i> Early Embryo and Endosperm Development through a Distinctive Gametophytic Maternal Effect. Plant Cell, 2012, 24, 4026-4043.	6.6	19
2884	Genome Sequence of <i>Legionella tunisiensis</i> Strain LegM ^T , a New <i>Legionella</i> Species Isolated from Hypersaline Lake Water. Journal of Bacteriology, 2012, 194, 5978-5978.	2.2	4
2885	Genome Sequence of <i>Rickettsia conorii</i> subsp. <i>israelensis</i> , the Agent of Israeli Spotted Fever. Journal of Bacteriology, 2012, 194, 5130-5131.	2.2	9
2886	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	14.5	490
2887	INFLUENZA A SUBTYPING AND HOST ORIGIN CLASSIFICATION USING PROFILE HIDDEN MARKOV MODELS. Journal of Mechanics in Medicine and Biology, 2012, 12, 1240009.	0.7	4
2888	Assignment of protein sequences to existing domain and family classification systems: Pfam and the PDB. Bioinformatics, 2012, 28, 2763-2772.	4.1	56
2889	Evolution of Viral Proteins Originated De Novo by Overprinting. Molecular Biology and Evolution, 2012, 29, 3767-3780.	8.9	125
2890	Visualizing the protein sequence universe. , 2012, , .		3
2891	TolC-Dependent Secretion of an Ankyrin Repeat-Containing Protein of <i>Rickettsia typhi</i> . Journal of Bacteriology, 2012, 194, 4920-4932.	2.2	51
2892	Accurate prediction of protein structural classes using functional domains and predicted secondary structure sequences. Journal of Biomolecular Structure and Dynamics, 2012, 29, 1127-1137.	3.5	17
2893	Identifying protein binding functionality of protein family sequences by aligned pattern clusters. , 2012, , .		0
2894	The binding of Varp to VAMP7 traps VAMP7 in a closed, fusogenically inactive conformation. Nature Structural and Molecular Biology, 2012, 19, 1300-1309.	8.2	68
2895	Provirophages and transpovirons as the diverse mobilome of giant viruses. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18078-18083.	7.1	194
2896	Garvieacin Q, a Novel Class II Bacteriocin from <i>Lactococcus garvieae</i> BCC 43578. Applied and Environmental Microbiology, 2012, 78, 1619-1623.	3.1	59
2897	Activator Role of the Pneumococcal Mga-Like Virulence Transcriptional Regulator. Journal of Bacteriology, 2012, 194, 4197-4207.	2.2	19
2898	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2012, 40, D445-D452.	14.5	166
2899	An adaptation of Pfam profiles to predict protein sub-cellular localization in Gram positive bacteria. , 2012, 2012, 5554-7.		4

#	ARTICLE	IF	CITATIONS
2900	DBETH: A Database of Bacterial Exotoxins for Human. <i>Nucleic Acids Research</i> , 2012, 40, D615-D620.	14.5	53
2901	Activation of the Carbon Concentrating Mechanism by CO ₂ Deprivation Coincides with Massive Transcriptional Restructuring in <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2012, 24, 1860-1875.	6.6	121
2902	Evolution of the FGF Gene Family. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-12.	1.0	42
2903	Novel domain combinations in proteins encoded by chimeric transcripts. <i>Bioinformatics</i> , 2012, 28, i67-i74.	4.1	35
2904	Myosinome: A Database of Myosins from Select Eukaryotic Genomes to Facilitate Analysis of Sequence-Structure-Function Relationships. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9902.	2.0	7
2905	EvoluCode: Evolutionary Barcodes as a Unifying Framework for Multilevel Evolutionary Data. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S8814.	1.2	4
2906	Determinants of Exon-Level Evolutionary Rates in <i>Arabidopsis</i> Species. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9743.	1.2	3
2907	Alternative Splicing: A Potential Source of Functional Innovation in the Eukaryotic Genome. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	66
2908	PDBTM: Protein Data Bank of transmembrane proteins after 8 years. <i>Nucleic Acids Research</i> , 2012, 41, D524-D529.	14.5	245
2909	Genomic Analysis of the Hydrocarbon-Producing, Cellulolytic, Endophytic Fungus <i>Ascocoryne sarcoides</i> . <i>PLoS Genetics</i> , 2012, 8, e1002558.	3.5	76
2910	Characterization of Protein Glycosylation in <i>Francisella tularensis</i> subsp. <i>holarctica</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015016-1-M111.015016-12.	3.8	36
2911	Novel search method for the discovery of functional relationships. <i>Bioinformatics</i> , 2012, 28, 269-276.	4.1	10
2912	Probabilistic suffix array: efficient modeling and prediction of protein families. <i>Bioinformatics</i> , 2012, 28, 1314-1323.	4.1	10
2913	Complete Genome Sequence of <i>Serratia plymuthica</i> Bacteriophage γ -MAM1. <i>Journal of Virology</i> , 2012, 86, 13872-13873.	3.4	8
2914	Independent Genome Reduction and Phylogenetic Reclassification of the Oceanic SAR11 Clade. <i>Molecular Biology and Evolution</i> , 2012, 29, 599-615.	8.9	105
2915	Lysophospholipid acyltransferases. <i>Current Opinion in Lipidology</i> , 2012, 23, 290-302.	2.7	50
2916	Analysis of yeast endocytic site formation and maturation through a regulatory transition point. <i>Molecular Biology of the Cell</i> , 2012, 23, 657-668.	2.1	75
2917	Characterization of Novel Phages Isolated in Coagulase-Negative Staphylococci Reveals Evolutionary Relationships with <i>Staphylococcus aureus</i> Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5829-5839.	2.2	50

#	ARTICLE	IF	CITATIONS
2918	Translating Mendelian and complex inheritance of Alzheimer's disease genes for predicting unique personal genome variants. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 306-316.	4.4	18
2919	Autoinhibition of the formin Cappuccino in the absence of canonical autoinhibitory domains. Molecular Biology of the Cell, 2012, 23, 3801-3813.	2.1	32
2920	C7orf30 specifically associates with the large subunit of the mitochondrial ribosome and is involved in translation. Nucleic Acids Research, 2012, 40, 4040-4051.	14.5	46
2921	Characterization of a Viral Synergism in the Monocot <i>Brachypodium distachyon</i> Reveals Distinctly Altered Host Molecular Processes Associated with Disease. Plant Physiology, 2012, 160, 1432-1452.	4.8	60
2922	Bacterial Cell Division Regulation by Ser/Thr Kinases: A Structural Perspective. Current Protein and Peptide Science, 2012, 13, 756-766.	1.4	52
2923	Incorporating molecular and functional context into the analysis and prioritization of human variants associated with cancer. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 275-283.	4.4	23
2924	Efficient alternatives to PSI-BLAST. Bulletin of the Polish Academy of Sciences: Technical Sciences, 2012, 60, 495-505.	0.8	0
2925	Adhesion of microbes to the intestinal surface: lessons from the paradigm probiotic <i>Lactobacillus rhamnosus</i> GG. Japanese Journal of Lactic Acid Bacteria, 2012, 23, 7-13.	0.1	0
2926	Protein complex prediction via improved verification methods using constrained domain-domain matching. International Journal of Bioinformatics Research and Applications, 2012, 8, 210.	0.2	1
2927	Human Retinoblastoma Binding Protein 9, a Serine Hydrolase Implicated in Pancreatic Cancers. Protein and Peptide Letters, 2012, 19, 194-197.	0.9	13
2928	Metagenomic Evidence for H ₂ Oxidation and H ₂ Production by Serpentinite-Hosted Subsurface Microbial Communities. Frontiers in Microbiology, 2012, 2, 268.	3.5	204
2929	Leucine-Rich Repeat (LRR) Domains Containing Intervening Motifs in Plants. Biomolecules, 2012, 2, 288-311.	4.0	74
2930	DICER-LIKE3 Activity in <i>Physcomitrella patens</i> DICER-LIKE4 Mutants Causes Severe Developmental Dysfunction and Sterility. Molecular Plant, 2012, 5, 1281-1294.	8.3	45
2931	Identification of viral biomarkers of hepatitis C virus (HCV) for liver cancer prediction. International Journal of Medical Engineering and Informatics, 2012, 4, 274.	0.3	2
2933	Hierarchical Motif Vectors for Prediction of Functional Sites in Amino Acid Sequences Using Quasi-Supervised Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1432-1441.	3.0	4
2934	Insect Genomics. , 2012, , 1-29.		0
2935	Structure of the <i>Archaeoglobus fulgidus</i> orphan ORF AF1382 determined by sulfur SAD from a moderately diffracting crystal. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1242-1252.	2.5	5
2936	Molecular Biology of Lignification in Grasses. Advances in Botanical Research, 2012, , 77-112.	1.1	9

#	ARTICLE	IF	CITATIONS
2937	Intrinsically disordered proteins in human mitochondria. <i>Genes To Cells</i> , 2012, 17, 817-825.	1.2	10
2938	Automated hierarchical classification of protein domain subfamilies based on functionally-divergent residue signatures. <i>BMC Bioinformatics</i> , 2012, 13, 144.	2.6	11
2939	Molecular characterization of ltp3 and ltp4, essential for C24-branched chain sterol-side-chain degradation in <i>Rhodococcus rhodochrous</i> DSM 43269. <i>Microbiology (United Kingdom)</i> , 2012, 158, 3054-3062.	1.8	23
2940	Bacterial Biosynthetic Gene Clusters Encoding the Anti-cancer Haterumalide Class of Molecules. <i>Journal of Biological Chemistry</i> , 2012, 287, 39125-39138.	3.4	80
2941	New cis-regulatory elements in the Rht-D1b locus region of wheat. <i>Functional and Integrative Genomics</i> , 2012, 12, 489-500.	3.5	13
2942	Fife, a <i>Drosophila</i> Piccolo-RIM Homolog, Promotes Active Zone Organization and Neurotransmitter Release. <i>Journal of Neuroscience</i> , 2012, 32, 17048-17058.	3.6	42
2943	Iterative orthology prediction uncovers new mitochondrial proteins and identifies C12orf62 as the human ortholog of COX14, a protein involved in the assembly of cytochrome c oxidase. <i>Genome Biology</i> , 2012, 13, R12.	9.6	100
2944	The Transcription Factor Encyclopedia. <i>Genome Biology</i> , 2012, 13, R24.	9.6	103
2945	Genome-wide identification and characterization of replication origins by deep sequencing. <i>Genome Biology</i> , 2012, 13, R27.	9.6	85
2946	Endosomal crosstalk: meeting points for signaling pathways. <i>Trends in Cell Biology</i> , 2012, 22, 447-456.	7.9	104
2947	Proteome variation among <i>Scaphylococcus</i> strains. <i>Proteomics</i> , 2012, 12, 3343-3364.	2.2	32
2948	MotViz: A Tool for Sequence Motif Prediction in Parallel to Structural Visualization and Analyses. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 35-43.	6.9	1
2949	Evolutionary history of exon shuffling. <i>Genetica</i> , 2012, 140, 249-257.	1.1	21
2950	Conservation of group XII phospholipase A2 from bacteria to human. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2012, 7, 340-350.	1.0	6
2951	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , 2012, 158, 248-258.	3.8	198
2952	Identification of aero-allergens from <i>Rhizopus oryzae</i> : An immunoproteomic approach. <i>Journal of Proteomics</i> , 2012, 77, 455-468.	2.4	44
2953	CancerProView: A graphical image database of cancer-related genes and proteins. <i>Genomics</i> , 2012, 100, 81-92.	2.9	2
2954	VIP DB – A viral protein domain usage and distribution database. <i>Genomics</i> , 2012, 100, 149-156.	2.9	0

#	ARTICLE	IF	CITATIONS
2955	Comparative Genomics of the Lipid-body-membrane Proteins Oleosin, Caleosin and Steroleosin in Magnoliophyte, Lycophyte and Bryophyte. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 345-353.	6.9	21
2956	Genome-wide Analysis of Ovate Family Proteins in Arabidopsis. <i>The Journal of Northeast Agricultural University</i> , 2012, 19, 49-59.	0.1	2
2957	Identification of the Replication Region of a 111-kb Circular Plasmid from <i>Rhodococcus opacus</i> B-4 by λ Red Recombination-Based Deletion Analysis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1758-1764.	1.3	3
2958	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	5.5	4,217
2959	RGRank: Ranking Semantically Related Genes. , 2012, , .		3
2960	Molecular characterization of 60 isolated wheat MYB genes and analysis of their expression during abiotic stress. <i>Journal of Experimental Botany</i> , 2012, 63, 203-214.	4.8	182
2961	Identification and Characterization of an RTX Toxinâ€“Like Gene and Its Operon from <i>Avibacterium paragallinarum</i> . <i>Avian Diseases</i> , 2012, 56, 537-544.	1.0	9
2962	Exploration of a Possible Partnership among Orphan Two-Component System Proteins in <i>Cyanobacterium</i> <i>Synechococcus elongatus</i> PCC 7942. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1484-1491.	1.3	16
2963	Automatic Prediction of Enzyme Functions from Domain Compositions Using Enzyme Reaction Prediction Scheme. , 2012, , .		0
2964	Using structural domains to predict obligate and non-obligate protein-protein interactions. , 2012, , .		4
2965	Drug-target network in myocardial infarction: A structural analysis. , 2012, , .		1
2966	Probabilistic Arithmetic Automata and Their Applications. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1737-1750.	3.0	11
2967	Two Isoforms of <i>Flk-1</i> Transcripts in Early Diabetic Rat Retinas. <i>Current Eye Research</i> , 2012, 37, 73-79.	1.5	2
2968	Cascaded walks in protein sequence space: use of artificial sequences in remote homology detection between natural proteins. <i>Molecular BioSystems</i> , 2012, 8, 2076.	2.9	9
2969	Predicting protein-RNA residue-base contacts using two-dimensional conditional random field. , 2012, , .		1
2970	Spiked-in Pulsed in Vivo Labeling Identifies a New Member of the CCN Family in Regenerating Newt Hearts. <i>Journal of Proteome Research</i> , 2012, 11, 4693-4704.	3.7	32
2971	Extracellular Polysaccharide-Degrading Proteome of <i>Butyrivibrio proteoclasticus</i> . <i>Journal of Proteome Research</i> , 2012, 11, 131-142.	3.7	21
2972	Regulated Assembly of the Transenvelope Protein Complex Required for Lipopolysaccharide Export. <i>Biochemistry</i> , 2012, 51, 4800-4806.	2.5	118

#	ARTICLE	IF	CITATIONS
2973	ProBiS-Database: Precalculated Binding Site Similarities and Local Pairwise Alignments of PDB Structures. <i>Journal of Chemical Information and Modeling</i> , 2012, 52, 604-612.	5.4	50
2974	Activity-Based Protein Profiling of the <i>Escherichia coli</i> GlpG Rhomboid Protein Delineates the Catalytic Core. <i>Biochemistry</i> , 2012, 51, 7794-7803.	2.5	43
2975	Basic leucine zipper transcription factor OsbZIP16 positively regulates drought resistance in rice. <i>Plant Science</i> , 2012, 193-194, 8-17.	3.6	98
2976	Genome organization, serology and phylogeny of Grapevine leafroll-associated viruses 4 and 6: Taxonomic implications. <i>Virus Research</i> , 2012, 163, 120-128.	2.2	44
2977	Distant plant homologues: don't throw out the baby. <i>Trends in Plant Science</i> , 2012, 17, 126-128.	8.8	3
2978	Parasites, proteomes and systems: has Descartes' clock run out of time?. <i>Parasitology</i> , 2012, 139, 1103-1118.	1.5	28
2979	Subversion of Cell Signaling by Pathogens. <i>Cold Spring Harbor Perspectives in Biology</i> , 2012, 4, a006114-a006114.	5.5	101
2980	Characterization of a Novel Bipartite Double-Stranded RNA Mycovirus Conferring Hypovirulence in the Phytopathogenic Fungus <i>Botrytis porri</i> . <i>Journal of Virology</i> , 2012, 86, 6605-6619.	3.4	115
2981	EFICAz2.5: application of a high-precision enzyme function predictor to 396 proteomes. <i>Bioinformatics</i> , 2012, 28, 2687-2688.	4.1	63
2982	Complex evolutionary history and diverse domain organization of SET proteins suggest divergent regulatory interactions. <i>New Phytologist</i> , 2012, 195, 248-263.	7.3	65
2983	Discovery of <i>Pyrobaculum</i> small RNA families with atypical pseudouridine guide RNA features. <i>Rna</i> , 2012, 18, 402-411.	3.5	25
2984	Role of Low-Complexity Sequences in the Formation of Novel Protein Coding Sequences. <i>Molecular Biology and Evolution</i> , 2012, 29, 883-886.	8.9	93
2985	Identification of a Ubiquitin-Binding Structure in the S-Locus F-Box Protein Controlling S-RNase-Based Self-Incompatibility. <i>Journal of Genetics and Genomics</i> , 2012, 39, 93-102.	3.9	12
2986	Structure of the Sensor Domain of <i>Mycobacterium tuberculosis</i> PknH Receptor Kinase Reveals a Conserved Binding Cleft. <i>Journal of Molecular Biology</i> , 2012, 422, 488-494.	4.2	18
2987	Elman RNN based classification of proteins sequences on account of their mutual information. <i>Journal of Theoretical Biology</i> , 2012, 311, 40-45.	1.7	3
2988	Identification of residues involved in water versus glycerol selectivity in aquaporins by differential residue pair co-evolution. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 907-914.	2.6	7
2989	Using machine learning techniques and genomic/proteomic information from known databases for defining relevant features for PPI classification. <i>Computers in Biology and Medicine</i> , 2012, 42, 639-650.	7.0	6
2990	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	3.9	140

#	ARTICLE	IF	CITATIONS
2991	Molecular characterizations and functional assessments of GATA-3 and its splice variant in Atlantic cod (<i>Gadus morhua</i> L.). <i>Developmental and Comparative Immunology</i> , 2012, 36, 491-501.	2.3	22
2992	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. <i>Cell</i> , 2012, 149, 1607-1621.	28.9	478
2993	Identification of a novel isoform of DHRS4 protein with a nuclear localization signal. <i>Gene</i> , 2012, 494, 161-167.	2.2	7
2994	Evolutionary analysis of prokaryotic heat-shock transcription regulatory protein ĩf32. <i>Gene</i> , 2012, 495, 49-55.	2.2	0
2995	The crystal structure of the periplasmic domain of <i>Vibrio parahaemolyticus</i> CpxA. <i>Protein Science</i> , 2012, 21, 1334-1343.	7.6	13
2996	Profile-based short linear protein motif discovery. <i>BMC Bioinformatics</i> , 2012, 13, 104.	2.6	14
2997	The origins of the evolutionary signal used to predict protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2012, 12, 238.	3.2	8
2998	Expansion and diversification of the SET domain gene family following whole-genome duplications in <i>Populus trichocarpa</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 51.	3.2	49
2999	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	2.8	80
3000	An elm EST database for identifying leaf beetle egg-induced defense genes. <i>BMC Genomics</i> , 2012, 13, 242.	2.8	27
3001	Combining laser microdissection and RNA-seq to chart the transcriptional landscape of fungal development. <i>BMC Genomics</i> , 2012, 13, 511.	2.8	73
3002	Genome-wide classification and expression analysis of MYB transcription factor families in rice and <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2012, 13, 544.	2.8	450
3003	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	2.8	52
3004	Dynamics of domain coverage of the protein sequence universe. <i>BMC Genomics</i> , 2012, 13, 634.	2.8	10
3005	Complete genome sequence of <i>Enterococcus faecium</i> strain TX16 and comparative genomic analysis of <i>Enterococcus faecium</i> genomes. <i>BMC Microbiology</i> , 2012, 12, 135.	3.3	126
3006	The <i>gpsX</i> gene encoding a glycosyltransferase is important for polysaccharide production and required for full virulence in <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>BMC Microbiology</i> , 2012, 12, 31.	3.3	67
3007	ST proteins, a new family of plant tandem repeat proteins with a DUF2775 domain mainly found in Fabaceae and Asteraceae. <i>BMC Plant Biology</i> , 2012, 12, 207.	3.6	11
3008	The tomato RLK superfamily: phylogeny and functional predictions about the role of the LRRIL-RLK subfamily in antiviral defense. <i>BMC Plant Biology</i> , 2012, 12, 229.	3.6	119

#	ARTICLE	IF	CITATIONS
3009	Interactions of an Arabidopsis RanBPM homologue with LisH-CTLH domain proteins revealed high conservation of CTLH complexes in eukaryotes. BMC Plant Biology, 2012, 12, 83.	3.6	29
3010	Statistical discovery of site inter-dependencies in sub-molecular hierarchical protein structuring. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 8.	1.4	5
3011	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. Biology Direct, 2012, 7, 32.	4.6	19
3012	A Toll/IL-1R/resistance domain-containing thioredoxin regulates phagocytosis in Entamoeba histolytica. Parasites and Vectors, 2012, 5, 224.	2.5	3
3013	Detection of dengue group viruses by fluorescence in situ hybridization. Parasites and Vectors, 2012, 5, 243.	2.5	20
3014	Environmental and Evolutionary Genomics of Microbial Algae: Power and Challenges of Metagenomics. Advances in Botanical Research, 2012, 64, 383-427.	1.1	11
3015	Single-domain α -chymosins: the family history. Annals of the New York Academy of Sciences, 2012, 1269, 7-15.	3.8	2
3016	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	12.0	1,474
3017	Enhancing Protein Domain Detection Using Domain Co-occurrence and Domain Exclusion. , 2012, , .		0
3018	The PWAPA cassette: Intimate association of a PHD-like finger and a winged-helix domain in proteins included in histone-modifying complexes. Biochimie, 2012, 94, 2006-2012.	2.6	5
3019	A novel big protein TPRBK possessing 25 units of TPR motif is essential for the progress of mitosis and cytokinesis. Gene, 2012, 511, 202-217.	2.2	15
3020	Homepeptide Repeats: Implications for Protein Structure, Function and Evolution. Genomics, Proteomics and Bioinformatics, 2012, 10, 217-225.	6.9	11
3021	Epitopic hexapeptide sequences from Baltic cod parvalbumin beta (allergen Gad c 1) are common in the universal proteome. Peptides, 2012, 38, 105-109.	2.4	6
3022	Structure of a Novel Winged-Helix Like Domain from Human NFRKB Protein. PLoS ONE, 2012, 7, e43761.	2.5	5
3024	Using Bioinformatics to Develop and Test Hypotheses: E. coli -Specific Virulence Determinants. Journal of Microbiology and Biology Education, 2012, 13, 161-169.	1.0	5
3026	Evolutionary Biology of Dyneins. , 2012, , 88-121.		6
3027	Molecular basis for fungicidal action of neothyonidioside, a triterpene glycoside from the sea cucumber, Australostichopus mollis. Molecular BioSystems, 2012, 8, 902.	2.9	19
3028	Predicted essential proteins of Plasmodium falciparum for potential drug targets. Asian Pacific Journal of Tropical Medicine, 2012, 5, 352-354.	0.8	2

#	ARTICLE	IF	CITATIONS
3029	Transdifferentiation of MALME-3M and MCF-7 Cells toward Adipocyte-like Cells is Dependent on Clathrin-mediated Endocytosis. SpringerPlus, 2012, 1, 44.	1.2	5
3030	Auxin response factor gene family in Brassica rapa: genomic organization, divergence, expression, and evolution. Molecular Genetics and Genomics, 2012, 287, 765-784.	2.1	57
3031	Recognition Rules for Binding of Homeodomains to Operator DNA. Journal of Biomolecular Structure and Dynamics, 2012, 29, 715-731.	3.5	7
3032	Molecular Evolution of Translin Superfamily Proteins Within the Genomes of Eubacteria, Archaea and Eukaryotes. Journal of Molecular Evolution, 2012, 75, 155-167.	1.8	14
3033	HeurisFCP — A heuristic approach to Identify Frequent Contiguous Patterns (FCP) in Sequence Database. , 2012, , .		1
3034	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. BMC Bioinformatics, 2012, 13, S12.	2.6	542
3035	Prediction of novel long non-coding RNAs based on RNA-Seq data of mouse Klf1 knockout study. BMC Bioinformatics, 2012, 13, 331.	2.6	117
3036	P2TF: a comprehensive resource for analysis of prokaryotic transcription factors. BMC Genomics, 2012, 13, 628.	2.8	52
3037	The protein interaction network of a taxis signal transduction system in a Halophilic Archaeon. BMC Microbiology, 2012, 12, 272.	3.3	37
3038	Organellar proteomics reveals hundreds of novel nuclear proteins in the malaria parasite Plasmodium falciparum. Genome Biology, 2012, 13, R108.	9.6	139
3039	The H-factor as a novel quality metric for homology modeling. Journal of Clinical Bioinformatics, 2012, 2, 18.	1.2	6
3040	Intrinsic Disorder in the Human Spliceosomal Proteome. PLoS Computational Biology, 2012, 8, e1002641.	3.2	73
3041	The Landscape of the Prion Protein's Structural Response to Mutation Revealed by Principal Component Analysis of Multiple NMR Ensembles. PLoS Computational Biology, 2012, 8, e1002646.	3.2	11
3042	Pleiotropic Roles of a Ribosomal Protein in Dictyostelium discoideum. PLoS ONE, 2012, 7, e30644.	2.5	4
3043	Roles of Major Facilitator Superfamily Transporters in Phosphate Response in Drosophila. PLoS ONE, 2012, 7, e31730.	2.5	19
3044	The Genome of Ganderma lucidum Provide Insights into Triterpense Biosynthesis and Wood Degradation. PLoS ONE, 2012, 7, e36146.	2.5	78
3045	Mapping the Mutual Information Network of Enzymatic Families in the Protein Structure to Unveil Functional Features. PLoS ONE, 2012, 7, e41430.	2.5	33
3046	Structures of Human DPP7 Reveal the Molecular Basis of Specific Inhibition and the Architectural Diversity of Proline-Specific Peptidases. PLoS ONE, 2012, 7, e43019.	2.5	23

#	ARTICLE	IF	CITATIONS
3047	A Bioinformatic Strategy for the Detection, Classification and Analysis of Bacterial Autotransporters. PLoS ONE, 2012, 7, e43245.	2.5	65
3048	The <i>Aspergillus fumigatus</i> Dihydroxyacid Dehydratase Ilv3A/IlvC Is Required for Full Virulence. PLoS ONE, 2012, 7, e43559.	2.5	41
3049	Phylogenetic and Functional Metagenomic Profiling for Assessing Microbial Biodiversity in Environmental Monitoring. PLoS ONE, 2012, 7, e43630.	2.5	47
3050	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. PLoS ONE, 2012, 7, e43866.	2.5	60
3051	System Wide Analysis of the Evolution of Innate Immunity in the Nematode Model Species <i>Caenorhabditis elegans</i> and <i>Pristionchus pacificus</i> . PLoS ONE, 2012, 7, e44255.	2.5	52
3052	Genome-Wide Identification and Analysis of the TIFY Gene Family in Grape. PLoS ONE, 2012, 7, e44465.	2.5	104
3053	An Insight into the Sialotranscriptome of the Cat Flea, <i>Ctenocephalides felis</i> . PLoS ONE, 2012, 7, e44612.	2.5	34
3054	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. PLoS ONE, 2012, 7, e45307.	2.5	93
3055	Detailed Transcriptome Description of the Neglected Cestode <i>Taenia multiceps</i> . PLoS ONE, 2012, 7, e45830.	2.5	27
3056	A Walk into the LuxR Regulators of Actinobacteria: Phylogenomic Distribution and Functional Diversity. PLoS ONE, 2012, 7, e46758.	2.5	61
3057	Transcriptional Profiles of Mating-Responsive Genes from Testes and Male Accessory Glands of the Mediterranean Fruit Fly, <i>Ceratitis capitata</i> . PLoS ONE, 2012, 7, e46812.	2.5	40
3058	A Non-Linear Deterministic Model for Regulation of Diauxic Lag on Cellobiose by the Pneumococcal Multidomain Transcriptional Regulator CelR. PLoS ONE, 2012, 7, e47393.	2.5	12
3059	Metagenomic Profiling of Microbial Composition and Antibiotic Resistance Determinants in Puget Sound. PLoS ONE, 2012, 7, e48000.	2.5	50
3060	Insights into the Evolutionary Features of Human Neurodegenerative Diseases. PLoS ONE, 2012, 7, e48336.	2.5	10
3061	A New Protein Superfamily: TPPP-Like Proteins. PLoS ONE, 2012, 7, e49276.	2.5	20
3062	TgpA, a Protein with a Eukaryotic-Like Transglutaminase Domain, Plays a Critical Role in the Viability of <i>Pseudomonas aeruginosa</i> . PLoS ONE, 2012, 7, e50323.	2.5	12
3063	Contribution of Lateral Gene Transfers to the Genome Composition and Parasitic Ability of Root-Knot Nematodes. PLoS ONE, 2012, 7, e50875.	2.5	57
3064	Development of Transcriptomic Resources for Interrogating the Biosynthesis of Monoterpene Indole Alkaloids in Medicinal Plant Species. PLoS ONE, 2012, 7, e52506.	2.5	150

#	ARTICLE	IF	CITATIONS
3065	Protein Phylogenetic Analysis of Ca ²⁺ /cation Antiporters and Insights into their Evolution in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 1.	3.6	490
3066	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	3.6	73
3067	Plant Glycosyltransferases Beyond CAZy: A Perspective on DUF Families. <i>Frontiers in Plant Science</i> , 2012, 3, 59.	3.6	84
3068	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. <i>Frontiers in Genetics</i> , 2012, 3, 283.	2.3	220
3069	Comparative genomic and transcriptional analyses of CRISPR systems across the genus <i>Pyrobaculum</i> . <i>Frontiers in Microbiology</i> , 2012, 3, 251.	3.5	28
3070	Tissue-Specific Transcriptome Profiling of <i>Plutella Xylostella</i> Third Instar Larval Midgut. <i>International Journal of Biological Sciences</i> , 2012, 8, 1142-1155.	6.4	52
3071	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 89.	3.9	67
3072	An intelligent data pre-processing of complex datasets. <i>Intelligent Data Analysis</i> , 2012, 16, 305-325.	0.9	14
3073	Abiotic Stress Responses in Plants: A Focus on the SRO Family. , 2012, , .		3
3074	Wnt Signaling Network in Homo Sapiens. , 0, , .		2
3075	Genomic Characterization for Parasitic Weeds of the Genus <i>Striga</i> by Sample Sequence Analysis. <i>Plant Genome</i> , 2012, 5, .	2.8	15
3076	The REACT Suite: A Software Toolkit for Microbial REgulon Annotation and Comparative Transcriptomics. , 0, , .		0
3077	The Unique Endosomal/Lysosomal System of <i>Giardia lamblia</i> . , 2012, , .		1
3078	Prots: A fragment based protein thermoâ€stability potential. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 81-92.	2.6	27
3079	Cell surface proteome of the marine planctomycete <i>Scopelodopirellula baltica</i> . <i>Proteomics</i> , 2012, 12, 1781-1791.	2.2	13
3080	required to maintain repression2 Is a Novel Protein That Facilitates Locus-Specific Paramutation in Maize. <i>Plant Cell</i> , 2012, 24, 1761-1775.	6.6	33
3081	Molecular Signatures of the Three Stem Cell Lineages in Hydra and the Emergence of Stem Cell Function at the Base of Multicellularity. <i>Molecular Biology and Evolution</i> , 2012, 29, 3267-3280.	8.9	140
3082	Characterization of the CRISPR/Cas Subtype I-A System of the Hyperthermophilic Crenarchaeon <i>Thermoproteus tenax</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2491-2500.	2.2	98

#	ARTICLE	IF	CITATIONS
3083	XatA, an ATP-binding autotransporter important for the virulence of <i>Xylella fastidiosa</i> . <i>MicrobiologyOpen</i> , 2012, 1, 33-45.	3.0	33
3084	Genome-wide and molecular evolution analysis of the <i>o</i> plax <i>K</i> <i>HAK</i> <i>KUP</i> potassium transporter gene family. <i>Ecology and Evolution</i> , 2012, 2, 1996-2004.	1.9	48
3085	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1798-1807.	3.3	19
3086	A Decade of the Human Genome Sequence—How Does the Medicinal Chemist Benefit?. <i>ChemMedChem</i> , 2012, 7, 194-203.	3.2	19
3087	A field guide to eukaryotic circular single-stranded DNA viruses: insights gained from metagenomics. <i>Archives of Virology</i> , 2012, 157, 1851-1871.	2.1	254
3088	QTLs for agronomic and cell wall traits in a maize RIL progeny derived from a cross between an old Minnesota13 line and a modern Iodent line. <i>Theoretical and Applied Genetics</i> , 2012, 125, 531-549.	3.6	41
3089	Structural and functional dissection of aminocoumarin antibiotic biosynthesis: a review. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 125-133.	1.2	4
3090	Synergy of multi-label hierarchical ensembles, data fusion, and cost-sensitive methods for gene functional inference. <i>Machine Learning</i> , 2012, 88, 209-241.	5.4	67
3091	A Study on Mutational Dynamics of Simple Sequence Repeats in Relation to Mismatch Repair System in Prokaryotic Genomes. <i>Journal of Molecular Evolution</i> , 2012, 74, 127-139.	1.8	7
3092	Two-component signal transduction in <i>Corynebacterium glutamicum</i> and other corynebacteria: on the way towards stimuli and targets. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1131-1150.	3.6	35
3093	Sucrose synthase in unicellular cyanobacteria and its relationship with salt and hypoxic stress. <i>Planta</i> , 2012, 235, 955-964.	3.2	45
3094	WUSCHEL-related genes are expressed during somatic embryogenesis of the basal angiosperm <i>Ocotea catharinensis</i> Mez. (Lauraceae). <i>Trees - Structure and Function</i> , 2012, 26, 493-501.	1.9	14
3095	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.	3.0	25
3096	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.	2.2	23
3097	A leucine-rich repeat receptor-like kinase gene is involved in the specification of outer cell layers in rice roots. <i>Plant Journal</i> , 2012, 69, 565-576.	5.7	21
3098	Experimental and analytical tools for studying the human microbiome. <i>Nature Reviews Genetics</i> , 2012, 13, 47-58.	16.3	601
3099	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. <i>FEMS Microbiology Ecology</i> , 2012, 79, 785-799.	2.7	130
3100	Conserved domains and evolution of secreted phospholipases A ₂ . <i>FEBS Journal</i> , 2012, 279, 636-649.	4.7	27

#	ARTICLE	IF	CITATIONS
3101	Ferlins: Regulators of Vesicle Fusion for Auditory Neurotransmission, Receptor Trafficking and Membrane Repair. <i>Traffic</i> , 2012, 13, 185-194.	2.7	119
3102	Detecting disease genes based on semi-supervised learning and protein-protein interaction networks. <i>Artificial Intelligence in Medicine</i> , 2012, 54, 63-71.	6.5	59
3103	A hyper-heuristic for the Longest Common Subsequence problem. <i>Computational Biology and Chemistry</i> , 2012, 36, 42-54.	2.3	22
3104	In silico sequence and structure analysis for mycobacteriophages. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2012, 2, S377-S379.	1.2	0
3105	Ecological structuring of bacterial and archaeal taxa in surface ocean waters. <i>FEMS Microbiology Ecology</i> , 2012, 81, 373-385.	2.7	22
3106	Functional bias of positively selected genes in <i>Streptococcus</i> genomes. <i>Infection, Genetics and Evolution</i> , 2012, 12, 274-277.	2.3	3
3107	Horizontal gene transfer confers fermentative metabolism in the respiratory-deficient plant trypanosomatid <i>Phytomonas serpens</i> . <i>Infection, Genetics and Evolution</i> , 2012, 12, 539-548.	2.3	5
3108	Immobilization of a recombinant endo-1,5-arabinanase secreted by <i>Aspergillus nidulans</i> strain A773. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2012, , .	1.8	2
3109	A novel quadripartite dsRNA virus isolated from a phytopathogenic filamentous fungus, <i>Rosellinia necatrix</i> . <i>Virology</i> , 2012, 426, 42-50.	2.4	87
3110	The ± 2 helix in the DNA ligase IV BRCT-1 domain is required for targeted degradation of ligase IV during adenovirus infection. <i>Virology</i> , 2012, 428, 128-135.	2.4	5
3111	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 637-648.	2.5	22
3112	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 744-750.	0.7	11
3113	A conformational switch controls cell wall-remodelling enzymes required for bacterial cell division. <i>Molecular Microbiology</i> , 2012, 85, 768-781.	2.5	98
3114	Beyond the genome: recent advances in <i>Toxoplasma gondii</i> functional genomics. <i>Parasite Immunology</i> , 2012, 34, 80-89.	1.5	9
3115	Polygalacturonase-inhibiting proteins - leucine-rich repeat proteins in plant defence. <i>Plant Biology</i> , 2012, 14, 22-30.	3.8	12
3116	A systematic comparison of genome-scale clustering algorithms. <i>BMC Bioinformatics</i> , 2012, 13, S7.	2.6	55
3117	Discovering patterns in drug-protein interactions based on their fingerprints. <i>BMC Bioinformatics</i> , 2012, 13, S4.	2.6	10
3118	Predict impact of single amino acid change upon protein structure. <i>BMC Genomics</i> , 2012, 13, S4.	2.8	48

#	ARTICLE	IF	CITATIONS
3119	Domain landscapes of somatic mutations in cancer. <i>BMC Genomics</i> , 2012, 13, S9.	2.8	51
3120	Inferring domain-domain interactions from protein-protein interactions in the complex network conformation. <i>BMC Systems Biology</i> , 2012, 6, S7.	3.0	8
3121	Characterization of Xyn10J, a Novel Family 10 Xylanase from a Compost Metagenomic Library. <i>Applied Biochemistry and Biotechnology</i> , 2012, 166, 1328-1339.	2.9	38
3122	Genome-scale identification of resistance gene analogs and the development of their intron length polymorphism markers in maize. <i>Molecular Breeding</i> , 2012, 29, 437-447.	2.1	23
3123	Putative xylosyltransferase genes in <i>Trichomonas vaginalis</i> . <i>Soft Computing</i> , 2012, 16, 381-391.	3.6	0
3124	SignatureClust: a tool for landmark gene-guided clustering. <i>Soft Computing</i> , 2012, 16, 411-418.	3.6	0
3125	Immunoglobulin domains in <i>Escherichia coli</i> and other enterobacteria: from pathogenesis to applications in antibody technologies. <i>FEMS Microbiology Reviews</i> , 2013, 37, 204-250.	8.6	84
3126	Interactome map uncovers phosphatidylserine transport by oxysterol-binding proteins. <i>Nature</i> , 2013, 501, 257-261.	27.8	279
3127	A human skeletal muscle interactome centered on proteins involved in muscular dystrophies: LGMD interactome. <i>Skeletal Muscle</i> , 2013, 3, 3.	4.2	36
3128	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.	2.3	22
3129	Comparative docking and ADMET study of some curcumin derivatives and herbal congeners targeting β -amyloid. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 13-27.	2.1	30
3130	Genome-Wide Analysis of Mitogen-Activated Protein Kinase Gene Family in Maize. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1446-1460.	1.8	74
3131	The family based variability in protein family expansion. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 121.	0.2	0
3132	Environmental responses and the control of iron homeostasis in fungal systems. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 939-955.	3.6	25
3133	IS-Dom: a dataset of independent structural domains automatically delineated from protein structures. <i>Journal of Computer-Aided Molecular Design</i> , 2013, 27, 419-426.	2.9	2
3134	Functional inference by ProtoNet family tree: the uncharacterized proteome of <i>Daphnia pulex</i> . <i>BMC Bioinformatics</i> , 2013, 14, S11.	2.6	1
3135	Inferring homologous protein-protein interactions through pair position specific scoring matrix. <i>BMC Bioinformatics</i> , 2013, 14, S11.	2.6	4
3136	Mining for class-specific motifs in protein sequence classification. <i>BMC Bioinformatics</i> , 2013, 14, 96.	2.6	21

#	ARTICLE	IF	CITATIONS
3137	Redundancy in electronic health record corpora: analysis, impact on text mining performance and mitigation strategies. BMC Bioinformatics, 2013, 14, 10.	2.6	80
3138	Transcriptome sequencing and de novo annotation of the critically endangered Adriatic sturgeon. BMC Genomics, 2013, 14, 407.	2.8	71
3139	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. BMC Genomics, 2013, 14, 379.	2.8	4
3140	Frequent loss of lineages and deficient duplications accounted for low copy number of disease resistance genes in Cucurbitaceae. BMC Genomics, 2013, 14, 335.	2.8	74
3141	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phytohormones in the resistance reaction. BMC Genomics, 2013, 14, 322.	2.8	56
3142	Genome-wide identification, characterization and expression analysis of populusleucine-rich repeat receptor-like protein kinase genes. BMC Genomics, 2013, 14, 318.	2.8	75
3143	P2RP: a web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. BMC Genomics, 2013, 14, 269.	2.8	69
3144	Genome sequencing of bacteria: sequencing, de novo assembly and rapid analysis using open source tools. BMC Genomics, 2013, 14, 211.	2.8	43
3145	5'-Serial Analysis of Gene Expression studies reveal a transcriptomic switch during fruiting body development in Coprinopsis cinerea. BMC Genomics, 2013, 14, 195.	2.8	65
3146	Draft genome sequence of the male-killing Wolbachia strain wBol1 reveals recent horizontal gene transfers from diverse sources. BMC Genomics, 2013, 14, 20.	2.8	65
3147	Pharmacophore Binding Motifs for Nicotinamide Adenine Dinucleotide Analogues Across Multiple Protein Families: A Detailed Contact-Based Analysis of the Interaction between Proteins and NAD(P) Cofactors. Journal of Medicinal Chemistry, 2013, 56, 6175-6189.	6.4	11
3148	Microtubule Affinity-Regulating Kinase 4: Structure, Function, and Regulation. Cell Biochemistry and Biophysics, 2013, 67, 485-499.	1.8	94
3149	Genome-Wide Analysis of Nucleotide-Binding Site (NBS) Disease Resistance (R) Genes in Sacred Lotus (Nelumbo nucifera Gaertn.) Reveals Their Transition Role During Early Evolution of Land Plants. Tropical Plant Biology, 2013, 6, 98-116.	1.9	10
3150	Genome-wide identification and expression profiling of ankyrin-repeat gene family in maize. Development Genes and Evolution, 2013, 223, 303-318.	0.9	29
3151	Long Noncoding RNA: a New Player of Heart Failure?. Journal of Cardiovascular Translational Research, 2013, 6, 876-883.	2.4	101
3152	Serine/threonine kinases and E2-ubiquitin conjugating enzymes in Planctomycetes: unexpected findings. Antonie Van Leeuwenhoek, 2013, 104, 509-520.	1.7	12
3153	Cloning of dfdA genes from Terrabacter sp. strain DBF63 encoding dibenzofuran 4,4a-dioxygenase and heterologous expression in Streptomyces lividans. Applied Microbiology and Biotechnology, 2013, 97, 4485-4498.	3.6	13
3154	A second quadrivirus strain from the phytopathogenic filamentous fungus Rosellinia necatrix. Archives of Virology, 2013, 158, 1093-1098.	2.1	34

#	ARTICLE	IF	CITATIONS
3155	The role of the N-terminal loop in the function of the colicin E7 nuclease domain. <i>Journal of Biological Inorganic Chemistry</i> , 2013, 18, 309-321.	2.6	13
3156	Detection of African swine fever virus-like sequences in ponds in the Mississippi Delta through metagenomic sequencing. <i>Virus Genes</i> , 2013, 46, 441-446.	1.6	21
3157	Predominant archaea in marine sediments degrade detrital proteins. <i>Nature</i> , 2013, 496, 215-218.	27.8	526
3158	Mutation study of DsrM from <i>Allochromatium vinosum</i> using the amino acid sequences. <i>Meta Gene</i> , 2013, 1, 33-42.	0.6	0
3159	Interplay of flagellar motility and mucin degradation stimulates the uassociation of <i>Pseudomonas aeruginosa</i> with human epithelial colorectal adenocarcinoma (Caco-2) cells. <i>Journal of Infection and Chemotherapy</i> , 2013, 19, 305-315.	1.7	15
3160	Comparative evaluation of commercially available homology modelling tools: A structural bioinformatics perspective. <i>Drug Invention Today (discontinued)</i> , 2013, 5, 207-211.	0.6	2
3161	PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. <i>Pain</i> , 2013, 154, 2586e1-2586e12.	4.2	50
3162	Microcephaly Thin Corpus Callosum Intellectual Disability Syndrome Caused by Mutated TAF2. <i>Pediatric Neurology</i> , 2013, 49, 411-416.e1.	2.1	36
3163	PPM-Dom: A novel method for domain position prediction. <i>Computational Biology and Chemistry</i> , 2013, 47, 8-15.	2.3	3
3164	Isolation and characterization of a carrot nucleolar protein with structural and sequence similarity to the vertebrate PESCADILLO protein. <i>Plant Science</i> , 2013, 208, 83-92.	3.6	0
3165	Computational determination of the orientation of a heat repeat-like domain of DNA-PKcs. <i>Computational Biology and Chemistry</i> , 2013, 42, 1-4.	2.3	1
3166	Cloning, molecular characterization, and expression analysis of the signal transducer and activator of transcription 3 (STAT3) gene from grass carp (<i>Ctenopharyngodon idellus</i>). <i>Fish and Shellfish Immunology</i> , 2013, 35, 1624-1634.	3.6	13
3167	Succinct interval-splitting tree for scalable similarity search of compound-protein pairs with property constraints. , 2013, , .		3
3168	IntApop: A web service for predicting apoptotic protein interactions in humans. <i>BioSystems</i> , 2013, 114, 238-244.	2.0	4
3169	Identification and Characterization of Five New Molecular Serogroups of <i>Cronobacter</i> spp.. <i>Foodborne Pathogens and Disease</i> , 2013, 10, 343-352.	1.8	37
3170	Atomistic Modelling of Phosphopeptide Recognition for Modular Domains. <i>Annual Reports in Computational Chemistry</i> , 2013, 9, 61-84.	1.7	1
3171	Identification and expression analysis of primary auxin-responsive Aux/IAA gene family in cucumber (<i>Cucumis sativus</i>). <i>Journal of Genetics</i> , 2013, 92, 513-521.	0.7	31
3172	LaAP2L1, a Heterosis-Associated AP2/EREBP Transcription Factor of <i>Larix</i> , Increases Organ Size and Final Biomass by Affecting Cell Proliferation in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2013, 54, 1822-1836.	3.1	33

#	ARTICLE	IF	CITATIONS
3173	PepBind: A Comprehensive Database and Computational Tool for Analysis of Protein-peptide Interactions. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 241-246.	6.9	72
3174	Residue correlation networks in nuclear receptors reflect functional specialization and the formation of the nematode-specific P-box. <i>BMC Genomics</i> , 2013, 14, S1.	2.8	5
3175	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.	2.8	109
3176	Understanding the sequential activation of Type III and Type VI Secretion Systems in <i>Salmonella typhimurium</i> using Boolean modeling. <i>Gut Pathogens</i> , 2013, 5, 28.	3.4	12
3177	Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (<i>Brassica</i>) Tj ETQq0 0 0 rgBT /Overlook 10 Tf 5	2.8	172
3178	Insight into the specific virulence related genes and toxin-antitoxin virulent pathogenicity islands in swine streptococcosis pathogen <i>Streptococcus equi</i> ssp. <i>zooepidemicus</i> strain ATCC35246. <i>BMC Genomics</i> , 2013, 14, 377.	2.8	23
3179	Fast error-tolerant quartet phylogeny algorithms. <i>Theoretical Computer Science</i> , 2013, 483, 104-114.	0.9	2
3180	Graph representation of high-dimensional alpha-helical membrane protein data. <i>BioData Mining</i> , 2013, 6, 21.	4.0	2
3181	Inferring protein domains associated with drug side effects based on drug-target interaction network. <i>BMC Systems Biology</i> , 2013, 7, S18.	3.0	23
3182	Scalable prediction of compound-protein interactions using minwise hashing. <i>BMC Systems Biology</i> , 2013, 7, S3.	3.0	37
3183	Transferring functional annotations of membrane transporters on the basis of sequence similarity and sequence motifs. <i>BMC Bioinformatics</i> , 2013, 14, 343.	2.6	20
3184	Phylogenomic analysis of Cation Diffusion Facilitator proteins uncovers Ni ²⁺ /Co ²⁺ transporters. <i>Metallomics</i> , 2013, 5, 1634.	2.4	60
3185	Two novel circo-like viruses detected in human feces: complete genome sequencing and electron microscopy analysis. <i>Virus Research</i> , 2013, 178, 364-373.	2.2	17
3186	Molecular cloning and characterization of major vault protein of <i>Echinococcus multilocularis</i> . <i>Experimental Parasitology</i> , 2013, 134, 102-108.	1.2	2
3187	ProtoNet: charting the expanding universe of protein sequences. <i>Nature Biotechnology</i> , 2013, 31, 290-292.	17.5	14
3188	Drug-Domain Interaction Networks in Myocardial Infarction. <i>IEEE Transactions on Nanobioscience</i> , 2013, 12, 182-188.	3.3	2
3189	GPU-Accelerated Protein Family Identification for Metagenomics. , 2013, , .		1
3190	Genetic determinants of swimming motility in the squid light organ symbiont <i>Vibrio fischeri</i> . <i>MicrobiologyOpen</i> , 2013, 2, 576-594.	3.0	58

#	ARTICLE	IF	CITATIONS
3191	Prediction of enzymatic activity of proteins based on structural and functional domains. , 2013, , .		1
3192	Characterization of a β -glucan recognition protein from the beet armyworm, <i>Spodoptera exigua</i> (Insecta: Lepidoptera: Noctuidae). <i>Insect Science</i> , 2013, 20, 575-584.	3.0	11
3193	Modeling the calcium and phosphate mineralization of American lobster cuticle. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 1601-1611.	1.4	13
3194	Mercury Methylation by the Methanogen <i>Methanospirillum hungatei</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 6325-6330.	3.1	119
3195	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	3.1	98
3196	Optimizing Big Data in Bioinformatics with Swarm Algorithms. , 2013, , .		8
3197	Identifying essential proteins based on protein domains in protein-protein interaction networks. , 2013, , .		3
3198	Cc.snf5, a gene encoding a putative component of the SWI/SNF chromatin remodeling complex, is essential for sexual development in the agaricomycete <i>Coprinopsis cinerea</i> . <i>Fungal Genetics and Biology</i> , 2013, 50, 82-89.	2.1	20
3199	LepChorionDB, a database of Lepidopteran chorion proteins and a set of tools useful for the identification of chorion proteins in Lepidopteran proteomes. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 189-196.	2.7	8
3200	Discovering Interacting Domains and Motifs in Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2013, 939, 9-20.	0.9	4
3201	Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature. <i>Natural Product Reports</i> , 2013, 30, 108-160.	10.3	1,692
3202	Mapping and candidate-gene screening of the novel Turnip mosaic virus resistance gene <i>retr02</i> in Chinese cabbage (<i>Brassica rapa</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 179-188.	3.6	47
3203	Density peaks of paralog pairs in human and mouse genomes. <i>Gene</i> , 2013, 527, 55-61.	2.2	3
3204	<i>Staphylococcus aureus</i> TMPK and TK showing distinct structural differences with human TMPK and TK – A probable explanation in the pathogenesis. <i>Journal of Pharmacy Research</i> , 2013, 7, 89-95.	0.4	0
3205	Identification of Immunity-related Genes in <i>Arabidopsis</i> and Cassava Using Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 345-353.	6.9	8
3206	Goose Toll-like receptor 7 (TLR7), myeloid differentiation factor 88 (MyD88) and antiviral molecules involved in anti-H5N1 highly pathogenic avian influenza virus response. <i>Veterinary Immunology and Immunopathology</i> , 2013, 153, 99-106.	1.2	22
3207	Protein dynamics – a moving target. <i>Physics of Life Reviews</i> , 2013, 10, 27-28.	2.8	2
3208	A proteomics approach to detect tissue-wide adaptive changes in the pancreas associated with increased pancreatic α -amylase activity in domestic cattle (<i>Bos taurus</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2013, 8, 65-71.	1.0	2

#	ARTICLE	IF	CITATIONS
3209	Cooperative scheduling mechanism for large-scale peer-to-peer computing systems. <i>Journal of Network and Computer Applications</i> , 2013, 36, 1620-1631.	9.1	14
3210	Her2p molecular modeling, mutant analysis and intramitochondrial localization. <i>Fungal Genetics and Biology</i> , 2013, 60, 133-139.	2.1	7
3211	Position-specific scoring matrix and hidden Markov model complement each other for the prediction of conopeptide superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 717-724.	2.3	12
3212	Characterization and disruption of the <i>cipC</i> gene in the ochratoxigenic fungus <i>Aspergillus carbonarius</i> . <i>Food Research International</i> , 2013, 54, 697-705.	6.2	18
3213	The photoconvertible water-soluble chlorophyll-binding protein of <i>Chenopodium album</i> is a member of DUF538, a superfamily that distributes in Embryophyta. <i>Journal of Plant Physiology</i> , 2013, 170, 1549-1552.	3.5	21
3214	Bcl2-associated Athanogene 3 Interactome Analysis Reveals a New Role in Modulating Proteasome Activity. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2804-2819.	3.8	62
3215	The superfamily of mitochondrial Complex1_LYR motif-containing (LYRM) proteins. <i>Biochemical Society Transactions</i> , 2013, 41, 1335-1341.	3.4	49
3216	Identification of Lysine Succinylation Substrates and the Succinylation Regulatory Enzyme CobB in <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3509-3520.	3.8	236
3217	A Zinc Lock on GGDEF Domain Dimerization Inhibits <i>E. coli</i> Biofilms. <i>Structure</i> , 2013, 21, 1067-1068.	3.3	1
3218	Helix Bundle Loops Determine Whether Histidine Kinases Autophosphorylate in cis or in trans. <i>Journal of Molecular Biology</i> , 2013, 425, 1198-1209.	4.2	61
3219	Genome-scale analysis of the metabolic networks of oleaginous Zygomycete fungi. <i>Gene</i> , 2013, 521, 180-190.	2.2	41
3220	Rho participates in chemoreceptor-induced changes in morphology to hair bundle mechanoreceptors of the sea anemone, <i>Nematostella vectensis</i> . <i>Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology</i> , 2013, 165, 139-148.	1.8	5
3221	Identification of susceptibility modules for coronary artery disease using a genome wide integrated network analysis. <i>Gene</i> , 2013, 531, 347-354.	2.2	17
3222	Regulation of ethylene biosynthesis at the level of 1-aminocyclopropane-1-carboxylate oxidase (ACO) gene. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 295-307.	2.1	94
3223	<sc>G</sc>sm<sc>R</sc>, a response regulator with an <sc>HD</sc>-related output domain in <i><sc>X</sc>anthomonas<sc>Acampestris</i>, is positively controlled by <sc>C</sc>lp and is involved in the expression of genes responsible for flagellum synthesis. <i>FEBS Journal</i> , 2013, 280, 199-213.	4.7	16
3224	Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.	3.8	99
3225	A Time to Scatter Genes and a Time to Gather Them. <i>Advances in Botanical Research</i> , 2013, 66, 1-35.	1.1	8
3226	Untangling the transcriptome from fungus-infected plant tissues. <i>Gene</i> , 2013, 519, 238-244.	2.2	6

#	ARTICLE	IF	CITATIONS
3227	Bioinformatics challenges in de novo transcriptome assembly using short read sequences in the absence of a reference genome sequence. <i>Natural Product Reports</i> , 2013, 30, 490.	10.3	62
3228	Global analysis of transcriptional regulators in <i>Staphylococcus aureus</i> . <i>BMC Genomics</i> , 2013, 14, 126.	2.8	66
3229	Bioinformatic survey for new physiological substrates of Cyclin-dependent kinase 5. <i>Genomics</i> , 2013, 101, 221-228.	2.9	13
3230	The acetylproteome of Gram-positive model bacterium <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2013, 13, 1726-1736.	2.2	115
3231	SH3 interactome conserves general function over specific form. <i>Molecular Systems Biology</i> , 2013, 9, 652.	7.2	61
3232	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to <i>Phytophthora infestans</i> . <i>Genomics</i> , 2013, 101, 249-255.	2.9	7
3233	Ecology of marine Bacteroidetes: a comparative genomics approach. <i>ISME Journal</i> , 2013, 7, 1026-1037.	9.8	614
3234	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.	2.0	20
3235	Recognition of Nontrivial Remote Homology Relationships Involving Proteins of <i>Helicobacter pylori</i> : Implications for Function Recognition. <i>Methods in Molecular Biology</i> , 2013, 993, 155-175.	0.9	0
3236	Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and development. <i>Toxicology and Applied Pharmacology</i> , 2013, 270, 149-157.	2.8	61
3237	Genome-wide identification and analysis of the B3 superfamily of transcription factors in Brassicaceae and major crop plants. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1305-1319.	3.6	42
3238	Novel inositol catabolic pathway in <i>Thermotoga maritima</i> . <i>Environmental Microbiology</i> , 2013, 15, 2254-2266.	3.8	23
3239	Identification of Human Protein Interaction Domains using an ORFeome-based Yeast Two-hybrid Fragment Library. <i>Journal of Proteome Research</i> , 2013, 12, 3181-3192.	3.7	14
3240	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	7.2	253
3241	Rational-Based Protein Engineering: Tips and Tools. <i>Methods in Molecular Biology</i> , 2013, 996, 233-250.	0.9	2
3242	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	17.5	1,176
3243	Genetic diversity in cultured and wild marine cyanomyoviruses reveals phosphorus stress as a strong selective agent. <i>ISME Journal</i> , 2013, 7, 1827-1841.	9.8	67
3244	Protein Engineering and Stabilization from Sequence Statistics. <i>Methods in Enzymology</i> , 2013, 523, 237-256.	1.0	25

#	ARTICLE	IF	CITATIONS
3245	Paleoproteomic study of the Iceman's brain tissue. Cellular and Molecular Life Sciences, 2013, 70, 3709-3722.	5.4	44
3246	wksl3, a New Biocontrol Agent for Salmonella enterica Serovars Enteritidis and Typhimurium in Foods: Characterization, Application, Sequence Analysis, and Oral Acute Toxicity Study. Applied and Environmental Microbiology, 2013, 79, 1956-1968.	3.1	75
3247	RECENT ADVANCES IN FUNCTIONAL REGION PREDICTION BY USING STRUCTURAL AND EVOLUTIONARY INFORMATION " REMAINING PROBLEMS AND FUTURE EXTENSIONS. Computational and Structural Biotechnology Journal, 2013, 8, e201308007.	4.1	8
3248	Emergence of novel domains in proteins. BMC Evolutionary Biology, 2013, 13, 47.	3.2	36
3249	Zinc Biochemistry: From a Single Zinc Enzyme to a Key Element of Life. Advances in Nutrition, 2013, 4, 82-91.	6.4	550
3251	Functional comparisons of proteins using the wavelet packet transform. , 2013, , .		0
3252	Inferring Chemogenomic Features from Drug-Target Interaction Networks. Molecular Informatics, 2013, 32, 991-999.	2.5	8
3253	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. ISME Journal, 2013, 7, 2287-2300.	9.8	113
3254	Viral Metagenome Annotation Pipeline. , 2013, , 1-12.		1
3255	Shape evolution with temperature of a thermotolerant protein (<i>PeaT</i> 1) in solution detected by small angle X-ray scattering. Proteins: Structure, Function and Bioinformatics, 2013, 81, 53-62.	2.6	3
3256	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. Intrinsically Disordered Proteins, 2013, 1, e25724.	1.9	12
3257	High-Quality Draft Genome Sequence of Vagococcus lutrae Strain LBD1, Isolated from the Largemouth Bass <i>Micropterus salmoides</i>. Genome Announcements, 2013, 1, .	0.8	8
3258	Draft Genome Sequence of Rhodococcus opacus Strain M213 Shows a Diverse Catabolic Potential. Genome Announcements, 2013, 1, .	0.8	10
3259	Kl. Comparison between Using Linear and Non-linear Features to Classify Uterine Electromyography Signals of Term and Preterm Deliveries. , 2013, , .		4
3260	Improving the Prediction of Kinase Binding Affinity Using Homology Models. , 2013, , .		2
3261	Evolution of Animal and Plant Dicers: Early Parallel Duplications and Recurrent Adaptation of Antiviral RNA Binding in Plants. Molecular Biology and Evolution, 2013, 30, 627-641.	8.9	138
3262	Conformational Coupling between Receptor and Kinase Binding Sites through a Conserved Salt Bridge in a Signaling Complex Scaffold Protein. PLoS Computational Biology, 2013, 9, e1003337.	3.2	13
3263	Defining the Core Proteome of the Chloroplast Envelope Membranes. Frontiers in Plant Science, 2013, 4, 11.	3.6	75

#	ARTICLE	IF	CITATIONS
3264	Investigating the beneficial traits of <i>Trichoderma hamatum</i> GD12 for sustainable agriculture—insights from genomics. <i>Frontiers in Plant Science</i> , 2013, 4, 258.	3.6	119
3265	A contribution to the study of plant development evolution based on gene co-expression networks. <i>Frontiers in Plant Science</i> , 2013, 4, 291.	3.6	22
3266	A comparison of the molecular organization of genomic regions associated with resistance to common bacterial blight in two <i>Phaseolus vulgaris</i> genotypes. <i>Frontiers in Plant Science</i> , 2013, 4, 318.	3.6	14
3267	Functional Analysis of Pneumococcal Drug Efflux Pumps Associates the MATE DinF Transporter with Quinolone Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 248-253.	3.2	37
3268	Comparative Genomic Analysis of the Endosymbionts of Herbivorous Insects Reveals Eco-Environmental Adaptations: Biotechnology Applications. <i>PLoS Genetics</i> , 2013, 9, e1003131.	3.5	56
3269	Discovery of diversity in xylan biosynthetic genes by transcriptional profiling of a heteroxylan containing mucilaginous tissue. <i>Frontiers in Plant Science</i> , 2013, 4, 183.	3.6	31
3270	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. <i>Genome Research</i> , 2013, 23, 1271-1282.	5.5	338
3271	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. <i>Bioinformatics</i> , 2013, 29, 1577-1579.	4.1	129
3272	KIDFamMap: a database of kinase-inhibitor-disease family maps for kinase inhibitor selectivity and binding mechanisms. <i>Nucleic Acids Research</i> , 2013, 41, D430-D440.	14.5	23
3273	The pneumococcal MgaSpn virulence transcriptional regulator generates multimeric complexes on linear double-stranded DNA. <i>Nucleic Acids Research</i> , 2013, 41, 6975-6991.	14.5	30
3274	Immune response of the Caribbean sea fan, <i>Gorgonia ventalina</i> , exposed to an <i>Aplanochytrium</i> parasite as revealed by transcriptome sequencing. <i>Frontiers in Physiology</i> , 2013, 4, 180.	2.8	58
3275	Phylogenetic Study of Polyketide Synthases and Nonribosomal Peptide Synthetases Involved in the Biosynthesis of Mycotoxins. <i>Toxins</i> , 2013, 5, 717-742.	3.4	86
3276	Short Toxin-like Proteins Attack the Defense Line of Innate Immunity. <i>Toxins</i> , 2013, 5, 1314-1331.	3.4	14
3277	The Genome and Development-Dependent Transcriptomes of <i>Pyronema confluens</i> : A Window into Fungal Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003820.	3.5	85
3278	Mutations in the UQCC1-Interacting Protein, UQCC2, Cause Human Complex III Deficiency Associated with Perturbed Cytochrome b Protein Expression. <i>PLoS Genetics</i> , 2013, 9, e1004034.	3.5	96
3279	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. <i>International Journal of Molecular Sciences</i> , 2013, 14, 15423-15458.	4.1	22
3280	Structural Disorder Provides Increased Adaptability for Vesicle Trafficking Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1003144.	3.2	46
3281	The Genome of <i>Spraguea lophii</i> and the Basis of Host-Microsporidian Interactions. <i>PLoS Genetics</i> , 2013, 9, e1003676.	3.5	66

#	ARTICLE	IF	CITATIONS
3282	TRIAD1 and HHARI bind to and are activated by distinct neddylated Cullin-RING ligase complexes. EMBO Journal, 2013, 32, 2848-2860.	7.8	84
3283	Combinatorial Clustering of Residue Position Subsets Predicts Inhibitor Affinity across the Human Kinome. PLoS Computational Biology, 2013, 9, e1003087.	3.2	14
3284	Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining. PLoS Pathogens, 2013, 9, e1003745.	4.7	90
3285	Construction of a rice glycoside hydrolase phylogenomic database and identification of targets for biofuel research. Frontiers in Plant Science, 2013, 4, 330.	3.6	35
3286	Structure and Function of a Novel <scp>Id</scp> -Carboxypeptidase A Involved in Peptidoglycan Recycling. Journal of Bacteriology, 2013, 195, 5555-5566.	2.2	16
3287	Systems biology methods and developments of filamentous fungi in relation to the production of food ingredients. , 2013, , 19-41.		0
3288	The Shells of BMC-Type Microcompartment Organelles in Bacteria. Journal of Molecular Microbiology and Biotechnology, 2013, 23, 290-299.	1.0	56
3289	Rfam 11.0: 10 years of RNA families. Nucleic Acids Research, 2013, 41, D226-D232.	14.5	745
3290	The Genetic Architecture of Degenerin/Epithelial Sodium Channels in<i>Drosophila</i>. G3: Genes, Genomes, Genetics, 2013, 3, 441-450.	1.8	85
3291	CG methylated microarrays identify a novel methylated sequence bound by the CEBPB ATF4 heterodimer that is active in vivo. Genome Research, 2013, 23, 988-997.	5.5	111
3292	FunGene: the functional gene pipeline and repository. Frontiers in Microbiology, 2013, 4, 291.	3.5	518
3293	Strategies and molecular tools to fight antimicrobial resistance: resistome, transcriptome, and antimicrobial peptides. Frontiers in Microbiology, 2013, 4, 412.	3.5	51
3294	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. Nucleic Acids Research, 2013, 41, D445-D451.	14.5	99
3295	Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387.	3.5	71
3296	A transcriptional regulator linking quorum sensing and chitin induction to render Vibrio cholerae naturally transformable. Nucleic Acids Research, 2013, 41, 3644-3658.	14.5	111
3297	A comparison of dense transposon insertion libraries in the Salmonella serovars Typhi and Typhimurium. Nucleic Acids Research, 2013, 41, 4549-4564.	14.5	108
3298	Structural studies of<i>Pseudomonas</i>and<i>Chromobacterium</i>γ-aminotransferases provide insights into their differing substrate specificity. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 564-576.	2.5	51
3299	Structure of Neisseria meningitidis lipoprotein GNA1162. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 362-368.	0.7	6

#	ARTICLE	IF	CITATIONS
3300	Crystallization and preliminary crystallographic analysis of an <i>Escherichia coli</i> -selected mutant of the nuclease domain of the metallo-nuclease colicin E7. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 551-554.	0.7	2
3301	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. <i>Journal of Bacteriology</i> , 2013, 195, 4466-4475.	2.2	16
3302	The <i>Escherichia coli</i> Lpt Transenvelope Protein Complex for Lipopolysaccharide Export Is Assembled via Conserved Structurally Homologous Domains. <i>Journal of Bacteriology</i> , 2013, 195, 1100-1108.	2.2	90
3303	Genes involved in host-parasite interactions can be revealed by their correlated expression. <i>Nucleic Acids Research</i> , 2013, 41, 1508-1518.	14.5	38
3304	Characterization of an M28 metalloprotease family member residing in the yeast vacuole. <i>FEMS Yeast Research</i> , 2013, 13, 471-484.	2.3	9
3305	Structure-function analysis of the <sc>LytM</sc> domain of <sc>EnvC</sc>, an activator of cell wall remodelling at the <i><sc>E</sc></i> <i>Escherichia coli</i> division site. <i>Molecular Microbiology</i> , 2013, 89, 690-701.	2.5	58
3306	A comparison of multi-label techniques based on problem transformation for protein functional prediction. , 2013, 2013, 2688-91.		2
3307	Comparative meta-analysis between human and mouse cancer microarray data reveals critical pathways. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 8, 349.	0.1	3
3308	In Silico Ionomics Segregates Parasitic from Free-Living Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 1902-1909.	2.5	4
3309	Metagenome Survey of a Multispecies and Alga-Associated Biofilm Revealed Key Elements of Bacterial-Algal Interactions in Photobioreactors. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6196-6206.	3.1	111
3310	Common and pathogen-specific virulence factors are different in function and structure. <i>Virulence</i> , 2013, 4, 473-482.	4.4	56
3311	EML1 (CNG-Modulin) Controls Light Sensitivity in Darkness and under Continuous Illumination in Zebrafish Retinal Cone Photoreceptors. <i>Journal of Neuroscience</i> , 2013, 33, 17763-17776.	3.6	33
3312	Structure and Function of the DUF2233 Domain in Bacteria and in the Human Mannose 6-Phosphate Uncovering Enzyme. <i>Journal of Biological Chemistry</i> , 2013, 288, 16789-16799.	3.4	7
3313	Characterization of the Yeast Actin Patch Protein App1p Phosphatidate Phosphatase. <i>Journal of Biological Chemistry</i> , 2013, 288, 6427-6437.	3.4	20
3314	The mutational landscape of phosphorylation signaling in cancer. <i>Scientific Reports</i> , 2013, 3, 2651.	3.3	149
3315	On the Origin of Large Flexibility of P-glycoprotein in the Inward-facing State. <i>Journal of Biological Chemistry</i> , 2013, 288, 19211-19220.	3.4	120
3316	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013, 41, e121-e121.	14.5	1,214
3317	DIALIGN at GOBICS multiple sequence alignment using various sources of external information. <i>Nucleic Acids Research</i> , 2013, 41, W3-W7.	14.5	45

#	ARTICLE	IF	CITATIONS
3318	Propeptides of eukaryotic proteases encode histidines to exploit organelle pH for regulation. <i>FASEB Journal</i> , 2013, 27, 2939-2945.	0.5	2
3319	Computational identification of functional RNA homologs in metagenomic data. <i>RNA Biology</i> , 2013, 10, 1170-1179.	3.1	56
3320	Random Matrix Theory Analysis of Cross Correlations in Molecular Dynamics Simulations of Macro-Biomolecules. <i>Journal of the Physical Society of Japan</i> , 2013, 82, 083801.	1.6	6
3321	The <i>Bdtf1</i> Gene in <i>Alternaria brassicicola</i> Is Important in Detoxifying Brassinin and Maintaining Virulence on <i>Brassica</i> Species. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1429-1440.	2.6	13
3322	UDP-galactopyranose mutase as a possible drug target for the human filarial parasite, <i>Brugia malayi</i> : an in silico evaluation. <i>International Journal of Medical Engineering and Informatics</i> , 2013, 5, 372.	0.3	3
3323	The Origin of Parasitism Gene in Nematodes: Evolutionary Analysis through the Construction of Domain Trees. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S13032.	1.2	0
3325	PlantTFcat: an online plant transcription factor and transcriptional regulator categorization and analysis tool. <i>BMC Bioinformatics</i> , 2013, 14, 321.	2.6	119
3326	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	2.8	408
3327	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
3328	Protamine-like Proteins in 12 Sequenced Species of <i>Drosophila</i> . <i>Protein and Peptide Letters</i> , 2013, 20, 17-35.	0.9	9
3329	A potential source for cellulolytic enzyme discovery and environmental aspects revealed through metagenomics of Brazilian mangroves. <i>AMB Express</i> , 2013, 3, 65.	3.0	40
3330	Cleaning evolutionary insights from the genome sequence of a probiotic yeast <i>Saccharomyces boulardii</i> . <i>Gut Pathogens</i> , 2013, 5, 30.	3.4	18
3331	MisPred: a resource for identification of erroneous protein sequences in public databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat053.	3.0	17
3332	Domain information based prediction of protein-protein interactions of glucosinolate biosynthesis. <i>International Journal of Computer Applications in Technology</i> , 2013, 48, 74.	0.5	0
3333	Proteinaceous determinants of surface colonization in bacteria: bacterial adhesion and biofilm formation from a protein secretion perspective. <i>Frontiers in Microbiology</i> , 2013, 4, 303.	3.5	162
3334	Identification and In-vivo Characterization of a Novel OhrR Transcriptional Regulator in <i>Burkholderia xenovorans</i> LB400. <i>Journal of Molecular Biology Research</i> , 2013, 3, .	0.1	3
3335	The Distribution of Polyhedral Bacterial Microcompartments Suggests Frequent Horizontal Transfer and Operon Reassembly. <i>Journal of Phylogenetics & Evolutionary Biology</i> , 2013, 01, .	0.2	22
3336	Feature-Based Classification of Amino Acid Substitutions outside Conserved Functional Protein Domains. <i>Scientific World Journal</i> , The, 2013, 2013, 1-10.	2.1	5

#	ARTICLE	IF	CITATIONS
3337	Cathelicidins Revisited. International Journal of Systems Biology and Biomedical Technologies, 2013, 2, 8-32.	0.2	1
3338	Comparative genome analysis of <i>Solanum lycopersicum</i> and <i>Solanum tuberosum</i> . Bioinformation, 2013, 9, 923-928.	0.5	1
3339	N-Acetylmuramoyl-l-alanine Amidase. , 2013, , 1401-1407.		1
3340	Identification and Characterisation CRN Effectors in <i>Phytophthora capsici</i> Shows Modularity and Functional Diversity. PLoS ONE, 2013, 8, e59517.	2.5	156
3341	Phylogeny of Toll-Like Receptor Signaling: Adapting the Innate Response. PLoS ONE, 2013, 8, e54156.	2.5	27
3342	Sequencing and De Novo Assembly of the Western Tarnished Plant Bug (<i>Lygus hesperus</i>) Transcriptome. PLoS ONE, 2013, 8, e55105.	2.5	49
3343	The Diversity and Evolution of <i>Wolbachia</i> Ankyrin Repeat Domain Genes. PLoS ONE, 2013, 8, e55390.	2.5	80
3344	Horizontal Transfer of a Subtilisin Gene from Plants into an Ancestor of the Plant Pathogenic Fungal Genus <i>Colletotrichum</i> . PLoS ONE, 2013, 8, e59078.	2.5	28
3345	Large-Scale Modelling of the Divergent Spectrin Repeats in Nesprins: Giant Modular Proteins. PLoS ONE, 2013, 8, e63633.	2.5	35
3346	Identification of Novel Adhesins of <i>M. tuberculosis</i> H37Rv Using Integrated Approach of Multiple Computational Algorithms and Experimental Analysis. PLoS ONE, 2013, 8, e69790.	2.5	29
3347	Homology Modeling of the CheW Coupling Protein of the Chemotaxis Signaling Complex. PLoS ONE, 2013, 8, e70705.	2.5	5
3348	Endogenous Retrovirus EAV-HP Linked to Blue Egg Phenotype in Mapuche Fowl. PLoS ONE, 2013, 8, e71393.	2.5	56
3349	DIRS and Ngara Retrotransposons in Fungi. PLoS ONE, 2013, 8, e76319.	2.5	16
3350	SIFT Indel: Predictions for the Functional Effects of Amino Acid Insertions/Deletions in Proteins. PLoS ONE, 2013, 8, e77940.	2.5	108
3351	Putative Sugar Transporters of the Mustard Leaf Beetle <i>Phaedon cochleariae</i> : Their Phylogeny and Role for Nutrient Supply in Larval Defensive Glands. PLoS ONE, 2013, 8, e84461.	2.5	16
3352	Inferring the <i>Brassica rapa</i> Interactome Using Protein-Protein Interaction Data from <i>Arabidopsis thaliana</i> . Frontiers in Plant Science, 2012, 3, 297.	3.6	25
3353	From Protein-Protein Interactions to Rational Drug Design: Are Computational Methods Up to the Challenge? Current Topics in Medicinal Chemistry, 2013, 13, 602-618.	2.1	23
3354	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. Frontiers in Genetics, 2013, 4, 62.	2.3	7

#	ARTICLE	IF	CITATIONS
3355	Meta4: a web application for sharing and annotating metagenomic gene predictions using web services. <i>Frontiers in Genetics</i> , 2013, 4, 168.	2.3	8
3356	Annotation extension through protein family annotation coherence metrics. <i>Frontiers in Genetics</i> , 2013, 4, 201.	2.3	5
3357	The Genome of <i>Nitrospina gracilis</i> Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. <i>Frontiers in Microbiology</i> , 2013, 4, 27.	3.5	243
3358	Interaction between the genomes of <i>Lactococcus lactis</i> and phages of the P335 species. <i>Frontiers in Microbiology</i> , 2013, 4, 257.	3.5	36
3359	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.	3.5	44
3360	The Clip-Segment of the von Willebrand Domain 1 of the BMP Modulator Protein Crossveinless 2 Is Preformed. <i>Molecules</i> , 2013, 18, 11658-11682.	3.8	9
3361	Influence of Mg ²⁺ ions on the interaction between 3,5-dicaffeoylquinic acid and HTLV-I integrase. <i>Universitas Scientiarum</i> , 2013, 17, 5.	0.4	3
3362	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. <i>PLoS ONE</i> , 2014, 9, e87723.	2.5	47
3363	Transcriptomics and Identification of the Chemoreceptor Superfamily of the Pupal Parasitoid of the Oriental Fruit Fly, <i>Spalangia endius</i> Walker (Hymenoptera: Pteromalidae). <i>PLoS ONE</i> , 2014, 9, e87800.	2.5	14
3364	Functionally Enigmatic Genes: A Case Study of the Brain Ignorome. <i>PLoS ONE</i> , 2014, 9, e88889.	2.5	77
3365	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. <i>PLoS ONE</i> , 2014, 9, e93907.	2.5	112
3366	Chitinase-Like (CTL) and Cellulose Synthase (CESA) Gene Expression in Gelatinous-Type Cellulosic Walls of Flax (<i>Linum usitatissimum</i> L.) Bast Fibers. <i>PLoS ONE</i> , 2014, 9, e97949.	2.5	59
3367	DUF581 Is Plant Specific FCS-Like Zinc Finger Involved in Protein-Protein Interaction. <i>PLoS ONE</i> , 2014, 9, e99074.	2.5	33
3368	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. <i>PLoS ONE</i> , 2014, 9, e104794.	2.5	43
3369	Hybrid and Rogue Kinases Encoded in the Genomes of Model Eukaryotes. <i>PLoS ONE</i> , 2014, 9, e107956.	2.5	3
3370	MacSyFinder: A Program to Mine Genomes for Molecular Systems with an Application to CRISPR-Cas Systems. <i>PLoS ONE</i> , 2014, 9, e110726.	2.5	315
3371	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. <i>PLoS ONE</i> , 2014, 9, e111122.	2.5	14
3372	Transcriptomic Analysis of the Mussel <i>Elliptio complanata</i> Identifies Candidate Stress-Response Genes and an Abundance of Novel or Noncoding Transcripts. <i>PLoS ONE</i> , 2014, 9, e112420.	2.5	13

#	ARTICLE	IF	CITATIONS
3373	De novo Assembly of the Grass Carp <i>Ctenopharyngodon idella</i> Transcriptome to Identify miRNA Targets Associated with Motile Aeromonad Septicemia. PLoS ONE, 2014, 9, e112722.	2.5	24
3374	Community Structure Detection for Overlapping Modules through Mathematical Programming in Protein Interaction Networks. PLoS ONE, 2014, 9, e112821.	2.5	18
3375	Toward Computational Cumulative Biology by Combining Models of Biological Datasets. PLoS ONE, 2014, 9, e113053.	2.5	8
3376	Structure of Putrescine Aminotransferase from <i>Escherichia coli</i> Provides Insights into the Substrate Specificity among Class III Aminotransferases. PLoS ONE, 2014, 9, e113212.	2.5	16
3377	Inferring Meaningful Communities from Topology-Constrained Correlation Networks. PLoS ONE, 2014, 9, e113438.	2.5	0
3378	Computational and Experimental Analysis of the Secretome of <i>Methylococcus capsulatus</i> (Bath). PLoS ONE, 2014, 9, e114476.	2.5	7
3379	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. Genes, 2014, 5, 957-981.	2.4	76
3380	Alternative splicing during <i>Arabidopsis</i> flower development results in constitutive and stage-regulated isoforms. Frontiers in Genetics, 2014, 5, 25.	2.3	45
3381	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep subseafloor sedimentary metagenomes. Frontiers in Microbiology, 2014, 5, 80.	3.5	61
3382	A Hypothetical Protein of <i>Alteromonas macleodii</i> AltDE1 (amad1_06475) Predicted to be a Cold-Shock Protein with RNA Chaperone Activity. Gene Regulation and Systems Biology, 2014, 8, GRSB.S20802.	2.3	2
3383	The Lipopolysaccharide Export Pathway in <i>Escherichia coli</i> : Structure, Organization and Regulated Assembly of the Lpt Machinery. Marine Drugs, 2014, 12, 1023-1042.	4.6	41
3384	Comprehensive analysis of patched domain-containing genes reveals a unique evolutionary pattern. Genetics and Molecular Research, 2014, 13, 7318-7331.	0.2	16
3385	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.	2.0	20
3386	Expressed sequence tags (EST) analysis of a normalized full-length cDNA library from the pinewood nematode (<i>Bursaphelenchus xylophilus</i>). African Journal of Biotechnology, 2014, 13, 3332-3343.	0.6	0
3387	Identification of novel and conserved microRNAs in <i>Coffea canephora</i> and <i>Coffea arabica</i> . Genetics and Molecular Biology, 2014, 37, 671-682.	1.3	15
3388	A Statistical Approach to Correcting Cross-Annotations in a Metagenomic Functional Profile Generated by Short Reads. Journal of Biometrics & Biostatistics, 2014, 05, .	4.0	2
3389	Detección de blancos moleculares en la ruta de señalización del fosfatidilinositol en <i>Leishmania</i> spp. a través de herramientas bioinformáticas y de modelado matemático. Biomedica, 2014, 35, .	0.7	1
3390	In-silico Structural and Functional Analysis of Hypothetical Proteins of <i>Leptospira Interrogans</i> . Biochemistry & Pharmacology: Open Access, 2014, 03, .	0.2	8

#	ARTICLE	IF	CITATIONS
3391	Structural Systems Biology: Modeling Interactions and Networks for Systems Studies. , 2014, , 9-19.		0
3392	CAMP: Collection of sequences and structures of antimicrobial peptides. Nucleic Acids Research, 2014, 42, D1154-D1158.	14.5	219
3393	A DEK Domain-Containing Protein Modulates Chromatin Structure and Function in <i>Arabidopsis</i> . Plant Cell, 2014, 26, 4328-4344.	6.6	57
3394	A Genomic Analysis Pipeline and Its Application to Pediatric Cancers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 826-839.	3.0	2
3395	Metatranscriptomic analysis of lignocellulolytic microbial communities involved in high-solids decomposition of rice straw. Biotechnology for Biofuels, 2014, 7, 495.	6.2	40
3396	Adaptive genomic structural variation in the grape powdery mildew pathogen, <i>Erysiphe necator</i> . BMC Genomics, 2014, 15, 1081.	2.8	162
3397	Genome wide in silico analysis of <i>Plasmodium falciparum</i> phosphatome. BMC Genomics, 2014, 15, 1024.	2.8	24
3398	Proteins: From sequence to structure. Chinese Physics B, 2014, 23, 078705.	1.4	2
3399	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. BMC Plant Biology, 2014, 14, 329.	3.6	42
3400	Genomewide identification and expression analysis of the ARF gene family in apple. Journal of Genetics, 2014, 93, 785-797.	0.7	40
3401	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. Genome Biology, 2014, 15, 512.	8.8	475
3402	Tomato nuclear proteome reveals the involvement of specific E2 ubiquitin-conjugating enzymes in fruit ripening. Genome Biology, 2014, 15, 548.	8.8	91
3403	Kinase domain-targeted isolation of defense-related receptor-like kinases (RLK/Pelle) in <i>Platanus acerifolia</i> : phylogenetic and structural analysis. BMC Research Notes, 2014, 7, 884.	1.4	7
3404	Functional genomics and microbiome profiling of the Asian longhorned beetle (<i>Anoplophora</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TF beetles. BMC Genomics, 2014, 15, 1096.	2.8	93
3405	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. BMC Genomics, 2014, 15, 901.	2.8	11
3406	Low frequency of paleoviral infiltration across the avian phylogeny. Genome Biology, 2014, 15, 539.	8.8	60
3407	Rapid Evolution of piRNA Pathway in the Teleost Fish: Implication for an Adaptation to Transposon Diversity. Genome Biology and Evolution, 2014, 6, 1393-1407.	2.5	46
3408	Bioinformatic characterisation of genes encoding cell wall degrading enzymes in the <i>Phytophthora parasitica</i> genome. BMC Genomics, 2014, 15, 785.	2.8	89

#	ARTICLE	IF	CITATIONS
3409	A novel approach for multi-domain and multi-gene family identification provides insights into evolutionary dynamics of disease resistance genes in core eudicot plants. <i>BMC Genomics</i> , 2014, 15, 966.	2.8	29
3410	The GPCR repertoire in the demosponge <i>Amphimedon queenslandica</i> : insights into the GPCR system at the early divergence of animals. <i>BMC Evolutionary Biology</i> , 2014, 14, 270.	3.2	42
3411	Exploring features and function of Ss-riok-3, an enigmatic kinase gene from <i>Strongyloides stercoralis</i> . <i>Parasites and Vectors</i> , 2014, 7, 561.	2.5	6
3412	Evolutionary pattern of four representative DNA repair proteins across six model organisms: an in silico analysis. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2014, 3, 1.	2.1	3
3413	A highly conserved family of domains related to the DNA-glycosylase fold helps predict multiple novel pathways for RNA modifications. <i>RNA Biology</i> , 2014, 11, 360-372.	3.1	35
3414	New Tricks for "Old" Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. <i>Genome Biology and Evolution</i> , 2014, 6, 2897-2917.	2.5	14
3415	Bicriteria data compression. , 2014, , .		6
3416	An antimicrobial protein of the gut symbiont <i>Bacteroides fragilis</i> with a MACPF domain of host immune proteins. <i>Molecular Microbiology</i> , 2014, 94, 1361-1374.	2.5	70
3417	Dissemination of 6S RNA among Bacteria. <i>RNA Biology</i> , 2014, 11, 1467-1478.	3.1	40
3418	A novel member of glycoside hydrolase family 30 subfamily 8 with altered substrate specificity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2950-2958.	2.5	25
3419	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 3122-3136.	2.5	24
3420	Phycoremediation Coupled with Generation of Value-Added Products. , 2014, , 341-387.		3
3421	DHCR24 associates strongly with the endoplasmic reticulum beyond predicted membrane domains: implications for the activities of this multi-functional enzyme. <i>Bioscience Reports</i> , 2014, 34, .	2.4	19
3422	Characterization and Bioinformatics Analysis of C-4 Sterol Methyl Oxidase from <i>Monascus purpureus</i> . <i>Applied Mechanics and Materials</i> , 2014, 522-524, 247-250.	0.2	1
3423	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014, 33, 648-664.	7.8	58
3424	ATPase Subdomain IA Is a Mediator of Interdomain Allostery in Hsp70 Molecular Chaperones. <i>PLoS Computational Biology</i> , 2014, 10, e1003624.	3.2	98
3425	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau022.	3.0	62
3426	Correcting for Differential Transcript Coverage Reveals a Strong Relationship between Alternative Splicing and Organism Complexity. <i>Molecular Biology and Evolution</i> , 2014, 31, 1402-1413.	8.9	124

#	ARTICLE	IF	CITATIONS
3427	Assembly of viral genomes from metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 714.	3.5	44
3428	Characterization of dehydrin AhDHN from Mediterranean saltbush (<i>Atriplex halimus</i>). <i>Turkish Journal of Biology</i> , 2014, 38, 469-477.	0.8	14
3429	dcGOR: An R Package for Analysing Ontologies and Protein Domain Annotations. <i>PLoS Computational Biology</i> , 2014, 10, e1003929.	3.2	18
3430	A mortise-tenon joint in the transmembrane domain modulates autotransporter assembly into bacterial outer membranes. <i>Nature Communications</i> , 2014, 5, 4239.	12.8	46
3431	Convergent Bacterial Microbiotas in the Fungal Agricultural Systems of Insects. <i>MBio</i> , 2014, 5, e02077.	4.1	96
3432	PLIC: protein-ligand interaction clusters. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau029.	3.0	37
3433	AromaDeg, a novel database for phylogenomics of aerobic bacterial degradation of aromatics. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau118.	3.0	57
3434	Manually curated database of rice proteins. <i>Nucleic Acids Research</i> , 2014, 42, D1214-D1221.	14.5	19
3435	Hierarchical Ensemble Methods for Protein Function Prediction. , 2014, 2014, 1-34.		32
3436	Discovery and Confirmation of Ligand Binding Specificities of the <i>Schistosoma japonicum</i> Polarity Protein Scribble. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2837.	3.0	5
3437	Improved Contact Predictions Using the Recognition of Protein Like Contact Patterns. <i>PLoS Computational Biology</i> , 2014, 10, e1003889.	3.2	142
3438	A Genome-Wide Screen for Bacterial Envelope Biogenesis Mutants Identifies a Novel Factor Involved in Cell Wall Precursor Metabolism. <i>PLoS Genetics</i> , 2014, 10, e1004056.	3.5	99
3439	Global Analysis of Photosynthesis Transcriptional Regulatory Networks. <i>PLoS Genetics</i> , 2014, 10, e1004837.	3.5	31
3440	Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. <i>Frontiers in Microbiology</i> , 2014, 5, 531.	3.5	87
3441	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 698.	3.5	62
3442	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. <i>Frontiers in Physiology</i> , 2013, 4, 315.	2.8	17
3443	Expression pattern of glycoside hydrolase genes in <i>Lutzomyia longipalpis</i> reveals key enzymes involved in larval digestion. <i>Frontiers in Physiology</i> , 2014, 5, 276.	2.8	24
3444	Analysis of two domains with novel RNA-processing activities throws light on the complex evolution of ribosomal RNA biogenesis. <i>Frontiers in Genetics</i> , 2014, 5, 424.	2.3	21

#	ARTICLE	IF	CITATIONS
3445	Network Assessor: An automated method for quantitative assessment of a network's potential for gene function prediction. <i>Frontiers in Genetics</i> , 2014, 5, 123.	2.3	10
3446	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2198-2212.	3.8	5
3447	Mutations Enabling Displacement of Tryptophan by 4-Fluorotryptophan as a Canonical Amino Acid of the Genetic Code. <i>Genome Biology and Evolution</i> , 2014, 6, 629-641.	2.5	31
3448	Quantitative Analysis of the Mitochondrial and Plastid Proteomes of the Moss <i>Physcomitrella patens</i> Reveals Protein Macrocompartmentation and Microcompartmentation. <i>Plant Physiology</i> , 2014, 164, 2081-2095.	4.8	61
3449	Genome Sequence of <i>Rickettsia hoogstraalii</i> , a Geographically Widely Distributed Tick-Associated Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
3450	Genome Sequence of <i>Bacillus simplex</i> Strain P558, Isolated from a Human Fecal Sample. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
3451	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	4.1	82
3452	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . <i>MBio</i> , 2014, 5, e01980.	4.1	39
3453	Regulatory interplay between soybean root and soybean cyst nematode during a resistant and susceptible reaction. <i>BMC Plant Biology</i> , 2014, 14, 300.	3.6	30
3454	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
3455	Immunoproteomics: current approach for subunit vaccine design. <i>International Journal of Immunological Studies</i> , 2014, 2, 16.	0.2	0
3456	Prediction of protein function by combining phylogenetic tree and mathematical inference. , 2014, , .		0
3457	Genome Sequence of the μ -Poly- L-Lysine-Producing Strain <i>Streptomyces albulus</i> NK660, Isolated from Soil in Gutian, Fujian Province, China. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
3458	A new insight into the zinc-dependent DNA-cleavage by the colicin E7 nuclease: a crystallographic and computational study. <i>Metallomics</i> , 2014, 6, 2090-2099.	2.4	7
3459	Distribution, classification, domain architectures and evolution of prolyl oligopeptidases in prokaryotic lineages. <i>BMC Genomics</i> , 2014, 15, 985.	2.8	15
3460	AlgaePath: comprehensive analysis of metabolic pathways using transcript abundance data from next-generation sequencing in green algae. <i>BMC Genomics</i> , 2014, 15, 196.	2.8	36
3461	Genome sequencing and comparative analysis of three <i>Chlamydia pecorum</i> strains associated with different pathogenic outcomes. <i>BMC Genomics</i> , 2014, 15, 23.	2.8	39
3462	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.	2.8	262

#	ARTICLE	IF	CITATIONS
3463	Characterization and regulation of the Resistance-Nodulation-Cell Division-type multidrug efflux pumps MdtABC and MdtUVW from the fire blight pathogen <i>Erwinia amylovora</i> . <i>BMC Microbiology</i> , 2014, 14, 185.	3.3	40
3464	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
3465	Comparison of gene expression of <i>Paramecium bursaria</i> with and without <i>Chlorella variabilis</i> symbionts. <i>BMC Genomics</i> , 2014, 15, 183.	2.8	57
3466	TIR-domain-containing protein repertoire of nine anthozoan species reveals coral-specific expansions and uncharacterized proteins. <i>Developmental and Comparative Immunology</i> , 2014, 46, 480-488.	2.3	80
3467	IndexedFCP - An Index Based Approach to Identify Frequent Contiguous Patterns (FCP) in Big Data. , 2014, , .		2
3468	DINIES: drug-target interaction network inference engine based on supervised analysis. <i>Nucleic Acids Research</i> , 2014, 42, W39-W45.	14.5	97
3469	A Bayesian Sampler for Optimization of Protein Domain Hierarchies. <i>Journal of Computational Biology</i> , 2014, 21, 269-286.	1.6	30
3470	Familial Isolated Growth Hormone Deficiency Due to A Novel Homozygous Missense Mutation in the Growth Hormone Releasing Hormone Receptor Gene: Clinical Presentation With Hypoglycemia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E2730-E2734.	3.6	11
3471	Decelerated genome evolution in modern vertebrates revealed by analysis of multiple lancelet genomes. <i>Nature Communications</i> , 2014, 5, 5896.	12.8	136
3472	The fungus gardens of leaf-cutter ants undergo a distinct physiological transition during biomass degradation. <i>Environmental Microbiology Reports</i> , 2014, 6, 389-395.	2.4	21
3473	The haemagglutinin of <i>Avibacterium paragallinarum</i> is a trimeric autotransporter adhesin that confers haemagglutination, cell adherence and biofilm formation activities. <i>Veterinary Microbiology</i> , 2014, 174, 474-482.	1.9	24
3474	Symbiotic adaptations in the fungal cultivar of leaf-cutting ants. <i>Nature Communications</i> , 2014, 5, 5675.	12.8	84
3475	Genome-wide identification and expression analyses of cytochrome <i>P450</i> genes in mulberry (<i>Morus notabilis</i>). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 887-901.	8.5	53
3476	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. <i>Nucleic Acids Research</i> , 2014, 42, D364-D373.	14.5	156
3477	Crystal structure of a putative quorum sensing-regulated protein (PA3611) from the <i>Pseudomonas</i> -specific DUF4146 family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1086-1092.	2.6	7
3478	Identification of a broad family of lipid <i>ACP</i> late acyltransferases with non-canonical substrate specificity. <i>Molecular Microbiology</i> , 2014, 91, 887-899.	2.5	17
3479	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	14.5	210
3480	Protein universe containing a <i>PUA</i> RNA-binding domain. <i>FEBS Journal</i> , 2014, 281, 74-87.	4.7	18

#	ARTICLE	IF	CITATIONS
3481	Benchmarking a Wide Range of Chemical Descriptors for Drug-Target Interaction Prediction Using a Chemogenomic Approach. <i>Molecular Informatics</i> , 2014, 33, 719-731.	2.5	49
3482	<i>Helicobacter pylori</i> Antigen HP0986 (TieA) Interacts with Cultured Gastric Epithelial Cells and Induces IL8 Secretion via NF- κ B Mediated Pathway. <i>Helicobacter</i> , 2014, 19, 26-36.	3.5	19
3483	Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. <i>Structure</i> , 2014, 22, 1799-1809.	3.3	10
3484	Candidate disease gene prediction using <i>Gentrepid</i> : application to a genome-wide association study on coronary artery disease. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 44-57.	1.2	11
3485	Structural basis and dynamics of multidrug recognition in a minimal bacterial multidrug resistance system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5498-507.	7.1	18
3486	<i>Phytophthora sojae</i> TatD Nuclease Positively Regulates Sporulation and Negatively Regulates Pathogenesis. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 1070-1080.	2.6	24
3487	Structural characterization of MepB from <i>Staphylococcus aureus</i> reveals homology to endonucleases. <i>Protein Science</i> , 2014, 23, 594-602.	7.6	6
3488	Genomic Characterization of Variable Surface Antigens Reveals a Telomere Position Effect as a Prerequisite for RNA Interference-Mediated Silencing in <i>Paramecium tetraurelia</i> . <i>MBio</i> , 2014, 5, e01328.	4.1	13
3489	3PFD \pm : improved search protocol and update for the identification of representatives of protein sequence domain families. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau026.	3.0	5
3490	Kin-Driver: a database of driver mutations in protein kinases. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau104-bau104.	3.0	23
3491	Evolutionary and Structural Analyses of Mammalian Haloacid Dehalogenase-type Phosphatases AUM and Chronophin Provide Insight into the Basis of Their Different Substrate Specificities. <i>Journal of Biological Chemistry</i> , 2014, 289, 3416-3431.	3.4	24
3492	Phylogenetic analysis of CDK and cyclin proteins in premetazoan lineages. <i>BMC Evolutionary Biology</i> , 2014, 14, 10.	3.2	114
3493	Novel and unique domains in aminoacyl-tRNA synthetases from human fungal pathogens <i>Aspergillus niger</i> , <i>Candida albicans</i> and <i>Cryptococcus neoformans</i> . <i>BMC Genomics</i> , 2014, 15, 1069.	2.8	14
3494	Alkane hydroxylase genes in psychrophile genomes and the potential for cold active catalysis. <i>BMC Genomics</i> , 2014, 15, 1120.	2.8	25
3495	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. <i>BMC Genomics</i> , 2014, 15, 1159.	2.8	10
3496	Conservation analysis of the CydX protein yields insights into small protein identification and evolution. <i>BMC Genomics</i> , 2014, 15, 946.	2.8	36
3497	Genome-wide cloning, identification, classification and functional analysis of cotton heat shock transcription factors in cotton (<i>Gossypium hirsutum</i>). <i>BMC Genomics</i> , 2014, 15, 961.	2.8	71
3498	Interspecific and host-related gene expression patterns in nematode-trapping fungi. <i>BMC Genomics</i> , 2014, 15, 968.	2.8	30

#	ARTICLE	IF	CITATIONS
3499	The <i>Vibrio cholerae</i> diguanylate cyclase VCA0965 has an AGDEF active site and synthesizes cyclic di-GMP. <i>BMC Microbiology</i> , 2014, 14, 22.	3.3	40
3500	The loose evolutionary relationships between transcription factors and other gene products across prokaryotes. <i>BMC Research Notes</i> , 2014, 7, 928.	1.4	2
3501	Unique features of apicoplast DNA gyrases from <i>Toxoplasma gondii</i> and <i>Plasmodium falciparum</i> . <i>BMC Bioinformatics</i> , 2014, 15, 416.	2.6	14
3502	Dynamic evolution of the GnRH receptor gene family in vertebrates. <i>BMC Evolutionary Biology</i> , 2014, 14, 215.	3.2	30
3503	Loss and retention of resistance genes in five species of the Brassicaceae family. <i>BMC Plant Biology</i> , 2014, 14, 298.	3.6	27
3504	In vivo functional analysis of a nuclear restorer PPR protein. <i>BMC Plant Biology</i> , 2014, 14, 313.	3.6	14
3505	Biophysics of protein evolution and evolutionary protein biophysics. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140419.	3.4	202
3506	Ancestral repeats have shaped epigenome and genome composition for millions of years in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2014, 5, 4104.	12.8	74
3507	3did: a catalog of domain-based interactions of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2014, 42, D374-D379.	14.5	249
3508	Comparative Genomics of the <i>Campylobacter lari</i> Group. <i>Genome Biology and Evolution</i> , 2014, 6, 3252-3266.	2.5	69
3509	MetaProx: the database of metagenomic proximons. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	3.0	7
3510	A Novel Mutation in the <i>ROGDI</i> Gene in a Patient with Kohlschütter-Törzsch Syndrome. <i>Molecular Syndromology</i> , 2014, 5, 293-298.	0.8	18
3511	Computational modeling and preliminary <i>iro N</i> , <i>fep A</i> , and <i>cir A</i> gene expression in <i>Salmonella</i> Enteritidis under iron-deficiency-induced conditions. <i>Poultry Science</i> , 2014, 93, 221-230.	3.4	9
3512	Complete genome sequence of the Radiation-Resistant bacterium <i>Rubrobacter radiotolerans</i> RSPS-4. <i>Standards in Genomic Sciences</i> , 2014, 9, 1062-1075.	1.5	43
3513	Transcript Profiling Reveals Auxin and Cytokinin Signaling Pathways and Transcription Regulation during In Vitro Organogenesis of Ramie (<i>Boehmeria nivea</i> L. Gaud). <i>PLoS ONE</i> , 2014, 9, e113768.	2.5	29
3514	Prediction of domain boundaries in protein sequences using predicted secondary structure and physicochemical properties of amino acids. , 2014, , .		0
3515	A novel missense mutation in <i>CCDC88C</i> activates the JNK pathway and causes a dominant form of spinocerebellar ataxia. <i>Journal of Medical Genetics</i> , 2014, 51, 590-595.	3.2	64
3516	Molecular Evolution of the Vertebrate FK506 Binding Protein 25. <i>International Journal of Genomics</i> , 2014, 2014, 1-9.	1.6	2

#	ARTICLE	IF	CITATIONS
3517	Analysis of Expressed Genes of the Bacterium <i>Candidatus Phytoplasma Mali</i> ™ Highlights Key Features of Virulence and Metabolism. PLoS ONE, 2014, 9, e94391.	2.5	29
3518	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	2.5	153
3520	Helminth Allergens, Parasite-Specific IgE, and Its Protective Role in Human Immunity. Frontiers in Immunology, 2014, 5, 61.	4.8	136
3521	Protein Domains of Unknown Function Are Essential in Bacteria. MBio, 2014, 5, e00744-13.	4.1	112
3522	Predicting virus mutations through statistical relational learning. BMC Bioinformatics, 2014, 15, 309.	2.6	6
3523	Comparative genomics of <i>Lactobacillus crispatus</i> suggests novel mechanisms for the competitive exclusion of <i>Gardnerella vaginalis</i> . BMC Genomics, 2014, 15, 1070.	2.8	101
3524	HMM-ModE: implementation, benchmarking and validation with HMMER3. BMC Research Notes, 2014, 7, 483.	1.4	10
3525	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. Nucleic Acids Research, 2014, 42, D1182-D1187.	14.5	800
3526	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	14.5	526
3527	Discovery of a Novel Bottlenose Dolphin Coronavirus Reveals a Distinct Species of Marine Mammal Coronavirus in Gammacoronavirus. Journal of Virology, 2014, 88, 1318-1331.	3.4	126
3528	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of the LRR domain of the LePRK1 receptor-like kinase from tomato. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 236-239.	0.8	1
3529	Preliminary crystallographic analysis of a double mutant of the acetyl xylo-oligosaccharide esterase Axe2 in its dimeric form. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 476-481.	0.8	8
3530	Long non-coding RNAs: modulators of nuclear structure and function. Current Opinion in Cell Biology, 2014, 26, 10-18.	5.4	219
3531	SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features. Journal of Molecular Biology, 2014, 426, 2692-2701.	4.2	189
3532	Functional Genomic Analysis of Human Mitochondrial RNA Processing. Cell Reports, 2014, 7, 918-931.	6.4	86
3533	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. Proteins: Structure, Function and Bioinformatics, 2014, 82, 103-118.	2.6	3
3534	Colocalizations Between Several QTLs for Cell Wall Degradability and Composition in the F288×F271 Early Maize RIL Progeny Raise the Question of the Nature of the Possible Underlying Determinants and Breeding Targets for Biofuel Capacity. Bioenergy Research, 2014, 7, 142-156.	3.9	27
3535	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. Molecular Neurobiology, 2014, 49, 88-102.	4.0	231

#	ARTICLE	IF	CITATIONS
3536	Cell Wall-Related Proteins of Unknown Function: Missing Links in Plant Cell Wall Development. <i>Plant and Cell Physiology</i> , 2014, 55, 1031-1043.	3.1	25
3537	Recombinant expression and purification of an ATP-dependent DNA ligase from <i>Aliivibrio salmonicida</i> . <i>Protein Expression and Purification</i> , 2014, 97, 29-36.	1.3	16
3538	Extracting data from the muck: deriving biological insight from complex microbial communities and non-model organisms with next generation sequencing. <i>Current Opinion in Biotechnology</i> , 2014, 28, 103-110.	6.6	31
3539	The Mi-2 Homolog Mit1 Actively Positions Nucleosomes within Heterochromatin To Suppress Transcription. <i>Molecular and Cellular Biology</i> , 2014, 34, 2046-2061.	2.3	29
3540	Dependency of codon usage on protein sequence patterns: a statistical study. <i>Theoretical Biology and Medical Modelling</i> , 2014, 11, 2.	2.1	2
3541	Land Use Type Significantly Affects Microbial Gene Transcription in Soil. <i>Microbial Ecology</i> , 2014, 67, 919-930.	2.8	48
3542	<i>Drechslerella stenobrocha</i> genome illustrates the mechanism of constricting rings and the origin of nematode predation in fungi. <i>BMC Genomics</i> , 2014, 15, 114.	2.8	72
3543	Functional Divergence and Evolutionary Dynamics of the Putative AAP Gene Family in <i>Brassica rapa</i> . <i>Plant Molecular Biology Reporter</i> , 2014, 32, 517-530.	1.8	7
3544	Comparative genomics of <i>Cylindrospermopsis raciborskii</i> strains with differential toxicities. <i>BMC Genomics</i> , 2014, 15, 83.	2.8	64
3545	Comparative Genomic Analysis of Two-Component Signal Transduction Systems in Probiotic <i>Lactobacillus casei</i> . <i>Indian Journal of Microbiology</i> , 2014, 54, 293-301.	2.7	7
3546	Improvement of a gene targeting system for genetic manipulation in <i>Penicillium digitatum</i> . <i>Journal of Zhejiang University: Science B</i> , 2014, 15, 116-124.	2.8	9
3547	Bacteriophage endolysin $\text{Lyt } \hat{1}/41/6$: characterization of the C-terminal binding domain. <i>FEMS Microbiology Letters</i> , 2014, 350, 199-208.	1.8	9
3548	Diversity and evolution of membrane intrinsic proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 1468-1481.	2.4	199
3549	The substrate specificity, enantioselectivity and structure of the α -selective amine:pyruvate transaminase from <i>Nectria haematococca</i> . <i>FEBS Journal</i> , 2014, 281, 2240-2253.	4.7	60
3550	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <i>Ecology Letters</i> , 2014, 17, 794-802.	6.4	243
3551	Transcriptome-wide identification of bread wheat WRKY transcription factors in response to drought stress. <i>Molecular Genetics and Genomics</i> , 2014, 289, 765-781.	2.1	116
3552	Genetically distinct pathways guide effector export through the type VI secretion system. <i>Molecular Microbiology</i> , 2014, 92, 529-542.	2.5	192
3553	<i>Trypanosoma brucei</i> adenine-phosphoribosyltransferases mediate adenine salvage and aminopurinol susceptibility but not adenine toxicity. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014, 4, 55-63.	3.4	26

#	ARTICLE	IF	CITATIONS
3554	High-throughput sequencing exclusively identified a novel Torque teno virus genotype in serum of a patient with fatal fever. <i>Virologica Sinica</i> , 2014, 29, 112-118.	3.0	16
3555	Structural Disorder in Viral Proteins. <i>Chemical Reviews</i> , 2014, 114, 6880-6911.	47.7	181
3556	The Genome of the Foraminiferan <i>Reticulomyxa filosa</i> . <i>Current Biology</i> , 2014, 24, 11-18.	3.9	73
3557	Interplay between phosphoinositide lipids and calcium signals at the leading edge of chemotaxing amoeboid cells. <i>Chemistry and Physics of Lipids</i> , 2014, 182, 73-79.	3.2	21
3558	Malaria proteomics: Insights into the parasite-host interactions in the pathogenic space. <i>Journal of Proteomics</i> , 2014, 97, 107-125.	2.4	27
3559	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. <i>Bioinformatics</i> , 2014, 30, 1112-1119.	4.1	57
3560	Marine Tubeworm Metamorphosis Induced by Arrays of Bacterial Phage Tail-Like Structures. <i>Science</i> , 2014, 343, 529-533.	12.6	223
3561	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92.	21.4	227
3562	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	16.2	82
3563	Selecting Protein Families for Environmental Features Based on Manifold Regularization. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 104-108.	3.3	1
3564	A SpoT polymorphism correlates with chill stress survival and is prevalent in clinical isolates of <i>Campylobacter jejuni</i> . <i>Poultry Science</i> , 2014, 93, 2900-2909.	3.4	2
3565	Different transcription regulation routes are exerted by L- and D-amino acid enantiomers of peptide hormones. <i>Journal of Experimental Biology</i> , 2014, 217, 4337-46.	1.7	7
3566	Unencapsulated <i>Streptococcus pneumoniae</i> from conjunctivitis encode variant traits and belong to a distinct phylogenetic cluster. <i>Nature Communications</i> , 2014, 5, 5411.	12.8	45
3567	The Ubiquitous Distribution of Late Embryogenesis Abundant Proteins across Cell Compartments in <i>Arabidopsis</i> Offers Tailored Protection against Abiotic Stress. <i>Plant Cell</i> , 2014, 26, 3148-3166.	6.6	179
3568	Basic characterization of avian NK-lysin (NKL) from the Japanese quail, <i>Coturnix japonica</i> . <i>Animal Science Journal</i> , 2014, 85, 90-95.	1.4	7
3569	Phenylethanol promotes adhesion and biofilm formation of the antagonistic yeast <i>Kloeckera apiculata</i> for the control of blue mold on citrus. <i>FEMS Yeast Research</i> , 2014, 14, 536-546.	2.3	63
3570	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. <i>Nature Communications</i> , 2014, 5, 4784.	12.8	118
3571	Comparative analysis of deep-sea bacterioplankton OMICS revealed the occurrence of habitat-specific genomic attributes. <i>Marine Genomics</i> , 2014, 17, 1-8.	1.1	11

#	ARTICLE	IF	CITATIONS
3572	The relationship between classification of multi-domain proteins using an alignment-free approach and their functions: a case study with immunoglobulins. <i>Molecular BioSystems</i> , 2014, 10, 1082.	2.9	8
3573	Data, Databases, Data Format, Database Search, Data Retrieval Systems, and Genome Browsers. , 2014, , 77-131.		0
3574	The landscape of kinase fusions in cancer. <i>Nature Communications</i> , 2014, 5, 4846.	12.8	769
3575	The cation diffusion facilitator protein EmfA of <i>Rhizobium etli</i> belongs to a novel subfamily of Mn ²⁺ /Fe ²⁺ transporters conserved in $\hat{\pm}$ -proteobacteria. <i>Metallomics</i> , 2014, 6, 1808-1815.	2.4	22
3576	Non-coding RNA: a new frontier in regulatory biology. <i>National Science Review</i> , 2014, 1, 190-204.	9.5	175
3577	Molecular characterization and expression analysis of the complement factor I (CpFI) in the whitespotted bamboo shark (<i>Chiloscyllium plagiosum</i>). <i>Fish and Shellfish Immunology</i> , 2014, 40, 414-423.	3.6	6
3578	Chemical synthesis, structureâ€“activity relationship, and properties of shepherdin I: a fungicidal peptide enriched in glycine-glycine-histidine motifs. <i>Amino Acids</i> , 2014, 46, 2573-2586.	2.7	34
3579	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	12.6	520
3580	Characterization and Phylogenetic Analysis of Allergenic Tryp_alpha_amyl Protein Family in Plants. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 270-278.	5.2	4
3581	GH51 Arabinofuranosidase and Its Role in the Methylglucuronarabinoxylan Utilization System in <i>Paenibacillus</i> sp. Strain JDR-2. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6114-6125.	3.1	7
3582	Evolutionarily Distinct Versions of the Multidomain Enzyme $\hat{\pm}$ -Isopropylmalate Synthase Share Discrete Mechanisms of V-Type Allosteric Regulation. <i>Biochemistry</i> , 2014, 53, 4847-4856.	2.5	10
3583	CutProtFam-Pred: Detection and classification of putative structural cuticular proteins from sequence alone, based on profile Hidden Markov Models. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 52, 51-59.	2.7	98
3584	Antagonistic roles of abscisic acid and cytokinin during response to nitrogen depletion in oleaginous microalga <i>Nannochloropsis oceanica</i> expand the evolutionary breadth of phytohormone function. <i>Plant Journal</i> , 2014, 80, 52-68.	5.7	101
3585	Differential gene expression profiles in the salivary gland of <i>Orius laevigatus</i> . <i>Journal of Asia-Pacific Entomology</i> , 2014, 17, 729-735.	0.9	6
3586	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies. , 2014, , 93-131.		1
3587	Identification of novel leads applying <i>in silico</i> studies for <i>Mycobacterium</i> multidrug resistant (MMR) protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1889-1906.	3.5	18
3588	Identification of Functional Modules by Integration of Multiple Data Sources Using a Bayesian Network Classifier. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 206-217.	5.1	5
3589	Genome-wide analysis of regulatory proteases sequences identified through bioinformatics data mining in <i>Taenia solium</i> . <i>BMC Genomics</i> , 2014, 15, 428.	2.8	6

#	ARTICLE	IF	CITATIONS
3590	LTR retroelements are intrinsic components of transcriptional networks in frogs. BMC Genomics, 2014, 15, 626.	2.8	4
3591	The reduced kinome of <i>Ostreococcus tauri</i> : core eukaryotic signalling components in a tractable model species. BMC Genomics, 2014, 15, 640.	2.8	18
3592	Inspecting the potential physiological and biomedical value of 44 conserved uncharacterised proteins of <i>Streptococcus pneumoniae</i> . BMC Genomics, 2014, 15, 652.	2.8	10
3593	Profiling the orphan enzymes. Biology Direct, 2014, 9, 10.	4.6	43
3594	Understanding the sequence requirements of protein families: insights from the BioVis 2013 contests. BMC Proceedings, 2014, 8, S1.	1.6	4
3595	Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. BMC Research Notes, 2014, 7, 493.	1.4	9
3596	Prediction and functional analysis of the sweet orange protein-protein interaction network. BMC Plant Biology, 2014, 14, 213.	3.6	30
3597	Biology of ferritin in mammals: an update on iron storage, oxidative damage and neurodegeneration. Archives of Toxicology, 2014, 88, 1787-1802.	4.2	135
3598	Integrative Network Analysis of the Signaling Cascades in Seedling Leaves of Bread Wheat by Large-Scale Phosphoproteomic Profiling. Journal of Proteome Research, 2014, 13, 2381-2395.	3.7	42
3599	Aggregation Factor as an Inhibitor of Bacterial Binding to Gut Mucosa. Microbial Ecology, 2014, 68, 633-644.	2.8	22
3600	Classification of Intrinsically Disordered Regions and Proteins. Chemical Reviews, 2014, 114, 6589-6631.	47.7	1,618
3601	Antibodies against CK1IRD, a receiver domain of the sensor histidine kinase in <i>Arabidopsis thaliana</i> : From antigen preparation to in planta immunolocalization. Phytochemistry, 2014, 100, 6-15.	2.9	2
3602	Cell Growth Inhibition upon Deletion of Four Toxin-Antitoxin Loci from the Megaplasms of <i>Sinorhizobium meliloti</i> . Journal of Bacteriology, 2014, 196, 811-824.	2.2	42
3603	Gene expression regulation of the PF00480 or PF14340 domain proteins suggests their involvement in sulfur metabolism. Computational Biology and Chemistry, 2014, 49, 7-13.	2.3	3
3604	Alginate-Dependent Gene Expression Mechanism in <i>Sphingomonas</i> sp. Strain A1. Journal of Bacteriology, 2014, 196, 2691-2700.	2.2	14
3605	Key components of the eight classes of type IV secretion systems involved in bacterial conjugation or protein secretion. Nucleic Acids Research, 2014, 42, 5715-5727.	14.5	200
3606	Aminopeptidase N1 (EtAPN1), an M1 Metalloprotease of the Apicomplexan Parasite <i>Eimeria tenella</i> , Participates in Parasite Development. Eukaryotic Cell, 2014, 13, 884-895.	3.4	19
3607	Exploration of the binding modes of buffalo PCRP1 receptor complexed with meso-diaminopimelic acid and lysine-type peptidoglycans by molecular dynamics simulation and free energy calculation. Chemico-Biological Interactions, 2014, 220, 255-268.	4.0	8

#	ARTICLE	IF	CITATIONS
3608	Virus proteins similar to human proteins as possible disturbance on human pathways. <i>Systems and Synthetic Biology</i> , 2014, 8, 283-295.	1.0	2
3609	A thermo-halo-tolerant and proteinase-resistant endoxylanase from <i>Bacillus</i> sp. HJ14. <i>Folia Microbiologica</i> , 2014, 59, 423-431.	2.3	17
3610	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	2.8	145
3611	Genome-scale metabolic reconstructions of <i>Bifidobacterium adolescentis</i> L2-32 and <i>Faecalibacterium prausnitzii</i> A2-165 and their interaction. <i>BMC Systems Biology</i> , 2014, 8, 41.	3.0	88
3612	pocketZebra: a web-server for automated selection and classification of subfamily-specific binding sites by bioinformatic analysis of diverse protein families. <i>Nucleic Acids Research</i> , 2014, 42, W344-W349.	14.5	28
3613	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. <i>Marine Genomics</i> , 2014, 18, 97-99.	1.1	14
3614	Repurposing TRASH: Emergence of the enzyme organomercurial lyase from a non-catalytic zinc finger scaffold. <i>Journal of Structural Biology</i> , 2014, 188, 16-21.	2.8	11
3615	Mechanistic and Bioinformatic Investigation of a Conserved Active Site Helix in β -Isopropylmalate Synthase from <i>Mycobacterium tuberculosis</i> , a Member of the DRE-TIM Metallolyase Superfamily. <i>Biochemistry</i> , 2014, 53, 2915-2925.	2.5	14
3616	LRRsearch: An asynchronous server-based application for the prediction of leucine-rich repeat motifs and an integrative database of NOD-like receptors. <i>Computers in Biology and Medicine</i> , 2014, 53, 164-170.	7.0	34
3617	Proteomic identification, characterization and expression analysis of <i>Ctenopharyngodon idella</i> VDAC1 upregulated by grass carp reovirus infection. <i>Fish and Shellfish Immunology</i> , 2014, 37, 96-107.	3.6	11
3618	Analysis and identification of toxin targets by topological properties in protein-protein interaction network. <i>Journal of Theoretical Biology</i> , 2014, 349, 82-91.	1.7	16
3619	The loss of the inducible <i>Aspergillus carbonarius</i> MFS transporter MfsA leads to ochratoxin A overproduction. <i>International Journal of Food Microbiology</i> , 2014, 181, 1-9.	4.7	10
3620	Assembly of Robust Bacterial Microcompartment Shells Using Building Blocks from an Organelle of Unknown Function. <i>Journal of Molecular Biology</i> , 2014, 426, 2217-2228.	4.2	102
3621	C19orf12 mutation leads to a pallido-pyramidal syndrome. <i>Gene</i> , 2014, 537, 352-356.	2.2	28
3622	Genome-wide analysis of the GRAS gene family in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Genomics</i> , 2014, 103, 135-146.	2.9	114
3623	A novel mycovirus closely related to viruses in the genus <i>Alphapartitivirus</i> confers hypovirulence in the phytopathogenic fungus <i>Rhizoctonia solani</i> . <i>Virology</i> , 2014, 456-457, 220-226.	2.4	104
3624	Proteome compression via protein domain compositions. <i>Methods</i> , 2014, 67, 380-385.	3.8	9
3625	Gene encoding a novel invertase from a xerophilic <i>Aspergillus niger</i> strain and production of the enzyme in <i>Pichia pastoris</i> . <i>Enzyme and Microbial Technology</i> , 2014, 63, 28-33.	3.2	16

#	ARTICLE	IF	CITATIONS
3626	Intrinsically Disordered Proteins and Intrinsically Disordered Protein Regions. Annual Review of Biochemistry, 2014, 83, 553-584.	11.1	850
3627	Metabolic Environments and Genomic Features Associated with Pathogenic and Mutualistic Interactions Between Bacteria and Plants. Molecular Plant-Microbe Interactions, 2014, 27, 664-677.	2.6	16
3628	Crystal structure of a member of a novel family of dioxygenases (PF10014) reveals a conserved cupin fold and active site. Proteins: Structure, Function and Bioinformatics, 2014, 82, 164-170.	2.6	15
3629	Crosstalk and the evolution of specificity in two-component signaling. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5550-5555.	7.1	95
3630	<i>Helicobacter pylori</i> RNA polymerase β -subunit C-terminal domain shows features unique to ϵ -proteobacteria and binds NikR/DNA complexes. Protein Science, 2014, 23, 454-463.	7.6	15
3631	Crystal structure of <i>Arabidopsis</i> glutamyl-tRNA reductase in complex with its stimulator protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6630-6635.	7.1	58
3632	Metatranscriptome profiling of a harmful algal bloom. Harmful Algae, 2014, 37, 75-83.	4.8	45
3633	Mining Association Rules from Gene Ontology and Protein Networks: Promises and Challenges.. Procedia Computer Science, 2014, 29, 1970-1980.	2.0	19
3634	Effective identification of kinase-specific phosphorylation sites based on domain-domain interactions. Chemometrics and Intelligent Laboratory Systems, 2014, 136, 97-103.	3.5	4
3635	Molybdenum cofactor: A key component of <i>Mycobacterium tuberculosis</i> pathogenesis?. Critical Reviews in Microbiology, 2014, 40, 18-29.	6.1	45
3636	Identifying Pathogenicity Islands in Bacterial Pathogenomics Using Computational Approaches. Pathogens, 2014, 3, 36-56.	2.8	78
3637	Accessing Microbial Communities Relevant to Biofuels Production. , 2014, , 565-576.		1
3639	Tn7. Microbiology Spectrum, 2014, 2, .	3.0	67
3640	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. Standards in Genomic Sciences, 2014, 9, 23.	1.5	4
3641	Bhageerath-H: A homology/ab initio hybrid server for predicting tertiary structures of monomeric soluble proteins. BMC Bioinformatics, 2014, 15, S7.	2.6	45
3642	The ins and outs of metal homeostasis by the root nodule actinobacterium <i>Frankia</i> . BMC Genomics, 2014, 15, 1092.	2.8	26
3643	Protein interaction networks associated with cardiovascular disease and cancer: exploring the effect of bias on shared network properties. International Journal of Data Mining and Bioinformatics, 2014, 9, 339.	0.1	2
3644	The complete genome sequence of the rumen methanogen <i>Methanobacterium formicicum</i> BRM9. Standards in Genomic Sciences, 2014, 9, 15.	1.5	27

#	ARTICLE	IF	CITATIONS
3645	Text Mining in Cancer Gene and Pathway Prioritization. <i>Cancer Informatics</i> , 2014, 13s1, CIN.S13874.	1.9	32
3646	Parallel algorithms for clustering biological graphs on distributed and shared memory architectures. <i>International Journal of High Performance Computing and Networking</i> , 2014, 7, 241.	0.4	21
3647	Genome Sequence of <i>Acanthamoeba</i> Strain 76713, Isolated in Hospital Water Using an Amoeba Co-Culture Procedure. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
3648	Discovering co-occurring patterns and their biological significance in protein families. <i>BMC Bioinformatics</i> , 2014, 15, S2.	2.6	5
3649	Robustness of birth-death and gain models for inferring evolutionary events. <i>BMC Genomics</i> , 2014, 15, S9.	2.8	2
3650	Genome Sequence of <i>Legionella anisa</i> , Isolated from a Respiratory Sample, Using an Amoebal Coculture Procedure. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
3651	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> HP T , the First Defined-Strain Dairy Starter Culture Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
3652	Explore protein-protein interaction network involved in glucosinolate biosynthesis. , 2014, , .		0
3653	Noncontiguous finished genome sequence and description of <i>Virgibacillus massiliensis</i> sp. nov., a moderately halophilic bacterium isolated from human gut. <i>New Microbes and New Infections</i> , 2015, 8, 78-88.	1.6	10
3654	Most partial domains in proteins are alignment and annotation artifacts. <i>Genome Biology</i> , 2015, 16, 99.	8.8	27
3655	Genomic and expression analysis of transition proteins in <i>Drosophila</i> . <i>Spermatogenesis</i> , 2015, 5, e1178518.	0.8	5
3656	Structure-guided selection of Specificity Determining Positions in the human kinome. , 2015, , .		0
3657	<i>Cryptococcus Agattii</i> urease as a virulence factor and the relevance of enzymatic activity in cryptococcosis pathogenesis. <i>FEBS Journal</i> , 2015, 282, 1406-1418.	4.7	47
3658	Combining RNA-seq and proteomic profiling to identify seminal fluid proteins in the migratory grasshopper <i>Melanoplus sanguinipes</i> (F). <i>BMC Genomics</i> , 2015, 16, 1096.	2.8	15
3659	The value of protein structure classification informationâ€”Surveying the scientific literature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2025-2038.	2.6	37
3660	Molecular marker associated with a deleterious recessive anomaly in <i>Eucalyptus grandis</i> seedlings. <i>Annals of Forest Science</i> , 2015, 72, 1043-1052.	2.0	4
3661	Biologyâ€”Driven Geneâ€”Gene Interaction Analysis of Ageâ€”Related Cataract in the eMERGE Network. <i>Genetic Epidemiology</i> , 2015, 39, 376-384.	1.3	20
3662	Pyrosequencing and de novo assembly of A ntartic krill (<i>E uphausia superba</i>) transcriptome to study the adaptability of krill to climateâ€”induced environmental changes. <i>Molecular Ecology Resources</i> , 2015, 15, 1460-1471.	4.8	30

#	ARTICLE	IF	CITATIONS
3663	An unusually simple HP1 gene set in Hymenopteran insects. <i>Biochemistry and Cell Biology</i> , 2015, 93, 596-603.	2.0	5
3664	Gene sequence analysis and screening of feature genes in spinal cord injury. <i>Molecular Medicine Reports</i> , 2015, 11, 3615-3620.	2.4	0
3665	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	3.3	69
3667	Regulation of transcription factors on sexual dimorphism of fig wasps. <i>Scientific Reports</i> , 2015, 5, 10696.	3.3	2
3668	Large scale transcriptome analysis reveals interplay between development of forest trees and a beneficial mycorrhiza helper bacterium. <i>BMC Genomics</i> , 2015, 16, 658.	2.8	28
3669	Comparative genome-based identification of a cell wall-anchored protein from <i>Lactobacillus plantarum</i> increases adhesion of <i>Lactococcus lactis</i> to human epithelial cells. <i>Scientific Reports</i> , 2015, 5, 14109.	3.3	29
3670	Functional and structural properties of a novel cellulosome-like multienzyme complex: efficient glycoside hydrolysis of water-insoluble 7-xylosyl-10-deacetylpaclitaxel. <i>Scientific Reports</i> , 2015, 5, 13768.	3.3	23
3671	Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. <i>Royal Society Open Science</i> , 2015, 2, 150377.	2.4	21
3672	Horizontal functional gene transfer from bacteria to fishes. <i>Scientific Reports</i> , 2015, 5, 18676.	3.3	9
3673	Molecular cloning and characterization of alpha - galactosidase gene from <i>Glaciozyma antarctica</i> . <i>AIP Conference Proceedings</i> , 2015, , .	0.4	0
3674	Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19.		1
3675	Tracing the structural evolution of eukaryotic ATP binding cassette transporter superfamily. <i>Scientific Reports</i> , 2015, 5, 16724.	3.3	55
3676	De novo transcriptome profiling of highly purified human lymphocytes primary cells. <i>Scientific Data</i> , 2015, 2, 150051.	5.3	33
3677	Regulatory RNA at the root of animals: dynamic expression of developmental lincRNAs in the calcsponge <i>Sycon ciliatum</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151746.	2.6	16
3678	OsbZIP33 is an ABA-Dependent Enhancer of Drought Tolerance in Rice. <i>Crop Science</i> , 2015, 55, 1673-1685.	1.8	9
3679	Homology-Based Prediction of Potential Protein-Protein Interactions between Human Erythrocytes and <i>Plasmodium falciparum</i> . <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S31880.	2.0	21
3680	Genome-wide Identification of WRKY Genes in the Desert Poplar <i>Populus euphratica</i> and Adaptive Evolution of the Genes in Response to Salt Stress. <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S22067.	1.2	20
3681	Systematic analyses reveal uniqueness and origin of the CFEM domain in fungi. <i>Scientific Reports</i> , 2015, 5, 13032.	3.3	46

#	ARTICLE	IF	CITATIONS
3682	Prioritization Of Nonsynonymous Single Nucleotide Variants For Exome Sequencing Studies Via Integrative Learning On Multiple Genomic Data. Scientific Reports, 2015, 5, 14955.	3.3	10
3683	Overview of the Cancer Genetics and Pathway Curation tasks of BioNLP Shared Task 2013. BMC Bioinformatics, 2015, 16, S2.	2.6	44
3684	Event inference in multidomain families with phylogenetic reconciliation. BMC Bioinformatics, 2015, 16, S8.	2.6	32
3685	Dimeric interactions and complex formation using direct coevolutionary couplings. Scientific Reports, 2015, 5, 13652.	3.3	75
3686	Genome wide discovery of long intergenic non-coding RNAs in Diamondback moth (Plutella Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 582 T	3.3	78
3687	Genome of the facultative scuticociliatosis pathogen Pseudocohnilembus persalinus provides insight into its virulence through horizontal gene transfer. Scientific Reports, 2015, 5, 15470.	3.3	46
3688	The Phylogenetic Signature Underlying ATP Synthase c-Ring Compliance. Biophysical Journal, 2015, 109, 975-987.	0.5	11
3689	Bos taurus papillomavirus (BPV) E6 protein: Sequence analysis and molecular evolution. Veterinary Microbiology, 2015, 181, 328-333.	1.9	0
3690	Pangenome analysis of Bifidobacterium longum and site-directed mutagenesis through by-pass of restriction-modification systems. BMC Genomics, 2015, 16, 832.	2.8	89
3691	Characterization and annotation of Babesia orientalis apicoplast genome. Parasites and Vectors, 2015, 8, 543.	2.5	25
3692	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). Standards in Genomic Sciences, 2015, 10, 86.	1.5	287
3693	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. Bioinformatics, 2015, 31, 926-932.	4.1	1,223
3694	dissectHMMER: a HMMER-based score dissection framework that statistically evaluates fold-critical sequence segments for domain fold similarity. Biology Direct, 2015, 10, 39.	4.6	18
3695	A novel RING finger in the C-terminal domain of the coatomer protein Î±-COP. Biology Direct, 2015, 10, 70.	4.6	7
3696	Draft genome sequence of Methylibium sp. strain T29, a novel fuel oxygenate-degrading bacterial isolate from Hungary. Standards in Genomic Sciences, 2015, 10, 39.	1.5	9
3697	Complete genome sequence of Salinicoccus halodurans H3B36, isolated from the Qaidam Basin in China. Standards in Genomic Sciences, 2015, 10, 116.	1.5	7
3698	Conformational thermodynamics of biomolecular complexes: The histogram-based method. Journal of Physics: Conference Series, 2015, 638, 012013.	0.4	3
3699	MnTEdb, a collective resource for mulberry transposable elements. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	3.0	25

#	ARTICLE	IF	CITATIONS
3700	Rare variants in the notch signaling pathway describe a novel type of autosomal recessive Klippelâ€Feil syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 2795-2799.	1.2	47
3701	Geneâ€based polymorphisms reveal limited genomic divergence in a species with a heritable lifeâ€history dimorphism. Evolution & Development, 2015, 17, 240-247.	2.0	11
3702	Draft Genome Sequence of Mycobacterium tuberculosis Strain MT43, a Representative of the Manu2 Genotype. Genome Announcements, 2015, 3, .	0.8	1
3703	Draft Genome Sequence of Mycobacterium mucogenicum Strain CSUR P2099. Genome Announcements, 2015, 3, .	0.8	1
3704	Pinpointing disease genes through phenomic and genomic data fusion. BMC Genomics, 2015, 16, S3.	2.8	14
3705	Better prediction of functional effects for sequence variants. BMC Genomics, 2015, 16, S1.	2.8	478
3706	High quality genome sequence and description of Enterobacter mori strain 5â€4, isolated from a mixture of formation water and crude-oil. Standards in Genomic Sciences, 2015, 10, 9.	1.5	6
3707	Phylogenomics and sequence-structure-function relationships in the GmrSD family of Type IV restriction enzymes. BMC Bioinformatics, 2015, 16, 336.	2.6	24
3708	Parameterizing sequence alignment with an explicit evolutionary model. BMC Bioinformatics, 2015, 16, 406.	2.6	26
3709	Comparative genomics between human and animal associated subspecies of the Mycobacterium avium complex: a basis for pathogenicity. BMC Genomics, 2015, 16, 695.	2.8	22
3710	Comparative genome analysis of the candidate functional starter culture strains Lactobacillus fermentum 222 and Lactobacillus plantarum 80 for controlled cocoa bean fermentation processes. BMC Genomics, 2015, 16, 766.	2.8	56
3711	Multifunctional polyketide synthase genes identified by genomic survey of the symbiotic dinoflagellate, Symbiodinium minutum. BMC Genomics, 2015, 16, 941.	2.8	28
3712	Metagenome from a Spirulina digesting biogas reactor: analysis via binning of contigs and classification of short reads. BMC Microbiology, 2015, 15, 277.	3.3	32
3713	Implications of ethylene biosynthesis and signaling in soybean drought stress tolerance. BMC Plant Biology, 2015, 15, 213.	3.6	110
3714	Three-dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. BMC Structural Biology, 2015, 15, 20.	2.3	4
3715	BioDB extractor: customized data extraction system for commonly used bioinformatics databases. BioData Mining, 2015, 8, 31.	4.0	2
3716	The UBR-box and its relationship to binuclear RING-like treble clef zinc fingers. Biology Direct, 2015, 10, 36.	4.6	7
3717	Pan-genomic analysis to redefine species and subspecies based on quantum discontinuous variation: the Klebsiella paradigm. Biology Direct, 2015, 10, 55.	4.6	33

#	ARTICLE	IF	CITATIONS
3718	Bacterial calpains and the evolution of the calpain (C2) family of peptidases. <i>Biology Direct</i> , 2015, 10, 66.	4.6	15
3719	The first draft genome of the aquatic model plant <i>Lemna minor</i> opens the route for future stress physiology research and biotechnological applications. <i>Biotechnology for Biofuels</i> , 2015, 8, 188.	6.2	112
3720	Saliva from nymph and adult females of <i>Haemaphysalis longicornis</i> : a proteomic study. <i>Parasites and Vectors</i> , 2015, 8, 338.	2.5	97
3721	Draft genome of <i>Brugia pahangi</i> : high similarity between <i>B. pahangi</i> and <i>B. malayi</i> . <i>Parasites and Vectors</i> , 2015, 8, 451.	2.5	19
3722	Gene expression changes in the salivary glands of <i>Anopheles coluzzii</i> elicited by <i>Plasmodium berghei</i> infection. <i>Parasites and Vectors</i> , 2015, 8, 485.	2.5	17
3723	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	1.4	38
3724	Genome sequence of <i>Oceanobacillus picturae</i> strain S1, an halophilic bacterium first isolated in human gut. <i>Standards in Genomic Sciences</i> , 2015, 10, 91.	1.5	16
3725	Draft genome sequence of <i>Halopiger salifodinae</i> KCY07-B2T, an extremely halophilic archaeon isolated from a salt mine. <i>Standards in Genomic Sciences</i> , 2015, 10, 124.	1.5	2
3726	Draft Genome Sequence of <i>Mycobacterium neworleansense</i> Strain ATCC 49404 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
3727	A refined genome-scale reconstruction of <i>Chlamydomonas</i> metabolism provides a platform for systems-level analyses. <i>Plant Journal</i> , 2015, 84, 1239-1256.	5.7	70
3728	SInCRE structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
3729	Draft Genome Sequence of <i>Streptomyces ahygroscopicus</i> subsp. <i>wuyiensis</i> CK-15, Isolated from Soil in Fujian Province, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
3730	Selection of recombinant anti- α SH3 domain antibodies by high-throughput phage display. <i>Protein Science</i> , 2015, 24, 1890-1900.	7.6	15
3731	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 629-638.	1.8	10
3732	Draft Genome Sequence of <i>Mycobacterium peregrinum</i> Strain CSUR P2098. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
3733	Complete Genome Sequences of <i>Campylobacter jejuni</i> Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barré Syndrome. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
3734	Identifying differentially expressed genes under heat stress and developing molecular markers in orchardgrass (<i>Dactylis glomerata</i> L.) through transcriptome analysis. <i>Molecular Ecology Resources</i> , 2015, 15, 1497-1509.	4.8	63
3735	Patterns of Wnt signaling in the life cycle of <i>Podocoryna carnea</i> and its implications for medusae evolution in Hydrozoa (Cnidaria). <i>Evolution & Development</i> , 2015, 17, 325-336.	2.0	24

#	ARTICLE	IF	CITATIONS
3736	EvoDB: a database of evolutionary rate profiles, associated protein domains and phylogenetic trees for PFAM-A. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav065.	3.0	1
3737	Draft Genome Sequence of Mycobacterium lentiflavum CSUR P1491. Genome Announcements, 2015, 3, .	0.8	1
3738	ProtoBug: functional families from the complete proteomes of insects. Database: the Journal of Biological Databases and Curation, 2015, 2015, bau122.	3.0	1
3739	Quantitative assessment of protein function prediction programs. Genetics and Molecular Research, 2015, 14, 17555-17566.	0.2	2
3740	Positive selection sites in tertiary structure of Leguminosae Chalcone isomerase 1. Genetics and Molecular Research, 2015, 14, 1957-1967.	0.2	2
3741	Genome-wide identification, classification, and analysis of heat shock transcription factor family in Chinese cabbage (<i>Brassica rapa pekinensis</i>). Genetics and Molecular Research, 2015, 14, 2189-2204.	0.2	24
3742	In silico characterization of hypothetical proteins from <i>Paracoccidioides lutzii</i> . Genetics and Molecular Research, 2015, 14, 17416-17425.	0.2	15
3743	Information of Surface Accessibility of the Peptide Fragments of Coat Protein from Alfalfa mosaic virus (AMV) at the Physicochemical and Immunochemical Levels. Drug Designing: Open Access, 2015, 04, .	0.2	2
3744	Barley molybdenum cofactor sulfurase (MCSU): sequencing, modeling, and its comparison to other higher plants. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2015, 39, 786-796.	2.1	3
3745	Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. Viruses, 2015, 7, 5388-5409.	3.3	16
3746	Review of Recent Protein-Protein Interaction Techniques. , 2015, , 99-121.		8
3747	Statistical Approaches to Detecting and Analyzing Tandem Repeats in Genomic Sequences. Frontiers in Bioengineering and Biotechnology, 2015, 3, 31.	4.1	19
3748	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. Frontiers in Bioengineering and Biotechnology, 2015, 3, 95.	4.1	26
3749	Census of solo LuxR genes in prokaryotic genomes. Frontiers in Cellular and Infection Microbiology, 2015, 5, 20.	3.9	82
3750	A Structure-Based Classification and Analysis of Protein Domain Family Binding Sites and Their Interactions. Biology, 2015, 4, 327-343.	2.8	5
3751	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. Biomolecules, 2015, 5, 1441-1466.	4.0	26
3752	How Common Is Disorder? Occurrence of Disordered Residues in Four Domains of Life. International Journal of Molecular Sciences, 2015, 16, 19490-19507.	4.1	24
3753	De Novo Transcriptome Sequencing of <i>Oryza officinalis</i> Wall ex Watt to Identify Disease-Resistance Genes. International Journal of Molecular Sciences, 2015, 16, 29482-29495.	4.1	21

#	ARTICLE	IF	CITATIONS
3754	Gene Expression, Protein Function and Pathways of <i>Arabidopsis thaliana</i> Responding to Silver Nanoparticles in Comparison to Silver Ions, Cold, Salt, Drought, and Heat. <i>Nanomaterials</i> , 2015, 5, 436-467.	4.1	104
3755	The Cytosolic Oligosaccharide-Degrading Proteome of <i>Butyrivibrio Proteoclasticus</i> . <i>Proteomes</i> , 2015, 3, 347-368.	3.5	7
3756	The Evolution of the Scavenger Receptor Cysteine-Rich Domain of the Class A Scavenger Receptors. <i>Frontiers in Immunology</i> , 2015, 6, 342.	4.8	31
3757	Identification of novel esterase-active enzymes from hot environments by use of the host bacterium <i>Thermus thermophilus</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 275.	3.5	65
3758	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.	3.5	58
3759	Discovery of new protein families and functions: new challenges in functional metagenomics for biotechnologies and microbial ecology. <i>Frontiers in Microbiology</i> , 2015, 6, 563.	3.5	52
3760	Changes in gene expression of <i>Prymnesium parvum</i> induced by nitrogen and phosphorus limitation. <i>Frontiers in Microbiology</i> , 2015, 6, 631.	3.5	46
3761	The polar and lateral flagella from <i>Plesiomonas shigelloides</i> are glycosylated with legionaminic acid. <i>Frontiers in Microbiology</i> , 2015, 6, 649.	3.5	16
3762	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192.	3.5	49
3763	Antibacterial phage ORFans of <i>Pseudomonas aeruginosa</i> phage LUZ24 reveal a novel MvaT inhibiting protein. <i>Frontiers in Microbiology</i> , 2015, 6, 1242.	3.5	31
3764	A Hormone-Responsive C1-Domain-Containing Protein At5g17960 Mediates Stress Response in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0115418.	2.5	13
3765	Genome and Transcriptome of <i>Clostridium phytofermentans</i> , Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. <i>PLoS ONE</i> , 2015, 10, e0118285.	2.5	28
3766	The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. <i>PLoS ONE</i> , 2015, 10, e0118606.	2.5	10
3767	Molecular Evolution and Phylogenetic Analysis of Eight COL Superfamily Genes in Group I Related to Photoperiodic Regulation of Flowering Time in Wild and Domesticated Cotton (<i>Gossypium</i>) Species. <i>PLoS ONE</i> , 2015, 10, e0118669.	2.5	18
3768	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. <i>PLoS ONE</i> , 2015, 10, e0120729.	2.5	2
3769	Genome-Wide Comparative Analysis Reveals Similar Types of NBS Genes in Hybrid <i>Citrus sinensis</i> Genome and Original <i>Citrus clementine</i> Genome and Provides New Insights into Non-TIR NBS Genes. <i>PLoS ONE</i> , 2015, 10, e0121893.	2.5	9
3770	Genome-Wide Transcriptome and Expression Profile Analysis of <i>Phalaenopsis</i> during Explant Browning. <i>PLoS ONE</i> , 2015, 10, e0123356.	2.5	16
3771	Building a Better Fragment Library for De Novo Protein Structure Prediction. <i>PLoS ONE</i> , 2015, 10, e0123998.	2.5	25

#	ARTICLE	IF	CITATIONS
3772	Transcriptome-Wide Identification of Salt-Responsive Members of the WRKY Gene Family in <i>Gossypium aridum</i> . PLoS ONE, 2015, 10, e0126148.	2.5	83
3773	Characterization of the Maize Chitinase Genes and Their Effect on <i>Aspergillus flavus</i> and Aflatoxin Accumulation Resistance. PLoS ONE, 2015, 10, e0126185.	2.5	64
3774	Est10: A Novel Alkaline Esterase Isolated from Bovine Rumen Belonging to the New Family XV of Lipolytic Enzymes. PLoS ONE, 2015, 10, e0126651.	2.5	10
3775	Phylogenomic Analysis Reveals Deep Divergence and Recombination in an Economically Important Grapevine Virus. PLoS ONE, 2015, 10, e0126819.	2.5	30
3776	Computational Analysis and Low-Scale Constitutive Expression of Laccases Synthetic Genes GILCC1 from <i>Ganoderma lucidum</i> and POXA 1B from <i>Pleurotus ostreatus</i> in <i>Pichia pastoris</i> . PLoS ONE, 2015, 10, e0116524.	2.5	36
3777	Characterization of the <i>Xylella fastidiosa</i> PD1671 Gene Encoding Degenerate c-di-GMP GGDEF/EAL Domains, and Its Role in the Development of Pierce's Disease. PLoS ONE, 2015, 10, e0121851.	2.5	13
3778	Functional Marker Detection and Analysis on a Comprehensive Transcriptome of Large Yellow Croaker by Next Generation Sequencing. PLoS ONE, 2015, 10, e0124432.	2.5	38
3779	Molecular Determinants Underlying Binding Specificities of the ABL Kinase Inhibitors: Combining Alanine Scanning of Binding Hot Spots with Network Analysis of Residue Interactions and Coevolution. PLoS ONE, 2015, 10, e0130203.	2.5	36
3780	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. PLoS Computational Biology, 2015, 11, e1004325.	3.2	80
3781	How Co-translational Folding of Multi-domain Protein Is Affected by Elongation Schedule: Molecular Simulations. PLoS Computational Biology, 2015, 11, e1004356.	3.2	22
3782	Identification of Ohnolog Genes Originating from Whole Genome Duplication in Early Vertebrates, Based on Synteny Comparison across Multiple Genomes. PLoS Computational Biology, 2015, 11, e1004394.	3.2	113
3783	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. PLoS Computational Biology, 2015, 11, e1004465.	3.2	17
3784	Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Computational Biology, 2015, 11, e1004467.	3.2	36
3785	Functional Basis of Microorganism Classification. PLoS Computational Biology, 2015, 11, e1004472.	3.2	37
3786	Reproductive Mode and the Evolution of Genome Size and Structure in <i>Caenorhabditis</i> Nematodes. PLoS Genetics, 2015, 11, e1005323.	3.5	102
3787	Genome-Wide Collation of the <i>Plasmodium falciparum</i> WDR Protein Superfamily Reveals Malarial Parasite-Specific Features. PLoS ONE, 2015, 10, e0128507.	2.5	9
3788	Large-Scale Evolutionary Analysis of Genes and Supergene Clusters from Terpenoid Modular Pathways Provides Insights into Metabolic Diversification in Flowering Plants. PLoS ONE, 2015, 10, e0128808.	2.5	19
3789	Proteins Related to the Type I Secretion System Are Associated with Secondary SecA_DEAD Domain Proteins in Some Species of Planctomycetes, Verrucomicrobia, Proteobacteria, Nitrospirae and Chlorobi. PLoS ONE, 2015, 10, e0129066.	2.5	1

#	ARTICLE	IF	CITATIONS
3790	Discovery of Chemosensory Genes in the Oriental Fruit Fly, <i>Bactrocera dorsalis</i> . PLoS ONE, 2015, 10, e0129794.	2.5	42
3791	A de novo Assembly of the Common Frog (<i>Rana temporaria</i>) Transcriptome and Comparison of Transcription Following Exposure to Ranavirus and <i>Batrachochytrium dendrobatidis</i> . PLoS ONE, 2015, 10, e0130500.	2.5	32
3792	The Polymerization of <i>Aeromonas hydrophila</i> AH-3 O-Antigen LPS: Concerted Action of WecP and Wzy. PLoS ONE, 2015, 10, e0131905.	2.5	5
3793	De Novo Transcriptome Analysis of <i>Warburgia ugandensis</i> to Identify Genes Involved in Terpenoids and Unsaturated Fatty Acids Biosynthesis. PLoS ONE, 2015, 10, e0135724.	2.5	1
3794	Citing a Data Repository: A Case Study of the Protein Data Bank. PLoS ONE, 2015, 10, e0136631.	2.5	26
3795	Genome-Wide Identification and Expression of <i>Xenopus</i> F-Box Family of Proteins. PLoS ONE, 2015, 10, e0136929.	2.5	3
3796	A Unique Set of the <i>Burkholderia</i> Collagen-Like Proteins Provides Insight into Pathogenesis, Genome Evolution and Niche Adaptation, and Infection Detection. PLoS ONE, 2015, 10, e0137578.	2.5	27
3797	Genome-Wide Characterization and Expression Analysis of Major Intrinsic Proteins during Abiotic and Biotic Stresses in Sweet Orange (<i>Citrus sinensis</i> L. Osb.). PLoS ONE, 2015, 10, e0138786.	2.5	65
3798	De Novo Assembly of the Whole Transcriptome of the Wild Embryo, <i>Preleptocephalus</i> , <i>Leptocephalus</i> , and Glass Eel of <i>Anguilla japonica</i> and Deciphering the Digestive and Absorptive Capacities during Early Development. PLoS ONE, 2015, 10, e0139105.	2.5	23
3799	Functional Advantages of Conserved Intrinsic Disorder in RNA-Binding Proteins. PLoS ONE, 2015, 10, e0139731.	2.5	100
3800	Extending Protein Domain Boundary Predictors to Detect Discontinuous Domains. PLoS ONE, 2015, 10, e0141541.	2.5	5
3801	De Novo Assembly and Characterization of the Invasive Northern Pacific Seastar Transcriptome. PLoS ONE, 2015, 10, e0142003.	2.5	16
3802	Coevolved Mutations Reveal Distinct Architectures for Two Core Proteins in the Bacterial Flagellar Motor. PLoS ONE, 2015, 10, e0142407.	2.5	8
3803	Relationships between predicted moonlighting proteins, human diseases, and comorbidities from a network perspective. <i>Frontiers in Physiology</i> , 2015, 6, 171.	2.8	14
3804	Genome-wide identification of CAMTA gene family members in <i>Medicago truncatula</i> and their expression during root nodule symbiosis and hormone treatments. <i>Frontiers in Plant Science</i> , 2015, 6, 459.	3.6	41
3805	Comparative analysis of the phytoeyanin gene family in 10 plant species: a focus on <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 515.	3.6	36
3806	The heat shock factor gene family in <i>Salix suchowensis</i> : a genome-wide survey and expression profiling during development and abiotic stresses. <i>Frontiers in Plant Science</i> , 2015, 6, 748.	3.6	40
3807	microProtein Prediction Program (miP3): A Software for Predicting microProteins and Their Target Transcription Factors. <i>International Journal of Genomics</i> , 2015, 2015, 1-4.	1.6	6

#	ARTICLE	IF	CITATIONS
3808	Divergence of the bZIP Gene Family in Strawberry, Peach, and Apple Suggests Multiple Modes of Gene Evolution after Duplication. <i>International Journal of Genomics</i> , 2015, 2015, 1-11.	1.6	21
3809	Comparative Analysis of Apicoplast-Targeted Protein Extension Lengths in Apicomplexan Parasites. <i>BioMed Research International</i> , 2015, 2015, 1-6.	1.9	7
3810	A Database of Plastid Protein Families from Red Algae and Apicomplexa and Expression Regulation of the <i>moeB</i> Gene. <i>BioMed Research International</i> , 2015, 2015, 1-5.	1.9	7
3811	A Large-Scale Structural Classification of Antimicrobial Peptides. <i>BioMed Research International</i> , 2015, 2015, 1-6.	1.9	123
3812	Developing of the Computer Method for Annotation of Bacterial Genes. <i>Advances in Bioinformatics</i> , 2015, 2015, 1-9.	5.7	15
3813	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. <i>ELife</i> , 2015, 4, e07966.	6.0	50
3814	SIFTER-T: A scalable and optimized framework for the SIFTER phylogenomic method of probabilistic protein domain annotation. <i>BioTechniques</i> , 2015, 58, 140-142.	1.8	1
3815	Molecular cloning of RBCS genes in <i>Selaginella</i> and the evolution of the <i>rbcS</i> gene family. <i>Archives of Biological Sciences</i> , 2015, 67, 373-383.	0.5	1
3816	RNA helicase A activity is inhibited by oncogenic transcription factor EWS-FLI1. <i>Nucleic Acids Research</i> , 2015, 43, 1069-1080.	14.5	30
3817	NrichD database: sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. <i>Nucleic Acids Research</i> , 2015, 43, D300-D305.	14.5	12
3818	Recognition rules for binding of Zn-Cys ² His ² transcription factors to operator DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 253-266.	3.5	10
3819	Comparative analysis of metagenomes from three methanogenic hydrocarbon-degrading enrichment cultures with 41 environmental samples. <i>ISME Journal</i> , 2015, 9, 2028-2045.	9.8	87
3820	Histone chaperones in <i>Arabidopsis</i> and rice: genome-wide identification, phylogeny, architecture and transcriptional regulation. <i>BMC Plant Biology</i> , 2015, 15, 42.	3.6	44
3821	Expression of extra-cellular levansucrase in <i>Pseudomonas syringae</i> is controlled by the in planta fitness-promoting metabolic repressor HexR. <i>BMC Microbiology</i> , 2015, 15, 48.	3.3	14
3822	Protein structure prediction guided by crosslinking restraints – A systematic evaluation of the impact of the crosslinking spacer length. <i>Methods</i> , 2015, 89, 79-90.	3.8	39
3823	Metagenomics: Tools and Insights for Analyzing Next-Generation Sequencing Data Derived from Biodiversity Studies. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S12462.	2.0	317
3824	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. <i>Molecular Biology and Evolution</i> , 2015, 32, 2195-2207.	8.9	48
3825	It's more than stamp collecting: how genome sequencing can unify biological research. <i>Trends in Genetics</i> , 2015, 31, 411-421.	6.7	37

#	ARTICLE	IF	CITATIONS
3826	Reinforcing the Egg-Timer: Recruitment of Novel Lophotrochozoa Homeobox Genes to Early and Late Development in the Pacific Oyster. <i>Genome Biology and Evolution</i> , 2015, 7, 677-688.	2.5	42
3827	Genome-wide survey and expression analysis of the PUB family in Chinese cabbage (<i>Brassica rapa</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overl	2.1	39
3828	Analysis of yeh Fimbrial Gene Cluster in <i>Escherichia coli</i> O157:H7 in Order to Find a Genetic Marker for this Serotype. <i>Current Microbiology</i> , 2015, 71, 274-282.	2.2	21
3829	The central nervous system transcriptome of the weakly electric brown ghost knifefish (<i>Apteronotus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	19
3830	A genetic map of cassava (<i>Manihot esculenta</i> Crantz) with integrated physical mapping of immunity-related genes. <i>BMC Genomics</i> , 2015, 16, 190.	2.8	65
3831	Pan-genome dynamics of <i>Pseudomonas</i> gene complements enriched across hexachlorocyclohexane dumpsite. <i>BMC Genomics</i> , 2015, 16, 313.	2.8	19
3832	Influence of in situ progressive N-terminal is still controversial truncation of glycogen branching enzyme in <i>Escherichia coli</i> DH5 α on glycogen structure, accumulation, and bacterial viability. <i>BMC Microbiology</i> , 2015, 15, 96.	3.3	26
3833	Predominant expression and activity of vacuolar H ⁺ -ATPases in the mixed segment of the wood-feeding termite <i>Nasutitermes takasagoensis</i> . <i>Journal of Insect Physiology</i> , 2015, 78, 1-8.	2.0	5
3834	Predicting Sub-cellular Location of Proteins Based on Hierarchical Clustering and Hidden Markov Models. <i>Lecture Notes in Computer Science</i> , 2015, , 256-263.	1.3	1
3835	Environmental Sensing in Actinobacteria: a Comprehensive Survey on the Signaling Capacity of This Phylum. <i>Journal of Bacteriology</i> , 2015, 197, 2517-2535.	2.2	54
3836	Prediction of protein solvent accessibility using PSO-SVR with multiple sequence-derived features and weighted sliding window scheme. <i>BioData Mining</i> , 2015, 8, 3.	4.0	17
3837	Complete genome and gene expression analyses of <i>Asaia bogorensis</i> reveal unique responses to culture with mammalian cells as a potential opportunistic human pathogen. <i>DNA Research</i> , 2015, 22, 357-366.	3.4	14
3838	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. <i>New Phytologist</i> , 2015, 208, 1227-1240.	7.3	165
3839	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	2.5	22
3840	Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <i>BMC Genomics</i> , 2015, 16, 540.	2.8	33
3841	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015, 528, 580-584.	27.8	227
3842	Comparative study of the effectiveness and limitations of current methods for detecting sequence coevolution. <i>Bioinformatics</i> , 2015, 31, 1929-1937.	4.1	22
3843	Improving compoundâ€“protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015, 31, i221-i229.	4.1	201

#	ARTICLE	IF	CITATIONS
3844	Protein contact prediction by integrating joint evolutionary coupling analysis and supervised learning. <i>Bioinformatics</i> , 2015, 31, 3506-3513.	4.1	101
3845	Epigenetic regulation of serotype expression antagonizes transcriptome dynamics in <i>Paramecium tetraurelia</i> . <i>DNA Research</i> , 2015, 22, 293-305.	3.4	18
3846	The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. <i>Genome Biology and Evolution</i> , 2015, 7, 1713-1727.	2.5	36
3847	Distinctive Genome Reduction Rates Revealed by Genomic Analyses of Two <i>Coxiella</i> -Like Endosymbionts in Ticks. <i>Genome Biology and Evolution</i> , 2015, 7, 1779-1796.	2.5	140
3848	Interspecific Differential Expression Analysis of RNA-Seq Data Yields Insight into Life Cycle Variation in Hydractiniid Hydrozoans. <i>Genome Biology and Evolution</i> , 2015, 7, 2417-2431.	2.5	22
3849	Developmentally regulated <i>HEART STOPPER</i> , a mitochondrially targeted L18 ribosomal protein gene, is required for cell division, differentiation, and seed development in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 5867-5880.	4.8	24
3850	A common tRNA modification at an unusual location: the discovery of wyosine biosynthesis in mitochondria. <i>Nucleic Acids Research</i> , 2015, 43, 4262-4273.	14.5	22
3851	By the company they keep: interaction networks define the binding ability of transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, e125-e125.	14.5	12
3852	Vascular expression of <i>Populus</i> LRR-RLK genes and the effects of their overexpression on wood formation. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	6
3853	Complete genome sequence of bacteriophage P8625, the first lytic phage that infects <i>Verrucomicrobia</i> . <i>Standards in Genomic Sciences</i> , 2015, 10, 96.	1.5	1
3854	Biochemical and Kinetic Characterization of the Eukaryotic Phosphotransacetylase Class IIa Enzyme from <i>Phytophthora ramorum</i> . <i>Eukaryotic Cell</i> , 2015, 14, 652-660.	3.4	2
3855	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MT11, Which Represents a New Lineage. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
3856	Complete Genome Sequences of Four Novel <i>Escherichia coli</i> Bacteriophages Belonging to New Phage Groups. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
3857	Draft Genome Sequence of <i>Mycobacterium europaeum</i> Strain CSUR P1344. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
3858	Draft Genome Sequence of the <i>Lactobacillus agilis</i> Strain Marseille. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
3859	Draft Genome Sequence of <i>Mycobacterium bohemicum</i> Strain DSM 44277 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
3860	The Intracellular Scots Pine Shoot Symbiont <i>Methylobacterium extorquens</i> DSM13060 Aggregates around the Host Nucleus and Encodes Eukaryote-Like Proteins. <i>MBio</i> , 2015, 6, .	4.1	44
3861	The Peptidoglycan-Binding Protein SjcF1 Influences Septal Junction Function and Channel Formation in the Filamentous Cyanobacterium <i>Anabaena</i> . <i>MBio</i> , 2015, 6, e00376.	4.1	33

#	ARTICLE	IF	CITATIONS
3862	The language of the protein universe. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 50-56.	3.3	27
3863	Predicting diverse M-best protein contact maps. , 2015, , .		0
3864	Predicting gene functions from multiple biological sources using novel ensemble methods. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 12, 184.	0.1	2
3865	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. <i>Standards in Genomic Sciences</i> , 2015, 10, 4.	1.5	4
3866	Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv100.	6.5	19
3867	Complete genome of the marine bacterium <i>Wenzhouxiangella marina</i> KCTC 42284T. <i>Marine Genomics</i> , 2015, 24, 277-280.	1.1	10
3868	Cloud computing service framework for bioinformatics tools. , 2015, , .		1
3869	Rice MEL2, the RNA recognition motif (RRM) protein, binds in vitro to meiosis-expressed genes containing U-rich RNA consensus sequences in the 3' UTR. <i>Plant Molecular Biology</i> , 2015, 89, 293-307.	3.9	10
3870	SpirPro: A <i>Spirulina</i> proteome database and web-based tools for the analysis of protein-protein interactions at the metabolic level in <i>Spirulina (Arthrospira) platensis</i> C1. <i>BMC Bioinformatics</i> , 2015, 16, 233.	2.6	14
3871	In-depth analysis of the critical genes and pathways in colorectal cancer. <i>International Journal of Molecular Medicine</i> , 2015, 36, 923-930.	4.0	20
3872	Sequence-based protein superfamily classification using computational intelligence techniques: a review. <i>International Journal of Data Mining and Bioinformatics</i> , 2015, 11, 424.	0.1	3
3873	Proteins involved in more domain types tend to be more essential. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 91.	0.2	3
3874	The YhhN protein of <i>Legionella pneumophila</i> is a Lysoplasmalogenase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 742-751.	2.6	22
3875	Identification and expression analyses of calmodulin-binding transcription activator genes in soybean. <i>Plant and Soil</i> , 2015, 386, 205-221.	3.7	52
3876	Codon usage and protein sequence pattern dependency in different organisms: A Bioinformatics approach. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550002.	0.8	1
3877	Robust Identification of Orthologues and Paralogues for Microbial Pan-Genomics Using GET_HOMOLOGUES: A Case Study of pIncA/C Plasmids. <i>Methods in Molecular Biology</i> , 2015, 1231, 203-232.	0.9	54
3878	Genomic Potential for Polysaccharide Deconstruction in Bacteria. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1513-1519.	3.1	155
3879	Gene Encoding Inulinase Isolated from <i>Penicillium citrinum</i> ESS and Its Molecular Phylogeny. <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 1358-1370.	2.9	5

#	ARTICLE	IF	CITATIONS
3880	Molecular insights into the binding of coenzyme F_{420} to the conserved protein R_{v1155} from <i>Mycobacterium tuberculosis</i> . Protein Science, 2015, 24, 729-740.	7.6	16
3881	<i>LiZIP3</i> is a cellular zinc transporter that mediates the tightly regulated import of zinc in <i>Leishmania infantum</i> parasites. Molecular Microbiology, 2015, 96, 581-595.	2.5	16
3882	Protein deimmunization via structure-based design enables efficient epitope deletion at high mutational loads. Biotechnology and Bioengineering, 2015, 112, 1306-1318.	3.3	29
3883	Arginine-rhamnosylation as new strategy to activate translation elongation factor P. Nature Chemical Biology, 2015, 11, 266-270.	8.0	116
3884	Molecular responses of <i>Frankia</i> sp. strain QA3 to naphthalene. Canadian Journal of Microbiology, 2015, 61, 281-292.	1.7	16
3885	Autophagy Regulatory Network "A systems-level bioinformatics resource for studying the mechanism and regulation of autophagy. Autophagy, 2015, 11, 155-165.	9.1	89
3886	mRNA secondary structure engineering of <i>Thermobifida fusca</i> endoglucanase (Cel6A) for enhanced expression in <i>Escherichia coli</i> . World Journal of Microbiology and Biotechnology, 2015, 31, 499-506.	3.6	3
3887	Genome-Wide Analysis of Alternative Splicing Landscapes Modulated during Plant-Virus Interactions in <i>Brachypodium distachyon</i> . Plant Cell, 2015, 27, 71-85.	6.6	145
3888	Discovery of a Novel Coronavirus, China Rattus Coronavirus HKU24, from Norway Rats Supports the Murine Origin of Betacoronavirus 1 and Has Implications for the Ancestor of Betacoronavirus Lineage A. Journal of Virology, 2015, 89, 3076-3092.	3.4	147
3889	A Similarity-Based Learning Algorithm Using Distance Transformation. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 1452-1464.	5.7	2
3890	PHOTOSYSTEM II PROTEIN33, a Protein Conserved in the Plastid Lineage, Is Associated with the Chloroplast Thylakoid Membrane and Provides Stability to Photosystem II Supercomplexes in Arabidopsis. Plant Physiology, 2015, 167, 481-492.	4.8	46
3891	Bioinformatic Techniques on Marine Genomics. , 2015, , 295-306.		0
3892	Genetic and genomic analysis of RNases in model cyanobacteria. Photosynthesis Research, 2015, 126, 171-183.	2.9	23
3893	New Mode of Energy Metabolism in the Seventh Order of Methanogens as Revealed by Comparative Genome Analysis of <i>Candidatus Methanoplasma termitum</i> . Applied and Environmental Microbiology, 2015, 81, 1338-1352.	3.1	235
3894	The Origin of CDR H3 Structural Diversity. Structure, 2015, 23, 302-311.	3.3	78
3895	Molecular Evolution of Nitrogen Assimilatory Enzymes in Marine Prasinophytes. Journal of Molecular Evolution, 2015, 80, 65-80.	1.8	8
3896	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. Bioinformatics, 2015, 31, 1411-1419.	4.1	167
3897	Current Functional Metagenomic Approaches Only Expand the Existing Protease Sequence Space, but does not Presently Add Any Novelty to it. Current Microbiology, 2015, 70, 19-26.	2.2	10

#	ARTICLE	IF	CITATIONS
3898	Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 76-81.	7.1	236
3899	UProC: tools for ultra-fast protein domain classification. <i>Bioinformatics</i> , 2015, 31, 1382-1388.	4.1	85
3900	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.	2.4	47
3901	Tannase Sequence from a Xerophilic <i>Aspergillus niger</i> Strain and Production of the Enzyme in <i>Pichia pastoris</i> . <i>Molecular Biotechnology</i> , 2015, 57, 439-447.	2.4	12
3902	RPI-Pred: predicting ncRNA-protein interaction using sequence and structural information. <i>Nucleic Acids Research</i> , 2015, 43, 1370-1379.	14.5	178
3903	Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses. <i>Briefings in Bioinformatics</i> , 2015, 16, 745-758.	6.5	66
3904	Regulation of the expression of the whole genome of <i>Ustilago maydis</i> by a MAPK pathway. <i>Archives of Microbiology</i> , 2015, 197, 575-588.	2.2	7
3905	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. <i>BMC Genomics</i> , 2015, 16, 77.	2.8	39
3906	Chemotactic signal transduction and phosphate metabolism as adaptive strategies during citrus canker induction by <i>Xanthomonas citri</i> . <i>Functional and Integrative Genomics</i> , 2015, 15, 197-210.	3.5	39
3907	Evolutionary and expression analysis of a MADS-box gene superfamily involved in ovule development of seeded and seedless grapevines. <i>Molecular Genetics and Genomics</i> , 2015, 290, 825-846.	2.1	46
3908	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <i>Nature Genetics</i> , 2015, 47, 416-422.	21.4	91
3909	Genome-wide analysis of bHLH transcription factor and involvement in the infection by yellow leaf curl virus in tomato (<i>Solanum lycopersicum</i>). <i>BMC Genomics</i> , 2015, 16, 39.	2.8	102
3910	A new method to improve network topological similarity search: applied to fold recognition. <i>Bioinformatics</i> , 2015, 31, 2106-2114.	4.1	12
3911	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. <i>ISME Journal</i> , 2015, 9, 2191-2205.	9.8	42
3912	Terminal-Repeat Retrotransposons with GAG Domain in Plant Genomes: A New Testimony on the Complex World of Transposable Elements. <i>Genome Biology and Evolution</i> , 2015, 7, 493-504.	2.5	23
3913	Genomic characterization of a temperate phage of the psychrotolerant deep-sea bacterium <i>Aurantimonas</i> sp.. <i>Extremophiles</i> , 2015, 19, 49-58.	2.3	15
3914	The Amaranthin-Like Lectin (LuALL) Genes of Flax: a Unique Gene Family with Members Inducible by Defence Hormones. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 731-741.	1.8	13
3915	Biosynthesis and genomic analysis of medium-chain hydrocarbon production by the endophytic fungal isolate <i>Nigrograna mackinnonii</i> E5202H. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3715-3728.	3.6	44

#	ARTICLE	IF	CITATIONS
3916	An overview on transcriptional regulators in <i>Streptomyces</i> . <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 1017-1039.	1.9	115
3917	The Lipoxygenase Gene Family in Poplar: Identification, Classification, and Expression in Response to MeJA Treatment. <i>PLoS ONE</i> , 2015, 10, e0125526.	2.5	57
3918	Physiological and proteomic analyses of leaves from the halophyte <i>Tangut Nitraria</i> reveals diverse response pathways critical for high salinity tolerance. <i>Frontiers in Plant Science</i> , 2015, 6, 30.	3.6	47
3919	The Origin and Evolution of Ribonucleotide Reduction. <i>Life</i> , 2015, 5, 604-636.	2.4	74
3920	RNA-seq for gene identification and transcript profiling in relation to root growth of bermudagrass (<i>Cynodon dactylon</i>) under salinity stress. <i>BMC Genomics</i> , 2015, 16, 575.	2.8	67
3921	Draft Genome Sequence of the <i>Lactobacillus mucosae</i> Strain Marseille. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
3922	C-S bond cleavage by a polyketide synthase domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10359-10364.	7.1	39
3923	CGMD: An integrated database of cancer genes and markers. <i>Scientific Reports</i> , 2015, 5, 12035.	3.3	6
3924	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. <i>EBioMedicine</i> , 2015, 2, 234-243.	6.1	20
3925	The insertion domain 1 of class IIA dimeric glycyl-tRNA synthetase is a rubredoxin-like zinc ribbon. <i>Journal of Structural Biology</i> , 2015, 190, 38-46.	2.8	5
3926	De novo assembly and characterization of germinating lettuce seed transcriptome using Illumina paired-end sequencing. <i>Plant Physiology and Biochemistry</i> , 2015, 96, 154-162.	5.8	10
3927	Identification and expression analysis of the <i>LRR-RLK</i> gene family in tomato (<i>Solanum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	33
3928	Genome-wide characterisation and analysis of bHLH transcription factors related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Scientific Reports</i> , 2015, 5, 11244.	3.3	97
3929	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015, 14, 2976-2987.	3.7	16
3930	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.	2.0	18
3931	AguR, a Transmembrane Transcription Activator of the Putrescine Biosynthesis Operon in <i>Lactococcus lactis</i> , Acts in Response to the Agmatine Concentration. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6145-6157.	3.1	20
3932	Map-based cloning and characterization of <i>BPH29</i> , a B3 domain-containing recessive gene conferring brown planthopper resistance in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 6035-6045.	4.8	148
3933	Genome-Wide Identification and Evolution of HECT Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2015, 16, 8517-8535.	4.1	15

#	ARTICLE	IF	CITATIONS
3934	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	6.5	6
3935	The Secreted Proteins of <i>Achlya hypogyna</i> and <i>Thraustotheca clavata</i> Identify the Ancestral Oomycete Secretome and Reveal Gene Acquisitions by Horizontal Gene Transfer. <i>Genome Biology and Evolution</i> , 2015, 7, 120-135.	2.5	34
3936	Structural insight into operator dre-sites recognition and effector binding in the GntR/HutC transcription regulator NagR. <i>Nucleic Acids Research</i> , 2015, 43, 1283-1296.	14.5	36
3937	In silico identification of AMPylating enzymes and study of their divergent evolution. <i>Scientific Reports</i> , 2015, 5, 10804.	3.3	32
3938	Characterization of Epidemic Inc11-Î ³ Plasmids Harboring Ambler Class A and C Genes in <i>Escherichia coli</i> and <i>Salmonella enterica</i> from Animals and Humans. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 5357-5365.	3.2	62
3939	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011.	3.5	29
3940	Analysis of Arabidopsis floral transcriptome: detection of new florally expressed genes and expansion of Brassicaceae-specific gene families. <i>Frontiers in Plant Science</i> , 2015, 5, 802.	3.6	28
3941	Combined transcriptome and metabolite profiling reveals that <i>PLR1</i> plays an important role in larciresinol accumulation in <i>Isatis indigotica</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 6259-6271.	4.8	38
3942	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015, 43, W134-W140.	14.5	73
3943	Lactococcal 949 Group Phages Recognize a Carbohydrate Receptor on the Host Cell Surface. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3299-3305.	3.1	35
3944	Functional characterization of two SOS-regulated genes involved in mitomycin C resistance in <i>Caulobacter crescentus</i> . <i>DNA Repair</i> , 2015, 33, 78-89.	2.8	10
3945	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. <i>Journal of Experimental Botany</i> , 2015, 66, 4239-4250.	4.8	10
3946	Genome Sequence of <i>Clostridium acetobutylicum</i> GXAS18-1, a Novel Biobutanol Production Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
3947	The functional landscape bound to the transcription factors of <i>Escherichia coli</i> K-12. <i>Computational Biology and Chemistry</i> , 2015, 58, 93-103.	2.3	16
3948	Identification of SlpB, a Cytotoxic Protease from <i>Serratia marcescens</i> . <i>Infection and Immunity</i> , 2015, 83, 2907-2916.	2.2	35
3949	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <i>Frontiers in Microbiology</i> , 2015, 6, 199.	3.5	24
3950	Mining proteomic data to expose protein modifications in <i>Methanosarcina mazei</i> strain GÄ¶1. <i>Frontiers in Microbiology</i> , 2015, 6, 149.	3.5	8
3951	Evolutionary dynamics of rhomboid proteases in Streptomycetes. <i>BMC Research Notes</i> , 2015, 8, 234.	1.4	0

#	ARTICLE	IF	CITATIONS
3952	The origin of the ADAR gene family and animal RNA editing. BMC Evolutionary Biology, 2015, 15, 4.	3.2	65
3953	An Integrated Approach to Reconstructing Genome-Scale Transcriptional Regulatory Networks. PLoS Computational Biology, 2015, 11, e1004103.	3.2	23
3954	Soybean kinome: functional classification and gene expression patterns. Journal of Experimental Botany, 2015, 66, 1919-1934.	4.8	43
3955	Protein Topology Determines Cysteine Oxidation Fate: The Case of Sulfenyl Amide Formation among Protein Families. PLoS Computational Biology, 2015, 11, e1004051.	3.2	39
3956	Predicting Peptide-Mediated Interactions on a Genome-Wide Scale. PLoS Computational Biology, 2015, 11, e1004248.	3.2	16
3957	The Aspartate-Less Receiver (ALR) Domains: Distribution, Structure and Function. PLoS Pathogens, 2015, 11, e1004795.	4.7	25
3958	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. Frontiers in Plant Science, 2014, 5, 759.	3.6	98
3959	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. Nature Reviews Microbiology, 2015, 13, 360-372.	28.6	544
3960	Batf3 deficiency is not critical for the generation of CD8 ⁺ dendritic cells. Immunobiology, 2015, 220, 518-524.	1.9	18
3961	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330
3962	Proteasome stress responses in <i>Schistosoma mansoni</i> . Parasitology Research, 2015, 114, 1747-1760.	1.6	8
3963	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
3964	PAV markers in <i>Sorghum bicolor</i> : genome pattern, affected genes and pathways, and genetic linkage map construction. Theoretical and Applied Genetics, 2015, 128, 623-637.	3.6	15
3965	Microbial Consortium Associated with the Antarctic Marine Ciliate <i>Euplotes focardii</i> : An Investigation from Genomic Sequences. Microbial Ecology, 2015, 70, 484-497.	2.8	42
3966	Diversity of the expression profiles of late embryogenesis abundant (LEA) protein encoding genes in the anhydrobiotic midge <i>Polypedilum vanderplanki</i> . Planta, 2015, 242, 451-459.	3.2	30
3967	Rapid turnover of antimicrobial-type cysteine-rich protein genes in closely related <i>Oryza</i> genomes. Molecular Genetics and Genomics, 2015, 290, 1753-1770.	2.1	6
3968	Molecular and Biochemical Characterization of a Novel Multidomain Xylanase from <i>Arthrobacter</i> sp. GN16 Isolated from the Feces of <i>Grus nigricollis</i> . Applied Biochemistry and Biotechnology, 2015, 175, 573-588.	2.9	10
3969	Genetic diversity of <i>Trichoderma atroviride</i> strains collected in Poland and identification of loci useful in detection of within-species diversity. Folia Microbiologica, 2015, 60, 297-307.	2.3	21

#	ARTICLE	IF	CITATIONS
3970	Studies on Deimmunization of Antileukaemic L-Asparaginase to have Reduced Clinical Immunogenicity- An in silico Approach. Pathology and Oncology Research, 2015, 21, 909-920.	1.9	20
3971	Structure-based function analysis of putative conserved proteins with isomerase activity from Haemophilus influenzae. 3 Biotech, 2015, 5, 741-763.	2.2	14
3972	Uncovering the novel characteristics of Asian honey bee, Apis cerana, by whole genome sequencing. BMC Genomics, 2015, 16, 1.	2.8	1,445
3973	MDAT- Aligning multiple domain arrangements. BMC Bioinformatics, 2015, 16, 19.	2.6	5
3974	MBBC: an efficient approach for metagenomic binning based on clustering. BMC Bioinformatics, 2015, 16, 36.	2.6	23
3975	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. BMC Bioinformatics, 2015, 16, 96.	2.6	6
3976	micropan: an R-package for microbial pan-genomics. BMC Bioinformatics, 2015, 16, 79.	2.6	165
3977	Genomic and transcriptomic analysis of the endophytic fungus Pestalotiopsis fici reveals its lifestyle and high potential for synthesis of natural products. BMC Genomics, 2015, 16, 28.	2.8	102
3978	Genome-wide analysis of the R2R3-MYB transcription factor genes in Chinese cabbage (Brassica rapa) Tj ETQq0 0 0.rgBT /Overclock 10 Tf	2.8	71
3979	The evolutionary and functional diversity of classical and lesser-known cytoplasmic and organellar translational GTPases across the tree of life. BMC Genomics, 2015, 16, 78.	2.8	48
3980	Genome-wide survey and expression analysis of F-box genes in chickpea. BMC Genomics, 2015, 16, 67.	2.8	68
3981	A novel Schistosoma japonicum endonuclease homologous to DNase II. BMC Genomics, 2015, 16, 126.	2.8	10
3982	Identification of three extra-chromosomal replicons in Leptospira pathogenic strain and development of new shuttle vectors. BMC Genomics, 2015, 16, 90.	2.8	17
3983	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49
3984	Retained duplicate genes in green alga Chlamydomonas reinhardtii tend to be stress responsive and experience frequent response gains. BMC Genomics, 2015, 16, 149.	2.8	12
3985	The genome of the basal agaricomycete Xanthophyllomyces dendrorhous provides insights into the organization of its acetyl-CoA derived pathways and the evolution of Agaricomycotina. BMC Genomics, 2015, 16, 233.	2.8	47
3986	Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (Pyrus bretschneideri) and five other Rosaceae species. BMC Plant Biology, 2015, 15, 12.	3.6	138
3987	The observation of evolutionary interaction pattern pairs in membrane proteins. BMC Structural Biology, 2015, 15, 6.	2.3	1

#	ARTICLE	IF	CITATIONS
3988	WallProtDB, a database resource for plant cell wall proteomics. <i>Plant Methods</i> , 2015, 11, 2.	4.3	70
3989	Mining the entire Protein DataBank for frequent spatially cohesive amino acid patterns. <i>BioData Mining</i> , 2015, 8, 4.	4.0	12
3990	The draft genome of <i>Primula veris</i> yields insights into the molecular basis of heterostyly. <i>Genome Biology</i> , 2015, 16, 12.	8.8	96
3991	K-core decomposition of a protein domain co-occurrence network reveals lower cancer mutation rates for interior cores. <i>Journal of Clinical Bioinformatics</i> , 2015, 5, 1.	1.2	16
3992	Habitat Visualization and Genomic Analysis of <i>Candidatus Pantoea carbekii</i> , the Primary Symbiont of the Brown Marmorated Stink Bug. <i>Genome Biology and Evolution</i> , 2015, 7, 620-635.	2.5	50
3993	X-Linked <i>TEX11</i> Mutations, Meiotic Arrest, and Azoospermia in Infertile Men. <i>New England Journal of Medicine</i> , 2015, 372, 2097-2107.	27.0	279
3994	Mannans and endo- β -mannanases (MAN) in <i>Brachypodium distachyon</i> : expression profiling and possible role of the BdMAN genes during coleorhiza-limited seed germination. <i>Journal of Experimental Botany</i> , 2015, 66, 3753-3764.	4.8	31
3995	Cancer3D: understanding cancer mutations through protein structures. <i>Nucleic Acids Research</i> , 2015, 43, D968-D973.	14.5	46
3996	Structural Features of the Receptor Tyrosine Kinase Ectodomains. , 2015, , 163-193.		6
3997	A Computational Domain-Based Feature Grouping Approach for Prediction of Stability of SCF Ligases. <i>Lecture Notes in Computer Science</i> , 2015, , 630-640.	1.3	1
3998	Genome Sequence, Comparative Analysis, and Evolutionary Insights into Chitinases of Entomopathogenic Fungus <i>Hirsutella thompsonii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 916-930.	2.5	39
3999	Evolutionary Patterns in Coiled-Coils. <i>Genome Biology and Evolution</i> , 2015, 7, 545-556.	2.5	27
4000	Lytic activity of the staphylolytic Twort phage endolysin CHAP domain is enhanced by the SH3b cell wall binding domain. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-8.	1.8	43
4001	Systematic identification and characterization of long intergenic non-coding RNAs in fetal porcine skeletal muscle development. <i>Scientific Reports</i> , 2015, 5, 8957.	3.3	154
4002	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. <i>Journal of Proteome Research</i> , 2015, 14, 1880-1887.	3.7	106
4003	Prediction of Human Gene - Phenotype Associations by Exploiting the Hierarchical Structure of the Human Phenotype Ontology. <i>Lecture Notes in Computer Science</i> , 2015, , 66-77.	1.3	3
4004	Faster sequence homology searches by clustering subsequences. <i>Bioinformatics</i> , 2015, 31, 1183-1190.	4.1	64
4005	Characterization of Novel Family IV Esterase and Family I.3 Lipase from an Oil-Polluted Mud Flat Metagenome. <i>Molecular Biotechnology</i> , 2015, 57, 781-792.	2.4	26

#	ARTICLE	IF	CITATIONS
4006	Widespread Proteome Remodeling and Aggregation in Aging <i>C.Âelegans</i> . <i>Cell</i> , 2015, 161, 919-932.	28.9	478
4007	Sensorâ€response regulator interactions in a cross-regulated signal transduction network. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1504-1515.	1.8	10
4008	Novel Transcriptional Regulons for Autotrophic Cycle Genes in Crenarchaeota. <i>Journal of Bacteriology</i> , 2015, 197, 2383-2391.	2.2	11
4009	The role of RNA conformation in RNA-protein recognition. <i>RNA Biology</i> , 2015, 12, 720-727.	3.1	31
4010	Mutations Associated with Reduced Surotomycin Susceptibility in <i>Clostridium difficile</i> and <i>Enterococcus</i> Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 4139-4147.	3.2	21
4011	Sequence and expression analysis of the AMT gene family in poplar. <i>Frontiers in Plant Science</i> , 2015, 6, 337.	3.6	43
4012	Feature extraction by statistical contact potentials and wavelet transform for predicting subcellular localizations in gram negative bacterial proteins. <i>Journal of Theoretical Biology</i> , 2015, 364, 121-130.	1.7	5
4013	Efficient Assembly of Ribosomes Is Inhibited by Deletion of <i><i>bipA</i></i> in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2015, 197, 1819-1827.	2.2	20
4014	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.	2.5	18
4015	Limited Portability of G-Patch Domains in Regulators of the Prp43 RNA Helicase Required for Pre-mRNA Splicing and Ribosomal RNA Maturation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015, 200, 135-147.	2.9	14
4016	Characterization of a new ViI-like <i>Erwinia amylovora</i> bacteriophage phiEa2809. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	18
4017	Molecular modeling, simulation and virtual screening of MurD ligase protein from <i>Salmonella typhimurium</i> LT2. <i>Journal of Pharmacological and Toxicological Methods</i> , 2015, 73, 34-41.	0.7	12
4018	MadR1, a <i>Mycobacterium tuberculosis</i> cell cycle stress response protein that is a member of a widely conserved protein class of prokaryotic, eukaryotic and archeal origin. <i>Tuberculosis</i> , 2015, 95, 251-258.	1.9	5
4019	A functional role of Rv1738 in <i><i>Mycobacterium tuberculosis</i></i> persistence suggested by racemic protein crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4310-4315.	7.1	43
4020	Loss of <i><i>Drosophila</i></i> pheromone reverses its role in sexual communication in <i><i>Drosophila suzukii</i></i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20143018.	2.6	70
4021	Genome-wide identification of auxin response factor (ARF) genes and its tissue-specific prominent expression in <i>Gossypium raimondii</i> . <i>Functional and Integrative Genomics</i> , 2015, 15, 481-493.	3.5	41
4022	Identification of the correct form of the mis-annotated response regulator Rre1 from the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	2
4023	Redox proteomic analysis of <i><i>mytilus edulis</i></i> gills: effects of the pharmaceutical diclofenac on a nonâ€target organism. <i>Drug Testing and Analysis</i> , 2015, 7, 957-966.	2.6	11

#	ARTICLE	IF	CITATIONS
4024	Personalized Biochemistry and Biophysics. <i>Biochemistry</i> , 2015, 54, 2551-2559.	2.5	31
4025	Amino- and Carboxyl-Terminal CCR5 Mutations in Brazilian HIV-1-Infected Women and Homology Model of p.L55Q CCR5 Mutant. <i>AIDS Research and Human Retroviruses</i> , 2015, 31, 685-691.	1.1	0
4026	Biomarker Panels and Multiple Readouts. , 2015, , 159-166.		0
4027	Single active-site mutants are sufficient to enhance serine:pyruvate α -ketotransaminase activity in an α -ketotransaminase. <i>FEBS Journal</i> , 2015, 282, 2512-2526.	4.7	23
4028	Computational tools for epitope vaccine design and evaluation. <i>Current Opinion in Virology</i> , 2015, 11, 103-112.	5.4	60
4029	Structural Determinants for Substrate Binding and Catalysis in Triphosphate Tunnel Metalloenzymes. <i>Journal of Biological Chemistry</i> , 2015, 290, 23348-23360.	3.4	30
4030	Genome-wide comparison of ferritin family from Archaea, Bacteria, Eukarya, and Viruses: its distribution, characteristic motif, and phylogenetic relationship. <i>Die Naturwissenschaften</i> , 2015, 102, 64.	1.6	21
4031	Functionally Structured Genomes in <i>Lactobacillus kunkeei</i> Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. <i>Genome Biology and Evolution</i> , 2015, 7, 1455-1473.	2.5	50
4032	Whole transcriptomic analysis of the plant-beneficial rhizobacterium <i>Bacillus amyloliquefaciens</i> SQR9 during enhanced biofilm formation regulated by maize root exudates. <i>BMC Genomics</i> , 2015, 16, 685.	2.8	139
4033	Associations of SNPs located at candidate genes to bovine growth traits, prioritized with an interaction networks construction approach. <i>BMC Genetics</i> , 2015, 16, 91.	2.7	16
4034	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. <i>BMC Genomics</i> , 2015, 16, 520.	2.8	173
4035	Plant Carbohydrate Active Enzyme (CAZyme) Repertoires: A Comparative Study. , 2015, , 115-134.		0
4036	Assessing sequence plasticity of a virus-like nanoparticle by evolution toward a versatile scaffold for vaccines and drug delivery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12360-12365.	7.1	117
4037	Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. <i>Nature Communications</i> , 2015, 6, 8285.	12.8	184
4038	Unravelling the genome of Holy basil: an "incomparable" elixir of life of traditional Indian medicine. <i>BMC Genomics</i> , 2015, 16, 413.	2.8	60
4039	TMFoldRec: a statistical potential-based transmembrane protein fold recognition tool. <i>BMC Bioinformatics</i> , 2015, 16, 201.	2.6	11
4040	Capturing coevolutionary signals in repeat proteins. <i>BMC Bioinformatics</i> , 2015, 16, 207.	2.6	24
4041	Prediction of host - pathogen protein interactions between <i>Mycobacterium tuberculosis</i> and <i>Homo sapiens</i> using sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 100.	2.6	51

#	ARTICLE	IF	CITATIONS
4042	Domain similarity based orthology detection. BMC Bioinformatics, 2015, 16, 154.	2.6	11
4043	Extensive intra-phylogroup diversity in lactobacilli and bifidobacteria from the honeybee gut. BMC Genomics, 2015, 16, 284.	2.8	111
4044	Aspergillus niger membrane-associated proteome analysis for the identification of glucose transporters. Biotechnology for Biofuels, 2015, 8, 150.	6.2	43
4045	Functional role of <i>oppA</i> encoding an oligopeptide-binding protein from <i>Lactobacillus salivarius</i> Ren in bile tolerance. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 1167-1174.	3.0	43
4046	Novel domain identification approach for protein-protein interaction prediction. , 2015, , .		2
4047	Transcriptome sequencing and annotation of the polychaete Hermodice carunculata (Annelida.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 10	2.8	23
4048	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. Cell Systems, 2015, 1, 197-209.	6.2	94
4049	Individual intestinal symbionts induce a distinct population of ROR γ regulatory T cells. Science, 2015, 349, 993-997.	12.6	707
4050	Identification and expression of the laboratory of genetics and physiology 2 gene in common carp <i>Cyprinus carpio</i> . Journal of Fish Biology, 2015, 86, 74-91.	1.6	8
4051	RNA-Seq UD: A bioinformatics platform for RNA-Seq analysis. , 2015, , .		0
4052	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. Genome Biology and Evolution, 2015, 7, 1815-1826.	2.5	27
4053	The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332.	2.5	70
4054	Exploring the rice dispensable genome using a metagenome-like assembly strategy. Genome Biology, 2015, 16, 187.	8.8	90
4055	Computing the origin and evolution of the ribosome from its structure " Uncovering processes of macromolecular accretion benefiting synthetic biology. Computational and Structural Biotechnology Journal, 2015, 13, 427-447.	4.1	26
4056	Insights into the evolution of enzyme substrate promiscuity after the discovery of (I 2 I $^+$) α isomerase evolutionary intermediates from a diverse metagenome. BMC Evolutionary Biology, 2015, 15, 107.	3.2	16
4057	Unearthing the genomes of plant-beneficial Pseudomonas model strains WCS358, WCS374 and WCS417. BMC Genomics, 2015, 16, 539.	2.8	184
4058	Whole transcriptome profiling of the vernalization process in Lilium longiflorum (cultivar White) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	2.8	45
4059	Trends in genome dynamics among major orders of insects revealed through variations in protein families. BMC Genomics, 2015, 16, 583.	2.8	5

#	ARTICLE	IF	CITATIONS
4060	REGULATOR: a database of metazoan transcription factors and maternal factors for developmental studies. BMC Bioinformatics, 2015, 16, 114.	2.6	13
4061	Light-assisted small-molecule screening against protein kinases. Nature Chemical Biology, 2015, 11, 952-954.	8.0	42
4062	Genome-Wide Analysis of<i>PHOSPHOLIPID</i>:<i>DIACYLGLYCEROL ACYLTRANSFERASE</i>(<i>PDAT</i>)<i> Genes in Plants Reveals the Eudicot-Wide<i>PDAT</i> Gene Expansion and Altered Selective Pressures Acting on the Core Eudicot<i>PDAT</i> Paralog s. Plant Physiology, 2015, 167, 887-904.	4.8	39
4063	Identification and characterization of TIFY family genes in Brachypodium distachyon. Journal of Plant Research, 2015, 128, 995-1005.	2.4	39
4064	Comparative Genomics Including the Early-Diverging Smut Fungus<i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes. Genome Biology and Evolution, 2015, 7, 2781-2798.	2.5	16
4065	Evolution and Diversity of the Ras Superfamily of Small GTPases in Prokaryotes. Genome Biology and Evolution, 2015, 7, 57-70.	2.5	51
4067	Structural modeling and in silico analysis of non-synonymous single nucleotide polymorphisms of human 3Î²-hydroxysteroid dehydrogenase type 2. Meta Gene, 2015, 5, 162-172.	0.6	37
4068	Identification of Proteinâ€Protein Interactions by Detecting Correlated Mutation at the Interface. Journal of Chemical Information and Modeling, 2015, 55, 2042-2049.	5.4	27
4069	Computational approaches to natural product discovery. Nature Chemical Biology, 2015, 11, 639-648.	8.0	373
4070	KLF/SP Transcription Factor Family Evolution: Expansion, Diversification, and Innovation in Eukaryotes. Genome Biology and Evolution, 2015, 7, 2289-2309.	2.5	93
4071	Inntags: small self-structured epitopes for innocuous protein tagging. Nature Methods, 2015, 12, 955-958.	19.0	22
4072	Distribution of putative xenogeneic silencers in prokaryote genomes. Computational Biology and Chemistry, 2015, 58, 167-172.	2.3	17
4073	CovRS-Regulated Transcriptome Analysis of a Hypervirulent M23 Strain of Group A Streptococcus pyogenes Provides New Insights into Virulence Determinants. Journal of Bacteriology, 2015, 197, 3191-3205.	2.2	17
4074	A novel RNA binding surface of the TAM domain of TIP5/BAZ2A mediates epigenetic regulation of rRNA genes. Nucleic Acids Research, 2015, 43, 5208-5220.	14.5	26
4075	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. Genome Announcements, 2015, 3, .	0.8	25
4076	Lipopolysaccharide transport to the cell surface: periplasmic transport and assembly into the outer membrane. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20150027.	4.0	58
4077	Computational approaches to study the effects of small genomic variations. Journal of Molecular Modeling, 2015, 21, 251.	1.8	21
4078	The Enterobacterium Trabulsiella odontotermitis Presents Novel Adaptations Related to Its Association with Fungus-Growing Termites. Applied and Environmental Microbiology, 2015, 81, 6577-6588.	3.1	18

#	ARTICLE	IF	CITATIONS
4079	Methods of processing mass spectrometry data to identify peptides and proteins. Moscow University Chemistry Bulletin, 2015, 70, 211-222.	0.6	0
4080	Identifying three-dimensional structures of autophosphorylation complexes in crystals of protein kinases. Science Signaling, 2015, 8, rs13.	3.6	38
4082	Robust sequence alignment using evolutionary rates coupled with an amino acid substitution matrix. BMC Bioinformatics, 2015, 16, 255.	2.6	0
4083	Polyketide synthesis genes associated with toxin production in two species of Gambierdiscus (Dinophyceae). BMC Genomics, 2015, 16, 410.	2.8	56
4084	A Chemical Proteomics Approach for Global Analysis of Lysine Monomethylome Profiling *. Molecular and Cellular Proteomics, 2015, 14, 329-339.	3.8	58
4085	CDvist: a webserver for identification and visualization of conserved domains in protein sequences. Bioinformatics, 2015, 31, 1475-1477.	4.1	69
4086	A new class of marine Euryarchaeota group II from the mediterranean deep chlorophyll maximum. ISME Journal, 2015, 9, 1619-1634.	9.8	95
4087	Terpene synthases are widely distributed in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 857-862.	7.1	441
4088	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. Applied and Environmental Microbiology, 2015, 81, 1375-1386.	3.1	206
4089	Identification and phylogenetic analysis of late embryogenesis abundant proteins family in tomato (Solanum lycopersicum). Planta, 2015, 241, 757-772.	3.2	93
4090	Novel Phage Group Infecting Lactobacillus delbrueckii subsp. lactis, as Revealed by Genomic and Proteomic Analysis of Bacteriophage Ldl1. Applied and Environmental Microbiology, 2015, 81, 1319-1326.	3.1	31
4091	A peptide ligase and the ribosome cooperate to synthesize the peptide pheganomycin. Nature Chemical Biology, 2015, 11, 71-76.	8.0	53
4092	MRFy: Remote Homology Detection for Beta-Structural Proteins Using Markov Random Fields and Stochastic Search. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 4-16.	3.0	8
4093	Receptor Tyrosine Kinases: Structure, Functions and Role in Human Disease. , 2015, , .		7
4094	Comparative genome analysis of <i>Pseudomonas knackmussii</i> 13, the first bacterium known to degrade chloroaromatic compounds. Environmental Microbiology, 2015, 17, 91-104.	3.8	52
4095	Genome wide in silico characterization of Dof gene families of pigeonpea (Cajanus cajan (L) Millsp.). Molecular Biology Reports, 2015, 42, 535-552.	2.3	31
4096	Molecular characterization of calponin in the catch muscle of the Yesso scallop Mizuhopecten yessoensis. Fisheries Science, 2015, 81, 155-162.	1.6	4
4097	Discovery, diversity and evolution of novel coronaviruses sampled from rodents in China. Virology, 2015, 474, 19-27.	2.4	116

#	ARTICLE	IF	CITATIONS
4098	Discovering Binding Cores in Protein-DNA Binding Using Association Rule Mining with Statistical Measures. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 142-154.	3.0	5
4099	Structure-based functional annotation of putative conserved proteins having lyase activity from Haemophilus influenzae. 3 Biotech, 2015, 5, 317-336.	2.2	15
4100	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. ISME Journal, 2015, 9, 207-216.	9.8	540
4101	Bacterial collagenases – A review. Critical Reviews in Microbiology, 2016, 42, 106-126.	6.1	136
4102	Circoviruses of Fish. , 2016, , 183-190.		0
4103	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Frontiers in Microbiology, 2016, 7, 238.	3.5	66
4104	Insights on the virulence of swine respiratory tract mycoplasmas through genome-scale metabolic modeling. BMC Genomics, 2016, 17, 353.	2.8	34
4105	RGAugury: a pipeline for genome-wide prediction of resistance gene analogs (RGAs) in plants. BMC Genomics, 2016, 17, 852.	2.8	162
4106	Structure Prediction and Binding Site Analysis of Hepatotoxic Microcystin-LR Degrading MlrC-Like Protein from <i>Burkholderia</i> sp. using Computational Approaches. Current Research in Bioinformatics, 2016, 5, 1-9.	0.1	1
4107	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. BMC Genomics, 2016, 17, 892.	2.8	14
4108	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted by <i>Lucilia sericata</i> Medical Maggots. BioMed Research International, 2016, 2016, 1-27.	1.9	24
4109	Genomic Analysis Unravels Reduced Inorganic Sulfur Compound Oxidation of Heterotrophic Acidophilic <i>Acidocaldococcus</i> sp. Strain DX-1. BioMed Research International, 2016, 2016, 1-8.	1.9	4
4110	QuaBingo: A Prediction System for Protein Quaternary Structure Attributes Using Block Composition. BioMed Research International, 2016, 2016, 1-10.	1.9	4
4111	Resistance of Permafrost and Modern <i>Acinetobacter lwoffii</i> Strains to Heavy Metals and Arsenic Revealed by Genome Analysis. BioMed Research International, 2016, 2016, 1-9.	1.9	42
4112	In silico identification and characterization of the WRKY gene superfamily in pepper (<i>Capsicum annuum</i>) Tj ETQq0 0.0 rgBT /Qverlock 100	0.2	22
4113	Red Algal Mitochondrial Genomes are More Complete than Previously Reported. Genome Biology and Evolution, 2017, 9, evw267.	2.5	19
4114	Steric Clash in the SET Domain of Histone Methyltransferase NSD1 as a Cause of Sotos Syndrome and Its Genetic Heterogeneity in a Brazilian Cohort. Genes, 2016, 7, 96.	2.4	9
4115	A transcriptional blueprint for a spiral-cleaving embryo. BMC Genomics, 2016, 17, 552.	2.8	20

#	ARTICLE	IF	CITATIONS
4116	Diagnostic Genomics and Clinical Bioinformatics. , 2016, , 37-50.		2
4117	Content and Variation of the Human Genome. , 2016, , 161-177.		3
4118	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	6.0	414
4119	Developmental Cycle and Genome Analysis of <i>Rubidus massiliensis</i> , a New <i>Vermamoeba vermiformis</i> Pathogen. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 31.	3.9	35
4120	Global Regulation of Gene Expression by the MafR Protein of <i>Enterococcus faecalis</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1521.	3.5	22
4121	Sister <i>Dehalobacter</i> Genomes Reveal Specialization in Organohalide Respiration and Recent Strain Differentiation Likely Driven by Chlorinated Substrates. <i>Frontiers in Microbiology</i> , 2016, 7, 100.	3.5	18
4122	Functional Analysis of the Citrate Activator CitO from <i>Enterococcus faecalis</i> Implicates a Divalent Metal in Ligand Binding. <i>Frontiers in Microbiology</i> , 2016, 7, 101.	3.5	18
4123	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016, 7, 118.	3.5	153
4124	Genomic Insights into a New <i>Citrobacter koseri</i> Strain Revealed Gene Exchanges with the Virulence-Associated <i>Yersinia pestis</i> pPCP1 Plasmid. <i>Frontiers in Microbiology</i> , 2016, 7, 340.	3.5	13
4125	Enantioselective Utilization of D-Amino Acids by Deep-Sea Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 511.	3.5	40
4126	The Role of Complement in Cnidarian-Dinoflagellate Symbiosis and Immune Challenge in the Sea Anemone <i>Aiptasia pallida</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 519.	3.5	66
4127	Proteomic Analysis of a Novel <i>Bacillus Jumbo</i> Phage Revealing Glycoside Hydrolase As Structural Component. <i>Frontiers in Microbiology</i> , 2016, 7, 745.	3.5	33
4128	The FlgT Protein Is Involved in <i>Aeromonas hydrophila</i> Polar Flagella Stability and Not Affects Anchorage of Lateral Flagella. <i>Frontiers in Microbiology</i> , 2016, 7, 1150.	3.5	9
4129	Bioinformatic Analyses of Unique (Orphan) Core Genes of the Genus <i>Acidithiobacillus</i> : Functional Inferences and Use As Molecular Probes for Genomic and Metagenomic/Transcriptomic Interrogation. <i>Frontiers in Microbiology</i> , 2016, 7, 2035.	3.5	16
4130	Comparative Genomic Analysis of <i>Bacillus amyloliquefaciens</i> and <i>Bacillus subtilis</i> Reveals Evolutional Traits for Adaptation to Plant-Associated Habitats. <i>Frontiers in Microbiology</i> , 2016, 7, 2039.	3.5	54
4131	Long Noncoding RNA and mRNA Expression Profiles in the Thyroid Gland of Two Phenotypically Extreme Pig Breeds Using Ribo-Zero RNA Sequencing. <i>Genes</i> , 2016, 7, 34.	2.4	36
4132	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. <i>Genes</i> , 2016, 7, 89.	2.4	51
4133	Identification of Novel Pathways in Plant Lectin-Induced Cancer Cell Apoptosis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 228.	4.1	12

#	ARTICLE	IF	CITATIONS
4134	Comparative Genomics of the Extreme Acidophile <i>Acidithiobacillus thiooxidans</i> Reveals Intraspecific Divergence and Niche Adaptation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1355.	4.1	39
4135	Genome-Wide Characterization and Expression Analysis of the Germin-Like Protein Family in Rice and Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1622.	4.1	39
4136	Reduction, alignment and visualisation of large diverse sequence families. <i>BMC Bioinformatics</i> , 2016, 17, 300.	2.6	4
4137	IGDD: a database of intronless genes in dicots. <i>BMC Bioinformatics</i> , 2016, 17, 289.	2.6	23
4138	Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. <i>Biology Direct</i> , 2016, 11, 27.	4.6	3
4139	Identification and functional characterization of novel xylose transporters from the cell factories <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 148.	6.2	71
4140	Identification of differentially expressed genes implicated in peel color (red and green) of <i>Dimocarpus confinis</i> . <i>SpringerPlus</i> , 2016, 5, 1088.	1.2	9
4141	Discovery and Characterization of a Thermostable and Highly Halotolerant GH5 Cellulase from an Icelandic Hot Spring Isolate. <i>PLoS ONE</i> , 2016, 11, e0146454.	2.5	61
4142	Cupincin: A Unique Protease Purified from Rice (<i>Oryza sativa</i> L.) Bran Is a New Member of the Cupin Superfamily. <i>PLoS ONE</i> , 2016, 11, e0152819.	2.5	14
4143	Dimerization and Transactivation Domains as Candidates for Functional Modulation and Diversity of Sox9. <i>PLoS ONE</i> , 2016, 11, e0156199.	2.5	8
4144	Identification of <i>Aedes aegypti</i> Long Intergenic Non-coding RNAs and Their Association with Wolbachia and Dengue Virus Infection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005069.	3.0	85
4145	A Factor Graph Approach to Automated GO Annotation. <i>PLoS ONE</i> , 2016, 11, e0146986.	2.5	5
4146	Computational Identification Raises a Riddle for Distribution of Putative NACHT NTPases in the Genome of Early Green Plants. <i>PLoS ONE</i> , 2016, 11, e0150634.	2.5	4
4147	Identification of a Non-Pentapeptide Region Associated with Rapid Mycobacterial Evolution. <i>PLoS ONE</i> , 2016, 11, e0154059.	2.5	1
4148	Ionotropic Receptors Identified within the Tentacle of the Freshwater Snail <i>Biomphalaria glabrata</i> , an Intermediate Host of <i>Schistosoma mansoni</i> . <i>PLoS ONE</i> , 2016, 11, e0156380.	2.5	7
4149	GPU-Acceleration of Sequence Homology Searches with Database Subsequence Clustering. <i>PLoS ONE</i> , 2016, 11, e0157338.	2.5	8
4150	Biochemical Characterization of a Family 15 Carbohydrate Esterase from a Bacterial Marine Arctic Metagenome. <i>PLoS ONE</i> , 2016, 11, e0159345.	2.5	32
4151	Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624. <i>PLoS ONE</i> , 2016, 11, e0162983.	2.5	76

#	ARTICLE	IF	CITATIONS
4152	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus <i>Aspergillus cristatus</i> . BMC Genomics, 2016, 17, 428.	2.8	55
4153	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in <i>Pigeonpea</i> (<i>Cajanus cajan</i> L.). Frontiers in Plant Science, 2015, 6, 1065.	3.6	39
4154	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. Frontiers in Plant Science, 2016, 7, 139.	3.6	81
4155	Transcriptome Analysis Identifies Candidate Genes Related to Triacylglycerol and Pigment Biosynthesis and Photoperiodic Flowering in the Ornamental and Oil-Producing Plant, <i>Camellia reticulata</i> (Theaceae). Frontiers in Plant Science, 2016, 7, 163.	3.6	29
4156	Diverse Evolutionary Trajectories for Small RNA Biogenesis Genes in the Oomycete Genus <i>Phytophthora</i> . Frontiers in Plant Science, 2016, 7, 284.	3.6	27
4157	Analyses of Old “Prokaryotic” Proteins Indicate Functional Diversification in <i>Arabidopsis</i> and <i>Oryza sativa</i> . Frontiers in Plant Science, 2016, 7, 304.	3.6	1
4158	Analysis of the Prefoldin Gene Family in 14 Plant Species. Frontiers in Plant Science, 2016, 7, 317.	3.6	20
4159	Genome-Wide Transcriptional Excavation of <i>Dipsacus asperoides</i> Unmasked both Cryptic Asperosaponin Biosynthetic Genes and SSR Markers. Frontiers in Plant Science, 2016, 7, 339.	3.6	7
4160	De novo Transcriptome Analysis and Molecular Marker Development of Two <i>Hemarthria</i> Species. Frontiers in Plant Science, 2016, 7, 496.	3.6	47
4161	SSH Analysis of Endosperm Transcripts and Characterization of Heat Stress Regulated Expressed Sequence Tags in Bread Wheat. Frontiers in Plant Science, 2016, 7, 1230.	3.6	14
4162	A Primary Sequence Analysis of the ARGONAUTE Protein Family in Plants. Frontiers in Plant Science, 2016, 7, 1347.	3.6	24
4163	Expansion and Functional Divergence of AP2 Group Genes in Spermatophytes Determined by Molecular Evolution and <i>Arabidopsis</i> Mutant Analysis. Frontiers in Plant Science, 2016, 7, 1383.	3.6	37
4164	A Developmental Transcriptome Map for Allotetraploid <i>Arachis hypogaea</i> . Frontiers in Plant Science, 2016, 7, 1446.	3.6	178
4165	Genome-Wide Investigation of Hsf Genes in Sesame Reveals Their Segmental Duplication Expansion and Their Active Role in Drought Stress Response. Frontiers in Plant Science, 2016, 7, 1522.	3.6	77
4166	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd), Poplar (<i>Populus</i>), Grape (<i>Vitis vinifera</i>), <i>Arabidopsis</i> and Rice (<i>Oryza sativa</i>). Frontiers in Plant Science, 2016, 7, 1750.	3.6	97
4167	Structural, Evolutionary, and Functional Analysis of the Class III Peroxidase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i>). Frontiers in Plant Science, 2016, 7, 1874.	3.6	83
4168	Glutathione S-transferases and UDP-glycosyltransferases Are Involved in Response to Aluminum Stress in Flax. Frontiers in Plant Science, 2016, 7, 1920.	3.6	55
4169	OsSGL, a Novel DUF1645 Domain-Containing Protein, Confers Enhanced Drought Tolerance in Transgenic Rice and <i>Arabidopsis</i> . Frontiers in Plant Science, 2016, 7, 2001.	3.6	46

#	ARTICLE	IF	CITATIONS
4170	Identification of genetic and environmental factors stimulating excision from <i>Sclerotinia sclerotiorum</i> chromosome of the toxicogenic region responsible for pathogenicity. <i>Molecular Plant Pathology</i> , 2016, 17, 501-509.	4.2	23
4171	DemaDb: an integrated dematiaceous fungal genomes database. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw008.	3.0	4
4172	Draft Genome Sequence of the Rumen Methanogen <i>Methanobrevibacter olleyae</i> YLM1. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
4173	Genome Sequence of a <i>Clostridium neonatale</i> Strain Isolated in a Canadian Neonatal Intensive Care Unit. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
4174	Identification of family determining residues in <i>Uromyces</i> lysine demethylases: A sequence-based, family wide classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 397-407.	2.6	4
4175	Identification and expression analysis of the <i>sting</i> gene, a sensor of viral DNA, in common carp <i>Cyprinus carpio</i> . <i>Journal of Fish Biology</i> , 2016, 88, 1949-1964.	1.6	10
4176	Draft Genome Sequence of <i>Actinobaculum massiliense</i> Strain FC3. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
4177	Role of magnesium ions in the reaction mechanism at the interface between Tm1631 protein and its DNA ligand. <i>Chemistry Central Journal</i> , 2016, 10, 41.	2.6	7
4178	bioassayR: Cross-Target Analysis of Small Molecule Bioactivity. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1237-1242.	5.4	13
4179	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. <i>Expert Review of Proteomics</i> , 2016, 13, 757-769.	3.0	67
4180	Investigating polymorphisms by bioinformatics is a potential cost-effective method to screen for germline mutations in Chinese familial adenomatous polyposis patients. <i>Oncology Letters</i> , 2016, 12, 421-428.	1.8	1
4181	Molecular cloning, heterologous expression, and enzymatic characterization of lysoplasmalogen-specific phospholipase D from <i>Thermococcus</i> sp.. <i>FEBS Open Bio</i> , 2016, 6, 1113-1130.	2.3	12
4182	xHMMER3x2: Utilizing HMMER3's speed and HMMER2's sensitivity and specificity in the global alignment mode for improved large-scale protein domain annotation. <i>Biology Direct</i> , 2016, 11, 63.	4.6	4
4183	Methuselah/Methuselah-like G protein-coupled receptors constitute an ancient metazoan gene family. <i>Scientific Reports</i> , 2016, 6, 21801.	3.3	24
4184	Identification and characterization of histone lysine methylation modifiers in <i>Fragaria vesca</i> . <i>Scientific Reports</i> , 2016, 6, 23581.	3.3	28
4185	Comparative phylogenetic analysis and transcriptional profiling of MADS-box gene family identified DAM and FLC-like genes in apple (<i>Malus domestica</i>). <i>Scientific Reports</i> , 2016, 6, 20695.	3.3	80
4186	FAMSA: Fast and accurate multiple sequence alignment of huge protein families. <i>Scientific Reports</i> , 2016, 6, 33964.	3.3	92
4187	A more efficient method for domain repeat detection in WD-40 proteins. , 2016, , .		0

#	ARTICLE	IF	CITATIONS
4188	RNA-seq-based evaluation of bicolor tepal pigmentation in Asiatic hybrid lilies (<i>Lilium</i> spp.). <i>BMC Genomics</i> , 2016, 17, 611.	2.8	65
4189	Genome-wide long non-coding RNA screening, identification and characterization in a model microorganism <i>Chlamydomonas reinhardtii</i> . <i>Scientific Reports</i> , 2016, 6, 34109.	3.3	43
4190	A genome-wide analysis of the ASYMMETRIC LEAVES2/LATERAL ORGAN BOUNDARIES (AS2/LOB) gene family in barley (<i>Hordeum vulgare</i> L.). <i>Journal of Zhejiang University: Science B</i> , 2016, 17, 763-774.	2.8	22
4191	Prediction and characterization of protein-protein interaction network in <i>Bacillus licheniformis</i> WX-02. <i>Scientific Reports</i> , 2016, 6, 19486.	3.3	12
4192	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , 2016, 6, 20915.	3.3	11
4193	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. <i>BMC Biotechnology</i> , 2016, 16, 47.	3.3	91
4194	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. <i>Scientific Reports</i> , 2016, 6, 22842.	3.3	21
4195	MTGpick allows robust identification of genomic islands from a single genome. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw118.	6.5	34
4196	Enhanced antimicrobial peptide-induced activity in the mollusc Toll-2 family through evolution via tandem Toll/interleukin-1 receptor. <i>Royal Society Open Science</i> , 2016, 3, 160123.	2.4	5
4197	Identification of protein secretion systems in bacterial genomes. <i>Scientific Reports</i> , 2016, 6, 23080.	3.3	315
4198	Synbiological systems for complex natural products biosynthesis. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 221-229.	3.7	3
4199	Orthologous and Paralogous AmpD Peptidoglycan Amidases from Gram-Negative Bacteria. <i>Microbial Drug Resistance</i> , 2016, 22, 470-476.	2.0	23
4200	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	3.4	38
4201	Toxin inhibition in <i>C. crescentus</i> VapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. <i>Nucleic Acids Research</i> , 2016, 45, gkw1266.	14.5	13
4202	Transcriptome analyses of the Dof-like gene family in grapevine reveal its involvement in berry, flower and seed development. <i>Horticulture Research</i> , 2016, 3, 16042.	6.3	25
4203	Structural and functional characterization of a novel gene, Hc-daf-22, from the strongylid nematode <i>Haemonchus contortus</i> . <i>Parasites and Vectors</i> , 2016, 9, 422.	2.5	14
4204	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. <i>Genome Biology and Evolution</i> , 2016, 8, 3323-3339.	2.5	42
4205	<i>Cryptosporidium hominis</i> gene catalog: a resource for the selection of novel <i>Cryptosporidium</i> vaccine candidates. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw137.	3.0	11

#	ARTICLE	IF	CITATIONS
4206	Global transcriptional analysis suggests <i>Lasiodiplodia theobromae</i> pathogenicity factors involved in modulation of grapevine defensive response. <i>BMC Genomics</i> , 2016, 17, 615.	2.8	51
4207	From Genomes to Phenotypes: Traitair, the Microbial Trait Analyzer. <i>MSystems</i> , 2016, 1, .	3.8	102
4208	The mechanism of the effect of U18666a on blocking the activity of 3Î²-hydroxysterol Î²-24-reductase (DHCR24): molecular dynamics simulation study and free energy analysis. <i>Journal of Molecular Modeling</i> , 2016, 22, 46.	1.8	12
4209	Identification of putative phosphoproteins in wheat spikes induced by <i>Fusarium graminearum</i> . <i>Planta</i> , 2016, 243, 719-731.	3.2	9
4210	A long noncoding RNA associated with susceptibility to celiac disease. <i>Science</i> , 2016, 352, 91-95.	12.6	211
4211	The tertiary structures of porcine AhR and ARNT proteins and molecular interactions within the TCDD/AhR/ARNT complex. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 67, 119-126.	2.4	1
4212	Next-generation biology: Sequencing and data analysis approaches for non-model organisms. <i>Marine Genomics</i> , 2016, 30, 3-13.	1.1	164
4213	Characterization of the Cadherinâ€Catenin Complex of the Sea Anemone <i>Nematostella vectensis</i> and Implications for the Evolution of Metazoan Cellâ€Cell Adhesion. <i>Molecular Biology and Evolution</i> , 2016, 33, 2016-2029.	8.9	22
4214	Phosphorylation of spore coat proteins by a family of atypical protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3482-91.	7.1	56
4215	Experimental validation of in silico modelâ€predicted isocitrate dehydrogenase and phosphomannose isomerase from <i>D. ehloccoides mccartyi</i> . <i>Microbial Biotechnology</i> , 2016, 9, 47-60.	4.2	1
4216	Nucleotide polymorphisms in the bovine lymphotoxin A gene and their distribution among <i>Bos indicus</i> zebu cattle breeds. <i>Gene</i> , 2016, 579, 82-94.	2.2	2
4217	Delineation of Polypharmacology across the Human Structural Kinome Using a Functional Site Interaction Fingerprint Approach. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4326-4341.	6.4	39
4218	Crystal Structure of the GRAS Domain of SCARECROW-LIKE7 in <i>Oryza sativa</i> . <i>Plant Cell</i> , 2016, 28, 1025-1034.	6.6	53
4219	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. <i>Nucleic Acids Research</i> , 2016, 44, 3513-3533.	14.5	54
4220	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the <i>Methanomassiliicoccales</i> , Isolated from a Sheep Rumen. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
4221	A comparative analysis of the other roles of transcriptional factors from pathogenic organisms. <i>Gene</i> , 2016, 586, 274-280.	2.2	1
4222	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.	3.1	22
4223	Genome-wide analysis of the BES1 transcription factor family in Chinese cabbage (<i>Brassica rapa</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overlo	3.4	35

#	ARTICLE	IF	CITATIONS
4224	Trait changes induced by species interactions in two phenotypically distinct strains of a marine dinoflagellate. <i>ISME Journal</i> , 2016, 10, 2658-2668.	9.8	15
4225	FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. <i>Nucleic Acids Research</i> , 2016, 44, 3534-3548.	14.5	60
4226	Evaluation of Descriptor Algorithms of Biological Sequences and Distance Measures for the Intelligent Cluster Index (IClx). <i>Communications in Computer and Information Science</i> , 2016, , 434-448.	0.5	0
4227	Protein Structure Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 31-53.	0.9	3
4228	Complete genome sequences and analysis of the <i>Fusobacterium nucleatum</i> subspecies <i>animalis</i> 7-1 bacteriophage Φ Funu1 and Φ Funu2. <i>Anaerobe</i> , 2016, 38, 125-129.	2.1	11
4229	Homology-Based Annotation of Large Protein Datasets. <i>Methods in Molecular Biology</i> , 2016, 1415, 153-176.	0.9	0
4230	Long-Term Warming Alters Carbohydrate Degradation Potential in Temperate Forest Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6518-6530.	3.1	68
4231	The Gearbox of the Bacterial Flagellar Motor Switch. <i>Structure</i> , 2016, 24, 1209-1220.	3.3	30
4232	Cryptophyte farming by symbiotic ciliate host detected in situ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12208-12213.	7.1	32
4233	Repeated Duplication of Argonaute2 Is Associated with Strong Selection and Testis Specialization in <i>Drosophila</i> . <i>Genetics</i> , 2016, 204, 757-769.	2.9	20
4234	GExplore 1.4: An expanded web interface for queries on <i>Caenorhabditis elegans</i> protein and gene function. <i>Worm</i> , 2016, 5, e1234659.	1.0	34
4235	Genome sequence of <i>Candidatus Arsenophonus lipopteni</i> , the exclusive symbiont of a blood sucking fly <i>Lipoptena cervi</i> (Diptera: Hippoboscidae). <i>Standards in Genomic Sciences</i> , 2016, 11, 72.	1.5	46
4236	Global transcriptional regulator TrmB family members in prokaryotes. <i>Journal of Microbiology</i> , 2016, 54, 639-645.	2.8	21
4237	Complete Genome Sequence of <i>Bacillus velezensis</i> CBMB205, a Phosphate-Solubilizing Bacterium Isolated from the Rhizoplane of Rice in the Republic of Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
4238	De novo transcriptome assembly of mangosteen (<i>Garcinia mangostana</i> L.) fruit. <i>Genomics Data</i> , 2016, 10, 35-37.	1.3	9
4239	LINEs between Species: Evolutionary Dynamics of LINE-1 Retrotransposons across the Eukaryotic Tree of Life. <i>Genome Biology and Evolution</i> , 2016, 8, 3301-3322.	2.5	66
4240	Genome-wide identification and functional analysis of the TIFY gene family in response to drought in cotton. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2173-2187.	2.1	34
4241	Identification and analysis of integrons and cassette arrays in bacterial genomes. <i>Nucleic Acids Research</i> , 2016, 44, 4539-4550.	14.5	235

#	ARTICLE	IF	CITATIONS
4242	Genomic identification, rapid evolution, and expression of Argonaute genes in the tilapia, <i>Oreochromis niloticus</i> . <i>Development Genes and Evolution</i> , 2016, 226, 339-348.	0.9	26
4243	Integrating metabolomics and transcriptomics data to discover a biocatalyst that can generate the amine precursors for alkamide biosynthesis. <i>Plant Journal</i> , 2016, 88, 775-793.	5.7	17
4244	Computational assessment of feature combinations for pathogenic variant prediction. <i>Molecular Genetics & Genomic Medicine</i> , 2016, 4, 431-446.	1.2	13
4245	Mitochondrial metabolites extend lifespan. <i>Aging Cell</i> , 2016, 15, 336-348.	6.7	52
4246	The conserved carboxyl domain of MorC, an inner membrane protein of <i>Aggregatibacter actinomycetemcomitans</i> , is essential for membrane function. <i>Molecular Oral Microbiology</i> , 2016, 31, 43-58.	2.7	9
4247	Transcriptome analysis of smooth cordgrass (<i>Spartina alterniflora</i> Loisel), a monocot halophyte, reveals candidate genes involved in its adaptation to salinity. <i>BMC Genomics</i> , 2016, 17, 657.	2.8	55
4248	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mammalian retinas. <i>Human Molecular Genetics</i> , 2016, 25, ddw268.	2.9	36
4249	Counting animal species with DNA barcodes: Canadian insects. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150333.	4.0	267
4250	Genomics and expression analysis of DHHC-cysteine-rich domain S-acyl transferase protein family in apple. <i>Genes and Genomics</i> , 2016, 38, 671-684.	1.4	0
4251	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	6.5	14
4252	UDoGeC:Essential Protein Prediction Using Domain and Gene Expression Profiles. <i>Procedia Computer Science</i> , 2016, 93, 1003-1009.	2.0	4
4253	Identification of antibacterial peptides from endophytic microbiome. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9283-9293.	3.6	11
4254	First high quality draft genome sequence of a plant growth promoting and cold active enzyme producing psychrotrophic <i>Arthrobacter agilis</i> strain L77. <i>Standards in Genomic Sciences</i> , 2016, 11, 54.	1.5	78
4255	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016, 20, 357-367.	11.0	123
4256	Improved glycerol to ethanol conversion by <i>E. coli</i> using a metagenomic fragment isolated from an anaerobic reactor. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 1405-1416.	3.0	18
4257	Extensive sequence divergence between the reference genomes of two elite <i>Oryza indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	7.1	211
4258	Genome sequence and comparative analysis of clavicipitaceous insect-pathogenic fungus <i>Aschersonia badia</i> with <i>Metarhizium</i> spp.. <i>BMC Genomics</i> , 2016, 17, 367.	2.8	12
4259	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. <i>BMC Genomics</i> , 2016, 17, 623.	2.8	35

#	ARTICLE	IF	CITATIONS
4260	First Comprehensive Proteome Analyses of Lysine Acetylation and Succinylation in Seedling Leaves of <i>Brachypodium distachyon</i> L.. Scientific Reports, 2016, 6, 31576.	3.3	62
4261	Characterization of long non-coding RNA transcriptome in high-energy diet induced nonalcoholic steatohepatitis minipigs. Scientific Reports, 2016, 6, 30709.	3.3	29
4262	Systematic identification and analysis of frequent gene fusion events in metabolic pathways. BMC Genomics, 2016, 17, 473.	2.8	13
4263	Substrate specificity characterization for eight putative nudix hydrolases. Evaluation of criteria for substrate identification within the Nudix family. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1810-1822.	2.6	10
4264	Mammalian Fe-S proteins: definition of a consensus motif recognized by the co-chaperone HSC20. Metallomics, 2016, 8, 1032-1046.	2.4	29
4265	Improve homology search sensitivity of PacBio data by correcting frameshifts. Bioinformatics, 2016, 32, i529-i537.	4.1	12
4266	The Evolution of Olfactory Gene Families in <i>Drosophila</i> and the Genomic Basis of chemical-Ecological Adaptation in <i>Drosophila suzukii</i> . Genome Biology and Evolution, 2016, 8, 2297-2311.	2.5	76
4267	Reconfigurable Hardware Accelerator for Profile Hidden Markov Models. Arabian Journal for Science and Engineering, 2016, 41, 3267-3277.	1.1	7
4268	A Combined Computational and Genetic Approach Uncovers Network Interactions of the Cyanobacterial Circadian Clock. Journal of Bacteriology, 2016, 198, 2439-2447.	2.2	16
4269	Structural insight with mutational impact on tyrosinase and PKC- η interaction from Homo sapiens : Molecular modeling and docking studies for melanogenesis, albinism and increased risk for melanoma. Gene, 2016, 592, 99-109.	2.2	5
4270	Mutation Drivers of Immunological Responses to Cancer. Cancer Immunology Research, 2016, 4, 789-798.	3.4	32
4271	Genomic location and expression analysis of expansin gene family reveals the evolutionary and functional significance in <i>Triticum aestivum</i> . Genes and Genomics, 2016, 38, 1021-1030.	1.4	12
4272	Genome Sequences of 12 Bacterial Isolates Obtained from the Urine of Pregnant Women. Genome Announcements, 2016, 4, .	0.8	3
4273	Genome Sequences of Nine Gram-Negative Vaginal Bacterial Isolates. Genome Announcements, 2016, 4, .	0.8	1
4274	Genome-wide identification, structural analysis and new insights into late embryogenesis abundant (LEA) gene family formation pattern in <i>Brassica napus</i> . Scientific Reports, 2016, 6, 24265.	3.3	91
4275	Evolution of Protein Domain Repeats in Metazoa. Molecular Biology and Evolution, 2016, 33, 3170-3182.	8.9	41
4276	An evaluation of the accuracy and speed of metagenome analysis tools. Scientific Reports, 2016, 6, 19233.	3.3	278
4277	A Nitrogen-Fixing Subunit Essential for Accumulating 4Fe-4S-Containing Photosystem I Core Proteins. Plant Physiology, 2016, 172, 2459-2470.	4.8	19

#	ARTICLE	IF	CITATIONS
4278	The <i>Gonium pectorale</i> genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity. <i>Nature Communications</i> , 2016, 7, 11370.	12.8	125
4279	DciA is an ancestral replicative helicase operator essential for bacterial replication initiation. <i>Nature Communications</i> , 2016, 7, 13271.	12.8	33
4280	Leaf transcriptome of two highly divergent genotypes of <i>Urochloa humidicola</i> (Poaceae), a tropical polyploid forage grass adapted to acidic soils and temporary flooding areas. <i>BMC Genomics</i> , 2016, 17, 910.	2.8	15
4281	Identification of candidate genes related to calanolide biosynthesis by transcriptome sequencing of <i>Calophyllum brasiliense</i> (Calophyllaceae). <i>BMC Plant Biology</i> , 2016, 16, 177.	3.6	7
4282	A Hybrid Monte Carlo Scheme for Multibackbone Protein Design. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 6035-6048.	5.3	14
4283	Computational analysis of translational readthrough proteins in <i>Drosophila</i> and yeast reveals parallels to alternative splicing. <i>Scientific Reports</i> , 2016, 6, 32142.	3.3	9
4284	A direct-sensing galactose chemoreceptor recently evolved in invasive strains of <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2016, 7, 13206.	12.8	49
4285	Evolution of Enzyme Superfamilies: Comprehensive Exploration of Sequence–Function Relationships. <i>Biochemistry</i> , 2016, 55, 6375-6388.	2.5	56
4286	Genome Sequences of 14 <i>Firmicutes</i> Strains Isolated from the Human Vagina. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
4287	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	8.2	51
4288	Characterisation of the immune compounds in koala milk using a combined transcriptomic and proteomic approach. <i>Scientific Reports</i> , 2016, 6, 35011.	3.3	25
4289	Analyses of Long Non-Coding RNA and mRNA profiling using RNA sequencing during the pre-implantation phases in pig endometrium. <i>Scientific Reports</i> , 2016, 6, 20238.	3.3	150
4290	Combining biophysical methods to analyze the disulfide bond in SH2 domain of C-terminal Src kinase. <i>Biophysics Reports</i> , 2016, 2, 33-43.	0.8	15
4292	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016, 7, 11491.	12.8	207
4293	Substrate prediction of <i>Ixodes ricinus</i> salivary lipocalins differentially expressed during <i>Borrelia afzelii</i> infection. <i>Scientific Reports</i> , 2016, 6, 32372.	3.3	29
4294	Characterization of Protein Lysine Propionylation in <i>Escherichia coli</i> : Global Profiling, Dynamic Change, and Enzymatic Regulation. <i>Journal of Proteome Research</i> , 2016, 15, 4696-4708.	3.7	50
4295	An efficient method for protein function annotation based on multilayer protein networks. <i>Human Genomics</i> , 2016, 10, 33.	2.9	29
4296	Computational Identification of Novel Genes: Current and Future Perspectives. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S39950.	2.0	32

#	ARTICLE	IF	CITATIONS
4297	Survey of Genes Involved in Biosynthesis, Transport, and Signaling of Phytohormones with Focus on <i>Solanum lycopersicum</i> . <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38425.	2.0	21
4298	Draft Genome Sequence of <i>Mycobacterium houstonense</i> Strain ATCC 49403 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
4299	Draft Genome Sequence of <i>Mycobacterium interjectum</i> Strain ATCC 51457 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
4300	Draft Genome Sequence of <i>Mycobacterium acapulcensis</i> Strain CSURP1424. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
4301	Rsite2: an efficient computational method to predict the functional sites of noncoding RNAs. <i>Scientific Reports</i> , 2016, 6, 19016.	3.3	15
4302	High frequency of +1 programmed ribosomal frameshifting in <i>Euplotes octocarinatus</i> . <i>Scientific Reports</i> , 2016, 6, 21139.	3.3	48
4303	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016, 6, 35076.	3.3	10
4304	Complete Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Strain RM1285 Isolated from Packaged Chicken. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
4305	Biochemical pathways supporting beta-lactam biosynthesis in the springtail <i>Folsomia candida</i> . <i>Biology Open</i> , 2016, 5, 1784-1789.	1.2	13
4306	The complete genome sequences of sulfur-oxidizing Gammaproteobacteria <i>Sulfurifustis variabilis</i> skN76T and <i>Sulfuricaulis limicola</i> HA5T. <i>Standards in Genomic Sciences</i> , 2016, 11, 71.	1.5	37
4307	The complete genome sequence of the rumen methanogen <i>Methanobrevibacter millerae</i> SM9. <i>Standards in Genomic Sciences</i> , 2016, 11, 49.	1.5	15
4308	Implementation and comparison of kernel-based learning methods to predict metabolic networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2016, 5, 26.	2.1	5
4309	A common theme in extracellular fluids of beetles: extracellular superoxide dismutases crucial for balancing ROS in response to microbial challenge. <i>Scientific Reports</i> , 2016, 6, 24082.	3.3	17
4310	Global inference of disease-causing single nucleotide variants from exome sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 468.	2.6	4
4311	The floral transcriptomes of four bamboo species (Bambusoideae; Poaceae): support for common ancestry among woody bamboos. <i>BMC Genomics</i> , 2016, 17, 384.	2.8	36
4312	Three DUF1996 Proteins Localize in Vacuoles and Function in Fungal Responses to Multiple Stresses and Metal Ions. <i>Scientific Reports</i> , 2016, 6, 20566.	3.3	14
4313	Structure-guided selection of specificity determining positions in the human Kinome. <i>BMC Genomics</i> , 2016, 17, 431.	2.8	4
4314	Whole genome shotgun sequence of <i>Bacillus amyloliquefaciens</i> TF28, a biocontrol entophytic bacterium. <i>Standards in Genomic Sciences</i> , 2016, 11, 73.	1.5	6

#	ARTICLE	IF	CITATIONS
4315	DOMMINO 2.0: integrating structurally resolved protein-, RNA-, and DNA-mediated macromolecular interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	34
4316	Positively charged residues within the MYO19 MyMOMA domain are essential for proper localization of MYO19 to the mitochondrial outer membrane. Cytoskeleton, 2016, 73, 286-299.	2.0	20
4317	Basic characterization of avian β -defensin genes in the Japanese quail, <i>Coturnix japonica</i> . Animal Science Journal, 2016, 87, 311-320.	1.4	7
4318	OsdR of <i>Streptomyces coelicolor</i> and the Dormancy Regulator DevR of <i>Mycobacterium tuberculosis</i> Control Overlapping Regulons. MSystems, 2016, 1, .	3.8	30
4319	Different evolutionary patterns of SNPs between domains and unassigned regions in human protein-coding sequences. Molecular Genetics and Genomics, 2016, 291, 1127-1136.	2.1	2
4320	PredRSA: a gradient boosted regression trees approach for predicting protein solvent accessibility. BMC Bioinformatics, 2016, 17, 8.	2.6	41
4321	LowMACA: exploiting protein family analysis for the identification of rare driver mutations in cancer. BMC Bioinformatics, 2016, 17, 80.	2.6	16
4322	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. BMC Bioinformatics, 2016, 17, 150.	2.6	0
4323	Type VI secretion systems of human gut Bacteroidales segregate into three genetic architectures, two of which are contained on mobile genetic elements. BMC Genomics, 2016, 17, 58.	2.8	121
4324	Recovering complete and draft population genomes from metagenome datasets. Microbiome, 2016, 4, 8.	11.1	254
4325	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). Standards in Genomic Sciences, 2016, 11, 17.	1.5	161
4326	A Hitchhiker's Guide to Metatranscriptomics. , 2016, , 313-342.		8
4327	Intrinsic disorder in biomarkers of insulin resistance, hypoadiponectinemia, and endothelial dysfunction among the type 2 diabetic patients. Intrinsically Disordered Proteins, 2016, 4, e1171278.	1.9	7
4328	Functional conservation of the apoptotic machinery from coral to man: the diverse and complex Bcl-2 and caspase repertoires of <i>Acropora millepora</i> . BMC Genomics, 2016, 17, 62.	2.8	45
4329	Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26.	3.0	46
4330	Duplication and Diversification of Dipteran Argonaute Genes, and the Evolutionary Divergence of Piwi and Aubergine. Genome Biology and Evolution, 2016, 8, 507-518.	2.5	98
4331	Putative function of hypothetical proteins expressed by <i>Clostridium perfringens</i> type A strains and their protective efficacy in mouse model. Infection, Genetics and Evolution, 2016, 44, 147-156.	2.3	3
4332	Towards synthesis of monoterpenes and derivatives using synthetic biology. Current Opinion in Chemical Biology, 2016, 34, 37-43.	6.1	89

#	ARTICLE	IF	CITATIONS
4333	Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016, 44, 6287-6297.	14.5	60
4334	Cloning, molecular characterization, and expression analysis of the unc45 myosin chaperone b(unc45b) gene of grass carp (<i>Ctenopharyngodon idellus</i>). <i>Journal of Muscle Research and Cell Motility</i> , 2016, 37, 71-81.	2.0	1
4335	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 34-44.	1.0	22
4336	Amplification and function analysis of N6-adenine-specific DNA methyltransferase gene in <i>Nilaparvata lugens</i> . <i>Journal of Integrative Agriculture</i> , 2016, 15, 591-599.	3.5	2
4337	De novo assembly of the blunt snout bream (<i>Megalobrama amblycephala</i>) gill transcriptome to identify ammonia exposure associated microRNAs and their targets. <i>Results in Immunology</i> , 2016, 6, 21-27.	2.2	12
4338	Genetic diversity of coronaviruses in <i>Miniopterus fuliginosus</i> bats. <i>Science China Life Sciences</i> , 2016, 59, 604-614.	4.9	20
4339	Characterisation of a novel enterobacteria phage, CAjan, isolated from rat faeces. <i>Archives of Virology</i> , 2016, 161, 2219-2226.	2.1	31
4340	CRISPR Screens Provide a Comprehensive Assessment of Cancer Vulnerabilities but Generate False-Positive Hits for Highly Amplified Genomic Regions. <i>Cancer Discovery</i> , 2016, 6, 900-913.	9.4	320
4341	Three Residues Make an Evolutionary Switch for Folding and RNA-Destabilizing Activity in the TTP Family of Proteins. <i>ACS Chemical Biology</i> , 2016, 11, 435-443.	3.4	7
4342	Characterization of multiple sequence alignment errors using complete-likelihood score and position-shift map. <i>BMC Bioinformatics</i> , 2016, 17, 133.	2.6	7
4343	Transcriptome sequencing based annotation and homologous evidence based scaffolding of <i>Anguilla japonica</i> draft genome. <i>BMC Genomics</i> , 2016, 17, 13.	2.8	9
4344	Genome-wide analysis of long non-coding RNAs at early stage of skin pigmentation in goats (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Overlacc	2.8	139
4345	Genomic and transcriptomic analysis of carbohydrate utilization by <i>Paenibacillus</i> sp. JDR-2: systems for bioprocessing plant polysaccharides. <i>BMC Genomics</i> , 2016, 17, 131.	2.8	11
4346	ChlamyNET: a <i>Chlamydomonas</i> gene co-expression network reveals global properties of the transcriptome and the early setup of key co-expression patterns in the green lineage. <i>BMC Genomics</i> , 2016, 17, 227.	2.8	45
4347	Red Sea Atlantis II brine pool nitrilase with unique thermostability profile and heavy metal tolerance. <i>BMC Biotechnology</i> , 2016, 16, 14.	3.3	19
4348	Transcriptome analysis reveals a ribosome constituents disorder involved in the RPL5 downregulated zebrafish model of Diamond-Blackfan anemia. <i>BMC Medical Genomics</i> , 2016, 9, 13.	1.5	32
4349	Draft genome sequences of <i>Pantoea agglomerans</i> and <i>Pantoea vagans</i> isolates associated with termites. <i>Standards in Genomic Sciences</i> , 2016, 11, 23.	1.5	29
4350	Wider than Thought Phylogenetic Occurrence of Apicortin, A Characteristic Protein of Apicomplexan Parasites. <i>Journal of Molecular Evolution</i> , 2016, 82, 303-314.	1.8	13

#	ARTICLE	IF	CITATIONS
4351	DUF3380 Domain from a Salmonella Phage Endolysin Shows Potent <i>N</i> -Acetylmuramidase Activity. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4975-4981.	3.1	49
4352	Fragment-based modelling of single stranded RNA bound to RNA recognition motif containing proteins. <i>Nucleic Acids Research</i> , 2016, 44, 4565-4580.	14.5	20
4353	Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera. <i>Systematic Biology</i> , 2016, 65, 1024-1040.	5.6	160
4354	Comparative transcript profiling of resistant and susceptible peanut post-harvest seeds in response to aflatoxin production by <i>Aspergillus flavus</i> . <i>BMC Plant Biology</i> , 2016, 16, 54.	3.6	41
4355	BLAST-based structural annotation of protein residues using Protein Data Bank. <i>Biology Direct</i> , 2016, 11, 4.	4.6	14
4356	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. <i>Standards in Genomic Sciences</i> , 2016, 11, 9.	1.5	2
4357	Cloning, characterization, and expression analysis of LGP2 cDNA from goose, <i>Anser cygnoides</i> . <i>Poultry Science</i> , 2016, 95, 2290-2296.	3.4	9
4358	Long noncoding RNAs: Central to nervous system development. <i>International Journal of Developmental Neuroscience</i> , 2016, 55, 109-116.	1.6	34
4359	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 235-244.	1.8	38
4360	Genome-Based Selection and Characterization of <i>Fusarium circinatum</i> -Specific Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 631-639.	1.8	14
4361	Comparative Protein Structure Modeling Using MODELLER. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 5.6.1-5.6.37.	25.8	2,248
4362	PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw013.	3.0	12
4363	Host specialization of the blast fungus <i>Magnaporthe oryzae</i> is associated with dynamic gain and loss of genes linked to transposable elements. <i>BMC Genomics</i> , 2016, 17, 370.	2.8	157
4364	Complete Genome Sequence of <i>Dyella thiooxydans</i> ATSB10, a Thiosulfate-Oxidizing Bacterium Isolated from Sunflower Fields in South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
4365	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. <i>Environmental Microbiology</i> , 2016, 18, 2825-2842.	3.8	72
4366	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.	3.4	4
4367	SeqTools: visual tools for manual analysis of sequence alignments. <i>BMC Research Notes</i> , 2016, 9, 39.	1.4	26
4368	Orphan Crops Browser: a bridge between model and orphan crops. <i>Molecular Breeding</i> , 2016, 36, 9.	2.1	18

#	ARTICLE	IF	CITATIONS
4369	Identification of catalytically important residues of the carotenoid 1,2-hydratases from <i>Rubrivivax gelatinosus</i> and <i>Thiocapsa roseopersicina</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 1275-1284.	3.6	21
4370	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. <i>Plant Physiology</i> , 2016, 170, 1878-1894.	4.8	63
4371	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	14.5	21
4372	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	9.8	66
4373	ELM 2016â€™ data update and new functionality of the eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2016, 44, D294-D300.	14.5	289
4374	An Extensive Empirical Comparison of Probabilistic Hierarchical Classifiers in Datasets of Ageing-Related Genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 1045-1058.	3.0	15
4375	HGTree: database of horizontally transferred genes determined by tree reconciliation. <i>Nucleic Acids Research</i> , 2016, 44, D610-D619.	14.5	45
4376	De novo analysis of transcriptome reveals genes associated with leaf abscission in sugarcane (<i>Saccharum officinarum</i> L.). <i>BMC Genomics</i> , 2016, 17, 195.	2.8	51
4377	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. <i>Nucleic Acids Research</i> , 2016, 44, D410-D414.	14.5	4
4378	Transmembrane START domain proteins:in silico identification, characterization and expression analysis under stress conditions in chickpea (<i>Cicer arietinum</i> L.). <i>Plant Signaling and Behavior</i> , 2016, 11, e992698.	2.4	8
4379	Evolutionary distinctiveness of fatty acid and polyketide synthesis in eukaryotes. <i>ISME Journal</i> , 2016, 10, 1877-1890.	9.8	72
4380	New features of desiccation tolerance in the lichen photobiont <i>Trebouxia gelatinosa</i> are revealed by a transcriptomic approach. <i>Plant Molecular Biology</i> , 2016, 91, 319-339.	3.9	69
4381	Identification and characterization of Lateral Organ Boundaries Domain genes in mulberry, <i>Morus notabilis</i> . <i>Meta Gene</i> , 2016, 8, 44-50.	0.6	15
4382	Genetic and life-history traits associated with the distribution of prophages in bacteria. <i>ISME Journal</i> , 2016, 10, 2744-2754.	9.8	314
4383	Signaling via the CytoR/JAK/STAT/SOCS pathway: Emergence during evolution. <i>Molecular Immunology</i> , 2016, 71, 166-175.	2.2	27
4384	KMAD: knowledge-based multiple sequence alignment for intrinsically disordered proteins. <i>Bioinformatics</i> , 2016, 32, 932-936.	4.1	27
4385	Biochemical characterization and structural analysis of a new cold-active and salt-tolerant esterase from the marine bacterium <i>Thalassospira</i> sp.. <i>Extremophiles</i> , 2016, 20, 323-336.	2.3	49
4386	The CopC Family: Structural and Bioinformatic Insights into a Diverse Group of Periplasmic Copper Binding Proteins. <i>Biochemistry</i> , 2016, 55, 2278-2290.	2.5	78

#	ARTICLE	IF	CITATIONS
4387	Genome Sequence and Analysis of <i>Escherichia coli</i> MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. <i>Genome Biology and Evolution</i> , 2016, 8, 742-752.	2.5	35
4388	A multi-objective optimization approach accurately resolves protein domain architectures. <i>Bioinformatics</i> , 2016, 32, 345-353.	4.1	45
4389	The Alba protein family: Structure and function. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 570-583.	2.3	46
4390	Bioinformatics Analysis of NBS-LRR Encoding Resistance Genes in <i>Setaria italica</i> . <i>Biochemical Genetics</i> , 2016, 54, 232-248.	1.7	18
4391	Short-Stalked <i>Prosthecomicrobium hirschii</i> Cells Have a <i>Caulobacter</i> -Like Cell Cycle. <i>Journal of Bacteriology</i> , 2016, 198, 1149-1159.	2.2	40
4392	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i> . <i>Plant Cell</i> , 2016, 28, 388-405.	6.6	163
4393	First structure of archaeal branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> specific for l-amino acids and R-amines. <i>Extremophiles</i> , 2016, 20, 215-225.	2.3	28
4394	Identification and Functional Prediction of Large Intergenic Noncoding RNAs (lincRNAs) in Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Marine Biotechnology</i> , 2016, 18, 271-282.	2.4	53
4395	Exome sequencing reveals genetic differentiation due to high-altitude adaptation in the Tibetan cashmere goat (<i>Capra hircus</i>). <i>BMC Genomics</i> , 2016, 17, 122.	2.8	87
4396	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
4397	A Developmental Switch of Gene Expression in the Barley Seed Mediated by HvVP1 (Viviparous-1) and HvGAMYB Interactions. <i>Plant Physiology</i> , 2016, 170, 2146-2158.	4.8	38
4398	Genome Content and Phylogenomics Reveal both Ancestral and Lateral Evolutionary Pathways in Plant-Pathogenic <i>Streptomyces</i> Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2146-2155.	3.1	44
4399	Knockdown of Five Genes Encoding Uncharacterized Proteins Inhibits <i>Entamoeba histolytica</i> Phagocytosis of Dead Host Cells. <i>Infection and Immunity</i> , 2016, 84, 1045-1053.	2.2	10
4400	Genome-wide analysis of CrRLK1L gene family in <i>Gossypium</i> and identification of candidate CrRLK1L genes related to fiber development. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1137-1154.	2.1	27
4401	Complete genome sequence and description of <i>Lactococcus garvieae</i> M14 isolated from Algerian fermented milk. <i>New Microbes and New Infections</i> , 2016, 10, 122-131.	1.6	9
4402	Horizontal Gene Transfer from Bacteria Has Enabled the Plant-Parasitic Nematode <i>Globodera pallida</i> to Feed on Host-Derived Sucrose. <i>Molecular Biology and Evolution</i> , 2016, 33, 1571-1579.	8.9	52
4403	Novel insights on ENTH domain-containing proteins in apicomplexan parasites. <i>Parasitology Research</i> , 2016, 115, 2191-2202.	1.6	3
4404	Transcript Abundance of Putative Lipid Phosphate Phosphatases During Development of <i>Trypanosoma brucei</i> in the Tsetse Fly. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 890-893.	1.4	4

#	ARTICLE	IF	CITATIONS
4405	Characterization of DNA methyltransferase and demethylase genes in <i>Fragaria vesca</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 1333-1345.	2.1	37
4406	Comparative genomics reveals new evolutionary and ecological patterns of selenium utilization in bacteria. <i>ISME Journal</i> , 2016, 10, 2048-2059.	9.8	54
4407	Mte1 interacts with Mph1 and promotes crossover recombination and telomere maintenance. <i>Genes and Development</i> , 2016, 30, 700-717.	5.9	27
4408	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.	1.1	3
4409	Bacterial ferrous iron transport: the Feo system. <i>FEMS Microbiology Reviews</i> , 2016, 40, 273-298.	8.6	301
4410	The Female Post-Mating Response Requires Genes Expressed in the Secondary Cells of the Male Accessory Gland in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 202, 1029-1041.	2.9	61
4411	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	21.4	235
4412	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	14.5	5,391
4413	Genome-wide analysis of WRKY family of transcription factors in common bean, <i>Phaseolus vulgaris</i> : Chromosomal localization, structure, evolution and expression divergence. <i>Plant Gene</i> , 2016, 5, 22-30.	2.3	22
4414	The role of the intestinal microbiota in type 1 diabetes mellitus. <i>Nature Reviews Endocrinology</i> , 2016, 12, 154-167.	9.6	335
4415	The structure of Resuscitation promoting factor B from <i>M. tuberculosis</i> reveals unexpected ubiquitin-like domains. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 445-451.	2.4	22
4416	Genome-wide analysis and expression patterns of ZF-HD transcription factors under different developmental tissues and abiotic stresses in Chinese cabbage. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1451-1464.	2.1	53
4417	Algorithms for modeling global and context-specific functional relationship networks. <i>Briefings in Bioinformatics</i> , 2016, 17, 686-695.	6.5	3
4418	Residue mutations of xylanase in <i>Aspergillus kawachii</i> alter its optimum pH. <i>Microbiological Research</i> , 2016, 182, 1-7.	5.3	14
4419	Molecular aspects of zygotic embryogenesis in sunflower (<i>Helianthus annuus</i> L.): correlation of positive histone marks with HaWUS expression and putative link HaWUS/HaL1L. <i>Planta</i> , 2016, 243, 199-215.	3.2	7
4420	Genomic survey and expression analysis of DNA repair genes in the genus <i>Leptospira</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 703-722.	2.1	8
4421	Identification of Genes Conferring Tolerance to Lignocellulose-Derived Inhibitors by Functional Selections in Soil Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 528-537.	3.1	20
4422	Dormancy-associated MADS-box genes and microRNAs jointly control dormancy transition in pear (<i>Pyrus pyrifolia</i>) white pear group) flower bud. <i>Journal of Experimental Botany</i> , 2016, 67, 239-257.	4.8	170

#	ARTICLE	IF	CITATIONS
4423	In silico analysis suggests that PH0702 and PH0208 encode for methylthioribose-1-phosphate isomerase and ribose-1,5-bisphosphate isomerase, respectively, rather than alF2B1 ² and alF2B1 ¹ . <i>Gene</i> , 2016, 575, 118-126.	2.2	7
4424	Using THz Spectroscopy, Evolutionary Network Analysis Methods, and MD Simulation to Map the Evolution of Allosteric Communication Pathways in c-Type Lysozymes. <i>Molecular Biology and Evolution</i> , 2016, 33, 40-61.	8.9	6
4425	Computational Analysis of Missense Variants of G Protein-Coupled Receptors Involved in the Neuroendocrine Regulation of Reproduction. <i>Neuroendocrinology</i> , 2016, 103, 230-239.	2.5	16
4426	Advances in long noncoding RNAs: identification, structure prediction and function annotation. <i>Briefings in Functional Genomics</i> , 2016, 15, 38-46.	2.7	111
4427	Deciphering the cause of evolutionary variance within intrinsically disordered regions in human proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 233-249.	3.5	9
4428	Review of the algal biology program within the National Alliance for Advanced Biofuels and Bioproducts. <i>Algal Research</i> , 2017, 22, 187-215.	4.6	69
4429	Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. <i>ISME Journal</i> , 2017, 11, 237-247.	9.8	298
4430	Fragmented protein sequence alignment using two-layer particle swarm optimization (FTLPSO). <i>Journal of King Saud University - Science</i> , 2017, 29, 191-205.	3.5	7
4431	De novo assembly of a tadpole shrimp (<i>Triops newberryi</i>) transcriptome and preliminary differential gene expression analysis. <i>Molecular Ecology Resources</i> , 2017, 17, 161-171.	4.8	28
4432	Nucleoplasmin-like domain of FKBP39 from <i>Drosophila melanogaster</i> forms a tetramer with partly disordered tentacle-like C-terminal segments. <i>Scientific Reports</i> , 2017, 7, 40405.	3.3	7
4433	Classification and Lineage Tracing of SH2 Domains Throughout Eukaryotes. <i>Methods in Molecular Biology</i> , 2017, 1555, 59-75.	0.9	0
4434	Mutations and interactions in human ER1 α and bZIP proteins: An in silico approach for cell signaling in breast oncology. <i>Gene</i> , 2017, 610, 90-102.	2.2	2
4435	Draft genome sequence of a human-associated isolate of <i>Haloferax alexandrinus</i> strain Arc-hr, an extremely halophilic archaea. <i>New Microbes and New Infections</i> , 2017, 15, 44-45.	1.6	10
4436	An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. <i>Protein Science</i> , 2017, 26, 677-699.	7.6	13
4437	Evolution of protein N-glycosylation process in Golgi apparatus which shapes diversity of protein N-glycan structures in plants, animals and fungi. <i>Scientific Reports</i> , 2017, 7, 40301.	3.3	27
4438	Aberrant coordination geometries discovered in the most abundant metalloproteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 885-907.	2.6	8
4439	De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. <i>Scientific Reports</i> , 2017, 7, 40472.	3.3	18
4440	Molecular cloning, phylogenetic analysis, and expression patterns of LATERAL SUPPRESSOR-LIKE and REGULATOR OF AXILLARY MERISTEM FORMATION-LIKE genes in sunflower (<i>Helianthus annuus</i> L.). <i>Development Genes and Evolution</i> , 2017, 227, 159-170.	0.9	8

#	ARTICLE	IF	CITATIONS
4441	New insights into marine group III Euryarchaeota, from dark to light. ISME Journal, 2017, 11, 1102-1117.	9.8	72
4442	Genome Sequence of <i>Christensenella minuta</i> DSM 22607 ^T . Genome Announcements, 2017, 5, .	0.8	19
4443	A comparative genomic analysis of putative pathogenicity genes in the host-specific sibling species <i>Colletotrichum graminicola</i> and <i>Colletotrichum sublineola</i> . BMC Genomics, 2017, 18, 67.	2.8	53
4444	Pharmacological profile of the aerial parts of <i>Rubus ulmifolius</i> Schott. BMC Complementary and Alternative Medicine, 2017, 17, 59.	3.7	13
4445	Exploring the genomic diversity of black yeasts and relatives (<i>Chaetothyriales</i> , <i>Ascomycota</i>). Studies in Mycology, 2017, 86, 1-28.	7.2	144
4446	Predicting Alpha Helical Transmembrane Proteins Using HMMs. Methods in Molecular Biology, 2017, 1552, 63-82.	0.9	2
4447	Complete genome sequence of <i>Lysinibacillus sphaericus</i> LMG 22257, a strain with ureolytic activity inducing calcium carbonate precipitation. Journal of Biotechnology, 2017, 246, 33-35.	3.8	5
4448	Screening and evaluating of long noncoding RNAs in the puberty of goats. BMC Genomics, 2017, 18, 164.	2.8	58
4449	Genome-wide identification and expression analysis of the GRAS family proteins in <i>Medicago truncatula</i> . Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	20
4450	Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Penner Serotype Reference Strain RM3420. Genome Announcements, 2017, 5, .	0.8	3
4451	In-silico screening, identification and validation of a novel vaccine candidate in the fight against <i>Plasmodium falciparum</i> . Parasitology Research, 2017, 116, 1293-1305.	1.6	13
4452	Heterologous production of kasugamycin, an aminoglycoside antibiotic from <i>Streptomyces kasugaensis</i> , in <i>Streptomyces lividans</i> and <i>Rhodococcus erythropolis</i> L-88 by constitutive expression of the biosynthetic gene cluster. Applied Microbiology and Biotechnology, 2017, 101, 4259-4268.	3.6	23
4453	Genome-wide analysis and expression patterns of the NAC transcription factor family in <i>Medicago truncatula</i> . Physiology and Molecular Biology of Plants, 2017, 23, 343-356.	3.1	40
4454	Lateral Gene Transfer in the Adaptation of the Anaerobic Parasite <i>Blastocystis</i> to the Gut. Current Biology, 2017, 27, 807-820.	3.9	94
4455	De novo transcriptome assemblies of four accessions of the metal hyperaccumulator plant <i>Noccaea caerulea</i> . Scientific Data, 2017, 4, 160131.	5.3	38
4456	Complete Annotated Genome Sequences of Three <i>Campylobacter jejuni</i> Strains Isolated from Naturally Colonized Farm-Raised Chickens. Genome Announcements, 2017, 5, .	0.8	4
4457	QuickProbs 2: Towards rapid construction of high-quality alignments of large protein families. Scientific Reports, 2017, 7, 41553.	3.3	9
4458	Seasonal patterns in Arctic prasinophytes and inferred ecology of <i>Bathycoccus</i> unveiled in an Arctic winter metagenome. ISME Journal, 2017, 11, 1372-1385.	9.8	54

#	ARTICLE	IF	CITATIONS
4459	Identification and functional analysis of the ICK gene family in maize. <i>Scientific Reports</i> , 2017, 7, 43818.	3.3	6
4460	Genome-wide identification of the TIFY gene family in three cultivated <i>Gossypium</i> species and the expression of JAZ genes. <i>Scientific Reports</i> , 2017, 7, 42418.	3.3	46
4461	Genome-Wide analysis of the AAAP gene family in moso bamboo (<i>Phyllostachys edulis</i>). <i>BMC Plant Biology</i> , 2017, 17, 29.	3.6	51
4462	Domain prediction with probabilistic directional context. <i>Bioinformatics</i> , 2017, 33, 2471-2478.	4.1	4
4463	Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to <i>Mycobacterium tuberculosis</i> . <i>BMC Bioinformatics</i> , 2017, 18, 201.	2.6	14
4464	Integrated host and viral transcriptome analyses reveal pathology and inflammatory response mechanisms to ALV-J injection in SPF chickens. <i>Scientific Reports</i> , 2017, 7, 46156.	3.3	24
4465	Transcriptome analyses of differential gene expression in the bursa of Fabricius between Silky Fowl and White Leghorn. <i>Scientific Reports</i> , 2017, 7, 45959.	3.3	18
4466	Spicule formation in calcareous sponges: Coordinated expression of biomineralization genes and spicule-type specific genes. <i>Scientific Reports</i> , 2017, 7, 45658.	3.3	19
4467	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. <i>Scientific Reports</i> , 2017, 7, 46562.	3.3	6
4468	Genome-wide identification, characterization of the MADS-box gene family in Chinese jujube and their involvement in flower development. <i>Scientific Reports</i> , 2017, 7, 1025.	3.3	42
4469	The SPOR Domain, a Widely Conserved Peptidoglycan Binding Domain That Targets Proteins to the Site of Cell Division. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	36
4470	Transcriptomic changes in an animal-bacterial symbiosis under modeled microgravity conditions. <i>Scientific Reports</i> , 2017, 7, 46318.	3.3	19
4471	Identification and expression analyses of the alanine aminotransferase (AlaAT) gene family in poplar seedlings. <i>Scientific Reports</i> , 2017, 7, 45933.	3.3	20
4472	Characterization of Methyltransferase AlmCII in Chalcomycin Biosynthesis: The First TylF Family Oâ€Methyltransferase Works on a 4â€2â€Deoxysugar. <i>ChemBioChem</i> , 2017, 18, 1510-1517.	2.6	4
4473	ThreaDomEx: a unified platform for predicting continuous and discontinuous protein domains by multiple-threading and segment assembly. <i>Nucleic Acids Research</i> , 2017, 45, W400-W407.	14.5	25
4474	Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in <i>Drosophila</i> Hybrids. <i>Genome Biology and Evolution</i> , 2017, 9, 1450-1470.	2.5	26
4475	In silico screening for candidate chassis strains of free fatty acid-producing cyanobacteria. <i>BMC Genomics</i> , 2017, 18, 33.	2.8	11
4476	Draft Genome Sequence of <i>Mycobacterium boenickei</i> CIP 107829. <i>Genome Announcements</i> , 2017, 5, .	0.8	3

#	ARTICLE	IF	CITATIONS
4477	Comparative transcriptomic analysis of <i>Gardnerella vaginalis</i> biofilms vs. planktonic cultures using RNA-seq. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 3.	6.4	66
4478	The Nucleoporin Nup2 Contains a Meiotic-Autonomous Region that Promotes the Dynamic Chromosome Events of Meiosis. <i>Genetics</i> , 2017, 206, 1319-1337.	2.9	18
4479	Systematic identification and characterization of cardiac long intergenic noncoding RNAs in zebrafish. <i>Scientific Reports</i> , 2017, 7, 1250.	3.3	12
4480	Bioinformatic and expression analyses on carotenoid dioxygenase genes in fruit development and abiotic stress responses in <i>Fragaria vesca</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 895-907.	2.1	27
4481	Comparative genomic analysis of SET domain family reveals the origin, expansion, and putative function of the arthropod-specific SmydA genes as histone modifiers in insects. <i>GigaScience</i> , 2017, 6, 1-16.	6.4	19
4482	The s48/45 six-cysteine proteins: mediators of interaction throughout the <i>Plasmodium</i> life cycle. <i>International Journal for Parasitology</i> , 2017, 47, 409-423.	3.1	45
4483	Structural conservation of the PIN domain active site across all domains of life. <i>Protein Science</i> , 2017, 26, 1474-1492.	7.6	33
4484	Network and role analysis of autophagy in <i>Phytophthora sojae</i> . <i>Scientific Reports</i> , 2017, 7, 1879.	3.3	19
4485	Complete genome of a metabolically-diverse marine bacterium <i>Shewanella japonica</i> KCTC 22435 T. <i>Marine Genomics</i> , 2017, 35, 39-42.	1.1	3
4486	On patterns and re-use in bioinformatics databases. <i>Bioinformatics</i> , 2017, 33, 2731-2736.	4.1	6
4487	Protein contact prediction by using information theory. <i>Journal of the Korean Physical Society</i> , 2017, 70, 876-879.	0.7	3
4488	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. <i>Nucleic Acids Research</i> , 2017, 45, e96-e96.	14.5	22
4489	Comparative and functional genomics of the <i>Lactococcus lactis</i> taxon; insights into evolution and niche adaptation. <i>BMC Genomics</i> , 2017, 18, 267.	2.8	117
4490	Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. <i>Journal of Virology</i> , 2017, 91, .	3.4	37
4491	In vitro and in silico characterization of metagenomic soil-derived cellulases capable of hydrolyzing oil palm empty fruit bunch. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2017, 15, 55-62.	4.4	8
4492	“ <i>Mycobacterium massiliopolynesiensis</i> ” sp. nov., a rapidly-growing mycobacterium of medical interest related to <i>Mycobacterium phlei</i> . <i>Scientific Reports</i> , 2017, 7, 40443.	3.3	6
4493	Sequencing, de novo assembling, and annotating the genome of the endangered Chinese crocodile lizard <i>Shinisaurus crocodilurus</i> . <i>GigaScience</i> , 2017, 6, 1-6.	6.4	23
4494	Genome-wide identification and phylogenetic, comparative genomic, alternative splicing, and expression analyses of TCP genes in plants. <i>Plant Gene</i> , 2017, 12, 23-32.	2.3	6

#	ARTICLE	IF	CITATIONS
4495	Comparative transcriptome analysis of <i>Rimicaris</i> sp. reveals novel molecular features associated with survival in deep-sea hydrothermal vent. <i>Scientific Reports</i> , 2017, 7, 2000.	3.3	28
4496	Comparative genomic analysis of innate immunity reveals novel and conserved components in crustacean food crop species. <i>BMC Genomics</i> , 2017, 18, 389.	2.8	37
4497	Molecular cloning, expression and insulin reduction activity of a thioredoxin 1 homologue (TRX1) from the pathogenic fungus <i>Paracoccidioides lutzii</i> . <i>International Journal of Biological Macromolecules</i> , 2017, 103, 683-691.	7.5	10
4498	ChiPPI: a novel method for mapping chimeric proteinâ€“protein interactions uncovers selection principles of protein fusion events in cancer. <i>Nucleic Acids Research</i> , 2017, 45, 7094-7105.	14.5	33
4499	Identifying relationships between unrelated pharmaceutical target proteins on the basis of shared active compounds. <i>Future Science OA</i> , 2017, 3, FSO212.	1.9	4
4500	Rapid and Recent Evolution of LTR Retrotransposons Drives Rice Genome Evolution During the Speciation of AA-Genome <i>Oryza</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1875-1885.	1.8	60
4501	Different expression patterns of sperm motility-related genes in testis of diploid and tetraploid cyprinid fish. <i>Biology of Reproduction</i> , 2017, 96, 907-920.	2.7	21
4502	Crystal structures of Î²-carboxysome shell protein CcmP: ligand binding correlates with the closed or open central pore. <i>Journal of Experimental Botany</i> , 2017, 68, 3857-3867.	4.8	40
4503	Methods for Microbiome Analysis. <i>Translational Medicine Research</i> , 2017, , 269-298.	0.0	1
4504	Testing for the Occurrence of Selective Episodes During the Divergence of Otophysan Fishes: Insights from Mitogenomics. <i>Journal of Molecular Evolution</i> , 2017, 84, 162-173.	1.8	5
4505	Draft genome sequence of <i>Cercospora soja</i> isolate S9, a fungus causing frog-eye leaf spot (FLS) disease of soybean. <i>Genomics Data</i> , 2017, 12, 79-80.	1.3	10
4506	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	139
4507	The Human CCHC-type Zinc Finger Nucleic Acid-Binding Protein Binds G-Rich Elements in Target mRNA Coding Sequences and Promotes Translation. <i>Cell Reports</i> , 2017, 18, 2979-2990.	6.4	106
4508	Expression of a MORN repeat protein from <i>Euplotes octocarinatus</i> requires a +1 programmed ribosomal frameshifting. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1327-1334.	1.3	0
4509	Genome Reduction and Microbe-Host Interactions Drive Adaptation of a Sulfur-Oxidizing Bacterium Associated with a Cold Seep Sponge. <i>MSystems</i> , 2017, 2, .	3.8	35
4510	Integration of mRNP formation and export. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 2875-2897.	5.4	64
4511	Comparative genomics of <i>Vibrio campbellii</i> strains and core species of the <i>Vibrio</i> Harveyi clade. <i>Scientific Reports</i> , 2017, 7, 41394.	3.3	42
4512	Structural insights into ligand binding of PGRP1 splice variants in Chinese giant salamander (<i>Andrias</i>) Tj ETQq1 1 0.784314 rgBT /Overdo 2017, 23, 135.	1.8	2

#	ARTICLE	IF	CITATIONS
4513	Topological knots and links in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3415-3420.	7.1	101
4514	Trypanosome outer kinetochore proteins suggest conservation of chromosome segregation machinery across eukaryotes. Journal of Cell Biology, 2017, 216, 379-391.	5.2	87
4515	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins “ extended Database. Journal of Molecular Biology, 2017, 429, 348-355.	4.2	85
4516	The evolution of function within the Nudix homology clan. Proteins: Structure, Function and Bioinformatics, 2017, 85, 775-811.	2.6	53
4517	Curd development associated gene (CDAG1) in cauliflower (Brassica oleracea L. var. botrytis) could result in enlarged organ size and increased biomass. Plant Science, 2017, 254, 82-94.	3.6	13
4518	Dynein light chain family genes in 15 plant species: Identification, evolution and expression profiles. Plant Science, 2017, 254, 70-81.	3.6	14
4519	Spontaneous circadian rhythms in a cold-adapted natural isolate of Aureobasidium pullulans. Scientific Reports, 2017, 7, 13837.	3.3	15
4520	Algorithms for matching partially labelled sequence graphs. Algorithms for Molecular Biology, 2017, 12, 24.	1.2	1
4521	Enzyme function and its evolution. Current Opinion in Structural Biology, 2017, 47, 151-156.	5.7	13
4522	Evolutionary Analysis of Pectin Lyases of the Genus Colletotrichum. Journal of Molecular Evolution, 2017, 85, 120-136.	1.8	5
4523	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	12.8	40
4524	MFIB: a repository of protein complexes with mutual folding induced by binding. Bioinformatics, 2017, 33, 3682-3684.	4.1	61
4525	Whole-genome comparison of urinary pathogenic Escherichia coli and faecal isolates of UTI patients and healthy controls. International Journal of Medical Microbiology, 2017, 307, 497-507.	3.6	57
4526	Chlamydomonas reinhardtii LFO1 Is an IsdG Family Heme Oxygenase. MSphere, 2017, 2, .	2.9	15
4527	Genomic characterization, phylogenetic analysis, and identification of virulence factors in Aerococcus sanguinicola and Aerococcus urinae strains isolated from infection episodes. Microbial Pathogenesis, 2017, 112, 327-340.	2.9	14
4528	Characterization of Trypanosoma cruzi MutY DNA glycosylase ortholog and its role in oxidative stress response. Infection, Genetics and Evolution, 2017, 55, 332-342.	2.3	6
4529	The chromosomal organization of horizontal gene transfer in bacteria. Nature Communications, 2017, 8, 841.	12.8	184
4530	Genome-wide identification and expression analyses of the homeobox transcription factor family during ovule development in seedless and seeded grapes. Scientific Reports, 2017, 7, 12638.	3.3	27

#	ARTICLE	IF	CITATIONS
4531	Oligo(cis-1,4-isoprene) aldehyde-oxidizing dehydrogenases of the rubber-degrading bacterium <i>Gordonia polyisoprenivorans</i> VH2. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7945-7960.	3.6	10
4532	THE PATTERN RECOGNITION OF PROBABILITY DISTRIBUTIONS OF AMINO ACIDS IN PROTEIN FAMILIES. , 2017, , 29-50.		1
4533	Both modular and single-domain Type I polyketide synthases are expressed in the brevetoxin-producing dinoflagellate, <i>Karenia brevis</i> (Dinophyceae). <i>Journal of Phycology</i> , 2017, 53, 1325-1339.	2.3	28
4534	Metagenome Assembly and Functional Annotation. , 2017, , 151-159.		0
4535	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	3.3	24
4536	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	7.1	111
4537	Draft Genome Sequences of 25 <i>Listeria monocytogenes</i> Isolates Associated with Human Clinical Listeriosis in Ireland. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
4538	A novel lipoate attachment enzyme is shared by <i>Plasmodium</i> and <i>Chlamydia</i> species. <i>Molecular Microbiology</i> , 2017, 106, 439-451.	2.5	11
4539	Molecular characterization of transport lectin vesicular integral membrane protein 36 kDa (VIP36) in the life cycle of <i>Schistosoma mansoni</i> . <i>Parasitology Research</i> , 2017, 116, 2765-2773.	1.6	3
4540	A Bacterial Multidomain NAD-Independent α -Lactate Dehydrogenase Utilizes Flavin Adenine Dinucleotide and Fe-S Clusters as Cofactors and Quinone as an Electron Acceptor for α -Lactate Oxidation. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	12
4541	Genome-wide identification and tissue-specific expression analysis of nucleotide binding site-leucine rich repeat gene family in <i>Cicer arietinum</i> (kabuli chickpea). <i>Genomics Data</i> , 2017, 14, 24-31.	1.3	16
4542	Shear force-based genetic screen reveals negative regulators of cell adhesion and protrusive activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7727-E7736.	7.1	19
4543	Evaluation of single-cell genomics to address evolutionary questions using three SAGs of the choanoflagellate <i>Monosiga brevicollis</i> . <i>Scientific Reports</i> , 2017, 7, 11025.	3.3	19
4544	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of <i>Drosophila</i> . <i>Current Biology</i> , 2017, 27, 2869-2877.e6.	3.9	37
4545	Structural and developmental expression of Ss-riok-2, an RIO protein kinase encoding gene of <i>Strongyloides stercoralis</i> . <i>Scientific Reports</i> , 2017, 7, 8693.	3.3	6
4546	Transcriptomic profiling of Tibetan highland fish (<i>Gymnocypris przewalskii</i>) in response to the infection of parasite ciliate <i>Ichthyophthirius multifiliis</i> . <i>Fish and Shellfish Immunology</i> , 2017, 70, 524-535.	3.6	23
4547	Genome reconstruction in <i>Cynara cardunculus</i> taxa gains access to chromosome-scale DNA variation. <i>Scientific Reports</i> , 2017, 7, 5617.	3.3	30
4548	Characterization of Phospholipid: Diacylglycerol Acyltransferases (PDATs) from <i>Camelina sativa</i> and Their Roles in Stress Responses. <i>Biology Open</i> , 2017, 6, 1024-1034.	1.2	31

#	ARTICLE	IF	CITATIONS
4549	A comparative genome analysis of <i>Cercospora sojina</i> with other members of the pathogen genus <i>Mycosphaerella</i> on different plant hosts. <i>Genomics Data</i> , 2017, 13, 54-63.	1.3	15
4550	Isolation and characterization of a novel endo- β -1,4-glucanase from a metagenomic library of the black-goat rumen. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 801-808.	2.0	22
4551	Draft Genome Sequence of <i>Mycobacterium colombiense</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0
4552	TbIRK is a signature sequence free potassium channel from <i>Trypanosoma brucei</i> locating to acidocalcisomes. <i>Scientific Reports</i> , 2017, 7, 656.	3.3	13
4553	Predicting the functional consequences of non-synonymous single nucleotide polymorphisms in IL8 gene. <i>Scientific Reports</i> , 2017, 7, 6525.	3.3	75
4554	Using RNA sequencing to identify putative competing endogenous RNAs (ceRNAs) potentially regulating fat metabolism in bovine liver. <i>Scientific Reports</i> , 2017, 7, 6396.	3.3	65
4555	Coronafacoyl Phytotoxin Biosynthesis and Evolution in the Common Scab Pathogen <i>Streptomyces scabiei</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	26
4556	<i>Dermatophagoides pteronyssinus</i> lytFM encoding an NlpC/P60 endopeptidase is also present in mite-associated bacteria that express LytFM variants. <i>FEBS Open Bio</i> , 2017, 7, 1267-1280.	2.3	8
4557	The hnRNP Q-like gene is retroinserted into the B chromosomes of the cichlid fish <i>Astatotilapia latifasciata</i> . <i>Chromosome Research</i> , 2017, 25, 277-290.	2.2	12
4558	FARME DB: a functional antibiotic resistance element database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw165.	3.0	40
4559	In silico characterization of tandem repeats in <i>Trichophyton rubrum</i> and related dermatophytes provides new insights into their role in pathogenesis. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	4
4560	Comparative analysis of double-stranded RNA degradation and processing in insects. <i>Scientific Reports</i> , 2017, 7, 17059.	3.3	153
4561	Genetic adaptation of microbial populations present in high-intensity catfish production systems with therapeutic oxytetracycline treatment. <i>Scientific Reports</i> , 2017, 7, 17491.	3.3	20
4562	Systematic CRISPR-Cas9-Mediated Modifications of <i>Plasmodium yoelii</i> ApiAP2 Genes Reveal Functional Insights into Parasite Development. <i>MBio</i> , 2017, 8, .	4.1	66
4563	Long noncoding RNAs that respond to <i>Fusarium oxysporum</i> infection in 'Cavendish' banana (<i>Musa</i>) Tj ETQq0.0.0 rgBT/Overlock 22	3.3	22
4564	Genomic assessment in <i>Lactobacillus plantarum</i> links the butyrogenic pathway with glutamine metabolism. <i>Scientific Reports</i> , 2017, 7, 15975.	3.3	25
4565	Computational design of fully overlapping coding schemes for protein pairs and triplets. <i>Scientific Reports</i> , 2017, 7, 15873.	3.3	22
4566	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	36

#	ARTICLE	IF	CITATIONS
4567	Complete Genome Sequences of <i>Vibrio cholerae</i> -Specific Bacteriophages 24 and X29. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
4568	Differential gene expression of Australian <i>Cricotopus draysoni</i> (Diptera: Chironomidae) populations reveals seasonal association in detoxification gene regulation. <i>Scientific Reports</i> , 2017, 7, 14263.	3.3	5
4569	Distinct <i>Campylobacter fetus</i> lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <i>Nature Communications</i> , 2017, 8, 1367.	12.8	56
4570	Plant polysaccharide degrading enzyme system of <i>Thermobifida cellulolytica</i> TB100T revealed by de novo genome project data. <i>Acta Alimentaria</i> , 2017, 46, 323-335.	0.7	3
4571	Signatures of adaptation and symbiosis in genomes and transcriptomes of <i>Symbiodinium</i> . <i>Scientific Reports</i> , 2017, 7, 15021.	3.3	35
4572	What Defines the "Kingdom" Fungi?. <i>Microbiology Spectrum</i> , 2017, 5, .	3.0	59
4573	Finding Similar Nucleotide Sequences Using Network BLAST Searches. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 3.3.1-3.3.25.	25.8	12
4574	Massive expansion and differential evolution of small heat shock proteins with wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.3	17
4575	Long noncoding RNA expression profile changes associated with dietary energy in the sheep testis during sexual maturation. <i>Scientific Reports</i> , 2017, 7, 5180.	3.3	51
4576	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	3.3	21
4577	Identification and expression analysis of the apple (<i>Malus</i> —domestica) basic helix-loop-helix transcription factor family. <i>Scientific Reports</i> , 2017, 7, 28.	3.3	43
4578	Insecticide resistance and resistance mechanisms in bed bugs, <i>Cimex</i> spp. (Hemiptera: Cimicidae). <i>Parasites and Vectors</i> , 2017, 10, 318.	2.5	159
4579	In silico approach to designing rational metagenomic libraries for functional studies. <i>BMC Bioinformatics</i> , 2017, 18, 267.	2.6	19
4580	Across-proteome modeling of dimer structures for the bottom-up assembly of protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017, 18, 257.	2.6	9
4581	Genetic and functional characterisation of the lactococcal P335 phage-host interactions. <i>BMC Genomics</i> , 2017, 18, 146.	2.8	29
4582	Genomic and transcriptomic analyses reveal distinct biological functions for cold shock proteins (VpaCspA and VpaCspD) in <i>Vibrio parahaemolyticus</i> CHN25 during low-temperature survival. <i>BMC Genomics</i> , 2017, 18, 436.	2.8	35
4583	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	2.8	33
4584	Genome-wide analysis of UDP-glycosyltransferase super family in <i>Brassica rapa</i> and <i>Brassica oleracea</i> reveals its evolutionary history and functional characterization. <i>BMC Genomics</i> , 2017, 18, 474.	2.8	54

#	ARTICLE	IF	CITATIONS
4585	Mining a differential sialotranscriptome of <i>Rhipicephalus microplus</i> guides antigen discovery to formulate a vaccine that reduces tick infestations. <i>Parasites and Vectors</i> , 2017, 10, 206.	2.5	46
4586	Complete genome sequence of <i>Pseudoalteromonas</i> phage vB_PspS-H40/1 (formerly H40/1) that infects <i>Pseudoalteromonas</i> sp. strain H40 and is used as biological tracer in hydrological transport studies. <i>Standards in Genomic Sciences</i> , 2017, 12, 20.	1.5	8
4587	Single-Cell Alternative Splicing Analysis with Expedition Reveals Splicing Dynamics during Neuron Differentiation. <i>Molecular Cell</i> , 2017, 67, 148-161.e5.	9.7	155
4588	Virus-host relationships of marine single-celled eukaryotes resolved from metatranscriptomics. <i>Nature Communications</i> , 2017, 8, 16054.	12.8	100
4589	Analysis of the grape (<i>Vitis vinifera</i> L.) thaumatin-like protein (TLP) gene family and demonstration that TLP29 contributes to disease resistance. <i>Scientific Reports</i> , 2017, 7, 4269.	3.3	75
4590	Identification of Protein Secretion Systems in Bacterial Genomes Using MacSyFinder. <i>Methods in Molecular Biology</i> , 2017, 1615, 1-21.	0.9	92
4591	Computational Functional Analysis of Lipid Metabolic Enzymes. <i>Methods in Molecular Biology</i> , 2017, 1609, 195-216.	0.9	2
4592	Use of restrained molecular dynamics to predict the conformations of phosphorylated receiver domains in two-component signaling systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 155-176.	2.6	12
4593	Metagenomic Insights into Effects of Chemical Pollutants on Microbial Community Composition and Function in Estuarine Sediments Receiving Polluted River Water. <i>Microbial Ecology</i> , 2017, 73, 791-800.	2.8	43
4594	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	2.7	21
4595	PASylation technology improves recombinant interferon- β 1b solubility, stability, and biological activity. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1975-1987.	3.6	28
4596	Genome scale identification, structural analysis, and classification of periplasmic binding proteins from <i>Mycobacterium tuberculosis</i> . <i>Current Genetics</i> , 2017, 63, 553-576.	1.7	1
4597	Isolation and characterization of a novel glycosyl hydrolase family 74 (GH74) cellulase from the black goat rumen metagenomic library. <i>Folia Microbiologica</i> , 2017, 62, 175-181.	2.3	19
4598	miRPathDB: a new dictionary on microRNAs and target pathways. <i>Nucleic Acids Research</i> , 2017, 45, D90-D96.	14.5	102
4599	The evolutionary divergence of STAT transcription factor in different <i>Anopheles</i> species. <i>Gene</i> , 2017, 596, 89-97.	2.2	6
4600	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.	2.2	20
4601	Overexpression of PSK1, a SKP1-like gene homologue, from <i>Paeonia suffruticosa</i> , confers salinity tolerance in <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2017, 36, 151-162.	5.6	20
4602	Genome-wide identification, characterisation and expression profiles of calcium-dependent protein kinase genes in barley (<i>Hordeum vulgare</i> L.). <i>Journal of Applied Genetics</i> , 2017, 58, 11-22.	1.9	17

#	ARTICLE	IF	CITATIONS
4603	Metazoan evolution of the armadillo repeat superfamily. Cellular and Molecular Life Sciences, 2017, 74, 525-541.	5.4	37
4604	Draft genome sequence of pectic polysaccharide-degrading moderate thermophilic bacterium <i>Geobacillus thermodenitrificans</i> DSM 101594. Brazilian Journal of Microbiology, 2017, 48, 7-8.	2.0	6
4605	Alternative Splicing May Not Be the Key to Proteome Complexity. Trends in Biochemical Sciences, 2017, 42, 98-110.	7.5	277
4606	Characterization of the <i>Xylella fastidiosa</i> PD1311 gene mutant and its suppression of Pierce's disease on grapevines. Molecular Plant Pathology, 2017, 18, 684-694.	4.2	8
4607	Structure and dynamics of the multi-domain resuscitation promoting factor RpfB from <i>Mycobacterium tuberculosis</i> . Journal of Biomolecular Structure and Dynamics, 2017, 35, 1322-1330.	3.5	20
4608	In-silico prediction of dual function of DksA like hypothetical protein in <i>V. cholerae</i> O395 genome. Microbiological Research, 2017, 195, 60-70.	5.3	1
4609	Family-specific scaling laws in bacterial genomes. Nucleic Acids Research, 2017, 45, 7615-7622.	14.5	8
4610	A metagenome-derived thermostable β -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. Scientific Reports, 2017, 7, 17306.	3.3	15
4611	MEBS, a software platform to evaluate large (meta)genomic collections according to their metabolic machinery: unraveling the sulfur cycle. GigaScience, 2017, 6, 1-17.	6.4	35
4612	Complete Genome Sequences of Seven <i>Vibrio cholerae</i> Phages Isolated in China. Genome Announcements, 2017, 5, .	0.8	1
4613	Comparative transcriptome analysis and identification of candidate effectors in two related rust species (<i>Gymnosporangium yamadae</i> and <i>Gymnosporangium asiaticum</i>). BMC Genomics, 2017, 18, 651.	2.8	20
4614	Genome-Based Analyses of Six Hexacorallian Species Reject the "Naked Coral" Hypothesis. Genome Biology and Evolution, 2017, 9, 2626-2634.	2.5	8
4615	Microbe Genomes Associated with Human Body. Evolutionary Studies, 2017, , 285-300.	0.1	0
4616	What Defines the "Kingdom" Fungi?. , 2017, , 57-77.		6
4617	Genome Wide Mapping of Peptidases in <i>Rhodnius prolixus</i> : Identification of Protease Gene Duplications, Horizontally Transferred Proteases and Analysis of Peptidase A1 Structures, with Considerations on Their Role in the Evolution of Hematophagy in Triatominae. Frontiers in Physiology, 2017, 8, 1051.	2.8	19
4618	Transcriptome-Wide Identification, Classification, and Characterization of AP2/ERF Family Genes in the Desert Moss <i>Syntrichia caninervis</i> . Frontiers in Plant Science, 2017, 8, 262.	3.6	25
4619	Identification of a Novel Alternative Splicing Variant of VvPMA1 in Grape Root under Salinity. Frontiers in Plant Science, 2017, 8, 605.	3.6	8
4620	Molecular Characterization and Expression Profiling of <i>Brachypodium distachyon</i> L. Cystatin Genes Reveal High Evolutionary Conservation and Functional Divergence in Response to Abiotic Stress. Frontiers in Plant Science, 2017, 8, 743.	3.6	15

#	ARTICLE	IF	CITATIONS
4621	Whole-Genome Identification and Expression Pattern of the Vicinal Oxygen Chelate Family in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 745.	3.6	16
4622	A Transcriptomics and Comparative Genomics Analysis Reveals Gene Families with a Role in Body Plan Complexity. <i>Frontiers in Plant Science</i> , 2017, 8, 869.	3.6	5
4623	YSK2 Type Dehydrin (SbDhn1) from Sorghum bicolor Showed Improved Protection under High Temperature and Osmotic Stress Condition. <i>Frontiers in Plant Science</i> , 2017, 8, 918.	3.6	45
4624	WHITE STRIPE LEAF4 Encodes a Novel P-Type PPR Protein Required for Chloroplast Biogenesis during Early Leaf Development. <i>Frontiers in Plant Science</i> , 2017, 8, 1116.	3.6	71
4625	Evolution of Daily Gene Co-expression Patterns from Algae to Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1217.	3.6	26
4626	De novo Assembly of the <i>Camellia nitidissima</i> Transcriptome Reveals Key Genes of Flower Pigment Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 1545.	3.6	43
4627	Comparative Genomics of <i>Ralstonia solanacearum</i> Identifies Candidate Genes Associated with Cool Virulence. <i>Frontiers in Plant Science</i> , 2017, 8, 1565.	3.6	25
4628	Overexpression of the Maize ZmNLP6 and ZmNLP8 Can Complement the Arabidopsis Nitrate Regulatory Mutant nlp7 by Restoring Nitrate Signaling and Assimilation. <i>Frontiers in Plant Science</i> , 2017, 8, 1703.	3.6	52
4629	Metagenomic Analysis of a Complex Community Present in Pond Sediment. <i>Journal of Genomics</i> , 2017, 5, 36-47.	0.9	12
4630	The purplish bifurcate mussel <i>Mytilisepta virgata</i> gene expression atlas reveals a remarkable tissue functional specialization. <i>BMC Genomics</i> , 2017, 18, 590.	2.8	32
4631	A Transcriptome Survey Spanning Life Stages and Sexes of the Harlequin Bug, <i>Murgantia histrionica</i> . <i>Insects</i> , 2017, 8, 55.	2.2	20
4632	Phage Biodiversity in Artisanal Cheese Wheys Reflects the Complexity of the Fermentation Process. <i>Viruses</i> , 2017, 9, 45.	3.3	21
4633	Integrated analysis of coding genes and non-coding RNAs during hair follicle cycle of cashmere goat (<i>Capra hircus</i>). <i>BMC Genomics</i> , 2017, 18, 767.	2.8	119
4634	Living Organisms Author Their Read-Write Genomes in Evolution. <i>Biology</i> , 2017, 6, 42.	2.8	44
4635	Genome-Wide Analysis Reveals Extensive Changes in LncRNAs during Skeletal Muscle Development in Hu Sheep. <i>Genes</i> , 2017, 8, 191.	2.4	41
4636	c-di-AMP: An Essential Molecule in the Signaling Pathways that Regulate the Viability and Virulence of Gram-Positive Bacteria. <i>Genes</i> , 2017, 8, 197.	2.4	97
4637	De Novo Assembly and Analysis of Tartary Buckwheat (<i>Fagopyrum tataricum</i> Garetn.) Transcriptome Discloses Key Regulators Involved in Salt-Stress Response. <i>Genes</i> , 2017, 8, 255.	2.4	42
4638	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in <i>Dendrobium officinale</i> . <i>Genes</i> , 2017, 8, 257.	2.4	20

#	ARTICLE	IF	CITATIONS
4639	Genome-Wide Comprehensive Analysis the Molecular Phylogenetic Evaluation and Tissue-Specific Expression of SABATH Gene Family in <i>Salvia miltiorrhiza</i> . <i>Genes</i> , 2017, 8, 365.	2.4	14
4640	Mutual Regulation of NOD2 and RIG-I in Zebrafish Provides Insights into the Coordination between Innate Antibacterial and Antiviral Signaling Pathways. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1147.	4.1	16
4641	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	6.0	121
4642	The Distinct Transcriptional Response of the Midgut of <i>Amblyomma sculptum</i> and <i>Amblyomma aureolatum</i> Ticks to <i>Rickettsia rickettsii</i> Correlates to Their Differences in Susceptibility to Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 129.	3.9	23
4643	Analysis of the Salivary Gland Transcriptome of Unfed and Partially Fed <i>Amblyomma sculptum</i> Ticks and Descriptive Proteome of the Saliva. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 476.	3.9	79
4644	Genome-Wide Analysis Suggests the Relaxed Purifying Selection Affect the Evolution of WOX Genes in <i>Pyrus bretschneideri</i> , <i>Prunus persica</i> , <i>Prunus mume</i> , and <i>Fragaria vesca</i> . <i>Frontiers in Genetics</i> , 2017, 8, 78.	2.3	68
4645	A Preliminary List of Horizontally Transferred Genes in Prokaryotes Determined by Tree Reconstruction and Reconciliation. <i>Frontiers in Genetics</i> , 2017, 8, 112.	2.3	11
4646	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. <i>Frontiers in Immunology</i> , 2017, 8, 1382.	4.8	25
4647	Responses of the Housefly, <i>Musca domestica</i> , to the Hytrosavirus Replication: Impacts on Host's Vitellogenesis and Immunity. <i>Frontiers in Microbiology</i> , 2017, 8, 583.	3.5	21
4648	In silico Prediction, in vitro Antibacterial Spectrum, and Physicochemical Properties of a Putative Bacteriocin Produced by <i>Lactobacillus rhamnosus</i> Strain L156.4. <i>Frontiers in Microbiology</i> , 2017, 8, 876.	3.5	29
4649	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in <i>Pasteurella multocida</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 961.	3.5	36
4650	Comparative Omics and Trait Analyses of Marine <i>Pseudoalteromonas</i> Phages Advance the Phage OTU Concept. <i>Frontiers in Microbiology</i> , 2017, 8, 1241.	3.5	34
4651	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. <i>Frontiers in Microbiology</i> , 2017, 8, 1279.	3.5	31
4652	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	3.5	15
4653	<i>Alternaria</i> Toxins: Potential Virulence Factors and Genes Related to Pathogenesis. <i>Frontiers in Microbiology</i> , 2017, 8, 1451.	3.5	163
4654	The Laclâ€‘Family Transcription Factor, RbsR, Is a Pleiotropic Regulator of Motility, Virulence, Siderophore and Antibiotic Production, Gas Vesicle Morphogenesis and Flotation in <i>Serratia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1678.	3.5	20
4655	Defining the Genetic Features of O-Antigen Biosynthesis Gene Cluster and Performance of an O-Antigen Serotyping Scheme for <i>Escherichia albertii</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1857.	3.5	16
4656	Insights into Microalga and Bacteria Interactions of Selected Phycosphere Biofilms Using Metagenomic, Transcriptomic, and Proteomic Approaches. <i>Frontiers in Microbiology</i> , 2017, 8, 1941.	3.5	97

#	ARTICLE	IF	CITATIONS
4657	The Sit-and-Wait Hypothesis in Bacterial Pathogens: A Theoretical Study of Durability and Virulence. <i>Frontiers in Microbiology</i> , 2017, 8, 2167.	3.5	24
4658	The Different Faces of Rolling-Circle Replication and Its Multifunctional Initiator Proteins. <i>Frontiers in Microbiology</i> , 2017, 8, 2353.	3.5	82
4659	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	3.5	60
4660	Agonist Binding to Chemosensory Receptors: A Systematic Bioinformatics Analysis. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 63.	3.5	36
4661	Exception to the Rule: Genomic Characterization of Naturally Occurring Unusual <i>Vibrio cholerae</i> Strains with a Single Chromosome. <i>International Journal of Genomics</i> , 2017, 2017, 1-14.	1.6	18
4662	Interaction of Recombinant <i>Gallus gallus</i> SEPT5 and Brain Proteins of H5N1-Avian Influenza Virus-Infected Chickens. <i>Proteomes</i> , 2017, 5, 23.	3.5	5
4663	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and <i>Brassica</i> species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	2.8	37
4664	Bioactive Nutrients and Nutrigenomics in Age-Related Diseases. <i>Molecules</i> , 2017, 22, 105.	3.8	61
4665	Transcriptome Analysis of <i>Taxillus chinensis</i> (DC.) Danser Seeds in Response to Water Loss. <i>PLoS ONE</i> , 2017, 12, e0169177.	2.5	31
4666	Mapping and Genetic Structure Analysis of the Anthracnose Resistance Locus Co-1HY in the Common Bean (<i>Phaseolus vulgaris</i> L.). <i>PLoS ONE</i> , 2017, 12, e0169954.	2.5	36
4667	Characterisation and genome sequence of the lytic <i>Acinetobacter baumannii</i> bacteriophage vB_AbaS_Loki. <i>PLoS ONE</i> , 2017, 12, e0172303.	2.5	26
4668	Bioinformatic prediction of G protein-coupled receptor encoding sequences from the transcriptome of the foreleg, including the Haller's organ, of the cattle tick, <i>Rhipicephalus australis</i> . <i>PLoS ONE</i> , 2017, 12, e0172326.	2.5	11
4669	RNA-Seq de novo assembly and differential transcriptome analysis of the nematode <i>Ascaridia galli</i> in relation to in vivo exposure to flubendazole. <i>PLoS ONE</i> , 2017, 12, e0185182.	2.5	11
4670	Relating protein functional diversity to cell type number identifies genes that determine dynamic aspects of chromatin organisation as potential contributors to organismal complexity. <i>PLoS ONE</i> , 2017, 12, e0185409.	2.5	4
4671	Ensemble-based modeling and rigidity decomposition of allosteric interaction networks and communication pathways in cyclin-dependent kinases: Differentiating kinase clients of the Hsp90-Cdc37 chaperone. <i>PLoS ONE</i> , 2017, 12, e0186089.	2.5	17
4672	Genomic features of <i>Candidatus Venteria ishoeyi</i> , a new sulfur-oxidizing macrobacterium from the Humboldt Sulfuretum off Chile. <i>PLoS ONE</i> , 2017, 12, e0188371.	2.5	12
4673	First insights into a type II toxin-antitoxin system from the clinical isolate <i>Mycobacterium</i> sp. MHSD3, similar to epsilon/zeta systems. <i>PLoS ONE</i> , 2017, 12, e0189459.	2.5	6
4674	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx006.	14.5	47

#	ARTICLE	IF	CITATIONS
4675	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . PLoS ONE, 2017, 12, e0186401.	2.5	35
4676	Inferring repeat-protein energetics from evolutionary information. PLoS Computational Biology, 2017, 13, e1005584.	3.2	11
4677	Identifying pathogenicity of human variants via paralog-based yeast complementation. PLoS Genetics, 2017, 13, e1006779.	3.5	30
4678	A highly specific phage defense system is a conserved feature of the <i>Vibrio cholerae</i> mobilome. PLoS Genetics, 2017, 13, e1006838.	3.5	101
4679	The <i>Biomphalaria glabrata</i> DNA methylation machinery displays spatial tissue expression, is differentially active in distinct snail populations and is modulated by interactions with <i>Schistosoma mansoni</i> . PLoS Neglected Tropical Diseases, 2017, 11, e0005246.	3.0	39
4680	Segmental duplications: evolution and impact among the current Lepidoptera genomes. BMC Evolutionary Biology, 2017, 17, 161.	3.2	13
4681	B-BOX genes: genome-wide identification, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i> Rehd.). BMC Plant Biology, 2017, 17, 156.	3.6	56
4682	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. BMC Biology, 2017, 15, 63.	3.8	238
4683	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . BMC Biology, 2017, 15, 111.	3.8	19
4684	Analysis of viral diversity for vaccine target discovery. BMC Medical Genomics, 2017, 10, 78.	1.5	14
4685	Generic amplification and next generation sequencing reveal Crimean-Congo hemorrhagic fever virus AP92-like strain and distinct tick phleboviruses in Anatolia, Turkey. Parasites and Vectors, 2017, 10, 335.	2.5	37
4686	The RIO protein kinase-encoding gene <i>Sj-riok-2</i> is involved in key reproductive processes in <i>Schistosoma japonicum</i> . Parasites and Vectors, 2017, 10, 604.	2.5	9
4687	Viral communities of the human gut: metagenomic analysis of composition and dynamics. Mobile DNA, 2017, 8, 12.	3.6	119
4688	Structural and functional annotation of hypothetical proteins of human adenovirus: prioritizing the novel drug targets. BMC Research Notes, 2017, 10, 706.	1.4	20
4689	Constructing an integrated gene similarity network for the identification of disease genes. Journal of Biomedical Semantics, 2017, 8, 32.	1.6	24
4690	Perturbed human sub-networks by <i>Fusobacterium nucleatum</i> candidate virulence proteins. Microbiome, 2017, 5, 89.	11.1	27
4691	Microbial phylogeny determines transcriptional response of resistome to dynamic composting processes. Microbiome, 2017, 5, 103.	11.1	60
4692	Differential gene expression in response to <i>Fusarium oxysporum</i> infection in resistant and susceptible genotypes of flax (<i>Linum usitatissimum</i> L.). BMC Plant Biology, 2017, 17, 253.	3.6	61

#	ARTICLE	IF	CITATIONS
4693	Transcriptome analysis of <i>Haloquadratum walsbyi</i> : vanity is but the surface. BMC Genomics, 2017, 18, 510.	2.8	10
4694	Draft genome sequences of two opportunistic pathogenic strains of <i>Staphylococcus cohnii</i> isolated from human patients. Standards in Genomic Sciences, 2017, 12, 49.	1.5	11
4695	Metagenomic analysis of intertidal hypersaline microbial mats from Elkhorn Slough, California, grown with and without molybdate. Standards in Genomic Sciences, 2017, 12, 67.	1.5	5
4696	Exploring general-purpose protein features for distinguishing enzymes and non-enzymes within the twilight zone. BMC Bioinformatics, 2017, 18, 349.	2.6	10
4697	Cancerous domains: comprehensive analysis of cancer type-specific recurrent somatic mutations in proteins and domains. BMC Bioinformatics, 2017, 18, 370.	2.6	8
4698	A sensitive short read homology search tool for paired-end read sequencing data. BMC Bioinformatics, 2017, 18, 414.	2.6	3
4699	LiverWiki: a wiki-based database for human liver. BMC Bioinformatics, 2017, 18, 452.	2.6	4
4700	Complete genome sequence of the sulfur-oxidizing chemolithoautotrophic <i>Sulfurovum lithotrophicum</i> 42BKTT. Standards in Genomic Sciences, 2017, 12, 54.	1.5	17
4701	RNA-seq-based genome annotation and identification of long-noncoding RNAs in the grapevine cultivar "Riesling". BMC Genomics, 2017, 18, 937.	2.8	15
4702	A dual transcript-discovery approach to improve the delimitation of gene features from RNA-seq data in the chicken model. Biology Open, 2018, 7, .	1.2	7
4703	Characterization of Cytosine Methylation and the DNA Methyltransferases of <i>Toxoplasma gondii</i> . International Journal of Biological Sciences, 2017, 13, 458-470.	6.4	13
4704	RNA-binding proteins and their role in the regulation of gene expression in <i>Trypanosoma cruzi</i> and <i>Saccharomyces cerevisiae</i> . Genetics and Molecular Biology, 2017, 40, 22-30.	1.3	38
4705	KiPho: malaria parasite kinome and phosphatome portal. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	1
4707	A biallelic <i>ANTXR1</i> variant expands the anthrax toxin receptor associated phenotype to tooth agenesis. American Journal of Medical Genetics, Part A, 2018, 176, 1015-1022.	1.2	11
4708	Diversity and motif conservation in protein 3D structural landscape: exploration by a new multivariate simulation method. Journal of Molecular Modeling, 2018, 24, 76.	1.8	3
4709	Studying AMPK in an Evolutionary Context. Methods in Molecular Biology, 2018, 1732, 111-142.	0.9	3
4710	Genome-wide identification and expression analysis of GRAS family transcription factors in tea plant (<i>Camellia sinensis</i>). Scientific Reports, 2018, 8, 3949.	3.3	62
4711	Cancer-Associated Long Noncoding RNA SMRT-2 Controls Epidermal Differentiation. Journal of Investigative Dermatology, 2018, 138, 1445-1449.	0.7	13

#	ARTICLE	IF	CITATIONS
4712	Comprehensive Redox Profiling of the Thiol Proteome of <i>Clostridium difficile</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1035-1046.	3.8	21
4713	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 519-531.	3.5	21
4714	Structural Basis for the Initiation of Glycosaminoglycan Biosynthesis by Human Xylosyltransferase 1. <i>Structure</i> , 2018, 26, 801-809.e3.	3.3	33
4715	The <i>Gastrodia elata</i> genome provides insights into plant adaptation to heterotrophy. <i>Nature Communications</i> , 2018, 9, 1615.	12.8	170
4716	A methanotrophic archaeon couples anaerobic oxidation of methane to Fe(III) reduction. <i>ISME Journal</i> , 2018, 12, 1929-1939.	9.8	266
4717	Genome-wide analyses of the bHLH superfamily in crustaceans: reappraisal of higher-order groupings and evidence for lineage-specific duplications. <i>Royal Society Open Science</i> , 2018, 5, 172433.	2.4	5
4718	Genome-wide Identification and Expression Analysis of the TRK Gene Family in <i>Aspergillus oryzae</i> . , 2018, , .		0
4719	Recurrent acquisition of cytosine methyltransferases into eukaryotic retrotransposons. <i>Nature Communications</i> , 2018, 9, 1341.	12.8	42
4720	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, <i>Scomber colias</i> . <i>Data in Brief</i> , 2018, 18, 276-284.	1.0	7
4721	Reconstruction of the sialylation pathway in the ancestor of eukaryotes. <i>Scientific Reports</i> , 2018, 8, 2946.	3.3	20
4722	Comprehensive analysis of the lysine acetylome and its potential regulatory roles in the virulence of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2018, 176, 46-55.	2.4	37
4723	Structural insights into the binding and catalytic mechanisms of the <i>Listeria monocytogenes</i> bacteriophage glycosyl hydrolase PlyP40. <i>Molecular Microbiology</i> , 2018, 108, 128-142.	2.5	12
4724	Novel global effector mining from the transcriptome of early life stages of the soybean cyst nematode <i>Heterodera glycines</i> . <i>Scientific Reports</i> , 2018, 8, 2505.	3.3	31
4725	Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. <i>DNA Research</i> , 2018, 25, 217-227.	3.4	33
4726	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. <i>Nature Communications</i> , 2018, 9, 448.	12.8	146
4727	Cell-type-resolved alternative splicing patterns in mouse liver. <i>DNA Research</i> , 2018, 25, 265-275.	3.4	14
4728	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.	4.4	12
4729	The reconstruction of 2,631 draft metagenome-assembled genomes from the global oceans. <i>Scientific Data</i> , 2018, 5, 170203.	5.3	449

#	ARTICLE	IF	CITATIONS
4730	Genome sequence and detection of peach rosette mosaic virus. Journal of Virological Methods, 2018, 254, 8-12.	2.1	8
4731	Insights from Ion Binding Site Network Analysis into Evolution and Functions of Proteins. Molecular Informatics, 2018, 37, e1700144.	2.5	4
4732	Genome sequence and description of Haloferax massiliense sp. nov., a new halophilic archaeon isolated from the human gut. Extremophiles, 2018, 22, 485-498.	2.3	14
4733	Novel Isoforms of N16 and N19 Families Implicated for the Nacreous Layer Formation in the Pearl Oyster Pinctada fucata. Marine Biotechnology, 2018, 20, 155-167.	2.4	5
4734	Function, distribution, and annotation of characterized cellulases, xylanases, and chitinases from CAZy. Applied Microbiology and Biotechnology, 2018, 102, 1629-1637.	3.6	109
4735	Complete Genome Sequence of <i>Bacillus methylotrophicus</i> Strain NKG-1, Isolated from the Changbai Mountains, China. Genome Announcements, 2018, 6, .	0.8	7
4736	Interactome INSIDER: a structural interactome browser for genomic studies. Nature Methods, 2018, 15, 107-114.	19.0	133
4737	Comparative transcriptomic analysis of two <i>Vicia sativa</i> L. varieties with contrasting responses to cadmium stress reveals the important role of metal transporters in cadmium tolerance. Plant and Soil, 2018, 423, 241-255.	3.7	34
4738	Characteristics of a PHD Finger Subtype. Biochemistry, 2018, 57, 525-539.	2.5	11
4739	Identification of a novel botulinum neurotoxin gene cluster in <i>Enterococcus</i> . FEBS Letters, 2018, 592, 310-317.	2.8	82
4740	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. Scientific Reports, 2018, 8, 85.	3.3	99
4741	PlanNET: homology-based predicted interactome for multiple planarian transcriptomes. Bioinformatics, 2018, 34, 1016-1023.	4.1	19
4742	A novel galactolipase from a green microalga <i>Chlorella kessleri</i> : purification, characterization, molecular cloning, and heterologous expression. Applied Microbiology and Biotechnology, 2018, 102, 1711-1723.	3.6	2
4743	RNA-seq analysis of lncRNA-controlled developmental gene expression during puberty in goat & rat. BMC Genetics, 2018, 19, 19.	2.7	24
4744	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (<i>Pyrus bretschneideri</i>). BMC Plant Biology, 2018, 18, 36.	3.6	6
4745	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. BMC Systems Biology, 2018, 12, 13.	3.0	1
4746	Flexible metagenome analysis using the MGX framework. Microbiome, 2018, 6, 76.	11.1	29
4747	Formation of chimeric genes with essential functions at the origin of eukaryotes. BMC Biology, 2018, 16, 30.	3.8	19

#	ARTICLE	IF	CITATIONS
4748	A novel chimaeric flocculation protein enhances flocculation in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2018, 6, 49-55.	3.6	3
4749	Effect of SrtA on Interspecies Adherence of Oral Bacteria. <i>Current Medical Science</i> , 2018, 38, 160-166.	1.8	4
4750	In silico comparative analysis of GGDEF and EAL domain signaling proteins from the <i>Azospirillum</i> genomes. <i>BMC Microbiology</i> , 2018, 18, 20.	3.3	18
4751	Functional Prediction of Hypothetical Transcription Factors of <i>Escherichia coli</i> K-12 Based on Expression Data. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 157-166.	4.1	6
4752	Biochemical and structural characterization of a novel cold-active esterase-like protein from the psychrophilic yeast <i>Glaciozyma antarctica</i> . <i>Extremophiles</i> , 2018, 22, 607-616.	2.3	24
4753	PANDA: Protein function prediction using domain architecture and affinity propagation. <i>Scientific Reports</i> , 2018, 8, 3484.	3.3	14
4754	Statistical correction for functional metagenomic profiling of a microbial community with short NGS reads. <i>Journal of Applied Statistics</i> , 2018, 45, 2521-2535.	1.3	0
4755	Genome-wide identification, putative functionality and interactions between lncRNAs and miRNAs in <i>Brassica</i> species. <i>Scientific Reports</i> , 2018, 8, 4960.	3.3	37
4756	Comparative Transcriptomics Among Four White Pine Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1461-1474.	1.8	35
4757	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain 3519A. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
4758	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain 4858. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
4759	Genetic Diversity and Functional Analysis of Sigma Factors in <i>Enterobacter cloacae</i> Complex Resourced From Various Niche. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431875487.	1.2	6
4760	A Decade of <i>Streptococcus thermophilus</i> Phage Evolution in an Irish Dairy Plant. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	35
4761	Large-scale computational drug repositioning to find treatments for rare diseases. <i>Npj Systems Biology and Applications</i> , 2018, 4, 13.	3.0	40
4762	Sequence- and structure-based analysis of proteins involved in miRNA biogenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 139-151.	3.5	5
4763	Genomewide analysis of the lateral organ boundaries domain gene family in <i>Eucalyptus grandis</i> reveals members that differentially impact secondary growth. <i>Plant Biotechnology Journal</i> , 2018, 16, 124-136.	8.3	44
4764	Immunohistochemical null-phenotype for mismatch repair proteins in colonic carcinoma associated with concurrent MLH1 hypermethylation and MSH2 somatic mutations. <i>Familial Cancer</i> , 2018, 17, 225-228.	1.9	17
4765	A dynamic microbial community with high functional redundancy inhabits the cold, oxic subseafloor aquifer. <i>ISME Journal</i> , 2018, 12, 1-16.	9.8	148

#	ARTICLE	IF	CITATIONS
4766	On the Early Evolution of Catabolic Pathways: A Comparative Genomics Approach. I. The Cases of Glucose, Ribose, and the Nucleobases Catabolic Routes. <i>Journal of Molecular Evolution</i> , 2018, 86, 27-46.	1.8	9
4767	Genome-wide identification and cadmium induced expression profiling of sulfate transporter (SULTR) genes in sorghum (<i>Sorghum bicolor</i> L.). <i>BioMetals</i> , 2018, 31, 91-105.	4.1	16
4768	Crystal structure of the Legionella effector Lem22. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 263-267.	2.6	3
4769	Gene expression profile and long non-coding RNA analysis, using RNA-Seq, in chicken embryonic fibroblast cells infected by avian leukosis virus J. <i>Archives of Virology</i> , 2018, 163, 639-647.	2.1	15
4770	Pectin methylesterase inhibitor (PMEI) family can be related to male sterility in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Molecular Genetics and Genomics</i> , 2018, 293, 343-357.	2.1	21
4771	Transcriptional profiling of antioxidant defense system and heat shock protein (Hsp) families in the cadmium- and copper-exposed marine ciliate <i>Euplotes crassus</i> . <i>Genes and Genomics</i> , 2018, 40, 85-98.	1.4	13
4772	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensor domain protein. <i>Protein Science</i> , 2018, 27, 568-572.	7.6	1
4773	Deciphering the tRNA-dependent lipid aminoacylation systems in bacteria: Novel components and structural advances. <i>RNA Biology</i> , 2018, 15, 480-491.	3.1	22
4774	Transcriptomic Characterization of the South American Freshwater Stingray <i>Potamotrygon motoro</i> Venom Apparatus. <i>Toxins</i> , 2018, 10, 544.	3.4	13
4775	VarQ: A Tool for the Structural and Functional Analysis of Human Protein Variants. <i>Frontiers in Genetics</i> , 2018, 9, 620.	2.3	10
4776	Improving Standard Progressive Multiple Sequence Alignment by Using Multithreading Techniques. , 2018, , .		0
4777	A new insight into the evolution and functional divergence of <i>FRK</i> genes in <i>Pyrus bretschneideri</i> . <i>Royal Society Open Science</i> , 2018, 5, 171463.	2.4	6
4778	Comparative Analysis of Genomic Island Prediction Tools. <i>Frontiers in Genetics</i> , 2018, 9, 619.	2.3	29
4779	Linking pangenomes and metagenomes: the <i>Prochlorococcus</i> metapangenome. <i>PeerJ</i> , 2018, 6, e4320.	2.0	318
4780	Physiological and protein responses in leaves of <i>Nitraria billardieri</i> seedlings to moderate salt stress. <i>Journal of Plant Interactions</i> , 2018, 13, 522-531.	2.1	0
4781	Draft Genome Sequence of <i>Paucibacter aquatilis</i> CR182 ^T , a Strain with Antimicrobial Activity Isolated from Freshwater of Nakdong River in South Korea. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
4782	A benchmark study of sequence alignment methods for protein clustering. <i>BMC Bioinformatics</i> , 2018, 19, 529.	2.6	26
4783	Identification and expression analysis of cDNA encoding insulin-like growth factor 2 in horses. <i>Journal of Reproduction and Development</i> , 2018, 64, 57-64.	1.4	0

#	ARTICLE	IF	CITATIONS
4784	Protein Design Assisted Residue Conservation and Functional Stability Analysis for Bacterial Chemotaxis. , 2018, , .		0
4785	A Survey of Phylogenetic Databases. , 2018, , .		0
4786	Mining Late Embryogenesis Abundant (LEA) Family Genes in <i>Cleistogenes songorica</i> , a Xerophyte Perennial Desert Plant. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3430.	4.1	28
4787	Expression profiling of lncRNAs and mRNAs reveals regulation of muscle growth in the Pacific abalone, <i>Haliotis discus hannai</i> . <i>Scientific Reports</i> , 2018, 8, 16839.	3.3	13
4788	Isolation of A Novel <i>Bacillus thuringiensis</i> Phage Representing A New Phage Lineage and Characterization of Its Endolysin. <i>Viruses</i> , 2018, 10, 611.	3.3	14
4789	Complete Genome Sequence of the <i>Arcobacter molluscorum</i> Type Strain LMG 25693. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	6
4790	Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. <i>Nature Communications</i> , 2018, 9, 4999.	12.8	205
4791	Combining bioinformatics, cheminformatics, functional genomics and whole organism approaches for identifying epigenetic drug targets in <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 559-570.	3.4	34
4792	Identification, Classification, and Functional Analysis of AP2/ERF Family Genes in the Desert Moss <i>Bryum argenteum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3637.	4.1	21
4793	Draft genome sequence of <i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain Fito_F321, an endophyte microorganism from <i>Vitis vinifera</i> with biocontrol potential. <i>Standards in Genomic Sciences</i> , 2018, 13, 30.	1.5	25
4794	Dissecting the Repertoire of DNA-Binding Transcription Factors of the Archaeon <i>Pyrococcus furiosus</i> DSM 3638. <i>Life</i> , 2018, 8, 40.	2.4	5
4795	Complete genome sequence of the halophile bacterium <i>Kushneria konosiri</i> X49T, isolated from salt-fermented <i>Konosirus punctatus</i> . <i>Standards in Genomic Sciences</i> , 2018, 13, 19.	1.5	8
4796	Characterization of Der f 22 - a paralogue of the major allergen Der f 2. <i>Scientific Reports</i> , 2018, 8, 11743.	3.3	5
4797	Transcriptome analysis of the typical freshwater rhodophytes <i>Sheathia arcuata</i> grown under different light intensities. <i>PLoS ONE</i> , 2018, 13, e0197729.	2.5	12
4798	SDADB: a functional annotation database of protein structural domains. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	9
4799	Expansion and Divergence of Argonaute Genes in the Oomycete Genus <i>Phytophthora</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2841.	3.5	14
4800	The crystal structure of <i>Mycobacterium tuberculosis</i> high-temperature requirement A protein reveals an autoregulatory mechanism. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 803-809.	0.8	1
4801	Complete Genome Sequence of the <i>Arcobacter suis</i> Type Strain LMG 26152. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	0

#	ARTICLE	IF	CITATIONS
4802	Complete Genome Sequence of the <i>Arcobacter skirrowii</i> Type Strain LMG 6621. Microbiology Resource Announcements, 2018, 7, .	0.6	0
4803	Analyses of long non-coding RNA and mRNA profiling in the spleen of diarrheic piglets caused by <i>Clostridium perfringens</i> type C. PeerJ, 2018, 6, e5997.	2.0	21
4804	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by <i>Pseudoalteromonas carrageenovora</i> 9T to Adapt to Macroalgal Niches. Frontiers in Microbiology, 2018, 9, 2740.	3.5	54
4805	Characterization of the Ubiquitin C-Terminal Hydrolase and Ubiquitin-Specific Protease Families in Rice (<i>Oryza sativa</i>). Frontiers in Plant Science, 2018, 9, 1636.	3.6	22
4806	Comparative Analysis of the Nodule Transcriptomes of <i>Ceanothus thyrsiflorus</i> (Rhamnaceae, Rosales) and <i>Datisca glomerata</i> (Datiscaceae, Cucurbitales). Frontiers in Plant Science, 2018, 9, 1629.	3.6	12
4807	Comparative Proteomic Analysis. , 2018, , .		2
4808	A two-level model for the role of complex and young genes in the formation of organism complexity and new insights into the relationship between evolution and development. EvoDevo, 2018, 9, 22.	3.2	12
4809	Genome-wide exploration of C2H2 zinc finger family in durum wheat (<i>Triticum turgidum</i> ssp. Durum): insights into the roles in biological processes especially stress response. BioMetals, 2018, 31, 1019-1042.	4.1	37
4810	Draft Genome Sequence of <i>Deinococcus koreensis</i> SJW1-2 ^T , a Gamma Radiation-Resistant Bacterium Isolated from River Water. Microbiology Resource Announcements, 2018, 7, .	0.6	1
4811	Multiple paralogues of Î±-SNAP in <i>Giardia lamblia</i> exhibit independent subcellular localization and redistribution during encystation and stress. Parasites and Vectors, 2018, 11, 539.	2.5	3
4812	TCP Transcription Factors in Moso Bamboo (<i>Phyllostachys edulis</i>): Genome-Wide Identification and Expression Analysis. Frontiers in Plant Science, 2018, 9, 1263.	3.6	60
4813	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. Genomics, Proteomics and Bioinformatics, 2018, 16, 283-293.	6.9	19
4814	DREB2 (dehydration-responsive element-binding protein 2) type transcription factor in sorghum (<i>Sorghum bicolor</i>): genome-wide identification, characterization and expression profiles under cadmium and salt stresses. 3 Biotech, 2018, 8, 426.	2.2	28
4815	Identifying Drivers of Parallel Evolution: A Regression Model Approach. Genome Biology and Evolution, 2018, 10, 2801-2812.	2.5	19
4816	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. Genetics, 2018, 210, 883-894.	2.9	21
4817	FINDSITE ^{comb2.0} : A New Approach for Virtual Ligand Screening of Proteins and Virtual Target Screening of Biomolecules. Journal of Chemical Information and Modeling, 2018, 58, 2343-2354.	5.4	35
4818	Genome-Wide Analysis of Glycine soja Response Regulator GsRR Genes Under Alkali and Salt Stresses. Frontiers in Plant Science, 2018, 9, 1306.	3.6	7
4819	Filamentous Aggregates of Tau Proteins Fulfil Standard Amyloid Criteria Provided by the Fuzzy Oil Drop (FOD) Model. International Journal of Molecular Sciences, 2018, 19, 2910.	4.1	19

#	ARTICLE	IF	CITATIONS
4820	Using transcriptomics to enable a plethodontid salamander (<i>Bolitoglossa ramosi</i>) for limb regeneration research. <i>BMC Genomics</i> , 2018, 19, 704.	2.8	20
4821	Genomic comparison of <i>Trypanosoma conorhini</i> and <i>Trypanosoma rangeli</i> to <i>Trypanosoma cruzi</i> strains of high and low virulence. <i>BMC Genomics</i> , 2018, 19, 770.	2.8	14
4822	Linear and Kernel Model Construction Methods for Predicting Drug-Target Interactions in a Chemogenomic Framework. <i>Methods in Molecular Biology</i> , 2018, 1825, 355-368.	0.9	3
4823	Refining cellular pathway models using an ensemble of heterogeneous data sources. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	1
4824	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. <i>Frontiers in Plant Science</i> , 2018, 9, 1376.	3.6	10
4825	Phytophthora methylomes are modulated by 6mA methyltransferases and associated with adaptive genome regions. <i>Genome Biology</i> , 2018, 19, 181.	8.8	61
4826	Deciphering the structure of the condensin protein complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11911-11916.	7.1	15
4827	Genetic Evidence Supporting the Role of the Calcium Channel, <i>CACNA1S</i> , in Tooth Cusp and Root Patterning. <i>Frontiers in Physiology</i> , 2018, 9, 1329.	2.8	10
4828	Forward Genetics by Genome Sequencing Uncovers the Central Role of the <i>Aspergillus niger</i> <i>goxB</i> Locus in Hydrogen Peroxide Induced Glucose Oxidase Expression. <i>Frontiers in Microbiology</i> , 2018, 9, 2269.	3.5	13
4829	Dissecting the functional domains of the <i>Arabidopsis thaliana</i> nonhost resistance 2B (<i>AtNHR2B</i>) protein. <i>Plant Signaling and Behavior</i> , 2018, 13, e1530024.	2.4	8
4830	Zinc Finger-Homeodomain Transcriptional Factors (ZHDs) in Upland Cotton (<i>Gossypium hirsutum</i>): Genome-Wide Identification and Expression Analysis in Fiber Development. <i>Frontiers in Genetics</i> , 2018, 9, 357.	2.3	23
4831	In silico approach to identify non-synonymous SNPs with highest predicted deleterious effect on protein function in human obesity related gene, neuronal growth regulator 1 (<i>NEGR1</i>). <i>3 Biotech</i> , 2018, 8, 466.	2.2	9
4832	Big data analysis of human mitochondrial DNA substitution models: a regression approach. <i>BMC Genomics</i> , 2018, 19, 759.	2.8	5
4833	Flexibility and constraint: Evolutionary remodeling of the sporulation initiation pathway in Firmicutes. <i>PLoS Genetics</i> , 2018, 14, e1007470.	3.5	13
4834	Tyrosine phosphorylation of a receptor-like cytoplasmic kinase, <i>BSR1</i> , plays a crucial role in resistance to multiple pathogens in rice. <i>Plant Journal</i> , 2018, 96, 1137-1147.	5.7	17
4835	Draft Genome Sequence of <i>Mycobacterium setense</i> CSUR47. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
4836	Global Transcriptome Analyses Reveal Differentially Expressed Genes of Six Organs and Putative Genes Involved in (Iso)flavonoid Biosynthesis in <i>Belamcanda chinensis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1160.	3.6	9
4837	Genome-Wide Identification and Functional Prediction of Novel Drought-Responsive lncRNAs in <i>Pyrus betulifolia</i> . <i>Genes</i> , 2018, 9, 311.	2.4	27

#	ARTICLE	IF	CITATIONS
4838	A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. <i>Microbiome</i> , 2018, 6, 149.	11.1	41
4839	Overexpressing lncRNA LAIR increases grain yield and regulates neighbouring gene cluster expression in rice. <i>Nature Communications</i> , 2018, 9, 3516.	12.8	170
4840	De novo assembly and annotation of <i>Hyalomma dromedarii</i> tick (Acari: Ixodidae) sialotranscriptome with regard to gender differences in gene expression. <i>Parasites and Vectors</i> , 2018, 11, 314.	2.5	21
4841	Phylogenomics Reveal the Dynamic Evolution of Fungal Nitric Oxide Reductases and Their Relationship to Secondary Metabolism. <i>Genome Biology and Evolution</i> , 2018, 10, 2474-2489.	2.5	44
4842	Molecular Signal Integration of Aging and Diabetes Mellitus. , 2018, , .		0
4843	Identification of transposons near predicted lncRNA and mRNA pools of <i>Prunus mume</i> using an integrative transposable element database constructed from Rosaceae plant genomes. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1301-1316.	2.1	3
4844	High pCO ₂ -induced exopolysaccharide-rich ballasted aggregates of planktonic cyanobacteria could explain Paleoproterozoic carbon burial. <i>Nature Communications</i> , 2018, 9, 2116.	12.8	19
4845	Introgression and gene family contraction drive the evolution of lifestyle and host shifts of hypocrealean fungi. <i>Mycology</i> , 2018, 9, 176-188.	4.4	35
4846	Sequential search leads to faster, more efficient fragment-based <i>de novo</i> protein structure prediction. <i>Bioinformatics</i> , 2018, 34, 1132-1140.	4.1	12
4847	Discovery and Sequence Analysis of Four Deltacoronaviruses from Birds in the Middle East Reveal Interspecies Jumping with Recombination as a Potential Mechanism for Avian-to-Avian and Avian-to-Mammalian Transmission. <i>Journal of Virology</i> , 2018, 92, .	3.4	62
4848	Molecular Mechanisms Preventing Senescence in Response to Prolonged Darkness in a Desiccation-Tolerant Plant. <i>Plant Physiology</i> , 2018, 177, 1319-1338.	4.8	26
4849	Discovery of Novel Cellulases Using Proteomic Strategies. <i>Methods in Molecular Biology</i> , 2018, 1796, 103-113.	0.9	1
4850	The floral transcriptome of <i>Machilus yunnanensis</i> , a tree in the magnoliid family Lauraceae. <i>Computational Biology and Chemistry</i> , 2018, 77, 456-465.	2.3	1
4851	Chinook salmon (<i>Oncorhynchus tshawytscha</i>) genome and transcriptome. <i>PLoS ONE</i> , 2018, 13, e0195461.	2.5	85
4852	Heterologous expression and enhanced production of Î²-1,4-glucanase of <i>Bacillus halodurans</i> C-125 in <i>Escherichia coli</i> . <i>Electronic Journal of Biotechnology</i> , 2018, 34, 29-36.	2.2	5
4853	Drug Side-effect Profiles Prediction: From Empirical Risk Minimization to Structural Risk Minimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	3.0	11
4854	Transcriptome Analysis Reveals Dynamic Gene Expression Profiles in Porcine Alveolar Macrophages in Response to the Chinese Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus. <i>BioMed Research International</i> , 2018, 2018, 1-23.	1.9	24
4855	Whole-Genome Sequencing and Comparative Genome Analysis Provided Insight into the Predatory Features and Genetic Diversity of Two <i>Bdellovibrio</i> Species Isolated from Soil. <i>International Journal of Genomics</i> , 2018, 2018, 1-10.	1.6	8

#	ARTICLE	IF	CITATIONS
4856	Early metazoan cell type diversity and the evolution of multicellular gene regulation. <i>Nature Ecology and Evolution</i> , 2018, 2, 1176-1188.	7.8	226
4857	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. <i>ELife</i> , 2018, 7, .	6.0	40
4858	Local and Systemic Effect of Cytokinins on Soybean Nodulation and Regulation of Their Isopentenyl Transferase (IPT) Biosynthesis Genes Following Rhizobia Inoculation. <i>Frontiers in Plant Science</i> , 2018, 9, 1150.	3.6	41
4859	Insights into Avian Incomplete Dosage Compensation: Sex-Biased Gene Expression Coevolves with Sex Chromosome Degeneration in the Common Whitethroat. <i>Genes</i> , 2018, 9, 373.	2.4	13
4860	Acquisition of MACPF domain-encoding genes is the main contributor to LPS glycan diversity in gut <i>Bacteroides</i> species. <i>ISME Journal</i> , 2018, 12, 2919-2928.	9.8	17
4861	Mixed evolutionary origins of endogenous biomass-depolymerizing enzymes in animals. <i>BMC Genomics</i> , 2018, 19, 483.	2.8	8
4862	Genomic characterization and pathogenicity of a porcine hemagglutinating encephalomyelitis virus strain isolated in China. <i>Virus Genes</i> , 2018, 54, 672-683.	1.6	10
4863	Transcriptome Reveals Long Non-coding RNAs and mRNAs Involved in Primary Wool Follicle Induction in Carpet Sheep Fetal Skin. <i>Frontiers in Physiology</i> , 2018, 9, 446.	2.8	72
4864	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.	3.6	14
4865	Molecular Mechanisms of Acclimatization to Phosphorus Starvation and Recovery Underlying Full-Length Transcriptome Profiling in Barley (<i>Hordeum vulgare</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 500.	3.6	57
4866	Altered Expression of the Malate-Permeable Anion Channel OsALMT4 Reduces the Growth of Rice Under Low Radiance. <i>Frontiers in Plant Science</i> , 2018, 9, 542.	3.6	10
4867	Sparse Modeling to Analyze Drug-Target Interaction Networks. <i>Methods in Molecular Biology</i> , 2018, 1807, 181-193.	0.9	1
4868	The Genome of a Thermo Tolerant, Pathogenic Albino <i>Aspergillus fumigatus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1827.	3.5	12
4869	Identification of WRKY Gene Family from <i>Dimocarpus longan</i> and Its Expression Analysis during Flower Induction and Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2169.	4.1	38
4870	Identification of likely pathogenic and known variants in TSPEAR, LAMB3, BCOR, and WNT10A in four Turkish families with tooth agenesis. <i>Human Genetics</i> , 2018, 137, 689-703.	3.8	24
4871	Functional characterisation of the actin-depolymerising factor from the apicomplexan <i>Neospora caninum</i> (NcADF). <i>Molecular and Biochemical Parasitology</i> , 2018, 224, 26-36.	1.1	2
4872	Genome Reduction in <i>Psychromonas</i> Species within the Gut of an Amphipod from the Ocean's Deepest Point. <i>MSystems</i> , 2018, 3, .	3.8	21
4873	Genome-wide analysis of differentially expressed profiles of mRNAs, lncRNAs and circRNAs during <i>Cryptosporidium baileyi</i> infection. <i>BMC Genomics</i> , 2018, 19, 356.	2.8	26

#	ARTICLE	IF	CITATIONS
4874	Two divergent Symbiodinium genomes reveal conservation of a gene cluster for sunscreen biosynthesis and recently lost genes. BMC Genomics, 2018, 19, 458.	2.8	114
4875	Comprehensive Insights Into Composition, Metabolic Potentials, and Interactions Among Archaeal, Bacterial, and Viral Assemblages in Meromictic Lake Shunet in Siberia. Frontiers in Microbiology, 2018, 9, 1763.	3.5	11
4876	SNP hot-spots in the clam parasite QPX. BMC Genomics, 2018, 19, 486.	2.8	2
4877	Development and validation of an updated computational model of Streptomyces coelicolor primary and secondary metabolism. BMC Genomics, 2018, 19, 519.	2.8	20
4878	Genomic Comparison Among Global Isolates of L. interrogans Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. Frontiers in Cellular and Infection Microbiology, 2018, 8, 193.	3.9	39
4879	Genome-Wide Analysis Characterization and Evolution of SBP Genes in Fragaria vesca, Pyrus bretschneideri, Prunus persica and Prunus mume. Frontiers in Genetics, 2018, 9, 64.	2.3	33
4880	Genome-Wide Identification and Classification of Soybean C2H2 Zinc Finger Proteins and Their Expression Analysis in Legume-Rhizobium Symbiosis. Frontiers in Microbiology, 2018, 9, 126.	3.5	40
4881	Membrane Topology and Heme Binding of the Histidine Kinases HrrS and ChrS in Corynebacterium glutamicum. Frontiers in Microbiology, 2018, 9, 183.	3.5	14
4882	Indigenous Pseudomonas spp. Strains from the Olive (Olea europaea L.) Rhizosphere as Effective Biocontrol Agents against Verticillium dahliae: From the Host Roots to the Bacterial Genomes. Frontiers in Microbiology, 2018, 9, 277.	3.5	79
4883	Distribution Patterns of Polyphosphate Metabolism Pathway and Its Relationships With Bacterial Durability and Virulence. Frontiers in Microbiology, 2018, 9, 782.	3.5	34
4884	Metagenomic Approaches to Investigate the Contribution of the Vineyard Environment to the Quality of Wine Fermentation: Potentials and Difficulties. Frontiers in Microbiology, 2018, 9, 991.	3.5	90
4885	Profiling of Long Non-coding RNAs and mRNAs by RNA-Sequencing in the Hippocampi of Adult Mice Following Propofol Sedation. Frontiers in Molecular Neuroscience, 2018, 11, 91.	2.9	9
4886	Dissection of Myogenic Differentiation Signatures in Chickens by RNA-Seq Analysis. Genes, 2018, 9, 34.	2.4	13
4887	Genome-Wide Identification of the Alba Gene Family in Plants and Stress-Responsive Expression of the Rice Alba Genes. Genes, 2018, 9, 183.	2.4	29
4888	A Possible Trifunctional Î²-Carotene Synthase Gene Identified in the Draft Genome of Aurantiochytrium sp. Strain KH105. Genes, 2018, 9, 200.	2.4	32
4889	Transcriptomic Analysis of Flower Bud Differentiation in Magnolia sinostellata. Genes, 2018, 9, 212.	2.4	24
4890	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two Pyrus Species. Genes, 2018, 9, 224.	2.4	16
4891	DeepFam: deep learning based alignment-free method for protein family modeling and prediction. Bioinformatics, 2018, 34, i254-i262.	4.1	86

#	ARTICLE	IF	CITATIONS
4892	Protein moonlighting elucidates the essential human pathway catalyzing lipoic acid assembly on its cognate enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7063-E7072.	7.1	33
4893	Genome-Wide Analysis of Long Non-Coding RNAs in Potato and Their Potential Role in Tuber Sprouting Process. <i>International Journal of Molecular Sciences</i> , 2018, 19, 101.	4.1	22
4894	Development of Versatile Vectors for Heterologous Expression in <i>Bacillus</i> . <i>Microorganisms</i> , 2018, 6, 51.	3.6	8
4895	Prediction of Disordered Regions and Their Roles in the Anti-Pathogenic and Immunomodulatory Functions of Butyrophilins. <i>Molecules</i> , 2018, 23, 328.	3.8	8
4896	PhcrTx2, a New Crab-Paralyzing Peptide Toxin from the Sea Anemone <i>Phymanthus crucifer</i> . <i>Toxins</i> , 2018, 10, 72.	3.4	7
4897	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	3.3	37
4898	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two <i>Pyrus</i> Species. <i>Cells</i> , 2018, 7, 77.	4.1	24
4899	Systematic Analysis of Long Non-Coding RNAs and mRNAs in the Ovaries of <i>Duroc</i> Pigs During Different Follicular Stages Using RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1722.	4.1	40
4900	Characterization of esterase activity from an <i>Acetomicrobium hydrogeniformans</i> enzyme with high structural stability in extreme conditions. <i>Extremophiles</i> , 2018, 22, 781-793.	2.3	10
4901	More than Rotating Flagella: Lipopolysaccharide as a Secondary Receptor for Flagellotropic Phage 7-7-1. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	40
4902	The Chaperone Activities of DsbG and Spy Restore Peptidoglycan Biosynthesis in the <i>elyC</i> Mutant by Preventing Envelope Protein Aggregation. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	7
4903	Deep Sequencing-Based Transcriptome Profiling Reveals Avian Interferon-Stimulated Genes and Provides Comprehensive Insight into Newcastle Disease Virus-Induced Host Responses. <i>Viruses</i> , 2018, 10, 162.	3.3	25
4904	Genome-wide identification and characterization of mRNAs and lncRNAs involved in cold stress in the wild banana (<i>Musa itinerans</i>). <i>PLoS ONE</i> , 2018, 13, e0200002.	2.5	61
4905	Transcriptome-Guided Identification of Carbohydrate Active Enzymes (CAZy) from the Christmas Island Red Crab, <i>Gecarcoidea natalis</i> and a Vote for the Inclusion of Transcriptome-Derived Crustacean CAZys in Comparative Studies. <i>Marine Biotechnology</i> , 2018, 20, 654-665.	2.4	21
4906	Structural insights into a novel functional dimer of <i>Staphylococcus aureus</i> RNase HII. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 1207-1213.	2.1	1
4907	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually reproducing species. <i>BMC Genomics</i> , 2018, 19, 321.	2.8	18
4908	<i>Ceratocystis cacaofunesta</i> genome analysis reveals a large expansion of extracellular phosphatidylinositol-specific phospholipase-C genes (PI-PLC). <i>BMC Genomics</i> , 2018, 19, 58.	2.8	19
4909	Acyl-CoA-binding protein family members in laticifers are possibly involved in lipid and latex metabolism of <i>Hevea brasiliensis</i> (the Para rubber tree). <i>BMC Genomics</i> , 2018, 19, 5.	2.8	8

#	ARTICLE	IF	CITATIONS
4910	The aquatic animalsâ€™ transcriptome resource for comparative functional analysis. BMC Genomics, 2018, 19, 103.	2.8	5
4911	Transcriptomic insights into citrus segment membraneâ€™s cell wall components relating to fruit sensory texture. BMC Genomics, 2018, 19, 280.	2.8	14
4912	Improving conditional random field model for prediction of proteinâ€“RNA residueâ€“base contacts. Quantitative Biology, 2018, 6, 155-162.	0.5	1
4913	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. Scientific Reports, 2018, 8, 6808.	3.3	10
4914	Acid-resistant genes of oral plaque microbiome from the functional metagenomics. Journal of Oral Microbiology, 2018, 10, 1424455.	2.7	4
4915	Identification of Streptococcus mitis321A vaccine antigens based on reverse vaccinology. Molecular Medicine Reports, 2018, 17, 7477-7486.	2.4	0
4916	BioPS: System for screening and assessment of biofuel-production potential of cyanobacteria. PLoS ONE, 2018, 13, e0202002.	2.5	4
4917	REVIEW: Novel sources and functions of microbial lipases and their role in the infection mechanisms. Physiological and Molecular Plant Pathology, 2018, 104, 119-126.	2.5	21
4918	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. Frontiers in Genetics, 2018, 9, 281.	2.3	30
4919	Transcriptome sequencing to detect the potential role of long non-coding RNAs in bovine mammary gland during the dry and lactation period. BMC Genomics, 2018, 19, 605.	2.8	54
4921	Comparative Genome Analysis of 2 <i>Mycobacterium Tuberculosis</i> Strains from Pakistan: Insights Globally Into Drug Resistance, Virulence, and Niche Adaptation. Evolutionary Bioinformatics, 2018, 14, 117693431879025.	1.2	3
4922	Novel Autotrophic Organisms Contribute Significantly to the Internal Carbon Cycling Potential of a Boreal Lake. MBio, 2018, 9, .	4.1	18
4923	Tangled history of a multigene family: The evolution of ISOPENTENYLTRANSFERASE genes. PLoS ONE, 2018, 13, e0201198.	2.5	25
4924	Essential Gene Clusters Identified in Stenotrophomonas MB339 for Multiple Metal/Antibiotic Resistance and Xenobiotic Degradation. Current Microbiology, 2018, 75, 1484-1492.	2.2	16
4925	Identification of Antifungal Targets Based on Computer Modeling. Journal of Fungi (Basel, Tj ETQq0 0 0 rgBT /Overlock 10 Tf, 50 182 Td	3.5	12
4927	TMC1 Forms the Pore of Mechanosensory Transduction Channels in Vertebrate Inner Ear Hair Cells. Neuron, 2018, 99, 736-753.e6.	8.1	250
4928	Localization and Regulation of the T1 Unimolecular Spanin. Journal of Virology, 2018, 92, .	3.4	11
4929	Assessment of an Organ-Specific <i>de Novo</i> Transcriptome of the Nematode Trap-Crop, <i>Solanum sisymbriifolium</i> . G3: Genes, Genomes, Genetics, 2018, 8, 2135-2143.	1.8	4

#	ARTICLE	IF	CITATIONS
4930	Cwp19 Is a Novel Lytic Transglycosylase Involved in Stationary-Phase Autolysis Resulting in Toxin Release in <i>Clostridium difficile</i> . MBio, 2018, 9, .	4.1	60
4931	Integrative Genome-Wide Analysis of Long Noncoding RNAs in Diverse Immune Cell Types of Melanoma Patients. Cancer Research, 2018, 78, 4411-4423.	0.9	39
4932	A recombinant isoform of the Ole e 7 olive pollen allergen assembled by de novo mass spectrometry retains the allergenic ability of the natural allergen. Journal of Proteomics, 2018, 187, 39-46.	2.4	8
4933	Identification of a seed maturation protein gene from Coffea arabica (CaSMP) and analysis of its promoter activity in tomato. Plant Cell Reports, 2018, 37, 1257-1268.	5.6	3
4934	Transcriptome profiling with focus on potential key genes for wing development and evolution in Megalopterus caeruleus, the damselfly species with the world's largest wings. PLoS ONE, 2018, 13, e0189898.	2.5	4
4935	Superior ab initio identification, annotation and characterisation of TEs and segmental duplications from genome assemblies. PLoS ONE, 2018, 13, e0193588.	2.5	27
4936	Proteomic endorsed transcriptomic profiles of venom glands from Tityus obscurus and T. serrulatus scorpions. PLoS ONE, 2018, 13, e0193739.	2.5	55
4937	Dicer-like and RNA-dependent RNA polymerase gene family identification and annotation in the cultivated Solanum tuberosum and its wild relative S. commersonii. Planta, 2018, 248, 729-743.	3.2	24
4938	De novo transcriptome assembly and functional annotation of the southern rock lobster (Jasus tjirri). BMC Genomics, 2018, 19, 111.	1.1	10
4939	In silico functional and tumor suppressor role of hypothetical protein PCNXL2 with regulation of the Notch signaling pathway. RSC Advances, 2018, 8, 21414-21430.	3.6	7
4940	Comprehensive search for accessory proteins encoded with archaeal and bacterial type III CRISPR-Cas gene cassettes reveals 39 new Cas gene families. RNA Biology, 2019, 16, 530-542.	3.1	97
4941	One-Step Bioprocess of Inulin to Product Inulo-Oligosaccharides Using Bacillus subtilis Secreting an Extracellular Endo-Inulinase. Applied Biochemistry and Biotechnology, 2019, 187, 116-128.	2.9	17
4942	Effusion: prediction of protein function from sequence similarity networks. Bioinformatics, 2019, 35, 442-451.	4.1	12
4943	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. Plant Biotechnology Journal, 2019, 17, 451-460.	8.3	89
4944	Adaptive responses along a depth and a latitudinal gradient in the endemic seagrass Posidonia oceanica. Heredity, 2019, 122, 233-243.	2.6	18
4945	Toward more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Briefings in Bioinformatics, 2019, 20, 1669-1684.	6.5	13
4946	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. RNA Biology, 2019, 16, 435-448.	3.1	45
4947	The Oxymonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. Molecular Biology and Evolution, 2019, 36, 2292-2312.	8.9	49

#	ARTICLE	IF	CITATIONS
4948	Hybrid sequencing of the <i>Gynostemma pentaphyllum</i> transcriptome provides new insights into gypenoside biosynthesis. <i>BMC Genomics</i> , 2019, 20, 632.	2.8	16
4949	Transcriptome profiling of the low-salinity stress responses in the gills of the juvenile <i>Pseudopleuronectes yokohamae</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 32, 100612.	1.0	18
4950	Regulation of phosphoribosyl ubiquitination by a calmodulin-dependent glutamylase. <i>Nature</i> , 2019, 572, 387-391.	27.8	91
4951	Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of <i>Mycobacterium tuberculosis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2420-2438.	2.5	29
4952	Characteristics and Expression Pattern of MYC Genes in <i>Triticum aestivum</i> , <i>Oryza sativa</i> , and <i>Brachypodium distachyon</i> . <i>Plants</i> , 2019, 8, 274.	3.5	25
4953	CasPDB: an integrated and annotated database for Cas proteins from bacteria and archaea. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	8
4954	Comprehensive Analysis of LncRNA Reveals the Temporal-Specific Module of Goat Skeletal Muscle Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3950.	4.1	25
4955	Combining Mutations That Inhibit Two Distinct Steps of the ATP Hydrolysis Cycle Restores Wild-Type Function in the Lipopolysaccharide Transporter and Shows that ATP Binding Triggers Transport. <i>MBio</i> , 2019, 10, .	4.1	17
4956	CsTFL1 inhibits determinate growth and terminal flower formation through interaction with CsNOT2a in cucumber (<i>Cucumis sativus</i> L.). <i>Development (Cambridge)</i> , 2019, 146, .	2.5	37
4957	Novel Tick Phlebovirus Genotypes Lacking Evidence for Vertebrate Infections in Anatolia and Thrace, Turkey. <i>Viruses</i> , 2019, 11, 703.	3.3	8
4958	Gene Families, Epistasis and the Amino Acid Preferences of Protein Homologs. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987048.	1.2	0
4959	Transcriptome Landscape Variation in the Genus <i>Thymus</i> . <i>Genes</i> , 2019, 10, 620.	2.4	11
4960	An iteration method for identifying yeast essential proteins from heterogeneous network. <i>BMC Bioinformatics</i> , 2019, 20, 355.	2.6	28
4961	T-box transcription factor eomesodermin/Tbr2 in Atlantic cod (<i>Gadus morhua</i> L.): Molecular characterization, promoter structure and function analysis. <i>Fish and Shellfish Immunology</i> , 2019, 93, 28-38.	3.6	1
4962	Sharing Programming Resources Between Bio* Projects. <i>Methods in Molecular Biology</i> , 2019, 1910, 747-766.	0.9	6
4963	A GntR-Like Transcription Factor HypR Regulates Expression of Genes Associated With L-Hydroxyproline Utilization in <i>Streptomyces coelicolor</i> A3(2). <i>Frontiers in Microbiology</i> , 2019, 10, 1451.	3.5	7
4964	Adaptive dif Modules in Permafrost Strains of <i>Acinetobacter lwoffii</i> and Their Distribution and Abundance Among Present Day <i>Acinetobacter</i> Strains. <i>Frontiers in Microbiology</i> , 2019, 10, 632.	3.5	22
4965	An interplay of structure and intrinsic disorder in the functionality of peptidylarginine deiminases, a family of key autoimmunity-related enzymes. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4635-4662.	5.4	27

#	ARTICLE	IF	CITATIONS
4966	Enzymatic Degradation of Biofilm by Metalloprotease From <i>Microbacterium</i> sp. SKS10. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 192.	4.1	67
4967	Flavonoid Biosynthesis Is Likely More Susceptible to Elevation and Tree Age Than Other Branch Pathways Involved in Phenylpropanoid Biosynthesis in Ginkgo Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 983.	3.6	31
4968	Two Novel Negative-Sense RNA Viruses Infecting Grapevine Are Members of a Newly Proposed Genus within the Family Phenuiviridae. <i>Viruses</i> , 2019, 11, 685.	3.3	27
4969	Whole genome sequence and de novo assembly revealed genomic architecture of Indian Mithun (<i>Bos</i>) Tj ETQq1 1 0,784314 rgBT /Overl	2.8	10
4970	The Parallel Molecular Adaptations to the Antarctic Cold Environment in Two Psychrophilic Green Algae. <i>Genome Biology and Evolution</i> , 2019, 11, 1897-1908.	2.5	19
4971	Genome-wide identification and functional analysis of oleosin genes in <i>Brassica napus</i> L.. <i>BMC Plant Biology</i> , 2019, 19, 294.	3.6	30
4972	Conjoint Analysis of Genome-Wide lncRNA and mRNA Expression of Heteromorphic Leaves in Response to Environmental Heterogeneity in <i>Populus euphratica</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5148.	4.1	16
4973	<p>Long noncoding RNA THAP9-AS1 is induced by Helicobacter pylori and promotes cell growth and migration of gastric cancer</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 6653-6663.	2.0	35
4974	The mixed liver and heart transcriptome dataset of the New Zealand brushtail possum, <i>Trichosurus vulpecula</i> . <i>Data in Brief</i> , 2019, 27, 104577.	1.0	1
4975	Reconstruction of protein domain evolution using single-cell amplified genomes of uncultured choanoflagellates sheds light on the origin of animals. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20190088.	4.0	36
4976	RFQAmoel: Random Forest Quality Assessment to identify a predicted protein structure in the correct fold. <i>PLoS ONE</i> , 2019, 14, e0218149.	2.5	3
4977	Phenotype Prediction and Genome-Wide Association Study Using Deep Convolutional Neural Network of Soybean. <i>Frontiers in Genetics</i> , 2019, 10, 1091.	2.3	78
4978	Dissecting the Genome-Wide Evolution and Function of R2R3-MYB Transcription Factor Family in <i>Rosa chinensis</i> . <i>Genes</i> , 2019, 10, 823.	2.4	14
4979	Identification of lncRNAs by RNA Sequencing Analysis During in Vivo Pre-Implantation Developmental Transformation in the Goat. <i>Frontiers in Genetics</i> , 2019, 10, 1040.	2.3	10
4980	Transcriptome-Based Identification and Molecular Evolution of the Cytochrome P450 Genes and Expression Profiling under Dimethoate Treatment in Amur Stickleback (<i>Pungitius sinensis</i>). <i>Animals</i> , 2019, 9, 873.	2.3	6
4981	The Impact of Type VI Secretion System, Bacteriocins and Antibiotics on Bacterial Competition of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> and the Regulation of Carbapenem Biosynthesis by Iron and the Ferric-Uptake Regulator. <i>Frontiers in Microbiology</i> , 2019, 10, 2379.	3.5	23
4982	Genome survey of resistance gene analogs in sugarcane: genomic features and differential expression of the innate immune system from a smut-resistant genotype. <i>BMC Genomics</i> , 2019, 20, 809.	2.8	22
4983	Genome-wide characterization and evolutionary analysis of heat shock transcription factors (HSFs) to reveal their potential role under abiotic stresses in radish (<i>Raphanus sativus</i> L.). <i>BMC Genomics</i> , 2019, 20, 772.	2.8	23

#	ARTICLE	IF	CITATIONS
4984	Identification of a Novel Betacoronavirus (Merbecovirus) in Amur Hedgehogs from China. <i>Viruses</i> , 2019, 11, 980.	3.3	42
4985	Small RNA inhibits infection by downy mildew pathogen <i>Hyaloperonospora arabidopsidis</i> . <i>Molecular Plant Pathology</i> , 2019, 20, 1523-1534.	4.2	28
4986	Gene Cascade Finder: A tool for identification of gene cascades and its application in <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2019, 14, e0215187.	2.5	5
4987	Genome-Wide Identification and Characterization of Cucumber BPC Transcription Factors and Their Responses to Abiotic Stresses and Exogenous Phytohormones. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5048.	4.1	11
4988	in silico screening and molecular dynamics simulations study to identify novel potent inhibitors against <i>Mycobacterium tuberculosis</i> DnaG primase. <i>Acta Tropica</i> , 2019, 199, 105154.	2.0	2
4989	Large-scale identification and functional analysis of <i>NLR</i> genes in blast resistance in the Tetep rice genome sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18479-18487.	7.1	63
4990	Measuring the impact of gene prediction on gene loss estimates in Eukaryotes by quantifying falsely inferred absences. <i>PLoS Computational Biology</i> , 2019, 15, e1007301.	3.2	43
4991	Molecular identification and expression of sesquiterpene pathway genes responsible for patchoulol biosynthesis and regulation in <i>Pogostemon cablin</i> . , 2019, 60, 11.		13
4992	Transcriptomic analyses of the acute ammonia stress response in the hepatopancreas of the kuruma shrimp (<i>Marsupenaeus japonicus</i>). <i>Aquaculture</i> , 2019, 513, 734328.	3.5	35
4993	Proteomics and Docking Study Targeting Penicillin-Binding Protein and Penicillin-Binding Protein2a of Methicillin-Resistant <i>Staphylococcus aureus</i> Strain SO-1977 Isolated from Sudan. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986494.	1.2	14
4994	Chicken Meat-Associated Enterococci: Influence of Agricultural Antibiotic Use and Connection to the Clinic. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	34
4995	Genome-Wide Analysis of the YABBY Gene Family in Grapevine and Functional Characterization of VvYABBY4. <i>Frontiers in Plant Science</i> , 2019, 10, 1207.	3.6	37
4996	Genome-wide identification and expression analysis of the <i>VQ</i> gene family in soybean (<i>Glycine</i>) Tj ETQq0.0.0 rgBT /Overlock 1	2.0	14
4997	RNA-Seq de Novo Assembly and Differential Transcriptome Analysis of Chaga (<i>Inonotus obliquus</i>) Cultured with Different Betulin Sources and the Regulation of Genes Involved in Terpenoid Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4334.	4.1	14
4998	ApicoTFdb: the comprehensive web repository of apicomplexan transcription factors and transcription-associated co-factors. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, .	3.0	2
4999	Protein Abundance Biases the Amino Acid Composition of Disordered Regions to Minimize Non-functional Interactions. <i>Journal of Molecular Biology</i> , 2019, 431, 4978-4992.	4.2	31
5000	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019, 11, 2306-2311.	2.5	11
5001	Enabling Web-scale data integration in biomedicine through Linked Open Data. <i>Npj Digital Medicine</i> , 2019, 2, 90.	10.9	19

#	ARTICLE	IF	CITATIONS
5002	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	3.6	13
5003	Immediate Effects of Ammonia Shock on Transcription and Composition of a Biogas Reactor Microbiome. <i>Frontiers in Microbiology</i> , 2019, 10, 2064.	3.5	18
5004	Haemophilus parasuis VtaA2 is involved in adhesion to extracellular proteins. <i>Veterinary Research</i> , 2019, 50, 69.	3.0	11
5005	Transcriptomic analysis of postharvest toon buds and key enzymes involved in terpenoid biosynthesis during cold storage. <i>Scientia Horticulturae</i> , 2019, 257, 108747.	3.6	10
5006	Genomic analysis of the tryptome reveals molecular mechanisms of gland cell evolution. <i>EvoDevo</i> , 2019, 10, 23.	3.2	21
5007	Integrative Analysis of the Core Fruit Lignification Toolbox in Pear Reveals Targets for Fruit Quality Bioengineering. <i>Biomolecules</i> , 2019, 9, 504.	4.0	28
5008	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	2.4	8
5009	Genomic diversity landscape of the honey bee gut microbiota. <i>Nature Communications</i> , 2019, 10, 446.	12.8	187
5010	Comparative transcriptomics in <i>Leishmania braziliensis</i> : disclosing differential gene expression of coding and putative noncoding RNAs across developmental stages. <i>RNA Biology</i> , 2019, 16, 639-660.	3.1	20
5011	Significant abundance of configurations of coding variants in diploid human genomes. <i>Nucleic Acids Research</i> , 2019, 47, 2981-2995.	14.5	5
5012	LncRNA expression profile and ceRNA analysis in tomato during flowering. <i>PLoS ONE</i> , 2019, 14, e0210650.	2.5	30
5013	The Genetic Structures of an Extensively Drug Resistant (XDR) <i>Klebsiella pneumoniae</i> and Its Plasmids. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 446.	3.9	28
5014	Secretome analysis of <i>Strongyloides venezuelensis</i> parasitic stages reveals that soluble and insoluble proteins are involved in its parasitism. <i>Parasites and Vectors</i> , 2019, 12, 21.	2.5	23
5015	Genomic Signals of Adaptation towards Mutualism and Sociality in Two Ambrosia Beetle Complexes. <i>Life</i> , 2019, 9, 2.	2.4	5
5016	The landscape of transposable elements and satellite DNAs in the genome of a dioecious plant spinach (<i>Spinacia oleracea</i> L.). <i>Mobile DNA</i> , 2019, 10, 3.	3.6	37
5017	Comparison of Open-Source Reverse Vaccinology Programs for Bacterial Vaccine Antigen Discovery. <i>Frontiers in Immunology</i> , 2019, 10, 113.	4.8	107
5018	LncRNA profile of <i>Apis mellifera</i> and its possible role in behavioural transition from nurses to foragers. <i>BMC Genomics</i> , 2019, 20, 393.	2.8	37
5019	Effect of expression of additional catalytic domain on characteristics of Xylanase Z of <i>Clostridium thermocellum</i> . <i>Biologia (Poland)</i> , 2019, 74, 1395-1403.	1.5	1

#	ARTICLE	IF	CITATIONS
5020	A genome-wide approach to the comprehensive analysis of GASA gene family in Glycine max. Plant Molecular Biology, 2019, 100, 607-620.	3.9	42
5021	Transcriptomic analysis provides insight into the mechanism of salinity adjustment in swimming crab Portunus trituberculatus. Genes and Genomics, 2019, 41, 961-971.	1.4	11
5022	Genome-wide analysis of the WRKY gene family and its response to abiotic stress in buckwheat (Fagopyrum tataricum). Open Life Sciences, 2019, 14, 80-96.	1.4	24
5023	Analysis of Long Non-Coding RNA and mRNA Expression Profiling in Immature and Mature Bovine (Bos) Tj ETQq1 1 0.784314 rgBT /Over 2.3 75	2.3	75
5024	Chemosensory Gene Families in the Oligophagous Pear Pest Cacopsylla chinensis (Hemiptera: Psyllidae). Insects, 2019, 10, 175.	2.2	16
5025	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. BMC Molecular and Cell Biology, 2019, 20, 18.	2.0	12
5026	Integrated analysis of long non-coding RNA and mRNA expression in different colored skin of koi carp. BMC Genomics, 2019, 20, 515.	2.8	44
5027	Comparative physiology and transcriptome analysis allows for identification of lncRNAs imparting tolerance to drought stress in autotetraploid cassava. BMC Genomics, 2019, 20, 514.	2.8	25
5028	Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family. Genome Research, 2019, 29, 1277-1286.	5.5	19
5029	Heterologous Microcompartment Assembly in <i>Bacillaceae</i>: Establishing the Components Necessary for Scaffold Formation. ACS Synthetic Biology, 2019, 8, 1642-1654.	3.8	9
5030	A survey of transcriptome complexity using PacBio single-molecule real-time analysis combined with Illumina RNA sequencing for a better understanding of ricinoleic acid biosynthesis in Ricinus communis. BMC Genomics, 2019, 20, 456.	2.8	25
5031	Proteomic Basis of Symbiosis: A Heterologous Partner Fails to Duplicate Homologous Colonization in a Novel Cnidarian Symbiodiniaceae Mutualism. Frontiers in Microbiology, 2019, 10, 1153.	3.5	22
5032	Comprehensive Genomic Survey, Characterization and Expression Analysis of the HECT Gene Family in Brassica rapa L. and Brassica oleracea L.. Genes, 2019, 10, 400.	2.4	15
5033	Transcriptome Profile Analysis Reveals that CsTCP14 Induces Susceptibility to Foliage Diseases in Cucumber. International Journal of Molecular Sciences, 2019, 20, 2582.	4.1	9
5034	Incorporating Distance-Based Top-n-gram and Random Forest To Identify Electron Transport Proteins. Journal of Proteome Research, 2019, 18, 2931-2939.	3.7	87
5035	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in Acomys cahirinus. PLoS ONE, 2019, 14, e0216228.	2.5	27
5036	Integrative Analyses of Long Non-coding RNA and mRNA Involved in Piglet Ileum Immune Response to Clostridium perfringens Type C Infection. Frontiers in Cellular and Infection Microbiology, 2019, 9, 130.	3.9	40
5037	Arboviral screening of invasive Aedes species in northeastern Turkey: West Nile virus circulation and detection of insect-only viruses. PLoS Neglected Tropical Diseases, 2019, 13, e0007334.	3.0	31

#	ARTICLE	IF	CITATIONS
5038	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. <i>Frontiers in Plant Science</i> , 2019, 10, 813.	3.6	24
5039	Long non-coding RNA and MicroRNA profiling provides comprehensive insight into non-coding RNA involved host immune responses in ALV-J-infected chicken primary macrophage. <i>Developmental and Comparative Immunology</i> , 2019, 100, 103414.	2.3	10
5040	The Class III Peroxidase (POD) Gene Family in Cassava: Identification, Phylogeny, Duplication, and Expression. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2730.	4.1	37
5041	Isolation, cultivation, and genome analysis of proteorhodopsin-containing SAR116-clade strain <i>Candidatus Puniceispirillum marinum</i> IMCC1322. <i>Journal of Microbiology</i> , 2019, 57, 676-687.	2.8	19
5042	HOT or not: examining the basis of high-occupancy target regions. <i>Nucleic Acids Research</i> , 2019, 47, 5735-5745.	14.5	41
5043	Iso-Seq analysis of the <i>Taxus cuspidata</i> transcriptome reveals the complexity of Taxol biosynthesis. <i>BMC Plant Biology</i> , 2019, 19, 210.	3.6	49
5044	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.	4.1	26
5045	Divergent Switchgrass Cultivars Modify Cereal Aphid Transcriptomes. <i>Journal of Economic Entomology</i> , 2019, 112, 1887-1901.	1.8	3
5046	Characteristics of Protein Fold Space Exhibits Close Dependence on Domain Usage. <i>Lecture Notes in Computer Science</i> , 2019, , 356-369.	1.3	0
5047	Superantigen SpeA attenuates the biofilm forming capacity of <i>Streptococcus pyogenes</i> . <i>Journal of Microbiology</i> , 2019, 57, 626-636.	2.8	10
5048	Geometric description of self-interaction potential in symmetric protein complexes. <i>Scientific Data</i> , 2019, 6, 64.	5.3	6
5049	Consensus sequence design as a general strategy to create hyperstable, biologically active proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11275-11284.	7.1	105
5050	Whirly (Why) transcription factors in tomato (<i>Solanum lycopersicum</i> L.): genome-wide identification and transcriptional profiling under drought and salt stresses. <i>Molecular Biology Reports</i> , 2019, 46, 4139-4150.	2.3	13
5051	The first draft genomes of the ant <i>Formica exsecta</i> , and its <i>Wolbachia</i> endosymbiont reveal extensive gene transfer from endosymbiont to host. <i>BMC Genomics</i> , 2019, 20, 301.	2.8	18
5052	Comparative Analysis of the aquaporin Gene Family in 12 Fish Species. <i>Animals</i> , 2019, 9, 233.	2.3	14
5053	An annual cycle of gene regulation in the red-legged salamander mental gland: from hypertrophy to expression of rapidly evolving pheromones. <i>BMC Developmental Biology</i> , 2019, 19, 10.	2.1	7
5054	Tracing the origin and evolution of pseudokinases across the tree of life. <i>Science Signaling</i> , 2019, 12, .	3.6	79
5055	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541

#	ARTICLE	IF	CITATIONS
5056	Genome-Wide Identification of Long Non-coding RNAs Responsive to <i>Lasiodiplodia theobromae</i> Infection in Grapevine. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431984136.	1.2	14
5057	Expression, purification, and subcellular localization of phospholipase C in <i>Dunaliella salina</i> . <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1363-1371.	1.3	0
5058	An Integrated Analysis of Cashmere Fineness lncRNAs in Cashmere Goats. <i>Genes</i> , 2019, 10, 266.	2.4	26
5059	Complete genome sequence of <i>Flavobacterium arcticum</i> SM1502T, exhibiting adaption to the Arctic marine salty environment. <i>Marine Genomics</i> , 2019, 47, 100670.	1.1	5
5060	In silico characterisation and functional validation of chilling tolerant divergence 1 (COLD1) gene in monocots during abiotic stress. <i>Functional Plant Biology</i> , 2019, 46, 524.	2.1	8
5061	Identification and characterization of pineapple leaf lncRNAs in crassulacean acid metabolism (CAM) photosynthesis pathway. <i>Scientific Reports</i> , 2019, 9, 6658.	3.3	17
5062	Transcriptome Profiles of <i>Alternaria oxytropis</i> Provides Insights into Swainsonine Biosynthesis. <i>Scientific Reports</i> , 2019, 9, 6021.	3.3	9
5063	Prevalence and Diversity Analysis of Candidate Prophages to Provide An Understanding on Their Roles in <i>Bacillus Thuringiensis</i> . <i>Viruses</i> , 2019, 11, 388.	3.3	17
5064	Key genes differential expressions and pathway involved in salt and water-deprivation stresses for renal cortex in camel. <i>BMC Molecular Biology</i> , 2019, 20, 11.	3.0	6
5065	Comparative analysis of the root and leaf transcriptomes in <i>Chelidonium majus</i> L.. <i>PLoS ONE</i> , 2019, 14, e0215165.	2.5	13
5066	Statistical mechanical properties of sequence space determine the efficiency of the various algorithms to predict interaction energies and native contacts from protein coevolution.. <i>Physical Biology</i> , 2019, 16, 046007.	1.8	4
5067	The <i>Lactococcus lactis</i> Pan-Plasmidome. <i>Frontiers in Microbiology</i> , 2019, 10, 707.	3.5	22
5068	O-Antigen Gene Clusters of <i>Plesiomonas shigelloides</i> Serogroups and Its Application in Development of a Molecular Serotyping Scheme. <i>Frontiers in Microbiology</i> , 2019, 10, 741.	3.5	7
5069	Aurora kinase protein family in <i>Trypanosoma cruzi</i> : Novel role of an AUK-B homologue in kinetoplast replication. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007256.	3.0	14
5070	Transcriptomic Analysis of Coding Genes and Non-Coding RNAs Reveals Complex Regulatory Networks Underlying the Black Back and White Belly Coat Phenotype in Chinese Wuzhishan Pigs. <i>Genes</i> , 2019, 10, 201.	2.4	6
5071	Diversified secondary metabolite biosynthesis gene repertoire revealed in symbiotic dinoflagellates. <i>Scientific Reports</i> , 2019, 9, 1204.	3.3	21
5072	Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). <i>PLoS ONE</i> , 2019, 14, e0211043.	2.5	5
5073	The golden death bacillus <i>Chryseobacterium nematophagum</i> is a novel matrix digesting pathogen of nematodes. <i>BMC Biology</i> , 2019, 17, 10.	3.8	12

#	ARTICLE	IF	CITATIONS
5074	Transcriptomic responses of regenerating earthworms (<i>Eisenia foetida</i>) to retinoic acid reveals the role of pluripotency genes. <i>Chemosphere</i> , 2019, 226, 47-59.	8.2	3
5075	Temporal variability of diazotroph community composition in the upwelling region off NW Iberia. <i>Scientific Reports</i> , 2019, 9, 3737.	3.3	18
5076	Classification of the human THAP protein family identifies an evolutionarily conserved coiled coil region. <i>BMC Structural Biology</i> , 2019, 19, 4.	2.3	15
5077	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	1.0	3
5078	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea <i>Geoglobus acetivorans</i> and <i>Archaeoglobus fulgidus</i> : Biochemical and Structural Characterization. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 7.	4.1	26
5079	A genome-wide analysis of coatomer protein (COP) subunits of apicomplexan parasites and their evolutionary relationships. <i>BMC Genomics</i> , 2019, 20, 98.	2.8	5
5080	Flax (<i>Linum usitatissimum</i> L.) response to non-optimal soil acidity and zinc deficiency. <i>BMC Plant Biology</i> , 2019, 19, 54.	3.6	28
5081	DDOT: A Swiss Army Knife for Investigating Data-Driven Biological Ontologies. <i>Cell Systems</i> , 2019, 8, 267-273.e3.	6.2	22
5082	Network-based characterization of drug-protein interaction signatures with a space-efficient approach. <i>BMC Systems Biology</i> , 2019, 13, 39.	3.0	13
5083	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. <i>Scientific Reports</i> , 2019, 9, 5953.	3.3	55
5084	Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	32
5085	Selection pressure causes differentiation of the SPL gene family in the Juglandaceae. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1037-1048.	2.1	6
5086	TriPepSVM: de novo prediction of RNA-binding proteins based on short amino acid motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4406-4417.	14.5	44
5087	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , 2019, 21, 2148-2170.	3.8	15
5088	Hce2 domain-containing effectors contribute to the full virulence of <i>Valsa mali</i> in a redundant manner. <i>Molecular Plant Pathology</i> , 2019, 20, 843-856.	4.2	20
5089	Flowering plant immune repertoires expand under mycorrhizal symbiosis. <i>Plant Direct</i> , 2019, 3, e00125.	1.9	2
5090	Neofunctionalization of Mitochondrial Proteins and Incorporation into Signaling Networks in Plants. <i>Molecular Biology and Evolution</i> , 2019, 36, 974-989.	8.9	17
5091	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. <i>Genome Biology</i> , 2019, 20, 64.	8.8	114

#	ARTICLE	IF	CITATIONS
5092	Genome-wide identification, classification and expression analysis of the JmjC domain-containing histone demethylase gene family in maize. BMC Genomics, 2019, 20, 256.	2.8	31
5093	An efficient genomic signature ranking method for genomic island prediction from a single genome. Journal of Theoretical Biology, 2019, 467, 142-149.	1.7	9
5094	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. PLoS ONE, 2019, 14, e0211635.	2.5	9
5095	Structureâ€‘function characterization of an insecticidal protein GNIP1Aa, a member of an MACPF and Î²-tripod families. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2897-2906.	7.1	19
5096	Genome-Wide Analysis of Domain-Swap Predicted Products in the Genome of Anti-Stress Medicinal Plant: <i>Ocimum tenuiflorum</i> . Bioinformatics and Biology Insights, 2019, 13, 117793221882136.	2.0	1
5097	Comparative transcriptome analysis reveals new molecular pathways for cucumber genes related to sex determination. Plant Reproduction, 2019, 32, 193-216.	2.2	25
5098	Bifunctional Chloroplastic DJ-1B from Arabidopsis thaliana is an Oxidation-Robust Holdase and a Glyoxalase Sensitive to H ₂ O ₂ . Antioxidants, 2019, 8, 8.	5.1	17
5099	Grammar of protein domain architectures. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3636-3645.	7.1	46
5100	Genome-wide analysis of the NAC transcription factor family in Tartary buckwheat (<i>Fagopyrum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	2.8	90
5101	Novel Insights reveal Anti-microbial Gene Regulation of Piglet Intestine Immune in response to Clostridium perfringens Infection. Scientific Reports, 2019, 9, 1963.	3.3	14
5102	Biochemical and Functional Characterization of Glycoside Hydrolase Family 16 Genes in Aedes aegypti Larvae: Identification of the Major Digestive Î²-1,3-Glucanase. Frontiers in Physiology, 2019, 10, 122.	2.8	10
5103	Structural characterization of plasmodial aminopeptidase: a combined molecular docking and QSAR-based in silico approaches. Molecular Diversity, 2019, 23, 965-984.	3.9	4
5104	Analysis of long non-coding RNA and mRNA expression in bovine macrophages brings up novel aspects of Mycobacterium avium subspecies paratuberculosis infections. Scientific Reports, 2019, 9, 1571.	3.3	24
5105	Hydrogenotrophic methanogenesis in archaeal phylum Verstraetearchaeota reveals the shared ancestry of all methanogens. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5037-5044.	7.1	187
5106	The Galleria mellonella Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. Cell Reports, 2019, 26, 2451-2464.e5.	6.4	103
5107	Isolation and Genomic Characterization of an Acinetobacter johnsonii Bacteriophage AJO2 From Bulking Activated Sludge. Frontiers in Microbiology, 2019, 10, 266.	3.5	7
5108	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) â€‘ A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	1.8	13
5109	Evaluating Precisicon and Recall through the Utility of msTALI via an Active Site Study on Fold Families. , 2019, , .		0

#	ARTICLE	IF	CITATIONS
5110	Complete Genome Sequence of <i>Phreatobacter</i> sp. Strain NMCR1094, a Formate-Utilizing Bacterium Isolated from a Freshwater Stream. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
5111	Cyberbiosecurity Challenges of Pathogen Genome Databases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 106.	4.1	17
5112	Transcriptomic Profile and Sexual Reproduction-Relevant Genes of <i>Alexandrium minutum</i> in Response to Nutritional Deficiency. <i>Frontiers in Microbiology</i> , 2019, 10, 2629.	3.5	14
5113	Survey and Characterization of Jingmen Tick Virus Variants. <i>Viruses</i> , 2019, 11, 1071.	3.3	38
5114	The Endophytic Fungus <i>Chaetomium cupreum</i> Regulates Expression of Genes Involved in the Tolerance to Metals and Plant Growth Promotion in <i>Eucalyptus globulus</i> Roots. <i>Microorganisms</i> , 2019, 7, 490.	3.6	28
5115	The transcriptomic signature of low aggression in honey bees resembles a response to infection. <i>BMC Genomics</i> , 2019, 20, 1029.	2.8	11
5116	UPObase: an online database of unspecific peroxygenases. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	5
5117	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>). <i>BMC Plant Biology</i> , 2019, 19, 517.	3.6	16
5118	Comparative Analysis of the YABBY Gene Family of <i>Bienertia sinuspersici</i> , a Single-Cell C4 Plant. <i>Plants</i> , 2019, 8, 536.	3.5	12
5119	Crystal Structure Of Photorespiratory Alanine:Glyoxylate Aminotransferase 1 (AGT1) From <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1229.	3.6	9
5120	Clinical Spectrum and Functional Consequences Associated with Bi-Allelic Pathogenic PNPT1 Variants. <i>Journal of Clinical Medicine</i> , 2019, 8, 2020.	2.4	16
5121	Dynamic Changes of DNA Methylation and Transcriptome Expression in Porcine Ovaries during Aging. <i>BioMed Research International</i> , 2019, 2019, 1-15.	1.9	9
5122	Identifying protein-protein interface via a novel multi-scale local sequence and structural representation. <i>BMC Bioinformatics</i> , 2019, 20, 483.	2.6	9
5123	The Transcription Factor Aabzip9 Positively Regulates the Biosynthesis of Artemisinin in <i>Artemisia annua</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1294.	3.6	14
5124	The expanding world of plant J-domain proteins. <i>Critical Reviews in Plant Sciences</i> , 2019, 38, 382-400.	5.7	18
5125	Protein-assisted RNA fragment docking (RnaX) for modeling RNA-protein interactions using ModelX. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24568-24573.	7.1	10
5126	A systems biology approach uncovers a gene co-expression network associated with cell wall degradability in maize. <i>PLoS ONE</i> , 2019, 14, e0227011.	2.5	2
5127	Comparative transcriptome analysis of TUCPs in <i>Gossypium hirsutum</i> Ligon-lintless-1 mutant and their proposed functions in cotton fiber development. <i>Molecular Genetics and Genomics</i> , 2019, 294, 23-34.	2.1	5

#	ARTICLE	IF	CITATIONS
5128	Comparative analysis of five <i>Mucor</i> species transcriptomes. <i>Genomics</i> , 2019, 111, 1306-1314.	2.9	14
5129	gcMeta: a Global Catalogue of Metagenomics platform to support the archiving, standardization and analysis of microbiome data. <i>Nucleic Acids Research</i> , 2019, 47, D637-D648.	14.5	70
5130	Comparative transcriptome analysis identifies genes associated with papilla development in the sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 255-263.	1.0	4
5131	Comparative genomics of the major parasitic worms. <i>Nature Genetics</i> , 2019, 51, 163-174.	21.4	377
5132	Dissecting the Genomic Diversification of Late Embryogenesis Abundant (LEA) Protein Gene Families in Plants. <i>Genome Biology and Evolution</i> , 2019, 11, 459-471.	2.5	102
5133	Transcriptome and Comparative Genomics Analyses Reveal New Functional Insights on Key Determinants of Pathogenesis and Interbacterial Competition in <i>Pectobacterium</i> and <i>Dickeya</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	61
5134	Genome-wide identification and expression analysis of StTCP transcription factors of potato (<i>Solanum tuberosum</i> L.). <i>Computational Biology and Chemistry</i> , 2019, 78, 53-63.	2.3	19
5135	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> 3107, Host for the Model Lactococcal P335 Bacteriophage TP901-1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
5136	Building Bridges Between Structural and Network-Based Systems Biology. <i>Molecular Biotechnology</i> , 2019, 61, 221-229.	2.4	10
5137	Genome-scale identification, classification, and tissue specific expression analysis of late embryogenesis abundant (LEA) genes under abiotic stress conditions in <i>Sorghum bicolor</i> L.. <i>PLoS ONE</i> , 2019, 14, e0209980.	2.5	59
5138	Gene expression changes elicited by a parasitic B chromosome in the grasshopper <i>Eyprepocnemis plorans</i> are consistent with its phenotypic effects. <i>Chromosoma</i> , 2019, 128, 53-67.	2.2	15
5139	Methods to Study Long Noncoding RNA Expression and Dynamics in Zebrafish Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1912, 77-110.	0.9	1
5140	A cross-sectional screening by next-generation sequencing reveals <i>Rickettsia</i> , <i>Coxiella</i> , <i>Francisella</i> , <i>Borrelia</i> , <i>Babesia</i> , <i>Theileria</i> and <i>Hemolivia</i> species in ticks from Anatolia. <i>Parasites and Vectors</i> , 2019, 12, 26.	2.5	25
5141	Bastion3: a two-layer ensemble predictor of type III secreted effectors. <i>Bioinformatics</i> , 2019, 35, 2017-2028.	4.1	69
5142	Long-term investigation of microbial community composition and transcription patterns in a biogas plant undergoing ammonia crisis. <i>Microbial Biotechnology</i> , 2019, 12, 305-323.	4.2	25
5143	Cross-strand disulfides in the hydrogen bonding site of antiparallel β -sheet (aCSDhs): Forbidden disulfides that are highly strained, easily broken. <i>Protein Science</i> , 2019, 28, 239-256.	7.6	4
5144	Strategies for Pathway Analysis Using GWAS and WGS Data. <i>Current Protocols in Human Genetics</i> , 2019, 100, e79.	3.5	26
5145	A map of constrained coding regions in the human genome. <i>Nature Genetics</i> , 2019, 51, 88-95.	21.4	201

#	ARTICLE	IF	CITATIONS
5146	Molecular Adaptations of Bacterial Mercuric Reductase to the Hypersaline Kebrit Deep in the Red Sea. Applied and Environmental Microbiology, 2019, 85, .	3.1	7
5147	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	6.4	108
5148	Genome analysis provides insights into crude oil degradation and biosurfactant production by extremely halotolerant Halomonas desertis G11 isolated from Chott El-Djerid salt-lake in Tunisian desert. Genomics, 2019, 111, 1802-1814.	2.9	42
5149	The genome of the jellyfish Aurelia and the evolution of animal complexity. Nature Ecology and Evolution, 2019, 3, 96-104.	7.8	86
5150	SCOPE: classification of large macromolecular structures in the structural classification of proteinsâ€™ extended database. Nucleic Acids Research, 2019, 47, D475-D481.	14.5	122
5151	Applications of Metagenomics in Microbial Bioremediation of Pollutants. , 2019, , 459-477.		84
5152	HMMCAS: A Web Tool for the Identification and Domain Annotations of CAS Proteins. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1313-1315.	3.0	43
5153	Identification and genetic analysis of alternative splicing of long non-coding RNAs in tomato initial flowering stage. Genomics, 2020, 112, 897-907.	2.9	25
5154	Disorder in milk proteins: adipophilin and TIP47, important constituents of the milk fat globule membrane. Journal of Biomolecular Structure and Dynamics, 2020, 38, 1214-1229.	3.5	3
5155	Structural and functional characterization of Tomato SUMO1 gene. Saudi Journal of Biological Sciences, 2020, 27, 352-357.	3.8	3
5156	Ontogenic succession of thermokarst thaw ponds is linked to dissolved organic matter quality and microbial degradation potential. Limnology and Oceanography, 2020, 65, S248.	3.1	15
5157	Expression patterns of octoploid strawberry TGA genes reveal a potential role in response to Podosphaera aphanis infection. Plant Biotechnology Reports, 2020, 14, 55-67.	1.5	13
5158	Comprehensive genomic analysis of the DUF4228 gene family in land plants and expression profiling of ATDUF4228 under abiotic stresses. BMC Genomics, 2020, 21, 12.	2.8	25
5159	Dataset on the formation of Thioredoxin interacting protein (Txnip) containing redox sensitive high molecular weight nucleoprotein complexes. Data in Brief, 2020, 28, 104893.	1.0	1
5160	Comparative transcriptomic analysis reveals novel insights into the response to Cr(VI) exposure in Cr(VI) tolerant ectomycorrhizal fungi Pisolithus sp. 1 LS-2017. Ecotoxicology and Environmental Safety, 2020, 188, 109935.	6.0	10
5161	Repositioning of a mucolytic drug to a selective antibacterial against Vibrio cholerae. Journal of Microbiology, 2020, 58, 61-66.	2.8	1
5162	Genome and population sequencing of a chromosome-level genome assembly of the Chinese tapertail anchovy (Coilia nasus) provides novel insights into migratory adaptation. GigaScience, 2020, 9, .	6.4	26
5163	Localization and enzyme kinetics of aminopeptidase N3 from Toxoplasma gondii. Parasitology Research, 2020, 119, 357-364.	1.6	3

#	ARTICLE	IF	CITATIONS
5164	Genome-wide identification, phylogenetic and expression analysis of SBP-box gene family in barley (<i>Hordeum vulgare</i> L.). <i>Plant Growth Regulation</i> , 2020, 90, 137-149.	3.4	9
5165	Esterase is a powerful tool for the biodegradation of pyrethroid insecticides. <i>Chemosphere</i> , 2020, 244, 125507.	8.2	148
5166	De novo transcriptome analysis of stressed blood clam (<i>Anadara broughtonii</i>) and identification of genes associated with hemoglobin. <i>Genes and Genomics</i> , 2020, 42, 189-202.	1.4	9
5167	Draft Genomes of Two Artocarpus Plants, Jackfruit (<i>A. heterophyllus</i>) and Breadfruit (<i>A. altilis</i>). <i>Genes</i> , 2020, 11, 27.	2.4	30
5168	Genome-Wide Characterization and Gene Expression Analyses of GATA Transcription Factors in Moso Bamboo (<i>Phyllostachys edulis</i>). <i>International Journal of Molecular Sciences</i> , 2020, 21, 14.	4.1	33
5169	Transcriptomic and Epigenomic Dynamics of Honey Bees in Response to Lethal Viral Infection. <i>Frontiers in Genetics</i> , 2020, 11, 566320.	2.3	16
5170	Genome-Wide Identification and Characterization of <i>Fusarium graminearum</i> -Responsive lncRNAs in <i>Triticum aestivum</i> . <i>Genes</i> , 2020, 11, 1135.	2.4	4
5171	Molecular evolutionary and structural analysis of human UCHL1 gene demonstrates the relevant role of intragenic epistasis in Parkinson's disease and other neurological disorders. <i>BMC Evolutionary Biology</i> , 2020, 20, 130.	3.2	7
5172	Integrative analysis of long non-coding RNA and mRNA in broilers with valgus-varus deformity. <i>PLoS ONE</i> , 2020, 15, e0239450.	2.5	10
5173	Fast and Flexible Protein Design Using Deep Graph Neural Networks. <i>Cell Systems</i> , 2020, 11, 402-411.e4.	6.2	121
5174	Design of novel viral attachment inhibitors of the spike glycoprotein (S) of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) through virtual screening and dynamics. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106177.	2.5	21
5175	Genomic characterization of a diazotrophic microbiota associated with maize aerial root mucilage. <i>PLoS ONE</i> , 2020, 15, e0239677.	2.5	13
5176	Computational identification of receptor-like kinases and receptor-like proteins in legumes. <i>BMC Genomics</i> , 2020, 21, 459.	2.8	16
5177	Transcriptomic and Ultrastructural Signatures of K ⁺ -Induced Aggregation in <i>Phytophthora parasitica</i> Zoospores. <i>Microorganisms</i> , 2020, 8, 1012.	3.6	7
5178	De novo transcriptome assembly and data for the blue-winged teal (<i>Spatula discors</i>). <i>Data in Brief</i> , 2020, 30, 105380.	1.0	2
5179	An insight into the genome of extensively drug-resistant and uropathogenic <i>Citrobacter werkmanii</i> . <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 785-791.	2.2	4
5180	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. <i>ISME Journal</i> , 2020, 14, 2907-2922.	9.8	51
5181	Long noncoding RNA MARL regulates antiviral responses through suppression miR-122-dependent MAVS downregulation in lower vertebrates. <i>PLoS Pathogens</i> , 2020, 16, e1008670.	4.7	65

#	ARTICLE	IF	CITATIONS
5182	Analysis and Screening of Reproductive Long Non-coding RNAs Through Genome-Wide Analyses of Goat Endometrium During the Pre-attachment Phase. <i>Frontiers in Genetics</i> , 2020, 11, 568017.	2.3	13
5183	Leaf shape in <i>Populus tremula</i> is a complex, omnigenic trait. <i>Ecology and Evolution</i> , 2020, 10, 11922-11940.	1.9	19
5184	Acinetobacter Plasmids: Diversity and Development of Classification Strategies. <i>Frontiers in Microbiology</i> , 2020, 11, 588410.	3.5	11
5185	A high-quality sponge gourd (<i>Luffa cylindrica</i>) genome. <i>Horticulture Research</i> , 2020, 7, 128.	6.3	35
5186	Molecular Evolution and Characterization of Fish Stathmin Genes. <i>Animals</i> , 2020, 10, 1328.	2.3	2
5187	Advances on systems metabolic engineering of <i>Bacillus subtilis</i> as a chassis cell. <i>Synthetic and Systems Biotechnology</i> , 2020, 5, 245-251.	3.7	29
5188	A Multiomics Approach Unravels New Toxins With Possible In Silico Antimicrobial, Antiviral, and Antitumoral Activities in the Venom of <i>Acanthoscurria rondoniae</i> . <i>Frontiers in Pharmacology</i> , 2020, 11, 1075.	3.5	18
5189	Functional Insight of Nitric-Oxide Induced DUF Genes in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1041.	3.6	24
5190	Comparative transcriptome profiling of pomegranate genotypes having resistance and susceptible reaction to <i>Xanthomonas axonopodis</i> pv. <i>punicae</i> . <i>Saudi Journal of Biological Sciences</i> , 2020, 27, 3514-3528.	3.8	5
5191	Whole-Genome Sequencing and Bioinformatics Analysis of <i>Apiotrichum mycotoxinivorans</i> : Predicting Putative Zearalenone-Degradation Enzymes. <i>Frontiers in Microbiology</i> , 2020, 11, 1866.	3.5	15
5192	Comprehensive Identification and Characterization of Long Non-coding RNAs Associated With Rice Black-Streaked Dwarf Virus Infection in <i>Laodelphax striatellus</i> (FallÅ©n) Midgut. <i>Frontiers in Physiology</i> , 2020, 11, 1011.	2.8	6
5193	NPF:network propagation for protein function prediction. <i>BMC Bioinformatics</i> , 2020, 21, 355.	2.6	11
5194	Transcriptome and Flavonoids Metabolomic Analysis Identifies Regulatory Networks and Hub Genes in Black and White Fruits of <i>Lycium ruthenicum</i> Murray. <i>Frontiers in Plant Science</i> , 2020, 11, 1256.	3.6	18
5195	COVID-19 and iron dysregulation: distant sequence similarity between hepcidin and the novel coronavirus spike glycoprotein. <i>Biology Direct</i> , 2020, 15, 19.	4.6	64
5196	Genome-Wide Identification of Barley ABC Genes and Their Expression in Response to Abiotic Stress Treatment. <i>Plants</i> , 2020, 9, 1281.	3.5	25
5197	Transcriptomic data on the transgenerational exposure of the keystone amphipod <i>Gammarus locusta</i> to simvastatin. <i>Data in Brief</i> , 2020, 32, 106248.	1.0	7
5198	Understanding the structural insights of enzymatic conformations for adenylosuccinate lyase receptor in malarial parasite <i>Plasmodium falciparum</i> . <i>Journal of Receptor and Signal Transduction Research</i> , 2020, 41, 1-8.	2.5	0
5199	Genome-Wide Identification of the <i>Gossypium hirsutum</i> NHX Genes Reveals That the Endosomal-Type GhNHX4A Is Critical for the Salt Tolerance of Cotton. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7712.	4.1	19

5201	The Infant-Derived Bifidobacterium bifidum Strain CNCM I-4319 Strengthens Gut Functionality. Microorganisms, 2020, 8, 1313.	3.6	10
5202	Transcriptomic Analysis of Rhodococcus opacus R7 Grown on o-Xylene by RNA-Seq. Frontiers in Microbiology, 2020, 11, 1808.	3.5	10
5203	Characterization and molecular evolution of claudin genes in the Pungitius sinensis. Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology, 2020, 190, 749-759.	1.5	2
5204	Genome-wide identification of lysin motif containing protein family genes in eight rosaceae species, and expression analysis in response to pathogenic fungus Botryosphaeria dothidea in Chinese white pear. BMC Genomics, 2020, 21, 612.	2.8	9
5205	Genome-Wide Characterization, Evolution, and Expression Analysis of the Leucine-Rich Repeat Receptor-Like Protein Kinase (LRR-RLK) Gene Family in Medicago truncatula. Life, 2020, 10, 176.	2.4	9
5206	Molecular characterisation and expression analysis of NAC transcription factor genes in wild Medicago falcata under abiotic stresses. Functional Plant Biology, 2020, 47, 327.	2.1	2
5207	Large-scale tethered function assays identify factors that regulate mRNA stability and translation. Nature Structural and Molecular Biology, 2020, 27, 989-1000.	8.2	51
5208	PINCER: improved CRISPR/Cas9 screening by efficient cleavage at conserved residues. Nucleic Acids Research, 2020, 48, 9462-9477.	14.5	6
5209	Classification and Computational Analysis of Arabidopsis thaliana Sperm Cell-Specific F-Box Protein Gene 3p.AtFBP113. Frontiers in Genetics, 2020, 11, 609668.	2.3	2
5210	Optimization of protease production and sequence analysis of the purified enzyme from the cold adapted yeast Rhodotorula mucilaginosa CBMAI 1528. Biotechnology Reports (Amsterdam,) Tj ETQq0 0 0 rgBT /Overclock 1017 50 33		
5211	Changing Expression Profiles of Messenger RNA, MicroRNA, Long Non-coding RNA, and Circular RNA Reveal the Key Regulators and Interaction Networks of Competing Endogenous RNA in Pulmonary Fibrosis. Frontiers in Genetics, 2020, 11, 558095.	2.3	9
5212	Genomic and transcriptomic landscapes and evolutionary dynamics of molluscan glycoside hydrolase families with implications for algae-feeding biology. Computational and Structural Biotechnology Journal, 2020, 18, 2744-2756.	4.1	2
5213	HpeNet: Co-expression Network Database for de novo Transcriptome Assembly of Paeonia lactiflora Pall. Frontiers in Genetics, 2020, 11, 570138.	2.3	6
5214	Identification of CCCH Zinc Finger Proteins Family in Moso Bamboo (Phyllostachys edulis), and PeC3H74 Confers Drought Tolerance to Transgenic Plants. Frontiers in Plant Science, 2020, 11, 579255.	3.6	17
5215	DNA topoisomerase III β promotes cyst generation by inducing cyst wall protein gene expression in <i>Giardia lamblia</i> . Open Biology, 2020, 10, 190228.	3.6	12
5216	An Out-of-Patagonia migration explains the worldwide diversity and distribution of Saccharomyces eubayanus lineages. PLoS Genetics, 2020, 16, e1008777.	3.5	34
5217	Horizontally Acquired Quorum-Sensing Regulators Recruited by the PhoP Regulatory Network Expand the Host Adaptation Repertoire in the Phytopathogen <i>Pectobacterium brasiliense</i> . MSystems, 2020, 5, .	3.8	11

#	ARTICLE	IF	CITATIONS
5218	The draft genome sequence of an upland wild rice species, <i>Oryza granulata</i> . <i>Scientific Data</i> , 2020, 7, 131.	5.3	21
5219	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. <i>Scientific Reports</i> , 2020, 10, 8164.	3.3	3
5220	Genome-Wide Analysis Reveals Changes in Polled Yak Long Non-coding RNAs in Skeletal Muscle Development. <i>Frontiers in Genetics</i> , 2020, 11, 365.	2.3	5
5221	Vitellogenins and choriogenins are biomarkers for monitoring <i>Oryzias curvinotus</i> juveniles exposed to 17 β -estradiol. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2020, 236, 108800.	2.6	6
5222	A Novel Computational Approach for Identifying Essential Proteins From Multiplex Biological Networks. <i>Frontiers in Genetics</i> , 2020, 11, 343.	2.3	6
5223	Long non-coding RNAs in the alkaline stress response in sugar beet (<i>Beta vulgaris</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 227.	3.6	13
5224	Ginkgo biloba Seeds. , 2020, , 241-254.		1
5225	The N ¹ -Methyladenosine Methylome of <i>Petunia</i> mRNA. <i>Plant Physiology</i> , 2020, 183, 1710-1724.	4.8	31
5226	Genomic and transcriptomic analyses in <i>Drosophila</i> suggest that the ecdysteroid kinase-like (EcKL) gene family encodes the “detoxification-by-phosphorylation”™ enzymes of insects. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 123, 103429.	2.7	24
5227	Comparative Genomics of <i>Acinetobacter baumannii</i> Clinical Strains From Brazil Reveals Polyclonal Dissemination and Selective Exchange of Mobile Genetic Elements Associated With Resistance Genes. <i>Frontiers in Microbiology</i> , 2020, 11, 1176.	3.5	24
5228	Shifting evolutionary sands: transcriptome characterization of the <i>Aptostichus atomarius</i> species complex. <i>BMC Evolutionary Biology</i> , 2020, 20, 68.	3.2	1
5229	Genetic and functional diversification of chemosensory pathway receptors in mosquito-borne filarial nematodes. <i>PLoS Biology</i> , 2020, 18, e3000723.	5.6	33
5230	Gill transcriptomes reveal expression changes of genes related with immune and ion transport under salinity stress in silvery pomfret (<i>Pampus argenteus</i>). <i>Fish Physiology and Biochemistry</i> , 2020, 46, 1255-1277.	2.3	19
5231	<i>Moniliophthora perniciosa</i> development: key genes involved in stress-mediated cell wall organization and autophagy. <i>International Journal of Biological Macromolecules</i> , 2020, 154, 1022-1035.	7.5	8
5232	Comparative Genomics of <i>Actinobacillus pleuropneumoniae</i> Serotype 8 Reveals the Importance of Prophages in the Genetic Variability of the Species. <i>International Journal of Genomics</i> , 2020, 2020, 1-12.	1.6	7
5233	Genome-Wide Detection of Key Genes and Epigenetic Markers for Chicken Fatty Liver. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1800.	4.1	11
5234	Comparative Genomic Analysis Confirms Five Genetic Populations of the Select Agent, <i>Rathayibacter toxicus</i> . <i>Microorganisms</i> , 2020, 8, 366.	3.6	3
5235	Hybrid histidine kinase activation by cyclic di-GMP“mediated domain liberation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1000-1008.	7.1	28

#	ARTICLE	IF	CITATIONS
5236	Identification of tissue-specific and cold-responsive lncRNAs in <i>Medicago truncatula</i> by high-throughput RNA sequencing. <i>BMC Plant Biology</i> , 2020, 20, 99.	3.6	29
5237	Improved hybrid <i>de novo</i> genome assembly and annotation of African wild rice, <i>Oryza longistaminata</i> , from Illumina and PacBio sequencing reads. <i>Plant Genome</i> , 2020, 13, e20001.	2.8	15
5238	Design protein-protein interaction network and protein-drug interaction network for common cancer diseases: A bioinformatics approach. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100311.	3.4	12
5239	Formate Utilization by the Crenarchaeon <i>Desulfurococcus amylolyticus</i> . <i>Microorganisms</i> , 2020, 8, 454.	3.6	4
5240	Targeted assemblies of <i>cas1</i> suggest CRISPR-Cas™s response to soil warming. <i>ISME Journal</i> , 2020, 14, 1651-1662.	9.8	6
5241	Complete genome sequence of Phobos: a novel bacteriophage with unusual genomic features that infects <i>Pseudomonas syringae</i> . <i>Archives of Virology</i> , 2020, 165, 1485-1488.	2.1	5
5242	Characterization of the Auxin Efflux Transporter PIN Proteins in Pear. <i>Plants</i> , 2020, 9, 349.	3.5	19
5243	Comparative functional genomics analysis of cytochrome P450 gene superfamily in wheat and maize. <i>BMC Plant Biology</i> , 2020, 20, 93.	3.6	52
5244	Molecular Evolution and Diversification of Proteins Involved in miRNA Maturation Pathway. <i>Plants</i> , 2020, 9, 299.	3.5	10
5245	Evidence from ileum and liver transcriptomes of resistance to high-salt and water-deprivation conditions in camel. <i>Zoological Letters</i> , 2020, 6, 8.	1.3	4
5246	Transcriptomic Analysis Reveals the Involvement of lncRNA-miRNA-mRNA Networks in Hair Follicle Induction in Aohan Fine Wool Sheep Skin. <i>Frontiers in Genetics</i> , 2020, 11, 590.	2.3	16
5247	A Chinese White Pear (<i>Pyrus bretschneideri</i>) BZR Gene PbBZR1 Act as a Transcriptional Repressor of Lignin Biosynthetic Genes in Fruits. <i>Frontiers in Plant Science</i> , 2020, 11, 1087.	3.6	16
5248	Comparison of the transcriptomes of different life history stages of the freshwater Rhodophyte <i>Thorea hispida</i> . <i>Genomics</i> , 2020, 112, 3978-3990.	2.9	3
5249	RNA-Seq analysis and development of SSR and KASP markers in lentil (<i>Lens culinaris</i> Medikus subsp.) Tj ETQq1 1 0.784314 rgBT /Overl...	3.2	15
5250	Insight into Evolution and Conservation Patterns of B1-Subfamily Members of GPCR. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2505-2517.	1.9	3
5251	Identification of a molecular marker associated with lignotuber in <i>Eucalyptus</i> ssp. <i>Scientific Reports</i> , 2020, 10, 3608.	3.3	4
5252	Genome-Wide Identification, Evolution and Expression of the Complete Set of Cytoplasmic Ribosomal Protein Genes in Nile Tilapia. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1230.	4.1	10
5253	Genome-wide identification and characterization of novel long non-coding RNA in Ruminal tissue affected with sub-acute Ruminal acidosis from Holstein cattle. <i>Veterinary Research Communications</i> , 2020, 44, 19-27.	1.6	5

#	ARTICLE	IF	CITATIONS
5254	Crystal structure of Alr1298, a pentapeptide repeat protein from the cyanobacterium <i>Nostoc</i> sp. PCC 7120, determined at 2.1 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1143-1153.	2.6	7
5255	Uncovering a hidden diversity: optimized protocols for the extraction of dsDNA bacteriophages from soil. <i>Microbiome</i> , 2020, 8, 17.	11.1	52
5256	Transcriptomic Analysis of the Grapevine LEA Gene Family in Response to Osmotic and Cold Stress Reveals a Key Role for VamDHN3. <i>Plant and Cell Physiology</i> , 2020, 61, 775-786.	3.1	26
5257	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of <i>Morchella crassipes</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 483.	4.1	27
5258	MMPdb and MitoPredictor: Tools for facilitating comparative analysis of animal mitochondrial proteomes. <i>Mitochondrion</i> , 2020, 51, 118-125.	3.4	2
5259	The round goby genome provides insights into mechanisms that may facilitate biological invasions. <i>BMC Biology</i> , 2020, 18, 11.	3.8	32
5260	A Possible Role of the Aleurone Expressed Gene HvMAN1 in the Hydrolysis of the Cell Wall Mannans of the Starchy Endosperm in Germinating <i>Hordeum vulgare</i> L. Seeds. <i>Frontiers in Plant Science</i> , 2019, 10, 1706.	3.6	9
5261	Evolutionary relationships between the transcriptional repressors of the polyhydroxyalkanoate reserve storage system in prokaryotes: Conserved but phylogenetically heterogeneous. <i>Gene</i> , 2020, 735, 144397.	2.2	2
5262	A comparative gene co-expression analysis using self-organizing maps on two congener filmy ferns identifies specific desiccation tolerance mechanisms associated to their microhabitat preference. <i>BMC Plant Biology</i> , 2020, 20, 56.	3.6	17
5263	Draft Genome of the Asian Buffalo Leech <i>Hirudinaria manillensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1321.	2.3	11
5264	The Great Oxidation Event expanded the genetic repertoire of arsenic metabolism and cycling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10414-10421.	7.1	96
5265	Transcriptomics-based identification and characterization of glucosyltransferases involved in betalain biosynthesis in <i>Hylocereus megalanthus</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 152, 112-124.	5.8	21
5266	Comparative Transcriptome Analyses of <i>Schistosoma japonicum</i> Derived From SCID Mice and BALB/c Mice: Clues to the Abnormality in Parasite Growth and Development. <i>Frontiers in Microbiology</i> , 2020, 11, 274.	3.5	5
5267	2SigFinder: the combined use of small-scale and large-scale statistical testing for genomic island detection from a single genome. <i>BMC Bioinformatics</i> , 2020, 21, 159.	2.6	29
5268	Genome-wide identification of long non-coding RNAs and circular RNAs reveal their ceRNA networks in response to cucumber green mottle mosaic virus infection in watermelon. <i>Archives of Virology</i> , 2020, 165, 1177-1190.	2.1	41
5269	Evolution and domestication of Tc1/mariner transposons in the genome of African coelacanth (<i>Latimeria chalumnae</i>). <i>Genome</i> , 2020, 63, 375-386.	2.0	1
5270	SPD_1495 Contributes to Capsular Polysaccharide Synthesis and Virulence in <i>Streptococcus pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	3.8	10
5271	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.	6.6	60

#	ARTICLE	IF	CITATIONS
5272	LncRNA regulates tomato fruit cracking by coordinating gene expression via a hormone-redox-cell wall network. BMC Plant Biology, 2020, 20, 162.	3.6	32
5273	Transcriptomic analysis of polyketide synthases in a highly ciguatoxic dinoflagellate, Gambierdiscus polynesiensis and low toxicity Gambierdiscus pacificus, from French Polynesia. PLoS ONE, 2020, 15, e0231400.	2.5	14
5274	Functional Divergence of Microtubule-Associated TPX2 Family Members in Arabidopsis thaliana. International Journal of Molecular Sciences, 2020, 21, 2183.	4.1	17
5275	Genome-wide identification and expression analysis of the NF- κ B transcription factor family in <i>Populus</i> . Physiologia Plantarum, 2021, 171, 309-327.	5.2	31
5276	Methods and Tools for Long Non-Coding RNA Detection and their Application in Systems Medicine. , 2021, , 40-51.		1
5277	ABC translation factors: from antibiotic resistance to immune response. FEBS Letters, 2021, 595, 675-706.	2.8	25
5278	Whole Genome Sequence Resource for <i>Fusarium oxysporum</i> f. sp. <i>capsici</i> 14003, the Causative Agent of Pepper Wilt. Plant Disease, 2021, 105, 1183-1186.	1.4	4
5279	Molecular mechanism of Chinese alligator (<i>Alligator sinensis</i>) adapting to hibernation. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2021, 336, 32-49.	1.3	7
5280	Genome-wide characterization and expression analysis of HAK K ⁺ transport family in Ipomoea. 3 Biotech, 2021, 11, 3.	2.2	13
5281	The transition to flowering in winter rapeseed during vernalization. Plant, Cell and Environment, 2021, 44, 506-518.	5.7	19
5282	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nature Biotechnology, 2021, 39, 578-585.	17.5	569
5283	Transcriptome profiling of Stevia rebaudiana MS007 revealed genes involved in flower development. Turkish Journal of Biology, 2021, 45, 314-322.	0.8	2
5284	Evolutionary Modeling of Protein Families by Chromosomal Translocation Events. , 2021, , 257-290.		0
5285	The Role of Omic Technologies in the Study of the Human Gut Microbiome. , 2021, , 469-481.		0
5286	Genome Recovery, Functional Profiling, and Taxonomic Classification from Metagenomes. Methods in Molecular Biology, 2021, 2242, 153-172.	0.9	2
5287	Genetics, molecular biomarkers, and artificial intelligence to improve diagnostic and prognostic efficacy. , 2021, , 167-176.		0
5288	Bulinus truncatus transcriptome – a resource to enable molecular studies of snail and schistosome biology. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100015.	1.9	5
5289	The C-terminal loop of <i>Arabidopsis thaliana</i> guanosine deaminase is essential to catalysis. Chemical Communications, 2021, 57, 9748-9751.	4.1	2

#	ARTICLE	IF	CITATIONS
5290	Histoplasma capsulatum Glycans From Distinct Genotypes Share Structural and Serological Similarities to Cryptococcus neoformans Glucuronoxylomannan. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 565571.	3.9	4
5291	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. <i>MSystems</i> , 2021, 6, .	3.8	24
5292	Construction of a reference transcriptome for the analysis of male sterility in sugi (<i>Cryptomeria japonica</i>). <i>Plant Biotechnology Journal</i> , 2021, 19, 1050-1060.	2.5	6
5293	Genome sequences of <i>Tropheus moorii</i> and <i>Petrochromis trewavasae</i> , two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. <i>Scientific Reports</i> , 2021, 11, 4309.	3.3	4
5294	Identifying Poly(ADP-ribose)-Binding Proteins with Photoaffinity-Based Proteomics. <i>Journal of the American Chemical Society</i> , 2021, 143, 3037-3042.	13.7	44
5295	Assessment of heterogeneity of two cultivars of <i>Olea europaea</i> based on the study of their Oleic acid protein content. <i>Environmental Science and Pollution Research</i> , 2021, 28, 33545-33556.	5.3	0
5296	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. <i>ISME Journal</i> , 2021, 15, 807-817.	9.8	28
5297	Genome-wide comparative analysis of Mg transporter gene family between <i>Triticum turgidum</i> and <i>Camelina sativa</i> . <i>BioMetals</i> , 2021, 34, 639-660.	4.1	20
5299	Additional description and genome analyses of <i>Caenorhabditis auriculariae</i> representing the basal lineage of genus <i>Caenorhabditis</i> . <i>Scientific Reports</i> , 2021, 11, 6720.	3.3	10
5300	High genomic diversity of novel phages infecting the plant pathogen <i>Ralstonia solanacearum</i> , isolated in Mauritius and Reunion islands. <i>Scientific Reports</i> , 2021, 11, 5382.	3.3	10
5301	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, <i>Harpalus pensylvanicus</i> . <i>Journal of Chemical Ecology</i> , 2021, 47, 334-349.	1.8	0
5302	Resequencing and SNP discovery of <i>Amur leuciscus</i> (<i>Leuciscus waleckii</i>) provides insights into local adaptations to extreme environments. <i>Scientific Reports</i> , 2021, 11, 5064.	3.3	15
5303	An Overview of Antennal Esterases in Lepidoptera. <i>Frontiers in Physiology</i> , 2021, 12, 643281.	2.8	14
5304	XlinkCyNET: A Cytoscape Application for Visualization of Protein Interaction Networks Based on Cross-Linking Mass Spectrometry Identifications. <i>Journal of Proteome Research</i> , 2021, 20, 1943-1950.	3.7	8
5305	Topological Analysis for Sequence Variability: Case Study on more than 2K SARS-CoV-2 sequences of COVID-19 infected 54 countries in comparison with SARS-CoV-1 and MERS-CoV. <i>Infection, Genetics and Evolution</i> , 2021, 88, 104708.	2.3	6
5306	A Roadmap for Genome-Based Phage Taxonomy. <i>Viruses</i> , 2021, 13, 506.	3.3	268
5307	Transcriptional profiling of two contrasting genotypes uncovers molecular mechanisms underlying salt tolerance in alfalfa. <i>Scientific Reports</i> , 2021, 11, 5210.	3.3	13
5310	The genome of <i>Magnolia biondii</i> Pamp. provides insights into the evolution of Magnoliales and biosynthesis of terpenoids. <i>Horticulture Research</i> , 2021, 8, 38.	6.3	32

#	ARTICLE	IF	CITATIONS
5311	Composition and function of ciliary innerâ€œdyneinâ€œ arm subunits studied in <i>Chlamydomonas reinhardtii</i>. Cytoskeleton, 2021, 78, 77-96.	2.0	19
5312	Improved de novo chromosomeâ€œlevel genome assembly of the vulnerable walnut tree <i>Juglans mandshurica</i> reveals gene family evolution and possible genome basis of resistance to lesion nematode. Molecular Ecology Resources, 2021, 21, 2063-2076.	4.8	20
5314	Identification of Genomic Islands in Synechococcus sp. WH8102 Using Genomic Barcode and Whole-Genome Microarray Analysis. Current Bioinformatics, 2021, 16, 24-30.	1.5	1
5315	A multi-omics approach to lignocellulolytic enzyme discovery reveals a new ligninase activity from <i>Parascedosporium putredinis</i> NO1. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	18
5318	Resilience in Greenland intertidal Mytilus: The hidden stress defense. Science of the Total Environment, 2021, 767, 144366.	8.0	25
5319	Genomic Resources for the North American Water Vole (Microtus richardsoni) and the Montane Vole (Microtus montanus). GigaByte, 0, 2021, 1-13.	0.0	1
5321	Genome-Wide Analysis of the DUF4228 Family in Soybean and Functional Identification of GmDUF4228â€œ70 in Response to Drought and Salt Stresses. Frontiers in Plant Science, 2021, 12, 628299.	3.6	19
5322	Whole-genome resequencing of Osmanthus fragrans provides insights into flower color evolution. Horticulture Research, 2021, 8, 98.	6.3	35
5323	Genomic Island Prediction via Chi-Square Test and Random Forest Algorithm. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9.	1.3	32
5324	Characterization of the pectin methylesterase inhibitor gene family in Rosaceae and role of PbrPMEI23/39/41 in methylesterified pectin distribution in pear pollen tube. Planta, 2021, 253, 118.	3.2	13
5325	Enterococcal PrgU Provides Additional Regulation of Pheromone-Inducible Conjugative Plasmids. MSphere, 2021, 6, e0026421.	2.9	4
5326	Simultaneous codon usage, the origin of the proteome, and the emergence of de-novo proteins. Current Opinion in Structural Biology, 2021, 68, 142-148.	5.7	14
5327	Evolution of networks of protein domain organization. Scientific Reports, 2021, 11, 12075.	3.3	23
5328	Improving sequence-based modeling of protein families using secondary-structure quality assessment. Bioinformatics, 2021, 37, 4083-4090.	4.1	6
5329	Highâ€œthroughput sequencing reveals differential expression of miRNAs in yak and cattleyak epididymis. Reproduction in Domestic Animals, 2021, , .	1.4	2
5330	Large-scale multiple inference of collective dependence with applications to protein function. Annals of Applied Statistics, 2021, 15, .	1.1	2
5331	Networkâ€œbased visualisation reveals new insights into transposable element diversity. Molecular Systems Biology, 2021, 17, e9600.	7.2	2
5332	The landscape and biological relevance of aberrant alternative splicing events in esophageal squamous cell carcinoma. Oncogene, 2021, 40, 4184-4197.	5.9	8

#	ARTICLE	IF	CITATIONS
5333	Identification and Comparative Analysis of Long Non-coding RNAs in High- and Low-Fecundity Goat Ovaries During Estrus. <i>Frontiers in Genetics</i> , 2021, 12, 648158.	2.3	4
5334	Learning the protein language: Evolution, structure, and function. <i>Cell Systems</i> , 2021, 12, 654-669.e3.	6.2	194
5335	IDOPS, a Profile HMM-Based Tool to Detect Pesticidal Sequences and Compare Their Genetic Context. <i>Frontiers in Microbiology</i> , 2021, 12, 664476.	3.5	5
5336	Long-read transcriptome and other genomic resources for the angiosperm <i>Silene noctiflora</i> . <i>C3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9
5337	Genomics and transcriptomics yields a system-level view of the biology of the pathogen <i>Naegleria fowleri</i> . <i>BMC Biology</i> , 2021, 19, 142.	3.8	18
5338	Comparative transcriptomic analysis brings new insights into the response to acute temperature acclimation in burbot (<i>Lota lota lota</i>). <i>Aquaculture Reports</i> , 2021, 20, 100657.	1.7	8
5339	Genome-wide analysis of the B3 transcription factors reveals that RcABI3/VP1 subfamily plays important roles in seed development and oil storage in castor bean (<i>Ricinus communis</i>). <i>Plant Diversity</i> , 2022, 44, 201-212.	3.7	8
5340	Genome-wide identification and analysis of the YABBY gene family in Moso Bamboo (<i>Phyllostachys</i>). <i>TJ ETQq1 1 0.784314 rgBT /Overl</i>	2.0	9
5341	Integrated Analysis of Long Non-Coding RNA and mRNA Expression Profiles in Testes of Calves and Sexually Mature Wandong Bulls (<i>Bos taurus</i>). <i>Animals</i> , 2021, 11, 2006.	2.3	6
5342	Diversity and function of arthropod endosymbiont toxins. <i>Trends in Microbiology</i> , 2022, 30, 185-198.	7.7	27
5343	Genome-wide identification of alcohol dehydrogenase (ADH) gene family under waterlogging stress in wheat (<i>Triticum aestivum</i>). <i>PeerJ</i> , 2021, 9, e11861.	2.0	11
5344	Transcriptome analysis of messenger RNA and long noncoding RNA related to different developmental stages of tail adipose tissues of sunite sheep. <i>Food Science and Nutrition</i> , 2021, 9, 5722-5734.	3.4	7
5345	Comparative transcriptome provides insights into the selection adaptation between wild and farmed foxes. <i>Ecology and Evolution</i> , 2021, 11, 13475-13486.	1.9	2
5346	Integrative overview of IFITMs family based on Bioinformatics analysis. <i>Intractable and Rare Diseases Research</i> , 2021, 10, 165-172.	0.9	6
5348	EvoProDom: evolutionary modeling of protein families by assessing translocations of protein domains. <i>FEBS Open Bio</i> , 2021, 11, 2507-2524.	2.3	0
5349	Full-length transcriptome analysis of <i>Spodoptera frugiperda</i> larval brain reveals detoxification genes. <i>PeerJ</i> , 2021, 9, e12069.	2.0	6
5350	Dynamic Diversity of NLR Genes in Triticum and Mining of Promising NLR Alleles for Disease Resistance. <i>Current Issues in Molecular Biology</i> , 2021, 43, 965-977.	2.4	0
5351	The DUF221 domain-containing (DDP) genes identification and expression analysis in tomato under abiotic and phytohormone stress. <i>GM Crops and Food</i> , 2021, 12, 586-599.	3.8	5

#	ARTICLE	IF	CITATIONS
5352	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	6.3	27
5353	High Arsenic Levels Increase Activity Rather than Diversity or Abundance of Arsenic Metabolism Genes in Paddy Soils. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0138321.	3.1	9
5354	The genomic basis of army ant chemosensory adaptations. <i>Molecular Ecology</i> , 2021, 30, 6627-6641.	3.9	9
5356	A Novel Sulfone Derivative Controls <i>Lasiodiplodia theobromae</i> in Tea Leaf Spot by Reducing the Ergosterol Content. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, MPMI-12-20-0343.	2.6	3
5357	Trends in the Application of “Omics” to Ecotoxicology and Stress Ecology. <i>Genes</i> , 2021, 12, 1481.	2.4	22
5359	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.	2.9	13
5360	Genome sequencing and identification of cellulase genes in <i>Bacillus paralicheniformis</i> strains from the Red Sea. <i>BMC Microbiology</i> , 2021, 21, 254.	3.3	10
5361	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	8.3	18
5362	Identification and Characterization of 24-Dehydrocholesterol Reductase (DHCR24) in the Two-Spotted Cricket, <i>Gryllus bimaculatus</i> . <i>Insects</i> , 2021, 12, 782.	2.2	3
5363	Metabolomics integrated with transcriptomics reveals the distribution of iridoid and crocin metabolic flux in <i>Gardenia jasminoides</i> Ellis. <i>PLoS ONE</i> , 2021, 16, e0256802.	2.5	15
5364	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	4.1	9
5365	Integrated analysis of lncRNA and mRNA in liver of <i>Megalobrama amblycephala</i> post <i>Aeromonas hydrophila</i> infection. <i>BMC Genomics</i> , 2021, 22, 653.	2.8	11
5367	Transcriptome and anatomical comparisons reveal the specific characteristics and genes involved in distinct types of growing culms. <i>Industrial Crops and Products</i> , 2021, 171, 113865.	5.2	3
5368	Draft genome analysis, poly-phasic study and lipid biosynthesis pathway of <i>Scenedesmus</i> sp. SVMICT1. <i>Bioresource Technology</i> , 2021, 341, 125809.	9.6	4
5369	A Novel Multiprotein Bridging Factor 1-Like Protein Induces Cyst Wall Protein Gene Expression and Cyst Differentiation in <i>Giardia lamblia</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 1370.	4.1	6
5370	The identification of novel immunogenic antigens as potential <i>Shigella</i> vaccine components. <i>Genome Medicine</i> , 2021, 13, 8.	8.2	9
5371	The Dfam community resource of transposable element families, sequence models, and genome annotations. <i>Mobile DNA</i> , 2021, 12, 2.	3.6	279
5372	Fluoxetine ameliorates depressive symptoms by regulating lncRNA expression in the mouse hippocampus. <i>Zoological Research</i> , 2021, 42, 28-42.	2.1	10

#	ARTICLE	IF	CITATIONS
5374	Protein Clustering and Classification. , 2004, , 203-226.		1
5375	Genome resources for the DT40 community. Sub-Cellular Biochemistry, 2006, 40, 25-37.	2.4	2
5377	A Technical Platform for Generating Reproducible Expression Data from Streptomyces coelicolor Batch Cultivations. Advances in Experimental Medicine and Biology, 2011, 696, 3-15.	1.6	8
5378	Metagenomics of the Human Body. , 2011, , .		18
5379	Bioinformatic Tools in Crop Improvement. , 2013, , 49-122.		6
5380	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.9	21
5381	Computational Prediction of Short Linear Motifs from Protein Sequences. Methods in Molecular Biology, 2015, 1268, 89-141.	0.9	39
5382	Structural Basis of Protein-Protein Interactions. Methods in Molecular Biology, 2015, 1278, 3-22.	0.9	2
5383	Protein Structure Prediction Based on Sequence Similarity. Methods in Molecular Biology, 2009, 569, 129-156.	0.9	16
5384	Integrated Tools for Biomolecular Sequence-Based Function Prediction as Exemplified by the ANNOTATOR Software Environment. Methods in Molecular Biology, 2010, 609, 257-267.	0.9	13
5385	An Introduction to Mitochondrial Informatics. Methods in Molecular Biology, 2010, 628, 259-274.	0.9	1
5386	A Functional Proteomic Study of the Trypanosoma brucei Nuclear Pore Complex: An Informatic Strategy. Methods in Molecular Biology, 2010, 673, 231-238.	0.9	11
5387	Computational Identification of Plant Transcription Factors and the Construction of the PlantTFDB Database. Methods in Molecular Biology, 2010, 674, 351-368.	0.9	16
5388	In Silico Protein Motif Discovery and Structural Analysis. Methods in Molecular Biology, 2011, 760, 341-353.	0.9	2
5389	Bioinformatics and Medicinal Plant Research: Current Scenario. , 2019, , 141-157.		1
5390	Obtaining Relevant Genes by Analysis of Expression Arrays with a Multi-agent System. Advances in Intelligent Systems and Computing, 2015, , 137-146.	0.6	6
5391	Antigens and Epitopes. , 2016, , 125-143.		1
5392	True Path Rule Hierarchical Ensembles. Lecture Notes in Computer Science, 2009, , 232-241.	1.3	28

#	ARTICLE	IF	CITATIONS
5393	Ensemble Based Data Fusion for Gene Function Prediction. Lecture Notes in Computer Science, 2009, , 448-457.	1.3	8
5394	A Bipartite Graph Based Model of Protein Domain Networks. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2009, , 525-535.	0.3	3
5396	Bacterial Autolysins. , 2010, , 383-406.		7
5397	Dual-topology: one sequence, two topologies. , 2010, , 137-150.		3
5398	Surviving in a sea of data: a survey of plant genome data resources and issues in building data management systems. , 2002, , 59-74.		6
5399	N-Acetylmuramoyl-l-alanine amidase. , 2004, , 866-868.		1
5400	The Structure and Function of Allergens. , 2014, , 398-429.		5
5401	A Practitioner's Guide to Data Management and Data Integration in Bioinformatics. , 2003, , 35-73.		12
5402	Novel protein domains and motifs in the marine planctomycete <i>Rhodopirellula baltica</i> . FEMS Microbiology Letters, 2004, 236, 333-340.	1.8	15
5403	Integrative bioinformatics for functional genome annotation: trawling for G protein-coupled receptors. Seminars in Cell and Developmental Biology, 2004, 15, 693-701.	5.0	19
5405	Anaerobic methane oxidation coupled to manganese reduction by members of the <i>Methanoperedenaceae</i> . ISME Journal, 2020, 14, 1030-1041.	9.8	203
5406	Viruses of the Nahant Collection, characterization of 251 marine Vibrionaceae viruses. Scientific Data, 2018, 5, 180114.	5.3	26
5407	Building an octaploid genome and transcriptome of the medicinal plant <i>Pogostemon cablin</i> from Lamiales. Scientific Data, 2018, 5, 180274.	5.3	17
5408	Draft genomic and transcriptome resources for marine chelicerate <i>Tachypleus tridentatus</i> . Scientific Data, 2019, 6, 190029.	5.3	15
5409	Cloning and identification of MYPT3: a prenylatable myosin targetting subunit of protein phosphatase 1. Biochemical Journal, 2001, 356, 257.	3.7	26
5410	Approaches to Fungal Genome Annotation. Mycology, 2011, 2, 118-141.	4.4	109
5411	<i>In silico</i> prediction of host-pathogen protein interactions in melioidosis pathogen <i>Burkholderia pseudomallei</i> and human reveals novel virulence factors and their targets. Briefings in Bioinformatics, 2021, 22, .	6.5	16
5412	A New Dinoflagellate Genome Illuminates a Conserved Gene Cluster Involved in Sunscreen Biosynthesis. Genome Biology and Evolution, 2021, 13, .	2.5	31

#	ARTICLE	IF	CITATIONS
5413	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , 2021, 33, 832-845.	6.6	11
5414	Comprehensive annotation of <i>Glossina pallidipes</i> salivary gland hypertrophy virus from Ethiopian tsetse flies: a proteogenomics approach. <i>Journal of General Virology</i> , 2016, 97, 1010-1031.	2.9	24
5415	A molecular-capsular-type prediction system for 90 <i>Streptococcus pneumoniae</i> serotypes using partial cpsA-cpsB sequencing and wzy- or wzx-specific PCR. <i>Journal of Medical Microbiology</i> , 2005, 54, 351-356.	1.8	52
5416	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. <i>Microbial Genomics</i> , 2016, 2, e000043.	2.0	162
5417	Deciphering the unexplored <i>Leptospira</i> diversity from soils uncovers genomic evolution to virulence. <i>Microbial Genomics</i> , 2018, 4, .	2.0	91
5418	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	2.0	18
5419	O-antigen biosynthesis gene clusters of <i>Escherichia albertii</i> : their diversity and similarity to <i>Escherichia coli</i> gene clusters and the development of an O-genotyping method. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
5420	Small RNA NcS27 co-regulates utilization of carbon sources in <i>Burkholderia cenocepacia</i> J2315. <i>Microbiology (United Kingdom)</i> , 2019, 165, 1135-1150.	1.8	4
5421	First detection and analysis of a fish circovirus. <i>Journal of General Virology</i> , 2011, 92, 1817-1821.	2.9	67
5445	Assembly, Annotation, and Integration of UNIGENE Clusters into the Human Genome Draft. <i>Genome Research</i> , 2001, 11, 904-918.	5.5	52
5446	Diversity of TITAN Functions in Arabidopsis Seed Development. <i>Plant Physiology</i> , 2002, 128, 38-51.	4.8	16
5447	A challenging interpretation of a hexagonally layered protein structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 203-208.	2.5	4
5448	The crystal structure of the <i>N</i> -acetylglucosamine 2-epimerase from <i>Nostoc</i> sp. KJ10 reveals the true dimer. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 90-100.	2.3	6
5449	Protein Structural Domain Assignment with a Delaunay Tessellation Derived Lattice. , 2006, , .		1
5451	MATCHING OF STRUCTURAL MOTIFS USING HASHING ON RESIDUE LABELS AND GEOMETRIC FILTERING FOR PROTEIN FUNCTION PREDICTION. , 2008, , .		11
5452	GOTREES: PREDICTING GO ASSOCIATIONS FROM PROTEIN DOMAIN COMPOSITION USING DECISION TREES. , 2004, , .		15
5453	Evolution and Classification of the Serpin Superfamily. , 2007, , 1-33.		4
5454	BIOSPIDER: A WEB SERVER FOR AUTOMATING METABOLOME ANNOTATIONS. , 2006, , .		8

#	ARTICLE	IF	CITATIONS
5456	CBS domains form energy-sensing modules whose binding of adenosine ligands is disrupted by disease mutations. <i>Journal of Clinical Investigation</i> , 2004, 113, 274-284.	8.2	622
5457	An automated protocol for modelling peptide substrates to proteases. <i>BMC Bioinformatics</i> , 2020, 21, 586.	2.6	7
5459	Systems Biology Application to Decipher Mechanisms and Novel Biomarkers in CNS Trauma. , 2015, , 448-461.		12
5460	ELIXIR pilot action: Marine metagenomics “ towards a domain specific set of sustainable services. <i>F1000Research</i> , 2017, 6, 70.	1.6	8
5461	A proposal to change the name of the NBPf/DUF1220 domain to the Olduvai domain. <i>F1000Research</i> , 2017, 6, 2185.	1.6	19
5462	A TALE of shrimps: Genome-wide survey of homeobox genes in 120 species from diverse crustacean taxa. <i>F1000Research</i> , 2018, 7, 71.	1.6	2
5463	Comparative genomic analysis of crustacean hyperglycemic hormone (CHH) neuropeptide genes across diverse crustacean species. <i>F1000Research</i> , 2018, 7, 100.	1.6	7
5464	Computational genome-wide identification of heat shock protein genes in the bovine genome. <i>F1000Research</i> , 2018, 7, 1504.	1.6	10
5465	IsoCleft Finder “ a web-based tool for the detection and analysis of protein binding-site geometric and chemical similarities. <i>F1000Research</i> , 2013, 2, 117.	1.6	10
5467	Cocos: Constructing multi-domain protein phylogenies. <i>PLOS Currents</i> , 2011, 3, RRN1240.	1.4	1
5468	Metabolic Complementarity and Genomics of the Dual Bacterial Symbiosis of Sharpshooters. <i>PLoS Biology</i> , 2006, 4, e188.	5.6	391
5469	Structural and Functional Diversity of the Microbial Kinome. <i>PLoS Biology</i> , 2007, 5, e17.	5.6	239
5470	The Structural Basis of Coenzyme A Recycling in a Bacterial Organelle. <i>PLoS Biology</i> , 2016, 14, e1002399.	5.6	40
5471	Extreme genome diversity in the hyper-prevalent parasitic eukaryote <i>Blastocystis</i> . <i>PLoS Biology</i> , 2017, 15, e2003769.	5.6	99
5472	Alternative Protein-Protein Interfaces Are Frequent Exceptions. <i>PLoS Computational Biology</i> , 2012, 8, e1002623.	3.2	26
5473	Evolutionary and Functional Relationships in the Truncated Hemoglobin Family. <i>PLoS Computational Biology</i> , 2016, 12, e1004701.	3.2	36
5474	Application of Rigidity Theory to the Thermostabilization of Lipase A from <i>Bacillus subtilis</i> . <i>PLoS Computational Biology</i> , 2016, 12, e1004754.	3.2	48
5475	Improvement in Protein Domain Identification Is Reached by Breaking Consensus, with the Agreement of Many Profiles and Domain Co-occurrence. <i>PLoS Computational Biology</i> , 2016, 12, e1005038.	3.2	38

#	ARTICLE	IF	CITATIONS
5476	Multiscale mutation clustering algorithm identifies pan-cancer mutational clusters associated with pathway-level changes in gene expression. PLoS Computational Biology, 2017, 13, e1005347.	3.2	14
5477	Learning causal networks with latent variables from multivariate information in genomic data. PLoS Computational Biology, 2017, 13, e1005662.	3.2	28
5478	Contact- and Protein Transfer-Dependent Stimulation of Assembly of the Gliding Motility Machinery in Myxococcus xanthus. PLoS Genetics, 2015, 11, e1005341.	3.5	49
5479	Comparative Genomic Analysis of Drechmeria coniospora Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. PLoS Genetics, 2016, 12, e1006017.	3.5	45
5480	Human IgG1 Responses to Surface Localised Schistosoma mansoni Ly6 Family Members Drop following Praziquantel Treatment. PLoS Neglected Tropical Diseases, 2015, 9, e0003920.	3.0	17
5481	Whole Genome Sequencing of Mycobacterium africanum Strains from Mali Provides Insights into the Mechanisms of Geographic Restriction. PLoS Neglected Tropical Diseases, 2016, 10, e0004332.	3.0	41
5482	A Post-Synaptic Scaffold at the Origin of the Animal Kingdom. PLoS ONE, 2007, 2, e506.	2.5	215
5483	Complete Genomic Characterization of a Pathogenic A.II Strain of Francisella tularensis Subspecies tularensis. PLoS ONE, 2007, 2, e947.	2.5	46
5484	Genome-Wide Detection of Serpentine Receptor-Like Proteins in Malaria Parasites. PLoS ONE, 2008, 3, e1889.	2.5	43
5485	Life-Cycle and Genome of OtV5, a Large DNA Virus of the Pelagic Marine Unicellular Green Alga Ostreococcus tauri. PLoS ONE, 2008, 3, e2250.	2.5	107
5486	Analysis of the Pseudoalteromonas tunicata Genome Reveals Properties of a Surface-Associated Life Style in the Marine Environment. PLoS ONE, 2008, 3, e3252.	2.5	126
5487	GeneDistiller—Distilling Candidate Genes from Linkage Intervals. PLoS ONE, 2008, 3, e3874.	2.5	98
5488	Impact of Pretreated Switchgrass and Biomass Carbohydrates on Clostridium thermocellum ATCC 27405 Cellulosome Composition: A Quantitative Proteomic Analysis. PLoS ONE, 2009, 4, e5271.	2.5	206
5489	Rapid Evolution of Virulence and Drug Resistance in the Emerging Zoonotic Pathogen Streptococcus suis. PLoS ONE, 2009, 4, e6072.	2.5	214
5490	ProteinArchitect: Protein Evolution above the Sequence Level. PLoS ONE, 2009, 4, e6176.	2.5	1
5491	Caenorhabditis elegans BAH-1 Is a DUF23 Protein Expressed in Seam Cells and Required for Microbial Biofilm Binding to the Cuticle. PLoS ONE, 2009, 4, e6741.	2.5	12
5492	Solution Structure and Phylogenetics of Prod1, a Member of the Three-Finger Protein Superfamily Implicated in Salamander Limb Regeneration. PLoS ONE, 2009, 4, e7123.	2.5	62
5493	Gene Context Analysis in the Integrated Microbial Genomes (IMG) Data Management System. PLoS ONE, 2009, 4, e7979.	2.5	54

#	ARTICLE	IF	CITATIONS
5494	The Evolutionary History of Protein Domains Viewed by Species Phylogeny. PLoS ONE, 2009, 4, e8378.	2.5	79
5495	The Imprinted Retrotransposon-Like Gene PEG11 (RTL1) Is Expressed as a Full-Length Protein in Skeletal Muscle from Callipyge Sheep. PLoS ONE, 2010, 5, e8638.	2.5	38
5496	Proteomic Analysis of Tardigrades: Towards a Better Understanding of Molecular Mechanisms by Anhydrobiotic Organisms. PLoS ONE, 2010, 5, e9502.	2.5	58
5497	Improved Microarray-Based Decision Support with Graph Encoded Interactome Data. PLoS ONE, 2010, 5, e10225.	2.5	6
5498	Computational Protein Design: Validation and Possible Relevance as a Tool for Homology Searching and Fold Recognition. PLoS ONE, 2010, 5, e10410.	2.5	16
5499	Prediction and Testing of Biological Networks Underlying Intestinal Cancer. PLoS ONE, 2010, 5, e12497.	2.5	11
5500	Genome-Wide Identification, Characterization and Phylogenetic Analysis of the Rice LRR-Kinases. PLoS ONE, 2011, 6, e16079.	2.5	69
5501	Genome-Wide Identification of Molecular Mimicry Candidates in Parasites. PLoS ONE, 2011, 6, e17546.	2.5	49
5502	Structure and Function of the First Full-Length Murein Peptide Ligase (Mpl) Cell Wall Recycling Protein. PLoS ONE, 2011, 6, e17624.	2.5	30
5503	Dissecting the Specificity of Protein-Protein Interaction in Bacterial Two-Component Signaling: Orphans and Crosstalks. PLoS ONE, 2011, 6, e19729.	2.5	91
5504	The Vein Patterning 1 (VEP1) Gene Family Laterally Spread through an Ecological Network. PLoS ONE, 2011, 6, e22279.	2.5	16
5505	Conservation of the Human Integrin-Type Beta-Propeller Domain in Bacteria. PLoS ONE, 2011, 6, e25069.	2.5	22
5506	Putting into Practice Domain-Linear Motif Interaction Predictions for Exploration of Protein Networks. PLoS ONE, 2011, 6, e25376.	2.5	37
5507	Bioinformatic Analysis of Pathogenic Missense Mutations of Activin Receptor Like Kinase 1 Ectodomain. PLoS ONE, 2011, 6, e26431.	2.5	14
5508	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624.	2.5	75
5509	Whole-Genome Comparison of Two <i>Campylobacter jejuni</i> Isolates of the Same Sequence Type Reveals Multiple Loci of Different Ancestral Lineage. PLoS ONE, 2011, 6, e27121.	2.5	25
5510	Expansion of Genes Encoding piRNA-Associated Argonaute Proteins in the Pea Aphid: Diversification of Expression Profiles in Different Plastic Morphs. PLoS ONE, 2011, 6, e28051.	2.5	38
5511	GlyGly-CTERM and Rhombosortase: A C-Terminal Protein Processing Signal in a Many-to-One Pairing with a Rhomboid Family Intramembrane Serine Protease. PLoS ONE, 2011, 6, e28886.	2.5	22

#	ARTICLE	IF	CITATIONS
5512	Regular Patterns for Proteome-Wide Distribution of Protein Abundance across Species. PLoS ONE, 2012, 7, e32423.	2.5	12
5513	Symbiodinium Transcriptomes: Genome Insights into the Dinoflagellate Symbionts of Reef-Building Corals. PLoS ONE, 2012, 7, e35269.	2.5	221
5514	Characterization of a Novel ArsR-Like Regulator Encoded by Rv2034 in Mycobacterium tuberculosis. PLoS ONE, 2012, 7, e36255.	2.5	48
5515	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	2.5	42
5516	Relating the Disease Mutation Spectrum to the Evolution of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). PLoS ONE, 2012, 7, e42336.	2.5	12
5517	Increasing Coverage of Transcription Factor Position Weight Matrices through Domain-level Homology. PLoS ONE, 2012, 7, e42779.	2.5	8
5518	Subcellular Localization of Extracytoplasmic Proteins in Monoderm Bacteria: Rational Secretomics-Based Strategy for Genomic and Proteomic Analyses. PLoS ONE, 2012, 7, e42982.	2.5	50
5519	Evolutionary Conservation of the Ribosomal Biogenesis Factor Rbm19/Mrd1: Implications for Function. PLoS ONE, 2012, 7, e43786.	2.5	10
5520	FunSAV: Predicting the Functional Effect of Single Amino Acid Variants Using a Two-Stage Random Forest Model. PLoS ONE, 2012, 7, e43847.	2.5	43
5521	Susceptibility towards Enterotoxigenic Escherichia coli F4ac Diarrhea Is Governed by the MUC13 Gene in Pigs. PLoS ONE, 2012, 7, e44573.	2.5	70
5522	Comparative proteome analysis of Milnesium tardigradum in early embryonic state versus adults in active and anhydrobiotic state. PLoS ONE, 2012, 7, e45682.	2.5	31
5523	ThioFinder: A Web-Based Tool for the Identification of Thiopeptide Gene Clusters in DNA Sequences. PLoS ONE, 2012, 7, e45878.	2.5	51
5524	Comparative Metagenomic Analysis of Soil Microbial Communities across Three Hexachlorocyclohexane Contamination Levels. PLoS ONE, 2012, 7, e46219.	2.5	97
5525	Analysis of the Organic Hydroperoxide Response of Chromobacterium violaceum Reveals That OhrR Is a Cys-Based Redox Sensor Regulated by Thioredoxin. PLoS ONE, 2012, 7, e47090.	2.5	43
5526	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	2.5	55
5527	Hybrid Sequencing Approach Applied to Human Fecal Metagenomic Clone Libraries Revealed Clones with Potential Biotechnological Applications. PLoS ONE, 2012, 7, e47654.	2.5	16
5528	Simultaneous RNA-Seq Analysis of a Mixed Transcriptome of Rice and Blast Fungus Interaction. PLoS ONE, 2012, 7, e49423.	2.5	242
5529	Lack of RsmA-Mediated Control Results in Constant Hypervirulence, Cell Elongation, and Hyperflagellation in Pectobacterium wasabiae. PLoS ONE, 2013, 8, e54248.	2.5	19

#	ARTICLE	IF	CITATIONS
5530	Eomesodermin of Atlantic Salmon: An Important Regulator of Cytolytic Gene and Interferon Gamma Expression in Spleen Lymphocytes. PLoS ONE, 2013, 8, e55893.	2.5	17
5531	The Myxococcus xanthus Two-Component System CorSR Regulates Expression of a Gene Cluster Involved in Maintaining Copper Tolerance during Growth and Development. PLoS ONE, 2013, 8, e68240.	2.5	13
5532	A Lover and a Fighter: The Genome Sequence of an Entomopathogenic Nematode Heterorhabditis bacteriophora. PLoS ONE, 2013, 8, e69618.	2.5	89
5533	Discovery of Microorganisms and Enzymes Involved in High-Solids Decomposition of Rice Straw Using Metagenomic Analyses. PLoS ONE, 2013, 8, e77985.	2.5	50
5534	Sequencing and De Novo Assembly of the Transcriptome of the Glassy-Winged Sharpshooter (Homalodisca vitripennis). PLoS ONE, 2013, 8, e81681.	2.5	15
5535	Functional Annotation of Conserved Hypothetical Proteins from Haemophilus influenzae Rd KW20. PLoS ONE, 2013, 8, e84263.	2.5	93
5536	QuickProbsâ€”A Fast Multiple Sequence Alignment Algorithm Designed for Graphics Processors. PLoS ONE, 2014, 9, e88901.	2.5	14
5537	Fast and Accurate Multivariate Gaussian Modeling of Protein Families: Predicting Residue Contacts and Protein-Interaction Partners. PLoS ONE, 2014, 9, e92721.	2.5	127
5538	Biochemical Properties and Atomic Resolution Structure of a Proteolytically Processed Î²-Mannanase from Cellulolytic Streptomyces sp. SirexAA-E. PLoS ONE, 2014, 9, e94166.	2.5	18
5539	Transcriptome Sequencing and Gene Expression Analysis of Trichoderma brevicompactum under Different Culture Conditions. PLoS ONE, 2014, 9, e94203.	2.5	42
5540	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PilO2Bp S-SAD Crystal Structure. PLoS ONE, 2014, 9, e94981.	2.5	4
5541	Identification of Divergent Protein Domains by Combining HMM-HMM Comparisons and Co-Occurrence Detection. PLoS ONE, 2014, 9, e95275.	2.5	6
5542	Genome-Wide Survey and Expression Analysis of Calcium-Dependent Protein Kinase in Gossypium raimondii. PLoS ONE, 2014, 9, e98189.	2.5	77
5543	Tissue-Specific Transcript Profiling for ABC Transporters in the Sequestering Larvae of the Phytophagous Leaf Beetle Chrysomela populi. PLoS ONE, 2014, 9, e98637.	2.5	37
5544	Establishing an In Vivo Assay System to Identify Components Involved in Environmental RNA Interference in the Western Corn Rootworm. PLoS ONE, 2014, 9, e101661.	2.5	72
5545	Physiological and Genomic Features of a Novel Sulfur-Oxidizing Gammaproteobacterium Belonging to a Previously Uncultivated Symbiotic Lineage Isolated from a Hydrothermal Vent. PLoS ONE, 2014, 9, e104959.	2.5	40
5546	Contrasting Metabolism in Perenniating Structures of Upland and Lowland Switchgrass Plants Late in the Growing Season. PLoS ONE, 2014, 9, e105138.	2.5	20
5547	Comparative Analysis of Functional Metagenomic Annotation and the Mappability of Short Reads. PLoS ONE, 2014, 9, e105776.	2.5	58

#	ARTICLE	IF	CITATIONS
5548	A Comparative Metagenome Survey of the Fecal Microbiota of a Breast- and a Plant-Fed Asian Elephant Reveals an Unexpectedly High Diversity of Glycoside Hydrolase Family Enzymes. PLoS ONE, 2014, 9, e106707.	2.5	80
5549	A Toolkit for ARB to Integrate Custom Databases and Externally Built Phylogenies. PLoS ONE, 2015, 10, e0109277.	2.5	1
5550	Metagenomic Insights into the RDX-Degrading Potential of the Ovine Rumen Microbiome. PLoS ONE, 2014, 9, e110505.	2.5	13
5551	The IQD Gene Family in Soybean: Structure, Phylogeny, Evolution and Expression. PLoS ONE, 2014, 9, e110896.	2.5	36
5552	Acanthamoeba castellanii STAT Protein. PLoS ONE, 2014, 9, e111345.	2.5	6
5553	Early Chordate Origin of the Vertebrate Integrin β Domains. PLoS ONE, 2014, 9, e112064.	2.5	7
5554	The pCri System: A Vector Collection for Recombinant Protein Expression and Purification. PLoS ONE, 2014, 9, e112643.	2.5	24
5555	A C2H2 Zinc Finger Protein FEMU2 Is Required for fox1 Expression in Chlamydomonas reinhardtii. PLoS ONE, 2014, 9, e112977.	2.5	6
5556	Genome-Wide Investigation and Expression Profiling of AP2/ERF Transcription Factor Superfamily in Foxtail Millet (<i>Setaria italica</i> L.). PLoS ONE, 2014, 9, e113092.	2.5	148
5557	Whole-Transcriptome Survey of the Putative ATP-Binding Cassette (ABC) Transporter Family Genes in the Latex-Producing Laticifers of <i>Hevea brasiliensis</i> . PLoS ONE, 2015, 10, e0116857.	2.5	20
5558	Quality Control Test for Sequence-Phenotype Assignments. PLoS ONE, 2015, 10, e0118288.	2.5	2
5559	Exome Analysis Reveals Differentially Mutated Gene Signatures of Stage, Grade and Subtype in Breast Cancers. PLoS ONE, 2015, 10, e0119383.	2.5	19
5560	Analysis and Prediction of the Critical Regions of Antimicrobial Peptides Based on Conditional Random Fields. PLoS ONE, 2015, 10, e0119490.	2.5	30
5561	In Silico Screening for Novel Inhibitors of DNA Polymerase III Alpha Subunit of <i>Mycobacterium tuberculosis</i> (MtbDnaE2, H37Rv). PLoS ONE, 2015, 10, e0119760.	2.5	15
5562	De novo Transcriptome Assembly and the Putative Biosynthetic Pathway of Steroidal Sapogenins of <i>Dioscorea composita</i> . PLoS ONE, 2015, 10, e0124560.	2.5	19
5563	Genome-Wide Analysis of the AP2/ERF Transcription Factors Family and the Expression Patterns of DREB Genes in Moso Bamboo (<i>Phyllostachys edulis</i>). PLoS ONE, 2015, 10, e0126657.	2.5	96
5564	Evolution of the SH3 Domain Specificity Landscape in Yeasts. PLoS ONE, 2015, 10, e0129229.	2.5	8
5565	β -PGA Hydrolases of Phage Origin in <i>Bacillus subtilis</i> and Other Microbial Genomes. PLoS ONE, 2015, 10, e0130810.	2.5	18

#	ARTICLE	IF	CITATIONS
5566	Structure and Assembly of TP901-1 Virion Unveiled by Mutagenesis. PLoS ONE, 2015, 10, e0131676.	2.5	19
5567	The Complete Genome of a New Betabaculovirus from Clostera anastomosis. PLoS ONE, 2015, 10, e0132792.	2.5	15
5568	The Inner Membrane Protein PilG Interacts with DNA and the Secretin PilQ in Transformation. PLoS ONE, 2015, 10, e0134954.	2.5	5
5569	Clustering and Differential Alignment Algorithm: Identification of Early Stage Regulators in the Arabidopsis thaliana Iron Deficiency Response. PLoS ONE, 2015, 10, e0136591.	2.5	13
5570	The Prediction and Validation of Small CDSs Expand the Gene Repertoire of the Smallest Known Eukaryotic Genomes. PLoS ONE, 2015, 10, e0139075.	2.5	3
5571	Rice-Infecting Pseudomonas Genomes Are Highly Accessorized and Harbor Multiple Putative Virulence Mechanisms to Cause Sheath Brown Rot. PLoS ONE, 2015, 10, e0139256.	2.5	10
5572	COGNIZER: A Framework for Functional Annotation of Metagenomic Datasets. PLoS ONE, 2015, 10, e0142102.	2.5	87
5573	Genome-Wide Identification, Phylogenetic and Expression Analyses of the Ubiquitin-Conjugating Enzyme Gene Family in Maize. PLoS ONE, 2015, 10, e0143488.	2.5	34
5574	SH3 Domains Differentially Stimulate Distinct Dynamin I Assembly Modes and G Domain Activity. PLoS ONE, 2015, 10, e0144609.	2.5	8
5575	Late Embryogenesis Abundant (LEA) Constitutes a Large and Diverse Family of Proteins Involved in Development and Abiotic Stress Responses in Sweet Orange (Citrus sinensis L. Osb.). PLoS ONE, 2015, 10, e0145785.	2.5	90
5576	Chamber Specific Gene Expression Landscape of the Zebrafish Heart. PLoS ONE, 2016, 11, e0147823.	2.5	24
5577	ENTPRISE: An Algorithm for Predicting Human Disease-Associated Amino Acid Substitutions from Sequence Entropy and Predicted Protein Structures. PLoS ONE, 2016, 11, e0150965.	2.5	23
5578	The HEX 110 Hexamerin Is a Cytoplasmic and Nucleolar Protein in the Ovaries of Apis mellifera. PLoS ONE, 2016, 11, e0151035.	2.5	15
5579	An Approach to Function Annotation for Proteins of Unknown Function (PUFs) in the Transcriptome of Indian Mulberry. PLoS ONE, 2016, 11, e0151323.	2.5	40
5580	Identification of VPS13C as a Galectin-12-Binding Protein That Regulates Galectin-12 Protein Stability and Adipogenesis. PLoS ONE, 2016, 11, e0153534.	2.5	35
5581	SVM-Prot 2016: A Web-Server for Machine Learning Prediction of Protein Functional Families from Sequence Irrespective of Similarity. PLoS ONE, 2016, 11, e0155290.	2.5	98
5582	The Kinome of Pacific Oyster Crassostrea gigas, Its Expression during Development and in Response to Environmental Factors. PLoS ONE, 2016, 11, e0155435.	2.5	17
5583	Cloning, Expression and Biochemical Characterization of Endomannanases from Thermobifida Species Isolated from Different Niches. PLoS ONE, 2016, 11, e0155769.	2.5	13

#	ARTICLE	IF	CITATIONS
5584	A Large and Phylogenetically Diverse Class of Type 1 Opsins Lacking a Canonical Retinal Binding Site. PLoS ONE, 2016, 11, e0156543.	2.5	11
5585	Genome-Wide Analysis of Long Noncoding RNAs and Their Responses to Drought Stress in Cotton (<i>Gossypium hirsutum</i> L.). PLoS ONE, 2016, 11, e0156723.	2.5	109
5586	Draft Genomes of <i>Anopheles cracens</i> and <i>Anopheles maculatus</i> : Comparison of Simian Malaria and Human Malaria Vectors in Peninsular Malaysia. PLoS ONE, 2016, 11, e0157893.	2.5	8
5587	Functional Comparison of Bacteria from the Human Gut and Closely Related Non-Gut Bacteria Reveals the Importance of Conjugation and a Paucity of Motility and Chemotaxis Functions in the Gut Environment. PLoS ONE, 2016, 11, e0159030.	2.5	9
5588	Machine Learning of Protein Interactions in Fungal Secretory Pathways. PLoS ONE, 2016, 11, e0159302.	2.5	7
5589	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. PLoS ONE, 2016, 11, e0159627.	2.5	5
5590	Sequencing and Characterization of the Invasive Sycamore Lace Bug <i>Corythucha ciliata</i> (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.5	10
5591	Characterization of Toxin Complex Gene Clusters and Insect Toxicity of Bacteria Representing Four Subgroups of <i>Pseudomonas fluorescens</i> . PLoS ONE, 2016, 11, e0161120.	2.5	43
5592	Genome-Wide Analysis of APETALA2/Ethylene-Responsive Factor (AP2/ERF) Gene Family in Barley (<i>Hordeum vulgare</i> L.). PLoS ONE, 2016, 11, e0161322.	2.5	108
5593	Comparative Genomics of <i>Acetobacterpasteurianus</i> Ab3, an Acetic Acid Producing Strain Isolated from Chinese Traditional Rice Vinegar Meiguichu. PLoS ONE, 2016, 11, e0162172.	2.5	12
5594	Differential Communications between Fungi and Host Plants Revealed by Secretome Analysis of Phylogenetically Related Endophytic and Pathogenic Fungi. PLoS ONE, 2016, 11, e0163368.	2.5	20
5595	DNA Barcodes for the Northern European Tachinid Flies (Diptera: Tachinidae). PLoS ONE, 2016, 11, e0164933.	2.5	20
5596	Large-scale bioactivity analysis of the small-molecule assayed proteome. PLoS ONE, 2017, 12, e0171413.	2.5	4
5597	Transcriptomes of three species of Tipuloidea (Diptera, Tipulomorpha) and implications for phylogeny of Tipulomorpha. PLoS ONE, 2017, 12, e0173207.	2.5	14
5598	De novo transcriptome analysis of the excretory tubules of <i>Carausius morosus</i> (Phasmatodea) and possible functions of the midgut "appendices". PLoS ONE, 2017, 12, e0174984.	2.5	9
5599	Major changes in microbial diversity and community composition across gut sections of a juvenile <i>Panchlora</i> cockroach. PLoS ONE, 2017, 12, e0177189.	2.5	20
5600	Characterization of the maize lipoxygenase gene family in relation to aflatoxin accumulation resistance. PLoS ONE, 2017, 12, e0181265.	2.5	44
5601	Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom <i>Thalassiosira oceanica</i> . PLoS ONE, 2017, 12, e0181753.	2.5	24

#	ARTICLE	IF	CITATIONS
5602	The role of core and accessory type IV pilus genes in natural transformation and twitching motility in the bacterium <i>Acinetobacter baylyi</i> . PLoS ONE, 2017, 12, e0182139.	2.5	43
5603	Comparative genomics and phylogenomic analyses of lysine riboswitch distributions in bacteria. PLoS ONE, 2017, 12, e0184314.	2.5	12
5604	Insight into cordycepin biosynthesis of <i>Cordyceps militaris</i> : Comparison between a liquid surface culture and a submerged culture through transcriptomic analysis. PLoS ONE, 2017, 12, e0187052.	2.5	29
5605	Evolutionary history of callose synthases in terrestrial plants with emphasis on proteins involved in male gametophyte development. PLoS ONE, 2017, 12, e0187331.	2.5	31
5606	The <i>Glaciozyma antarctica</i> genome reveals an array of systems that provide sustained responses towards temperature variations in a persistently cold habitat. PLoS ONE, 2018, 13, e0189947.	2.5	45
5607	ProtDataTherm: A database for thermostability analysis and engineering of proteins. PLoS ONE, 2018, 13, e0191222.	2.5	22
5608	Identification and expression analyses of WRKY genes reveal their involvement in growth and abiotic stress response in watermelon (<i>Citrullus lanatus</i>). PLoS ONE, 2018, 13, e0191308.	2.5	61
5609	Variability in metagenomic samples from the Puget Sound: Relationship to temporal and anthropogenic impacts. PLoS ONE, 2018, 13, e0192412.	2.5	9
5611	Bves: ten years after. Histology and Histopathology, 2009, 24, 777-87.	0.7	28
5612	Genomics Confounds Gene Classification. American Scientist, 2008, 96, 466.	0.1	5
5613	In <i>Entamoeba histolytica</i> , a BspA family protein is required for chemotaxis toward tumour necrosis factor. Microbial Cell, 2015, 2, 235-246.	3.2	27
5615	Differential gene expression in response to water deficit in leaf and root tissues of soybean genotypes with contrasting tolerance profiles. Genetics and Molecular Biology, 2020, 43, e20180290.	1.3	5
5616	Metals from cell to environment: Connecting Metallomics with other omics. Open Journal of Plant Science, 0, , 001-014.	0.2	3
5617	Modeling studies of potato nucleoside triphosphate diphosphohydrolase NTPDase1: an insight into the catalytic mechanism.. Acta Biochimica Polonica, 2008, 55, 141-150.	0.5	12
5618	Unexpected domain composition of MACC1 links MET signaling and apoptosis.. Acta Biochimica Polonica, 2009, 56, .	0.5	38
5619	<i>Lactococcus lactis</i> IBB477 presenting adhesive and muco-adhesive properties as a candidate carrier strain for oral vaccination against influenza virus.. Acta Biochimica Polonica, 2014, 61, .	0.5	9
5620	Computational Analysis of PTEN Gene Mutation. International Journal on Advanced Science, Engineering and Information Technology, 2012, 2, 383.	0.4	2
5621	Visual Characterization of Misclassified Class C GPCRs through Manifold-based Machine Learning Methods. Genomics and Computational Biology, 2015, 1, 19.	0.7	3

#	ARTICLE	IF	CITATIONS
5622	LncRNA mediated regulation of aging pathways in <i>Drosophila melanogaster</i> during dietary restriction. <i>Aging</i> , 2016, 8, 2182-2203.	3.1	36
5623	Downregulated long noncoding RNA ALDBGALG0000005049 induces inflammation in chicken muscle suffered from selenium deficiency by regulating stearyl-CoA desaturase. <i>Oncotarget</i> , 2017, 8, 52761-52774.	1.8	16
5624	Identification of the PAK4 interactome reveals PAK4 phosphorylation of N-WASP and promotion of Arp2/3-dependent actin polymerization. <i>Oncotarget</i> , 2017, 8, 77061-77074.	1.8	23
5625	LncRNA and mRNA profiling during activation of tilapia macrophages by HSP70 and <i>Streptococcus agalactiae</i> antigen. <i>Oncotarget</i> , 2017, 8, 98455-98470.	1.8	22
5626	Functional characterization of a short peptidoglycan recognition protein from Chinese giant salamander (<i>Andrias davidianus</i>). <i>Oncotarget</i> , 2017, 8, 99323-99335.	1.8	10
5627	Comprehensive transcriptional landscape of porcine cardiac and skeletal muscles reveals differences of aging. <i>Oncotarget</i> , 2018, 9, 1524-1541.	1.8	41
5628	FGF8 promotes colorectal cancer growth and metastasis by activating YAP1. <i>Oncotarget</i> , 2015, 6, 935-952.	1.8	52
5629	Systems biology network-based discovery of a small molecule activator BL-AD008 targeting AMPK/ZIPK and inducing apoptosis in cervical cancer. <i>Oncotarget</i> , 2015, 6, 8071-8088.	1.8	30
5630	Novel HER3/MUC4 oncogenic signaling aggravates the tumorigenic phenotypes of pancreatic cancer cells. <i>Oncotarget</i> , 2015, 6, 21085-21099.	1.8	31
5631	The drug target genes show higher evolutionary conservation than non-target genes. <i>Oncotarget</i> , 2016, 7, 4961-4971.	1.8	16
5632	The cytomegalovirus protein UL138 induces apoptosis of gastric cancer cells by binding to heat shock protein 70. <i>Oncotarget</i> , 2016, 7, 5630-5645.	1.8	10
5633	Role of recA/RAD51 family proteins in mammals. <i>Acta Medica Okayama</i> , 2005, 59, 1-9.	0.2	55
5634	Genomic classification of protein-coding gene families. <i>WormBook</i> , 2005, , 1-23.	5.3	19
5637	Protein-Protein Interactions and Prediction: A Comprehensive Overview. <i>Protein and Peptide Letters</i> , 2013, 21, 779-789.	0.9	19
5638	Phytocystatins and their Potential to Control Plant Diseases Caused by Fungi. <i>Protein and Peptide Letters</i> , 2015, 22, 104-111.	0.9	19
5639	Leptin and the Ob-Receptor as Anti-Obesity Target: Recent In Silico Advances in the Comprehension of the Protein-Protein Interaction and Rational Drug Design of Anti- Obesity Lead Compounds. <i>Current Pharmaceutical Design</i> , 2014, 20, 136-145.	1.9	9
5640	Diverse Distribution of Resistomes in the Human and Environmental Microbiomes. <i>Current Genomics</i> , 2018, 19, 701-711.	1.6	10
5641	Rescue of the activity of HNH nuclease mutants - towards controlled enzymes for gene therapy. <i>Current Protein and Peptide Science</i> , 2016, 17, 191-197.	1.4	1

#	ARTICLE	IF	CITATIONS
5642	Characterization of a Bacteriophage-Derived Murein Peptidase for Elimination of Antibiotic-Resistant <i>Staphylococcus aureus</i> . <i>Current Protein and Peptide Science</i> , 2016, 17, 183-190.	1.4	20
5643	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.	2.1	35
5644	Structural Characterization, Homology Modeling and Docking Studies of ARG674 Mutation in MyH8 Gene Associated with Trismus-Pseudocamptodactyly Syndrome. <i>Letters in Drug Design and Discovery</i> , 2014, 11, 1177-1187.	0.7	15
5645	Computational RNA Structure Prediction. <i>Current Bioinformatics</i> , 2008, 3, 32-45.	1.5	37
5646	Using Pseudo Amino Acid Composition to Predict Protein Attributes Via Cellular Automata and Other Approaches. <i>Current Bioinformatics</i> , 2011, 6, 251-260.	1.5	22
5647	Identifying Coevolution Between Amino Acid Residues in Protein Families: Advances in the Improvement and Evaluation of Correlated Mutation Algorithms. <i>Current Bioinformatics</i> , 2013, 8, 148-160.	1.5	3
5648	Identification of Fungal DNA Barcode Targets and PCR Primers Based on Pfam Protein Families and Taxonomic Hierarchy. <i>The Open Applied Informatics Journal</i> , 2011, 5, 30-44.	1.0	7
5649	SWISS-PROT: Connecting Biomolecular Knowledge Via a Protein Database. <i>Current Issues in Molecular Biology</i> , 2001, , .	2.4	62
5650	Expression, divergence and evolution of the caleosin gene family in <i>Brassica rapa</i> . <i>Archives of Biological Sciences</i> , 2013, 65, 863-876.	0.5	6
5651	Key2Ann: a tool to process sequence sets by replacing database identifiers with a human-readable annotation. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, .	1.5	2
5652	<i>Plasmodium</i> DEH is ER-localized and crucial for oocyst mitotic division during malaria transmission. <i>Life Science Alliance</i> , 2020, 3, e202000879.	2.8	6
5653	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
5654	Genome-wide identification and characterization of eukaryotic protein kinases. <i>Frontiers in Bioscience - Landmark</i> , 2020, 25, 1787-1827.	3.0	5
5655	Lysosomal protein trafficking in <i>Giardia lamblia</i> : common and distinct features. <i>Frontiers in Bioscience - Elite</i> , 2012, E4, 1898.	1.8	11
5656	Nitrogenase genes in non-cyanobacterial plankton: prevalence, diversity and regulation in marine waters. <i>Aquatic Microbial Ecology</i> , 2010, 61, 235-247.	1.8	165
5657	Gammaproteobacterial methanotrophs dominate methanotrophy in aerobic and anaerobic layers of boreal lake waters. <i>Aquatic Microbial Ecology</i> , 2018, 81, 257-276.	1.8	72
5658	Identification of icp11, the most highly expressed gene of shrimp white spot syndrome virus (WSSV). <i>Diseases of Aquatic Organisms</i> , 2007, 74, 179-189.	1.0	36
5659	Differential gene expression between squamous cell carcinoma of esophagus and its normal epithelium; altered pattern of mal, akr1c2, and rab11a expression. <i>World Journal of Gastroenterology</i> , 2004, 10, 1716.	3.3	27

#	ARTICLE	IF	CITATIONS
5660	Characterization of human gene encoding SLA/LP autoantigen and its conserved homologs in mouse, fish, fly, and worm. World Journal of Gastroenterology, 2006, 12, 902.	3.3	6
5661	Computational prediction and experimental validation of novel markers for detection of STEC O157:H7. World Journal of Gastroenterology, 2011, 17, 1910.	3.3	12
5662	Predicting a novel pathogenicity island in <i>Helicobacter pylori</i> by genomic barcoding. World Journal of Gastroenterology, 2013, 19, 5006.	3.3	5
5663	Topology of Performance Indicators of All Irrigation Schemes in Turkey. Pakistan Journal of Biological Sciences, 2004, 7, 163-173.	0.5	1
5665	A modeling strategy for G-protein coupled receptors. AIMS Biophysics, 2016, 3, 211-231.	0.6	1
5666	Biochemical Characterization of Recombinant L-Asparaginase (AnsA) from <i>Rhizobium etli</i> , a Member of an Increasing Rhizobial-Type Family of L-Asparaginases. Journal of Microbiology and Biotechnology, 2012, 22, 292-300.	2.1	37
5667	Molecular and Biochemical Characterization of a Novel Intracellular Low-Temperature-Active Xylanase. Journal of Microbiology and Biotechnology, 2012, 22, 501-509.	2.1	16
5668	Algorithm for Predicting Functionally Equivalent Proteins from BLAST and HMMER Searches. Journal of Microbiology and Biotechnology, 2012, 22, 1054-1058.	2.1	6
5669	High-Throughput GRID Computing for Life Sciences. , 2009, , 187-205.		1
5670	GO-Based Term Semantic Similarity. , 2011, , 174-185.		2
5671	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. Standards in Genomic Sciences, 2013, 7, 382-398.	1.5	12
5672	iRhoms; Its Functions and Essential Roles. Biomolecules and Therapeutics, 2016, 24, 109-114.	2.4	13
5673	Collagen-Induced Arthritis Analysis in <i>Rhbd2</i> Knockout Mouse. Biomolecules and Therapeutics, 2018, 26, 298-305.	2.4	9
5674	Bioinformatics for Viral Metagenomics. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	14
5676	Computational Annotation for Hypothetical Proteins of <i>Mycobacterium Tuberculosis</i> . Journal of Computer Science and Systems Biology, 2008, 01, .	0.0	8
5677	Emerging Trends in Various Fields with Systems Biology Approach. Journal of Computer Science and Systems Biology, 2011, 4, .	0.0	2
5678	Protein Fold Classification with Backbone Torsional Characters Using Multi- Class Linear Discriminant Analysis. Journal of Proteomics and Bioinformatics, 2013, 06, 196-209.	0.4	42
5679	Helical Parameters and Correlations of Tandem Leucine Rich Repeats in Proteins. Journal of Proteomics and Bioinformatics, 2014, 07, .	0.4	13

#	ARTICLE	IF	CITATIONS
5680	World's Hottest Chilli Bhut Jolokia (<i>Capsicum assamicum</i>) Proteome Revealed: Comparative Proteomic Analysis of Differentially Expressed Proteins. <i>Journal of Proteomics and Bioinformatics</i> , 2014, 07, .	0.4	1
5681	MegaFiller: A Retrofitted Protein Function Predictor for Filling Gaps in Metabolic Networks. <i>Journal of Proteomics and Bioinformatics</i> , 0, s9, .	0.4	5
5683	Genome sequencing and next-generation sequence data analysis: A comprehensive compilation of bioinformatics tools and databases. <i>American Journal of Molecular Biology</i> , 2013, 03, 115-130.	0.3	8
5684	Homology-based cloning and expression analysis of Rf genes encoding PPR-containing proteins in tobacco. <i>Genetics and Molecular Research</i> , 2014, 13, 2310-2322.	0.2	5
5685	Transcriptome sequencing and analysis of the coconut leaf beetle, <i>Brontispa longissima</i> . <i>Genetics and Molecular Research</i> , 2015, 14, 8359-8365.	0.2	3
5686	Identification and expression analysis of YABBY family genes associated with fruit shape in tomato (<i>Solanum lycopersicum</i> L.). <i>Genetics and Molecular Research</i> , 2015, 14, 7079-7091.	0.2	26
5687	SVM-based Automatic Annotation of Multiple Sequence Alignments. <i>Journal of Computers</i> , 2014, 9, .	0.4	3
5688	Data Mining Techniques for Informative Motif Discovery. <i>International Journal of Computer Applications</i> , 2014, 88, 21-24.	0.2	2
5689	Designing Novel Antibacterials: Application of Omics Science. <i>Klinik Dergisi</i> , 2014, 26, 2-8.	0.4	1
5690	Cloning and Sequence Analysis of the Cellulase Genes Isolated from Two Cellulolytic <i>Streptomyces</i> and Their Heterologous Expression in <i>Streptomyces lividans</i> . <i>International Journal of the Society of Materials Engineering for Resources</i> , 2014, 20, 213-218.	0.1	5
5691	Structure and Function of Exo-BETA.-glucosaminidase from <i>Amycolatopsis orientalis</i> . <i>Journal of Applied Glycoscience</i> (1999), 2007, 54, 133-138.	0.7	3
5692	Predicting conformation of protein complexes by determining statistically significant domain-domain interactions. <i>Plant Biotechnology</i> , 2009, 26, 495-501.	1.0	1
5696	Application of HMM to the Study of Three-Dimensional Protein Structure. , 0, , .		1
5697	Prediction and Experimental Detection of Structural and Functional Motifs in Intrinsically Unfolded Proteins. , 0, , .		2
5698	Computational Methods for Prediction of Protein-Protein Interaction Sites. , 0, , .		10
5699	Sequence Analysis of Hypothetical Proteins from <i>Helicobacter pylori</i> 26695 to Identify Potential Virulence Factors. <i>Genomics and Informatics</i> , 2016, 14, 125.	0.8	28
5700	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.	0.8	11
5701	Bioinformatic Identification of Rare Codon Clusters (RCCs) in HBV Genome and Evaluation of RCCs in Proteins Structure of Hepatitis B Virus. <i>Hepatitis Monthly</i> , 2016, 16, e39909.	0.2	12

#	ARTICLE	IF	CITATIONS
5702	A Polyketide cyclase/dehydrase and lipid transport superfamily gene of Arabidopsis and its orthologue of chickpea exhibit rapid response to wounding. Indian Journal of Genetics and Plant Breeding, 2014, 74, 463.	0.5	5
5703	Homology modeling, comparative genomics and functional annotation of Mycoplasma genitalium hypothetical protein MG_237. Bioinformation, 2011, 7, 299-303.	0.5	14
5704	HNHDb: A database on pattern based classification of HNH domains reveals functional relevance of sequence patterns and domain associations.. Bioinformation, 2009, 4, 80-83.	0.5	12
5705	Predicting highly-connected hubs in protein interaction networks by QSAR and biological data descriptors. Bioinformation, 2009, 4, 164-168.	0.5	6
5706	DNA polymerase III a subunit from Mycobacterium tuberculosis H37Rv: Homology modeling and molecular docking of its inhibitor. Bioinformation, 2011, 6, 69-73.	0.5	5
5707	Characterization of Lovastatin biosynthetic cluster proteins in Aspergillus terreus strain ATCC 20542. Bioinformation, 2011, 6, 250-254.	0.5	12
5708	Resistome analysis of Mycobacterium tuberculosis: Identification of aminoglycoside 2â€™-N-acetyltransferase (AAC) as co-target for drug designing. Bioinformation, 2013, 9, 174-181.	0.5	7
5709	SVM based model generation for binding site prediction on helix turn helix motif type of transcription factors in eukaryotes. Bioinformation, 2013, 9, 500-505.	0.5	2
5710	Domain analyses of Usher syndrome causing Clarin-1 and GPR98 protein models. Bioinformation, 2014, 10, 491-495.	0.5	2
5711	Structure and functional annotation of hypothetical proteins having putative Rubisco activase function from Vitis vinifera. Bioinformation, 2015, 11, 11-16.	0.5	5
5712	Homology modeling and assigned functional annotation of an uncharacterized antitoxin protein from Streptomyces xinghaiensis. Bioinformation, 2015, 11, 493-500.	0.5	2
5713	Expression and in silico characterization of Phenylalanine ammonium lyase against karnal bunt (Tilletia indica) in wheat (Triticum aestivum). Bioinformation, 2013, 9, 1013-1018.	0.5	6
5715	Identification of Prostate Cancer LncRNAs by RNA-Seq. Asian Pacific Journal of Cancer Prevention, 2014, 15, 9439-9444.	1.2	12
5716	Coupled ion binding and structural transitions along the transport cycle of glutamate transporters. ELife, 2014, 3, e02283.	6.0	105
5717	YcgC represents a new protein deacetylase family in prokaryotes. ELife, 2015, 4, .	6.0	52
5718	Mapping and analysis of Caenorhabditis elegans transcription factor sequence specificities. ELife, 2015, 4, .	6.0	85
5719	Many lncRNAs, 5â€™UTRs, and pseudogenes are translated and some are likely to express functional proteins. ELife, 2015, 4, e08890.	6.0	439
5720	Comparative genomics explains the evolutionary success of reef-forming corals. ELife, 2016, 5, .	6.0	169

#	ARTICLE	IF	CITATIONS
5721	Dynamics of venom composition across a complex life cycle. <i>ELife</i> , 2018, 7, .	6.0	83
5722	Functional metagenomics-guided discovery of potent Cas9 inhibitors in the human microbiome. <i>ELife</i> , 2019, 8, .	6.0	56
5723	Myofibril diameter is set by a finely tuned mechanism of protein oligomerization in <i>Drosophila</i> . <i>ELife</i> , 2019, 8, .	6.0	27
5724	Isolation and transcriptomic analysis of <i>Anopheles gambiae</i> oenocytes enables the delineation of hydrocarbon biosynthesis. <i>ELife</i> , 2020, 9, .	6.0	20
5725	Exploring the transcriptomic data of the Australian paralysis tick, <i>Ixodes holocyclus</i> . <i>GSTF Journal of Veterinary Science</i> , 2016, 3, .	0.1	5
5726	Genome-wide identification and expression analysis of the ERF transcription factor family in pineapple (<i>Ananas comosus</i> (L.) Merr.). <i>PeerJ</i> , 2020, 8, e10014.	2.0	10
5727	Perilipin-related protein regulates lipid metabolism in <i>C. elegans</i> . <i>PeerJ</i> , 2015, 3, e1213.	2.0	25
5728	Intrinsically disordered caldesmon binds calmodulin via the "buttons on a string" mechanism. <i>PeerJ</i> , 2015, 3, e1265.	2.0	9
5729	Genome-wide identification and characterization of WRKY gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2016, 4, e2437.	2.0	52
5730	<i>Burkholderia pseudomallei</i> type III secreted protein BipC: role in actin modulation and translocation activities required for the bacterial intracellular lifecycle. <i>PeerJ</i> , 2016, 4, e2532.	2.0	6
5731	Genome-wide identification and characterization of TIFY family genes in Moso Bamboo (<i>Phyllostachys edulis</i>) and expression profiling analysis under dehydration and cold stresses. <i>PeerJ</i> , 2016, 4, e2620.	2.0	37
5732	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquillettii</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. <i>PeerJ</i> , 2017, 5, e2951.	2.0	23
5733	A Profile Hidden Markov Model to investigate the distribution and frequency of LanB-encoding lantibiotic modification genes in the human oral and gut microbiome. <i>PeerJ</i> , 2017, 5, e3254.	2.0	24
5734	Genome-wide analysis suggests high level of microsynteny and purifying selection affect the evolution of <i>Ein3/EIL</i> family in Rosaceae. <i>PeerJ</i> , 2017, 5, e3400.	2.0	16
5735	Genome-wide identification of CBL family and expression analysis of <i>CBLs</i> in response to potassium deficiency in cotton. <i>PeerJ</i> , 2017, 5, e3653.	2.0	36
5736	Genome-wide identification of the <i>MADS-box</i> transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	38
5737	Integration of lncRNA-miRNA-mRNA reveals novel insights into oviposition regulation in honey bees. <i>PeerJ</i> , 2017, 5, e3881.	2.0	49
5738	Genome-wide identification and characterization of GRAS transcription factors in tomato (<i>Solanum lycopersicum</i>). <i>PeerJ</i> , 2017, 5, e3955.	2.0	50

#	ARTICLE	IF	CITATIONS
5739	Comparative genomic analysis of the PKS genes in five species and expression analysis in upland cotton. <i>PeerJ</i> , 2017, 5, e3974.	2.0	17
5740	Genome-wide characterization and expression profiling of <i>NAC</i> transcription factor genes under abiotic stresses in radish (<i>Raphanus sativus</i> L.). <i>PeerJ</i> , 2017, 5, e4172.	2.0	20
5741	<i>In silico</i> structural and functional prediction of African swine fever virus protein-B263R reveals features of a TATA-binding protein. <i>PeerJ</i> , 2018, 6, e4396.	2.0	12
5742	Sexually dimorphic venom proteins in long-jawed orb-weaving spiders (<i>Tetragnatha</i>) comprise novel gene families. <i>PeerJ</i> , 2018, 6, e4691.	2.0	21
5743	Identification and comparative analysis of the <i>CIPK</i> gene family and characterization of the cold stress response in the woody plant <i>Prunus mume</i> . <i>PeerJ</i> , 2019, 7, e6847.	2.0	20
5744	Comprehensive transcriptional profiling of aging porcine liver. <i>PeerJ</i> , 2019, 7, e6949.	2.0	6
5745	Enzyme characterization and biological activities of a resuscitation promoting factor from an oil degrading bacterium <i>Rhodococcus erythropolis</i> KB1. <i>PeerJ</i> , 2019, 7, e6951.	2.0	7
5746	Molecular characterization of bacterial leaf streak resistance in hard winter wheat. <i>PeerJ</i> , 2019, 7, e7276.	2.0	19
5747	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015, 3, e740.	2.0	157
5748	Cyclic nucleotide binding and structural changes in the isolated GAF domain of <i>Anabaena</i> adenylyl cyclase, CyaB2. <i>PeerJ</i> , 2015, 3, e882.	2.0	26
5749	Genome-wide identification and characterization of TCP family genes in <i>Brassica juncea</i> var. <i>tumida</i> . <i>PeerJ</i> , 2020, 8, e9130.	2.0	11
5751	Exploration of Chemosensory Ionotropic Receptors in Cephalopods: the IR25 gene is expressed in the Olfactory Organs, Suckers, and Fins of <i>Sepia officinalis</i> . <i>Chemical Senses</i> , 2021, 46, .	2.0	1
5752	ConVarT: a search engine for matching human genetic variants with variants from non-human species. <i>Nucleic Acids Research</i> , 2022, 50, D1172-D1178.	14.5	16
5753	Insertions and deletions in the RNA sequenceâ€‘structure map. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210380.	3.4	15
5754	The novel anti-CRISPR AcrIIA22 relieves DNA torsion in target plasmids and impairs SpyCas9 activity. <i>PLoS Biology</i> , 2021, 19, e3001428.	5.6	13
5755	Sequence Engineering of an <i>Aspergillus niger</i> Tannase to Produce in <i>Pichia pastoris</i> a Single-Chain Enzyme with High Specific Activity. <i>Molecular Biotechnology</i> , 2022, 64, 388-400.	2.4	1
5756	De novo transcriptome analysis provides insights into the salt tolerance of <i>Podocarpus macrophyllus</i> under salinity stress. <i>BMC Plant Biology</i> , 2021, 21, 489.	3.6	9
5757	A Genomic Survey of <i>Mayetiola destructor</i> Mobilome Provides New Insights into the Evolutionary History of Transposable Elements in the Cecidomyiid Midges. <i>PLoS ONE</i> , 2021, 16, e0257996.	2.5	6

#	ARTICLE	IF	CITATIONS
5758	The chromosome-scale genome assembly, annotation and evolution of <i>Rhododendron henanense</i> subsp. <i>lingbaoense</i> . Molecular Ecology Resources, 2022, 22, 988-1001.	4.8	14
5759	Genome-Wide Identification and Expression Analysis of AP2/ERF Transcription Factor Related to Drought Stress in Cultivated Peanut (<i>Arachis hypogaea</i> L.). Frontiers in Genetics, 2021, 12, 750761.	2.3	21
5760	Heterotrophic bacterial diazotrophs are more abundant than their cyanobacterial counterparts in metagenomes covering most of the sunlit ocean. ISME Journal, 2022, 16, 927-936.	9.8	41
5761	MCRL: using a reference library to compress a metagenome into a non-redundant list of sequences, considering viruses as a case study. Bioinformatics, 2022, 38, 631-647.	4.1	3
5762	Sulfur cycling and host-virus interactions in <i>Aquificales</i> -dominated biofilms from Yellowstone's hottest ecosystems. ISME Journal, 2022, 16, 842-855.	9.8	8
5764	STRUCTURE-BASED COMPARISON OF FOUR EUKARYOTIC GENOMES. , 2001, , .		2
5765	Molecular characterization of calponin from molluscan catch muscle. Fisheries Science, 2002, 68, 1609-1610.	1.6	2
5766	IDENTIFYING STRUCTURAL MOTIFS IN PROTEINS. , 2002, , .		4
5767	Analysis of functional domains of <i>Streptococcus sobrinus</i> glucosyltransferase U. International Journal of Oral-Medical Sciences, 2003, 1, 152-156.	0.1	0
5768	Dragon and Dragon View: Methods for the Annotation, Analysis, and Visualization of Large-Scale Gene Expression Data. Statistics in the Health Sciences, 2003, , 185-209.	0.2	2
5769	Identificaci3n de sitios en prote3nas usando m3quinas con vectores de soporte. Nova, 2015, 1, 65-71.	0.1	0
5770	Temporal Assessment of Irrigation Schemes in Cukurova Region of Turkey. Pakistan Journal of Biological Sciences, 2004, 7, 174-181.	0.5	0
5772	BAYESIAN JOINT PREDICTION OF ASSOCIATED TRANSCRIPTION FACTORS IN <i>BACILLUS SUBTILIS</i> . , 2004, , 507-18.		2
5773	A BETTER GAP PENALTY FOR PAIRWISE SVM. , 2005, , .		2
5774	Genomic Characterization of Chromosome 1 of <i>Plasmodium falciparum</i> by Computational Methods. The Internet Journal of Microbiology, 2005, 1, .	0.1	0
5776	A +1 Programmed Ribosomal Frameshifting of a Human C2H2 Zinc Finger Gene Discovered by Computational Analysis. Biotechnology, 2005, 4, 316-324.	0.1	0
5777	Structural And Functional Characterization Of Cation-Transporting Atpase Of <i>Mycobacterium Tuberculosis</i> CDC 1551 By <i>In Silico</i> Methods. Internet Journal of Genomics and Proteomics, 2006, 2, .	0.1	0
5778	Collaborative Discovery Through Biological Language Modeling Interface. Lecture Notes in Computer Science, 2006, , 300-321.	1.3	0

#	ARTICLE	IF	CITATIONS
5779	BIOMEDIATOR DATA INTEGRATION AND INFERENCE FOR FUNCTIONAL ANNOTATION OF ANONYMOUS SEQUENCES. , 2006, , .		9
5780	DISCOVERING MAXIMIZED PROGRESSIVE HIGH-ORDER PATTERNS IN BIOSEQUENCES. , 2007, , 110-115.		5
5781	Modern genome annotation: the BioSapiens network. , 2008, , 213-238.		2
5782	Data Mining of SubQTL Region on Chromosome 9: Dissecting Gene Structure and Protein Function. Asian Journal of Plant Sciences, 2008, 7, 268-275.	0.4	1
5783	A Bioinformatics Resource for Crop Functional Genomics: GFSelector Module in Automated Annotation System, RiceGAAS. Japan Agricultural Research Quarterly, 2009, 43, 103-113.	0.4	0
5784	Incorporating Graph Features for Predicting Protein-Protein Interactions. , 2009, , 45-63.		0
5785	Proteomic Tools for the Analysis of Cytoskeleton Proteins. Methods in Molecular Biology, 2009, 586, 375-388.	0.9	0
5786	Ontological Enrichment of the Genes-to-Systems Breast Cancer Database. Communications in Computer and Information Science, 2009, , 171-182.	0.5	1
5787	A Medium-Throughput Structural Proteomics Approach Applied to the Genome of E. coli. , 2009, , 59-86.		0
5788	An Empirical Evaluation of the Effectiveness of Different Types of Predictor Attributes in Protein Function Prediction. Studies in Computational Intelligence, 2009, , 339-357.	0.9	0
5789	UNSUPERVISED CLASSIFICATION OF TREE STRUCTURED OBJECTS. , 2009, , .		1
5790	A database for human Y chromosome protein data. Bioinformation, 2009, 4, 184-186.	0.5	0
5791	Pangenomic Reverse Vaccinology. , 2010, , 203-221.		1
5792	Computational Methods for Predicting Domain-Domain Interactions. Computational Biology, 2010, , 157-173.	0.2	0
5793	In Silico Modeling of Ligand Molecule for Target Protein in Diabetes Mellitus Type II Insight Mechanism. The Open Nutraceuticals Journal, 2010, 3, 76-80.	0.2	1
5794	Sequence Alignment. Computational Biology, 2010, , 89-155.	0.2	0
5795	ANALYSIS OF A LIPID BIOSYNTHESIS PROTEIN FAMILY AND PHOSPHOLIPID STRUCTURAL VARIATIONS. , 2010, , .		1
5796	Modularity and Distribution of Sulfur Metabolism Genes in Bacterial Populations: Search and Design. Journal of Computer Science and Systems Biology, 2010, 03, .	0.0	2

#	ARTICLE	IF	CITATIONS
5797	CO-EVOLUTION IN HIV ENZYMES. , 2010, , .		1
5798	Genome Annotation. , 2010, , 4281-4288.		0
5799	Whole-Genome Sequence Characterization of Primary Auxin-Responsive <i>Aux/IAA</i> Gene Family in Sorghum (<i>Sorghum bicolor</i> L.). Acta Agronomica Sinica(China), 2010, 36, 688-694.	0.3	1
5800	Selection and Sequencing of Strains as References for Human Microbiome Studies. , 2011, , 79-90.		0
5801	Allergens in Peanut, Soybean and Lupin. , 2010, , 29-76.		0
5802	An Optimal Mesh Algorithm for Remote Protein Homology Detection. Communications in Computer and Information Science, 2011, , 471-497.	0.5	0
5804	FPGA-Based Accelerators for Bioinformatics Applications. , 2011, , 311-341.		0
5805	SUBSET SEED EXTENSION TO PROTEIN BLAST. , 2011, , .		3
5806	Protein Fold Classification with Backbone Torsional Characters Using Multi- Class Linear Discriminant Analysis. Journal of Proteomics and Bioinformatics, 2011, 6, .	0.4	0
5807	XML-Based Approaches for the Integration of Heterogeneous Bio-Molecular Data. , 2011, , 206-241.		0
5808	Selected Works in Bioinformatics. , 2011, , .		1
5809	Disease Gene Prioritization. , 0, , .		0
5810	Bioinformatics Domain Structure Prediction and Homology Modeling of Human Ryanodine Receptor 2. , 0, , .		1
5811	Island Injection Genetic Algorithm with Relaxed Coordination for the Multiple Sequence Alignment Problem. Studies in Computational Intelligence, 2012, , 67-87.	0.9	0
5812	High-Throughput GRID Computing for Life Sciences. , 2012, , 821-840.		2
5813	Irr1/Scc3 cohesin interacts with Rec8 in meiotic prophase of <i>Saccharomyces cerevisiae</i>. Open Journal of Genetics, 2012, 02, 1-6.	0.1	1
5814	Cloning and expression of a Trichoderma longibrachiatum β -mannanase gene in Pichia pastoris. African Journal of Biotechnology, 2012, 11, .	0.6	2
5815	cswHMM: A NOVEL CONTEXT SWITCHING HIDDEN MARKOV MODEL FOR BIOLOGICAL SEQUENCE ANALYSIS. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
5816	Estimation of False Discovery Rate of Protein Identification. , 0, , .		0
5817	PROTEIN LOCAL TERTIARY STRUCTURE PREDICTION BY SUPER GRANULE SUPPORT VECTOR MACHINES WITH CHOU-FASMAN PARAMETER. International Journal for Computational Biology, 2012, 1, 14.	0.1	1
5818	Protein Interactome and Its Application to Protein Function Prediction. , 0, , .		0
5819	BRNN-SVM: Increasing the Strength of Domain Signal to Improve Protein Domain Prediction Accuracy. , 0, , .		0
5820	Computational Analysis of Proteases Domains using Hidden Markov Model. International Journal of Computer Applications, 2012, 43, 32-35.	0.2	0
5821	Recurrent Neural Network based Classification of Protein-Protein Interactions. International Journal of Computer Applications, 2012, 52, 6-11.	0.2	0
5822	Predicting Protein Functions from Protein Interaction Networks. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 50-70.	0.8	4
5823	USING BIOBIN TO EXPLORE RARE VARIANT POPULATION STRATIFICATION. , 2012, , .		7
5824	Data Fusion with Optimized Block Kernels in LS-SVM for Protein Classification. Engineering, 2013, 05, 223-236.	0.8	1
5825	Bioinformatics Analysis of the Ribosomal Proteins,RPL27, RPL37a and RPL41: 3-D Protein Modeling and Protein-protein Interaction Prediction. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 2013, , 10-15.	0.2	1
5826	SET domain-containing Protein 4 (SETD4) is a Newly Identified Cytosolic and Nuclear Lysine Methyltransferase involved in Breast Cancer Cell Proliferation. Journal of Cancer Science & Therapy, 2013, 05, .	1.7	10
5827	Predicting Long Non-coding RNAs Based on Genomic Sequence Information. Computational Molecular Biology, 0, , .	0.0	0
5828	Differential Fusion Expression and Purification of a Cystatin in Two Different Bacterial Strains. Prikladnaia Biokhimiia I Mikrobiologiia, 2013, 49, 353-357.	0.4	0
5830	A fragmented alignment method detects a phosphorylation site and a new BRC repeat in the Drosophila melanogaster BRCA2 protein, and a new HAT repeat in Utp6 from yeast. F1000Research, 2013, 2, 143.	1.6	0
5831	Method of Search for Substrate Specificity Regions in Cellulase Class Enzymes Based on their Primary and Tertiary Structures. Mathematical Biology and Bioinformatics, 2013, 8, 407-418.	0.6	0
5832	Bioinformatic Methods and Resources for Neuroscience Research. Springer Protocols, 2014, , 453-463.	0.3	0
5833	And and And**, 2013, , 198-213.		4
5834	Chapter 9: Characterization and Prediction of Human Protein-Protein Interactions. Science, Engineering, and Biology Informatics, 2014, , 237-261.	0.1	1

#	ARTICLE	IF	CITATIONS
5835	Molecular modelling techniques in environmental research. Environmental Biotechnology, 2014, 9, 39-51.	1.5	0
5836	Evolution of PE35 and PPE68 Gene Families in Mycobacterium: Roles of Horizontal Gene Transfer and Evolutionary Constraints. Journal of Tuberculosis Research, 2014, 02, 181-198.	0.2	1
5838	Predicting residue contacts for protein-protein interactions by integration of multiple information. Journal of Biomedical Science and Engineering, 2014, 07, 28-37.	0.4	0
5839	In Silico Proteomic Functional Re-annotation of <i>Escherichia coli</i> K-12 using Dynamic Biological Data Fusion Strategy. Computational Molecular Biology, 0, , .	0.0	0
5841	Using Sequence Information to Identify Motifs. , 2014, , 1-6.		0
5842	Relationship between Physico-chemical Parameters and Phylogenetics Study of Human Low Density Lipoprotein Receptor-Related Protein (LRP). British Biotechnology Journal, 2014, 4, 289-304.	0.4	2
5843	Novel Inorganic Pyrophosphatase from Soil Metagenomic and Family and Subfamily Prediction. Open Journal of Applied Sciences, 2014, 04, 68-75.	0.4	1
5845	A Comprehensive Bioinformatics Analysis of the Lipxygenases Superfamily in Shewanella Woodyi Strain (Strain ATCC 51908/MS32). Journal of Materials Science and Engineering B, 2014, 4, .	0.3	0
5847	Ubiquity of Cyclic Di-GMP Pathways: a Bioinformatic Analysis. , 0, , 24-36.		0
5848	Extra-Ribosomal Functions of the Ribosomal Protein, RPS3 as Predicted by In Silico Analysis. Borneo Journal of Resource Science and Technology, 2016, 4, 62-69.	0.1	1
5849	Quantum Computing Approach for Alignment-Free Sequence Search and Classification. , 2012, , 279-300.		0
5850	The Core Pathway: Diguanylate Cyclases, Cyclic Di-GMP-Specific Phosphodiesterases, and Cyclic Di-GMP-Binding Proteins. , 0, , 37-56.		2
5851	SMDB: SOYBEAN MARKER DATABASE. International Journal for Computational Biology, 2014, 3, 44.	0.1	0
5853	Rapid Assembly and Cloning of Zinc Finger Proteins with Multiple Finger Modules. Bulletin of the Korean Chemical Society, 2014, 35, 2197-2200.	1.9	0
5854	"Diabetes Associated Genes from the Dark Matter of the Human Proteome". MOJ Proteomics & Bioinformatics, 2014, 1, .	0.1	6
5859	Sequence Alignment. Computational Biology, 2015, , 107-174.	0.2	0
5860	Annotation Pipelines for Next-Generation Sequencing Projects. Computational Biology, 2015, , 325-367.	0.2	0
5861	Atlas of the Open Reading Frames in Human Diseases: Dark Matter of the Human Genome. MOJ Proteomics & Bioinformatics, 2015, 2, .	0.1	1

#	ARTICLE	IF	CITATIONS
5862	Molecular characterization, tissue distribution, and immune reaction expression of karyopherins in the domestic silkworm (<i>Bombyx mori</i>). <i>Genetics and Molecular Research</i> , 2015, 14, 13049-13065.	0.2	0
5863	Combining Disparate Data Types: Protein Sequences and Protein Structures. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2015, 06, .	0.5	0
5864	GO-WAR: A Tool for Mining Weighted Association Rules from Gene Ontology Annotations. <i>Lecture Notes in Computer Science</i> , 2015, , 3-18.	1.3	1
5867	MULISA : A New Strategy for Discovery of Protein Functional Motifs and Residues. , 2015, , .		0
5869	Estimando dom�nio de prote�nas por abordagem estat�stica. , 0, , .		0
5871	Genomic Analysis of the Moderately Haloalkaliphilic Bacterium <i>Oceanobacillus kimchii</i> Strain X50T with Improved High-Quality Draft Genome Sequences. <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 1971-1976.	2.1	1
5872	An Optimized In Silico Neuroinformatics Approach. <i>Advances in Computational Intelligence and Robotics Book Series</i> , 2016, , 802-820.	0.4	0
5873	Grundlagen nat�rlicher Allergene. , 2016, , 177-191.		0
5874	In Silico Perspective into Interactions and Mutations in Human TLR4 and Ebola Glycoprotein. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> , 2016, , 209-231.	0.3	0
5875	Overview of Cellular Computing-Basic Principles and Applications. <i>Advances in Computational Intelligence and Robotics Book Series</i> , 2016, , 637-662.	0.4	0
5876	Characterization of DsrK and DsrO from <i>Allochromatium vinosum</i> and other Proteobacteria Using the Amino Acid Sequences. <i>Research & Reviews Journal of Material Sciences</i> , 2016, 01, .	0.1	0
5888	Sequence Information to Identify Motifs. , 2018, , 1121-1126.		0
5890	Biosynthesis of protein in plants under different environmental factors. <i>Journal of Medicinal Plants Studies</i> , 2018, 6, 261-264.	0.4	3
5895	Microbial Treatment of Waste by Culture-Dependent and Culture-Independent Approaches: Opportunities and Challenges. , 2019, , 415-446.		6
5897	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. , 2019, , 406-427.		0
5898	Alternative Splicing. , 2019, , 1-8.		0
5903	Proteomics and bioinformatics analysis reveal potential roles of cadmium-binding proteins in cadmium tolerance and accumulation of <i>Enterobacter cloacae</i> . <i>PeerJ</i> , 2019, 7, e6904.	2.0	7
5904	Identification of Chimeric RNAs Using RNA-Seq Reads and Protein��Protein Interactions of Translated Chimeras. <i>Methods in Molecular Biology</i> , 2020, 2079, 27-40.	0.9	0

#	ARTICLE	IF	CITATIONS
5908	SH3 BINDING DOMAINS FROM PHAGE ENDOLYSINS: HOW TO USE THEM FOR DETECTION OF GRAM-POSITIVE PATHOGENS. <i>Journal of Microbiology, Biotechnology and Food Sciences</i> , 2020, 9, 1215-1220.	0.8	1
5910	Comprehensive analysis and identification of heat-responsive genes in <i>Agarophyton vermiculophyllum</i> by RNA-sequencing. <i>Botanica Marina</i> , 2020, 63, 479-490.	1.2	3
5913	Comparative RNA-Seq Analysis Reveals Potentially Resistance-Related Genes in Response to Bacterial Canker of Tomato. <i>Genes</i> , 2021, 12, 1745.	2.4	5
5914	The endophytome (plant-associated microbiome): methodological approaches, biological aspects, and biotech applications. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 206.	3.6	7
5915	A High Rate Algal Pond Hosting a Dynamic Community of RNA Viruses. <i>Viruses</i> , 2021, 13, 2163.	3.3	6
5916	Pneumococcal Extracellular Serine Proteases: Molecular Analysis and Impact on Colonization and Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 763152.	3.9	4
5917	Quick and efficient approach to develop genomic resources in orphan species: Application in <i>Lavandula angustifolia</i> . <i>PLoS ONE</i> , 2020, 15, e0243853.	2.5	4
5918	The effect of oxidized fish oil on antioxidant ability, histology and transcriptome in intestine of the juvenile hybrid grouper (<i>Epinephelus fuscoguttatus</i> × <i>Epinephelus lanceolatus</i>). <i>Aquaculture Reports</i> , 2022, 22, 100921.	1.7	5
5919	Transcriptome sequencing flower petals reveals insights into regulation of flavonoid biosynthesis in <i>Osmanthus fragrans</i> . <i>Biologia Plantarum</i> , 0, 63, 765-775.	1.9	4
5921	Overview of Cellular Computing-Basic Principles and Applications. , 2020, , 1895-1920.		0
5924	Computational Analysis of the Hypothetical Protein P9303_05031 from Marine Cyanobacterium <i>Prochlorococcus Marinus</i> MIT 9303. <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.5	3
5925	Identification and heavy metals-induced expression analysis of the oligopeptide transporters (OPT) gene family in tomato. <i>Pakistan Journal of Botany</i> , 2020, 52, .	0.5	4
5927	Tomato COI gene family identification and expression under abiotic and phytohormone stress. <i>Journal of Genetics</i> , 2021, 100, 1.	0.7	1
5928	Transcriptomic Profile of the Cockle <i>Cerastoderma edule</i> Exposed to Seasonal Diarrhetic Shellfish Toxin Contamination. <i>Toxins</i> , 2021, 13, 784.	3.4	3
5929	A Novel Spo11 Homologue Functions as a Positive Regulator in Cyst Differentiation in <i>Giardia lamblia</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 11902.	4.1	2
5931	High-Throughput GRID Computing for Life Sciences. , 0, , 821-840.		0
5932	A Transfer Learning Approach and Selective Integration of Multiple Types of Assays for Biological Network Inference. , 0, , 188-202.		1
5933	GO-Based Term Semantic Similarity. , 0, , 93-104.		0

#	ARTICLE	IF	CITATIONS
5934	FPGA-Based Accelerators for Bioinformatics Applications. , 0, , 605-635.		0
5935	Quantum Computing Approach for Alignment-Free Sequence Search and Classification. , 0, , 1705-1726.		0
5936	Developing Resources for Analysis of Secreted Proteins from <i>Magnaporthe oryzae</i> . , 2009, , 113-124.		0
5937	Of Proteins, Genomes, and Proteomes. <i>Computational Biology</i> , 2009, , 189-210.	0.2	0
5938	Whole-Genome Sequence Characterization of Primary Auxin-Responsive Aux/IAA Gene Family in <i>Sorghum</i> (Sorghum bicolor L.). <i>Acta Agronomica Sinica</i> (China), 2010, 36, 688-694.	0.3	0
5939	Multiple Graph Alignment for the Structural Analysis of Protein Active Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 310-320.	3.0	9
5941	Evolutionary history of dimethylsulfoniopropionate (DMSP) demethylation enzyme DmdA in marine bacteria. <i>PeerJ</i> , 2020, 8, e9861.	2.0	4
5942	An integrated dataset for in silico drug discovery. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	9
5943	Biofilter: a knowledge-integration system for the multi-locus analysis of genome-wide association studies. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 368-79.	0.7	79
5945	Genetic and epigenetic association studies suggest a role of microRNA biogenesis gene exportin-5 (XPO5) in breast tumorigenesis. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2011, 2, 9-18.	0.4	42
5947	SET domain-containing Protein 4 (SETD4) is a Newly Identified Cytosolic and Nuclear Lysine Methyltransferase involved in Breast Cancer Cell Proliferation. <i>Journal of Cancer Science & Therapy</i> , 2013, 5, 58-65.	1.7	25
5951	Phenotypic Screening of Molecular Docking Enriched Chemical Libraries from Targets Identified in Ischemic Stroke Genome Data by Network-Based Method. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-9.	1.9	0
5952	Artemisinin Binds and Inhibits the Activity of <i>Plasmodium falciparum</i> Ddi1, a Retroviral Aspartyl Protease. <i>Pathogens</i> , 2021, 10, 1465.	2.8	5
5953	Genome-Wide Identification, Characterization, and Expression Analysis of DDE_Tnp_4 Family Genes in <i>Eriocheir sinensis</i> . <i>Antibiotics</i> , 2021, 10, 1430.	3.7	2
5955	ElyC and Cyclic Enterobacterial Common Antigen Regulate Synthesis of Phosphoglyceride-Linked Enterobacterial Common Antigen. <i>MBio</i> , 2021, 12, e0284621.	4.1	6
5956	Accurate expression quantification from nanopore direct RNA sequencing with NanoCount. <i>Nucleic Acids Research</i> , 2022, 50, e19-e19.	14.5	44
5958	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. <i>American Journal of Human Genetics</i> , 2021, 108, 2301-2318.	6.2	21
5960	Recurrent expansions of B30.2-associated immune receptor families in fish. <i>Immunogenetics</i> , 2022, 74, 129-147.	2.4	6

#	ARTICLE	IF	CITATIONS
5962	Genome-wide identification and expression profiles of AP2/ERF transcription factor family in mung bean (<i>Vigna radiata</i> L.). <i>Journal of Applied Genetics</i> , 2022, , 1.	1.9	1
5963	Epigenomic and transcriptomic analyses reveal differences between low-grade inflammation and severe exhaustion in LPS-challenged murine monocytes. <i>Communications Biology</i> , 2022, 5, 102.	4.4	20
5964	A Micrarchaeon Isolate Is Covered by a Proteinaceous S-Layer. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0155321.	3.1	4
5965	Transcription Factor RrANT1 of <i>Rosa rugosa</i> Positively Regulates Flower Organ Size in <i>Petunia hybrida</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 1236.	4.1	0
5966	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.	2.2	5
5967	Chromosome-level genome assembly of the shuttles hopfish, <i>Periophthalmus modestus</i> . <i>GigaScience</i> , 2022, 11, .	6.4	4
5968	A High-Density Genetic Map Enables Genome Synteny and QTL Mapping of Vegetative Growth and Leaf Traits in <i>Gardenia</i> . <i>Frontiers in Genetics</i> , 2021, 12, 802738.	2.3	2
5969	Differential Expression of lncRNAs and miRNAs Between Self-Rooting Juvenile and Donor Clones Unveils Novel Insight Into the Molecular Regulation of Rubber Biosynthesis in <i>Hevea brasiliensis</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 740597.	3.6	2
5970	Comparative transcriptomics reveal tissue level specialization towards diet in prickleback fishes. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2022, 192, 275-295.	1.5	10
5971	Transcriptomic profiling suggests candidate molecular responses to waterlogging in cassava. <i>PLoS ONE</i> , 2022, 17, e0261086.	2.5	11
5972	Habitat Adaptation Drives Speciation of a <i>Streptomyces</i> Species with Distinct Habitats and Disparate Geographic Origins. <i>MBio</i> , 2022, 13, e0278121.	4.1	15
5973	<i>Schistosoma mansoni</i> Î±-N-acetylgalactosaminidase (SmNAGAL) regulates coordinated parasite movement and egg production. <i>PLoS Pathogens</i> , 2022, 18, e1009828.	4.7	14
5974	Characterizing the oral and distal gut microbiota of the threatened southern sea otter (<i>Enhydra</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2.0 9	2.0	9
5975	Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. <i>BMC Genomics</i> , 2022, 23, 42.	2.8	11
5976	Systematic analysis of the Serine/Arginine-Rich Protein Splicing Factors (SRs) and focus on salt tolerance of PtSC27 in <i>Populus trichocarpa</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 173, 97-109.	5.8	5
5977	SPOT-Contact-LM: improving single-sequence-based prediction of protein contact map using a transformer language model. <i>Bioinformatics</i> , 2022, 38, 1888-1894.	4.1	25
5978	Isolation, Characterization and Draft Genome Analysis of Bacteriophages Infecting <i>Acidovorax citrulli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 803789.	3.5	3
5979	Identification of sodium homeostasis genes in <i>Camelus bactrianus</i> by whole transcriptome sequencing. <i>FEBS Open Bio</i> , 2022, 12, 864-876.	2.3	0

#	ARTICLE	IF	CITATIONS
5980	Haplotype-Resolved Genome Analyses Reveal Genetically Distinct Nuclei within a Commercial Cultivar of <i>Lentinula edodes</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 167.	3.5	5
5981	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	6.4	8
5982	Deep generative models for peptide design. , 2022, 1, 195-208.		34
5983	Genome-wide identification of CAMTA gene family members in rice (<i>Oryza sativa</i> L.) and in silico study on their versatility in respect to gene expression and promoter structure. <i>Functional and Integrative Genomics</i> , 2022, 22, 193-214.	3.5	9
5984	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.	3.6	1
5985	Genome-Wide Identification and Expression Profiling of Germin-Like Proteins Reveal Their Role in Regulating Abiotic Stress Response in Potato. <i>Frontiers in Plant Science</i> , 2021, 12, 831140.	3.6	9
5986	Genome-Wide Identification, Characterization and Expression Analysis of Lipoxygenase Gene Family in <i>Artemisia annua</i> L.. <i>Plants</i> , 2022, 11, 655.	3.5	6
5987	Time-resolved and multi-tissue RNAseq provides new insights on the immune responses of European eels following infection with <i>Aeromonas hydrophila</i> . , 2022, 1, 100003.		3
5988	Analysis of global <i>Aeromonas veronii</i> genomes provides novel information on source of infection and virulence in human gastrointestinal diseases. <i>BMC Genomics</i> , 2022, 23, 166.	2.8	15
5989	Hydroxyl Radical Overproduction in the Envelope: an Achilles'™ Heel in Peptidoglycan Synthesis. <i>Microbiology Spectrum</i> , 2022, 10, e0120321.	3.0	3
5990	Genome-wide analysis of sucrose synthase family in soybean and their expression in response to abiotic stress and seed development. <i>PLoS ONE</i> , 2022, 17, e0264269.	2.5	2
5991	Discovery of ultrafast myosin, its amino acid sequence, and structural features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
5992	Transcriptomics Analysis of Wheat Tassel Response to <i>Tilletia laevis</i> ¼hn, Which Causes Common Bunt of Wheat. <i>Frontiers in Plant Science</i> , 2022, 13, 823907.	3.6	4
5993	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. <i>ELife</i> , 2022, 11, .	6.0	43
5994	Identification and regulatory network analysis of SPL family transcription factors in <i>Populus euphratica</i> Oliv. heteromorphic leaves. <i>Scientific Reports</i> , 2022, 12, 2856.	3.3	7
5995	Transcriptome analysis reveals the potential roles of long non-coding RNAs in feed efficiency of chicken. <i>Scientific Reports</i> , 2022, 12, 2558.	3.3	6
5996	Genome-Wide Analyses of Aspartic Proteases on Potato Genome (<i>Solanum tuberosum</i>): Generating New Tools to Improve the Resistance of Plants to Abiotic Stress. <i>Plants</i> , 2022, 11, 544.	3.5	4
5997	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. <i>Horticulture Research</i> , 2022, 9, uhac067.	6.3	12

#	ARTICLE	IF	CITATIONS
5998	Odorant Binding Proteins (OBPs) and Odorant Receptors (ORs) of <i>Anopheles stephensi</i> : Identification and comparative insights. <i>PLoS ONE</i> , 2022, 17, e0265896.	2.5	6
5999	ATGPred-FL: sequence-based prediction of autophagy proteins with feature representation learning. <i>Amino Acids</i> , 2022, 54, 799-809.	2.7	3
6000	DUF1005 Family Identification, Evolution Analysis in Plants, and Primary Root Elongation Regulation of CiDUF1005 From <i>Caragana intermedia</i> . <i>Frontiers in Genetics</i> , 2022, 13, 807293.	2.3	2
6001	Chromosome-Level Genome Assembly for <i>Acer pseudosieboldianum</i> and Highlights to Mechanisms for Leaf Color and Shape Change. <i>Frontiers in Plant Science</i> , 2022, 13, 850054.	3.6	7
6002	Species Persistence with Hybridization in Toad-Headed Lizards Driven by Divergent Selection and Low Recombination. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
6003	Genome-Wide Analysis of Late Embryogenesis Abundant Protein Gene Family in <i>Vigna</i> Species and Expression of VrLEA Encoding Genes in <i>Vigna glabrescens</i> Reveal Its Role in Heat Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 843107.	3.6	9
6004	Genome-Wide Survey and Development of the First Microsatellite Markers Database (AnCorDB) in <i>Anemone coronaria</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3126.	4.1	13
6005	Comparative Transcriptome Profiling Analysis Reveals the Adaptive Molecular Mechanism of Yellow-Green Leaf in <i>Rosa beggeriana</i> "Aurea"™. <i>Frontiers in Plant Science</i> , 2022, 13, 845662.	3.6	5
6006	Diversity and origins of bacterial and archaeal viruses on sinking particles reaching the abyssal ocean. <i>ISME Journal</i> , 2022, 16, 1627-1635.	9.8	18
6007	Partially Resistant Avocado Rootstock Dusa® Shows Prolonged Upregulation of Nucleotide Binding-Leucine Rich Repeat Genes in Response to <i>Phytophthora cinnamomi</i> Infection. <i>Frontiers in Plant Science</i> , 2022, 13, 793644.	3.6	6
6008	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	14.5	34
6009	High diversity in the regulatory region of Shiga toxin encoding bacteriophages. <i>BMC Genomics</i> , 2022, 23, 230.	2.8	8
6010	Genome-wide identification, characterization of expansin gene family of banana and their expression pattern under various stresses. <i>3 Biotech</i> , 2022, 12, 101.	2.2	1
6011	Identification of TIFY gene family in walnut and analysis of its expression under abiotic stresses. <i>BMC Genomics</i> , 2022, 23, 190.	2.8	6
6012	A high-quality reference genome for the fish pathogen <i>Streptococcus iniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
6013	Transcriptome analysis of the bivalve <i>Placuna placenta</i> mantle reveals potential biomineralization-related genes. <i>Scientific Reports</i> , 2022, 12, 4743.	3.3	6
6014	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	3.6	8
6015	The long non-coding RNA LNC_000397 negatively regulates PRRSV replication through induction of interferon-stimulated genes. <i>Virology Journal</i> , 2022, 19, 40.	3.4	7

#	ARTICLE	IF	CITATIONS
6016	In Silico Characterisation of the Late Embryogenesis Abundant (LEA) Protein Families and Their Role in Desiccation Tolerance in <i>Ramonda serbica</i> Panc. International Journal of Molecular Sciences, 2022, 23, 3547.	4.1	11
6017	Snake Venomics: Fundamentals, Recent Updates, and a Look to the Next Decade. Toxins, 2022, 14, 247.	3.4	19
6018	The importance of biofilm formation for cultivation of a Micrarchaeon and its interactions with its Thermoplasmatales host. Nature Communications, 2022, 13, 1735.	12.8	12
6019	The <i>Gastrodia menghaiensis</i> (Orchidaceae) genome provides new insights of orchid mycorrhizal interactions. BMC Plant Biology, 2022, 22, 179.	3.6	13
6020	Hybridization and introgression are prevalent in Southern European <i>Erysimum</i> (Brassicaceae) species. Annals of Botany, 2023, 131, 171-184.	2.9	10
6021	Genome-wide transcriptional profiling and functional analysis reveal miR-330-MAPK15 axis involving in cellular responses to deoxynivalenol exposure. Chemosphere, 2022, 298, 134199.	8.2	3
6022	High-Performance Deep Learning Toolbox for Genome-Scale Prediction of Protein Structure and Function. , 2021, 2021, 46-57.		8
6023	AU-Rich Element RNA Binding Proteins: At the Crossroads of Post-Transcriptional Regulation and Genome Integrity. International Journal of Molecular Sciences, 2022, 23, 96.	4.1	19
6024	Benchmark Evaluation of Protein-Protein Interaction Prediction Algorithms. Molecules, 2022, 27, 41.	3.8	22
6025	Unique roles of vaginal <i>Megasphaera</i> phylotypes in reproductive health. Microbial Genomics, 2021, 7, .	2.0	6
6026	High Molecular Weight Kininogen: A Review of the Structural Literature. International Journal of Molecular Sciences, 2021, 22, 13370.	4.1	15
6027	Phylogenetic Analysis with Prediction of Cofactor or Ligand Binding for <i>Pseudomonas aeruginosa</i> PAS and Cache Domains. Microbiology Spectrum, 2021, 9, e0102621.	3.0	4
6028	Analyses of Lysin-motif Receptor-like Kinase (LysM-RLK) Gene Family in Allotetraploid <i>Brassica napus</i> L. and Its Progenitor Species: An In Silico Study. Cells, 2022, 11, 37.	4.1	8
6029	Molecular Characterization and Functional Localization of a Novel SUMOylation Gene in <i>Oryza sativa</i> . Biology, 2022, 11, 53.	2.8	2
6030	Mutations in PpAGO3 Lead to Enhanced Virulence of <i>Phytophthora parasitica</i> by Activation of 25â€“26â€“ont sRNA-Associated Effector Genes. Frontiers in Microbiology, 2022, 13, 856106.	3.5	0
6031	Integrated Analysis of the ceRNA Network and M-7474 Function in Testosterone-Mediated Fat Deposition in Pigs. Genes, 2022, 13, 668.	2.4	2
6032	Identification and Characterization of the MIKC-Type MADS-Box Gene Family in <i>Brassica napus</i> and Its Role in Floral Transition. International Journal of Molecular Sciences, 2022, 23, 4289.	4.1	9
6033	Genome-Wide Screening of Transposable Elements in the Whitefly, <i>Bemisia tabaci</i> (Hemiptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 396.	2.2	5

#	ARTICLE	IF	CITATIONS
6034	R gene triplication confers European fodder turnip with improved clubroot resistance. <i>Plant Biotechnology Journal</i> , 2022, 20, 1502-1517.	8.3	15
6035	A chromosome-level genome assembly of chia provides insights into high omega-3 content and coat color variation of its seeds. <i>Plant Communications</i> , 2022, 3, 100326.	7.7	14
6036	Systematic identification and characterization of long noncoding RNAs (lncRNAs) during <i>Aedes albopictus</i> development. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010245.	3.0	6
6037	Cisplatin resistance-related multi-omics differences and the establishment of machine learning models. <i>Journal of Translational Medicine</i> , 2022, 20, 171.	4.4	18
6038	The Importance of Weakly Co-Evolving Residue Networks in Proteins is Revealed by Visual Analytics. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	2
6039	Simple, efficient and thorough shotgun proteomic analysis with PatternLab V. <i>Nature Protocols</i> , 2022, 17, 1553-1578.	12.0	26
6040	Genome-wide analysis and functional characterization of CHYR gene family associated with abiotic stress tolerance in bread wheat (<i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2022, 22, 204.	3.6	8
6041	Lentil allergens identification and quantification: An update from omics perspective. <i>Food Chemistry Molecular Sciences</i> , 2022, 4, 100109.	2.1	3
6097	Fungal genome resources at NCBI. <i>Mycology</i> , 2011, 2, 142-160.	4.4	4
6098	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. <i>Environmental Microbiomes</i> , 2022, 17, 19.	5.0	6
6100	Integrative visual analysis of the effects of alternative splicing on protein domain interaction networks. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.5	2
6101	Noise tolerance of multiple classifier systems in data integration-based gene function prediction. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.5	1
6102	Predicting protein distance maps according to physicochemical properties. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 181.	1.5	3
6103	A hierarchical approach to protein fold prediction. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 185.	1.5	4
6104	Efficient mapping of genomic sequences to optimize multiple pairwise alignment in hybrid cluster platforms. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 251.	1.5	0
6105	Multi-agent System for Obtaining Relevant Genes in Expression Analysis between Young and Older Women with Triple Negative Breast Cancer. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 278.	1.5	2
6107	PpePL1 and PpePL15 Are the Core Members of the Pectate Lyase Gene Family Involved in Peach Fruit Ripening and Softening. <i>Frontiers in Plant Science</i> , 2022, 13, 844055.	3.6	9
6108	Advances in phylogenomics. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2014, 36, 669-78.	0.2	0

#	ARTICLE	IF	CITATIONS
6109	RBP-TSTL is a two-stage transfer learning framework for genome-scale prediction of RNA-binding proteins. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	6
6110	Evaluating hierarchical machine learning approaches to classify biological databases. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
6111	Human Protein-<scp>l</scp>-isoaspartate <i>O</i>-Methyltransferase Domain-Containing Protein 1 (PCMTD1) Associates with Cullin-RING Ligase Proteins. <i>Biochemistry</i> , 2022, 61, 879-894.	2.5	2
6112	Transcriptome annotation reveals minimal immunogenetic diversity among Wyoming toads, <i>Anaxyrus baxteri</i> . <i>Conservation Genetics</i> , 2022, 23, 669-681.	1.5	2
6113	Functional dissection of human mitotic genes using CRISPRâ€Cas9 tiling screens. <i>Genes and Development</i> , 2022, 36, 495-510.	5.9	2
6114	Thyroid Transcriptomic Profiling Reveals the Follicular Phase Differential Regulation of lncRNA and mRNA Related to Prolificacy in Small Tail Han Sheep with Two FecB Genotypes. <i>Genes</i> , 2022, 13, 849.	2.4	4
6115	Reaching alignment-profile-based accuracy in predicting protein secondary and tertiary structural properties without alignment. <i>Scientific Reports</i> , 2022, 12, 7607.	3.3	14
6116	Analysis of the Î²-Glucosidase Family Reveals Genes Involved in the Lignification of Stone Cells in Chinese White Pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	2
6117	Whole-Transcriptome Analysis Reveals Long Noncoding RNAs Involved in Female Floral Development of Hickory (<i>Carya cathayensis</i> Sarg.). <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	2
6118	Combined GWAS and Transcriptome Analyses Provide New Insights Into the Response Mechanisms of Sunflower Against Drought Stress. <i>Frontiers in Plant Science</i> , 2022, 13, 847435.	3.6	14
6119	Engineering processive cellulase of <i>Clostridium thermocellum</i> to divulge the role of the carbohydrateâ€binding module. <i>Biotechnology and Applied Biochemistry</i> , 2023, 70, 290-305.	3.1	2
6120	Evaluation of the Major Seed Storage Proteins, the Conglutins, Across Genetically Diverse Narrow-Leafed Lupin Varieties. <i>Frontiers in Nutrition</i> , 2022, 9, .	3.7	4
6121	Synergistic Effects of Bacteriophage vB_Eco4-M7 and Selected Antibiotics on the Biofilm Formed by Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Antibiotics</i> , 2022, 11, 712.	3.7	8
6122	HDACs Gene Family Analysis of Eight Rosaceae Genomes Reveals the Genomic Marker of Cold Stress in <i>Prunus mume</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 5957.	4.1	7
6123	Transcriptomic Analysis of Trigeminal Ganglion and Spinal Trigeminal Nucleus Caudalis in Mice with Inflammatory Temporomandibular Joint Pain. <i>Journal of Pain Research</i> , 0, Volume 15, 1487-1502.	2.0	2
6124	Genome Assembly and Evolutionary Analysis of the Mandarin Duck <i>Aix galericulata</i> Reveal Strong Genome Conservation among Ducks. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	1
6125	Heterologous Expression of a Thermostable Î±-Galactosidase from <i>Parageobacillus thermoglucosidasius</i> Isolated from the Lignocellulolytic Microbial Consortium TMC7. <i>Journal of Microbiology and Biotechnology</i> , 2022, , .	2.1	2
6126	A tensor-based bi-random walks model for protein function prediction. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	4

#	ARTICLE	IF	CITATIONS
6127	<i>mebipred</i> : identifying metal-binding potential in protein sequence. <i>Bioinformatics</i> , 2022, 38, 3532-3540.	4.1	15
6128	Polyloid giant cancer cells are dependent on cholesterol for progeny formation through amitotic division. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
6129	Plasmodium manipulates the expression of host long non-coding RNA during red blood cell intracellular infection. <i>Parasites and Vectors</i> , 2022, 15, .	2.5	8
6130	Catching a Walker in the ActDNA Partitioning by ParA Family of Proteins. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	8
6131	Genome-Wide Identification and Expression Pattern Analysis of KNOX Gene Family in Orchidaceae. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	12
6132	Prediction of Plant Resistance Proteins Based on Pairwise Energy Content and Stacking Framework. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
6133	Comparative Transcriptomics and Metabolites Analysis of Two Closely Related Euphorbia Species Reveal Environmental Adaptation Mechanism and Active Ingredients Difference. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	5
6134	Antioxidant potential of <i>Pediococcus pentosaceus</i> strains from the sow milk bacterial collection in weaned piglets. <i>Microbiome</i> , 2022, 10, .	11.1	16
6135	High-throughput analysis of lncRNA in cows with naturally infected <i>Staphylococcus aureus</i> mammary gland. <i>Animal Biotechnology</i> , 0, , 1-9.	1.5	0
6136	The chromosome-level genome for <i>Toxicodendron vernicifluum</i> provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. <i>IScience</i> , 2022, 25, 104512.	4.1	6
6137	<i>Trypanosoma cruzi</i> iron superoxide dismutases: insights from phylogenetics to chemotherapeutic target assessment. <i>Parasites and Vectors</i> , 2022, 15, .	2.5	2
6138	A consensus view of the proteome of the last universal common ancestor. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	10
6146	The landscape of isoform switches in sepsis: a multicenter cohort study. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
6147	Analysis of the <i>Arabidopsis</i> <i>coilin</i> mutant reveals a positive role of AtCOILIN in plant immunity. <i>Plant Physiology</i> , 2022, 190, 745-761.	4.8	6
6148	Development of a High Oleic Cardoon Cell Culture Platform by SAD Overexpression and RNAi-Mediated FAD2.2 Silencing. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
6149	The evolution of multi-gene families and metabolic pathways in the evening primroses (<i>Oenothera</i>): Tj ETQq1 1 0.784314 rgBT /Overl	2.5	3
6150	N-Methyltransferase CaASHH3 Acts as a Positive Regulator of Immunity against Bacterial Pathogens in Pepper. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6492.	4.1	3
6151	Genome-Wide Characterization of Superoxide Dismutase (SOD) Genes in <i>Daucus carota</i> : Novel Insights Into Structure, Expression, and Binding Interaction With Hydrogen Peroxide (H2O2) Under Abiotic Stress Condition. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	13

#	ARTICLE	IF	CITATIONS
6152	Combined transcriptome and metabolome analysis of <i>Nerium indicum</i> L. elaborates the key pathways that are activated in response to witches' broom disease. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	5
6153	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	7.8	26
6154	Exploring the SiCCT Gene Family and Its Role in Heading Date in Foxtail Millet. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	0
6155	Transcriptional Basis for Haustorium Formation and Host Establishment in Hemiparasitic <i>Psittacanthus schiedeanus</i> Mistletoes. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	4
6156	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.	8.3	74
6157	Genome-Wide Study of Hsp90 Gene Family in Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.) and Their Imperative Roles in Response to Cold Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	6
6158	Systematic Analysis of NB-ARC Gene Family in Rice and Functional Characterization of GNP12. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	3
6159	Effects of turning over intensity on fatty acid metabolites in postharvest leaves of Tieguanyin oolong tea (<i>Camellia sinensis</i>). <i>PeerJ</i> , 0, 10, e13453.	2.0	6
6160	New Mutations in <i>cls</i> Lead to Daptomycin Resistance in a Clinical Vancomycin- and Daptomycin-Resistant <i>Enterococcus faecium</i> Strain. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	4
6161	The Long Read Transcriptome of Rice (<i>Oryza sativa</i> ssp. <i>japonica</i> var. <i>Nipponbare</i>) Reveals Novel Transcripts. <i>Rice</i> , 2022, 15, .	4.0	2
6162	Exploration of the Mechanisms of Differential Indole Alkaloid Biosynthesis in Dedifferentiated and Cambial Meristematic Cells of <i>Catharanthus roseus</i> Using Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
6163	Comparative physiology and transcriptome analysis reveals that chloroplast development influences silver-white leaf color formation in <i>Hydrangea macrophylla</i> var. <i>maculata</i> . <i>BMC Plant Biology</i> , 2022, 22, .	3.6	1
6164	Deciphering polymorphism in 61,157 <i>Escherichia coli</i> genomes via epistatic sequence landscapes. <i>Nature Communications</i> , 2022, 13, .	12.8	6
6165	Oligomeric interactions maintain active-site structure in a noncooperative enzyme family. <i>EMBO Journal</i> , 2022, 41, .	7.8	10
6166	Genome wide and evolutionary analysis of heat shock protein 70 proteins in tomato and their role in response to heat and drought stress. <i>Molecular Biology Reports</i> , 2022, 49, 11229-11241.	2.3	3
6167	Chromosome-Level Genome Assembly and Transcriptome Comparison Analysis of <i>Cephalopholis sonnerati</i> and Its Related Grouper Species. <i>Biology</i> , 2022, 11, 1053.	2.8	4
6168	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. <i>Nature Communications</i> , 2022, 13, .	12.8	17
6170	The clove (<i>Syzygium aromaticum</i>) genome provides insights into the eugenol biosynthesis pathway. <i>Communications Biology</i> , 2022, 5, .	4.4	6

#	ARTICLE	IF	CITATIONS
6171	Transcriptome comparison for identification of pigmentation-related genes in different color varieties of Siamese fighting fish <i>Betta splendens</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, , 101014.	1.0	1
6172	Chromosome-level assembly and analysis of the <i>Thymus</i> genome provide insights into glandular secretory trichome formation and monoterpenoid biosynthesis in thyme. <i>Plant Communications</i> , 2022, 3, 100413.	7.7	20
6173	Conserved and lineage-specific hypothetical proteins may have played a central role in the rise and diversification of major archaeal groups. <i>BMC Biology</i> , 2022, 20, .	3.8	4
6174	Transcriptome and Metabolome Analyses of <i>Codonopsis convolvulacea</i> Kurz Tuber, Stem, and Leaf Reveal the Presence of Important Metabolites and Key Pathways Controlling Their Biosynthesis. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
6175	Investigation of rumen long noncoding RNA before and after weaning in cattle. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
6176	Transcriptome analysis revealed the roles of long non-coding RNA and mRNA in the bursa of Fabricius during pigeon (<i>Columba livia</i>) development. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	3
6178	ArsR Family Regulator MSMEG_6762 Mediates the Programmed Cell Death by Regulating the Expression of HNH Nuclease in <i>Mycobacteria</i> . <i>Microorganisms</i> , 2022, 10, 1535.	3.6	1
6179	The Genome of the Mimosoid Legume <i>Prosopis cineraria</i> , a Desert Tree. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8503.	4.1	5
6180	Comparative Transcriptome Analysis Reveals Gene Expression Differences in Eggplant (<i>Solanum</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	4.3	3
6181	Identification and Analysis of Long Non-Coding RNAs Related to UV-B-Induced Anthocyanin Biosynthesis During Blood-Fleshed Peach (<i>Prunus persica</i>) Ripening. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
6182	Expression plasticity regulates intraspecific variation in the acclimatization potential of a reef-building coral. <i>Nature Communications</i> , 2022, 13, .	12.8	10
6183	The gill transcriptome of threatened European freshwater mussels. <i>Scientific Data</i> , 2022, 9, .	5.3	10
6184	Genomic analysis reveals the role of integrative and conjugative elements in plant pathogenic bacteria. <i>Mobile DNA</i> , 2022, 13, .	3.6	6
6185	Characterizing isoform switching events in esophageal adenocarcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 29, 749-768.	5.1	5
6186	Possible Contribution of Alternative Transcript Isoforms in Mature Biofilm Growth Phase of <i>Candida glabrata</i> . <i>Indian Journal of Microbiology</i> , 2022, 62, 583-601.	2.7	1
6187	Analysis of Protein Sequence Identity, Binding Sites, and 3D Structures Identifies Eight Pollen Species and Ten Fruit Species with High Risk of Cross-Reactive Allergies. <i>Genes</i> , 2022, 13, 1464.	2.4	1
6188	Structural and Functional Annotation and Molecular Docking Analysis of a Hypothetical Protein from <i>Neisseria gonorrhoeae</i> : An In-Silico Approach. <i>BioMed Research International</i> , 2022, 2022, 1-12.	1.9	6
6189	Delineating specific regions of N- terminal domain of T3SS ATPase YsaN of <i>Yersinia enterocolitica</i> governing its different oligomerization states. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	0

#	ARTICLE	IF	CITATIONS
6191	Genome sequencing and comparative analysis of <i>Ficus benghalensis</i> and <i>Ficus religiosa</i> species reveal evolutionary mechanisms of longevity. <i>IScience</i> , 2022, 25, 105100.	4.1	12
6192	Identification of a novel fusion Iduronidase with improved activity in the cardiovascular system. <i>Molecular Genetics and Metabolism Reports</i> , 2022, 33, 100917.	1.1	0
6193	A Fast Heuristic Search Algorithm for Finding the Longest Common Subsequence of Multiple Strings. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2010, 24, 1287-1292.	4.9	15
6194	Network metrics, structural dynamics and density functional theory calculations identified a novel Ursodeoxycholic Acid derivative against therapeutic target Parkin for Parkinson's disease. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4271-4287.	4.1	18
6195	Proteomic and Transcriptomic Analyses in the Slipper Snail <i>Crepidula fornicata</i> Uncover Shell Matrix Genes Expressed During Adult and Larval Biomineralization. <i>Integrative Organismal Biology</i> , 2022, 4, .	1.8	3
6196	Identification of candidate sex-specific genomic regions in male and female Asian arowana genomes. <i>GigaScience</i> , 2022, 11, .	6.4	0
6197	Genome wide analysis of BnAPs gene family in <i>Brassica napus</i> . <i>Acta Agronomica Sinica</i> (China), 2022, 48, 597-607.	0.3	1
6198	How to Completely Squeeze a Fungus"Advanced Genome Mining Tools for Novel Bioactive Substances. <i>Pharmaceutics</i> , 2022, 14, 1837.	4.5	9
6199	Identification of Novel Multi-Omics Expression Landscapes and Meta-Analysis of Landscape-Based Competitive Endogenous RNA Networks in ALDH+ Lung Adenocarcinoma Stem Cells. <i>BioMed Research International</i> , 2022, 2022, 1-20.	1.9	1
6200	Transcriptomic Analysis of Radish (<i>Raphanus sativus</i> L.) Roots with CLE41 Overexpression. <i>Plants</i> , 2022, 11, 2163.	3.5	4
6201	Genome-Wide Identification and Characterization of Heat Shock Protein 20 Genes in Maize. <i>Life</i> , 2022, 12, 1397.	2.4	3
6202	A Plasmid Carrying bla _{IMP-56} in <i>Pseudomonas aeruginosa</i> Belonging to a Novel Resistance Plasmid Family. <i>Microorganisms</i> , 2022, 10, 1863.	3.6	3
6203	Microbial cytosine deaminase is a programmable anticancer prodrug mediating enzyme: antibody, and gene directed enzyme prodrug therapy. <i>Heliyon</i> , 2022, 8, e10660.	3.2	5
6204	Development of de-novo transcriptome assembly and SSRs in allohexaploid Brassica with functional annotations and identification of heat-shock proteins for thermotolerance. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	2
6205	Characterization of a metagenome-derived thermostable xylanase from Tengchong hot spring. <i>Biomass Conversion and Biorefinery</i> , 0, , .	4.6	2
6206	Genome-wide identification of AOX family genes in Moso bamboo and functional analysis of PeAOX1b_2 in drought and salinity stress tolerance. <i>Plant Cell Reports</i> , 2022, 41, 2321-2339.	5.6	5
6207	Disease resistance in coral is mediated by distinct adaptive and plastic gene expression profiles. <i>Science Advances</i> , 2022, 8, .	10.3	8
6208	Genome-wide identification of the ZIP gene family in lettuce (<i>Lactuca sativa</i> L.) and expression analysis under different element stress. <i>PLoS ONE</i> , 2022, 17, e0274319.	2.5	5

#	ARTICLE	IF	CITATIONS
6209	Enzymatic properties and biological activity of resuscitation-promoting factor B of <i>Rhodococcus</i> sp. (GX12401). <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
6210	Transcriptional regulation underlying the temperature response of embryonic development rate in the winter moth. <i>Molecular Ecology</i> , 0, , .	3.9	2
6211	Different skeletal protein toolkits achieve similar structure and performance in the tropical coral <i>Stylophora pistillata</i> and the temperate <i>Oculina patagonica</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	2
6212	Application of virus-induced gene silencing in <i>Pogostemon cablin</i> advances our understanding of patchoulol and sesquiterpene metabolism. <i>Journal of Horticultural Science and Biotechnology</i> , 2023, 98, 322-333.	1.9	1
6213	Genome-Wide Investigation and Expression Analysis of the <i>Nitraria sibirica</i> Pall. CIPK Gene Family. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11599.	4.1	3
6214	Comparative transcriptomic analysis of normal and abnormal in vitro flowers in <i>Cymbidium nanulum</i> Y. S. Wu et S. C. Chen identifies differentially expressed genes and candidate genes involved in flower formation. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
6215	Investigating NAC Transcription Factor Role in Redox Homeostasis in <i>Solanum lycopersicum</i> L.: Bioinformatics, Physiological and Expression Analysis under Drought Stress. <i>Plants</i> , 2022, 11, 2930.	3.5	1
6216	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, .	3.8	15
6218	Expansion and Neofunctionalization of Actinoporin-like Genes in Mediterranean Mussel (<i>Mytilus</i>) Tj ETQq0 0 0 rgBT /Overlck 10 Tf 5	2.5	1
6219	Antibacterial T6SS effectors with a VRR-Nuc domain are structure-specific nucleases. <i>ELife</i> , 0, 11, .	6.0	10
6220	mTOR Contributes to the Proteome Diversity through Transcriptome-Wide Alternative Splicing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12416.	4.1	2
6221	Genome-Wide Identification and Characterization of YUCCA Gene Family in <i>Mikania micrantha</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13037.	4.1	4
6222	ROS generated from biotic stress: Effects on plants and alleviation by endophytic microbes. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	44
6223	The Chromosome-level genome of <i>Aesculus wilsonii</i> provides new insights into terpenoid biosynthesis and <i>Aesculus</i> evolution. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	1
6224	In silico functional annotation of hypothetical proteins from the <i>Bacillus paralicheniformis</i> strain Bac84 reveals proteins with biotechnological potentials and adaptational functions to extreme environments. <i>PLoS ONE</i> , 2022, 17, e0276085.	2.5	5
6225	Computational Methods and Deep Learning for Elucidating Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2023, , 285-323.	0.9	1
6226	De Novo Transcriptome Dataset Generation of the Swamp Buffalo Brain and Non-Brain Tissues. <i>BioMed Research International</i> , 2022, 2022, 1-15.	1.9	1
6227	Nutrient regulation of lipochitooligosaccharide recognition in plants via NSP1 and NSP2. <i>Nature Communications</i> , 2022, 13, .	12.8	18

#	ARTICLE	IF	CITATIONS
6228	Transcriptome analysis reveals the proline metabolic pathway and its potential regulation TF-hub genes in salt-stressed potato. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	4
6229	Shared Patterns of Gene Expression and Protein Evolution Associated with Adaptation to Desert Environments in Rodents. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
6230	Ribovirus classification by a polymerase barcode sequence. <i>PeerJ</i> , 0, 10, e14055.	2.0	20
6231	Integrated analysis of the whole transcriptome of skeletal muscle reveals the ceRNA regulatory network related to the formation of muscle fibers in Tan sheep. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	4
6232	A comprehensive Bioconductor ecosystem for the design of CRISPR guide RNAs across nucleases and technologies. <i>Nature Communications</i> , 2022, 13, .	12.8	10
6233	Gene Expression in the Developing Seed of Wild and Domesticated Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13351.	4.1	3
6234	Genomic insights into phage-host interaction in the deep-sea chemolithoautotrophic <i>Campylobacterota</i> , <i>Nitratiruptor</i> . <i>ISME Communications</i> , 2022, 2, .	4.2	1
6235	Transcriptome and Regional Association Analyses Reveal the Effects of Oleosin Genes on the Accumulation of Oil Content in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 3140.	3.5	5
6236	Vetinformatics from functional genomics to drug discovery: Insights into decoding complex molecular mechanisms of livestock systems in veterinary science. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	7
6237	Combined Transcriptome and Metabolome Profiling Provide Insights into Cold Responses in Rapeseed (<i>Brassica napus</i> L.) Genotypes with Contrasting Cold-Stress Sensitivity. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13546.	4.1	5
6238	Nearest neighbor search on embeddings rapidly identifies distant protein relations. <i>Frontiers in Bioinformatics</i> , 0, 2, .	2.1	13
6239	CRISPR-Cas9 Technology for the Creation of Biological Avatars Capable of Modeling and Treating Pathologies: From Discovery to the Latest Improvements. <i>Cells</i> , 2022, 11, 3615.	4.1	4
6240	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. <i>Communications Biology</i> , 2022, 5, .	4.4	3
6241	Identification of CAMTA Gene Family in <i>Heimia myrtifolia</i> and Expression Analysis under Drought Stress. <i>Plants</i> , 2022, 11, 3031.	3.5	1
6242	Revealing the Regulatory Mechanism of lncRNA-LMEP on Melanin Deposition Based on High-Throughput Sequencing in Xichuan Chicken Skin. <i>Genes</i> , 2022, 13, 2143.	2.4	4
6243	Reconstructing horizontal gene flow network to understand prokaryotic evolution. <i>Open Biology</i> , 2022, 12, .	3.6	2
6244	Rice TCD8 Encoding a Multi-Domain GTPase Is Crucial for Chloroplast Development of Early Leaf Stage at Low Temperatures. <i>Biology</i> , 2022, 11, 1738.	2.8	0
6245	Discovery, Structure, and Mechanism of a Class II Sesquiterpene Cyclase. <i>Journal of the American Chemical Society</i> , 2022, 144, 22067-22074.	13.7	15

#	ARTICLE	IF	CITATIONS
6246	Insights on variant analysis in silico tools for pathogenicity prediction. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	17
6247	Investigating isoform switching in <i>RHBDF2</i> and its role in neoplastic growth in breast cancer. <i>PeerJ</i> , 0, 10, e14124.	2.0	1
6248	Mining key genes related to root morphogenesis through genome-wide identification and expression analysis of RR gene family in citrus. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6249	Approaches for the Identification of Intrinsically Disordered Protein Domains. <i>Methods in Molecular Biology</i> , 2023, , 403-412.	0.9	0
6250	Genome-wide identification and expression analysis of the SPL transcription factor family and its response to abiotic stress in Quinoa (<i>Chenopodium quinoa</i>). <i>BMC Genomics</i> , 2022, 23, .	2.8	11
6251	A common transcriptional mechanism involving R-loop and RNA abasic site regulates an enhancer RNA of <i>APOE</i> . <i>Nucleic Acids Research</i> , 2022, 50, 12497-12514.	14.5	9
6252	The nuclear factor of activated T cells 5 (NFAT5) contributes to the renal corticomedullary differences in gene expression. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
6253	Analysis of mRNA and lncRNA Expression Profiles of Breast Muscle during Pigeon (<i>Columba livia</i>) Development. <i>Genes</i> , 2022, 13, 2314.	2.4	1
6254	Unsupervised Machine Learning Organization of the Functional Dark Proteome of Gram-Negative "Superbugs": Six Protein Clusters Amenable for Distinct Scientific Applications. <i>ACS Omega</i> , 2022, 7, 46131-46145.	3.5	0
6255	Metagenomics and metatranscriptomics reveal broadly distributed, active, novel methanotrophs in the Gulf of Mexico hypoxic zone and in the marine water column. <i>FEMS Microbiology Ecology</i> , 2023, 99, .	2.7	5
6256	A shotgun approach to explore the bacterial diversity and a brief insight into the glycoside hydrolases of Samiti lake located in the Eastern Himalayas. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 162.	3.3	1
6257	How to survive in the world's third poplar: Insights from the genome of the highest altitude woody plant, <i>Hippophae tibetana</i> (Elaeagnaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6258	Population diversity analyses provide insights into key horticultural traits of Chinese native thymes. <i>Horticulture Research</i> , 2023, 10, .	6.3	2
6259	Transcriptome-wide identification of WRKY transcription factors and their expression profiles under different stress in <i>Cynanchum thesioides</i> . <i>PeerJ</i> , 0, 10, e14436.	2.0	3
6260	Characterization and genomic analysis of a novel halovirus infecting <i>Chromohalobacter beijerinckii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
6261	Differentially expressed long noncoding RNAs in RAW264.7 macrophages during <i>Brucella</i> infection and functional analysis on the bacterial intracellular replication. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
6262	Identification of hub genes associated with follicle development in multiple births sheep by WGCNA. <i>Frontiers in Veterinary Science</i> , 0, 9, .	2.2	3
6263	Draft genome sequencing and secretome profiling of <i>Sclerotinia sclerotiorum</i> revealed effector repertoire diversity and allied broad-host range necrotrophy. <i>Scientific Reports</i> , 2022, 12, .	3.3	8

#	ARTICLE	IF	CITATIONS
6264	Looking for the mechanism of arsenate respiration of <i>Fusibacter</i> sp. strain 3D3, independent of ArrAB. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	2
6265	Multi-locus genome-wide association studies reveal genomic regions and putative candidate genes associated with leaf spot diseases in African groundnut (<i>Arachis hypogaea</i> L.) germplasm. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	2
6266	RNA-Seq and genetic diversity analysis of faba bean (<i>Vicia faba</i> L.) varieties in China. <i>PeerJ</i> , 0, 11, e14259.	2.0	0
6267	Connecting genomic islands across prokaryotic and phage genomes via protein families. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
6268	Genomic Structure, Protein Character, Phylogenic Implication, and Embryonic Expression Pattern of a Zebrafish New Member of Zinc Finger BED-Type Gene Family. <i>Genes</i> , 2023, 14, 179.	2.4	2
6269	Overexpression of a DUF740 family gene (LOC_Os04g59420) imparts enhanced climate resilience through multiple stress tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
6270	CRISPR/Cas9-targeted mutagenesis of <i>TaDCL4</i> , <i>TaDCL5</i> and <i>TaRDR6</i> induces male sterility in common wheat. <i>Plant Biotechnology Journal</i> , 2023, 21, 839-853.	8.3	10
6271	Genome-wide characterization of <i>Ficus carica</i> MADS-box transcription factors with a focus on their roles during fruit development. <i>Horticulture Environment and Biotechnology</i> , 0, , .	2.1	0
6272	<i>coth</i> Genes Are Necessary for Normal Spore Formation and Virulence in <i>Mucor lusitanicus</i> . <i>MBio</i> , 2023, 14, .	4.1	10
6273	Identification and expression of the CCO family during development, ripening and stress response in banana. <i>Genetica</i> , 0, , .	1.1	0
6274	Genome-wide identification and expression analysis of two-component system genes in sweet potato (<i>Ipomoea batatas</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
6275	Comprehensive Analysis of Whole-Transcriptome Profiles in Response to Acute Hypersaline Challenge in Chinese Razor Clam <i>Sinonovacula constricta</i> . <i>Biology</i> , 2023, 12, 106.	2.8	5
6276	Comparative genome analysis reveals high-level drug resistance markers in a clinical isolate of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> MF GZ001. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	1
6277	High-quality genome sequence reveals a young polyploidization and provides insights into cellulose and lignin biosynthesis in water dropwort (<i>Oenanthe sinensis</i>). <i>Industrial Crops and Products</i> , 2023, 193, 116203.	5.2	7
6278	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.	8.3	19
6279	Phylogenetic, Structural and Functional Evolution of the LHC Gene Family in Plant Species. <i>International Journal of Molecular Sciences</i> , 2023, 24, 488.	4.1	2
6280	The inside scoop: Comparative genomics of two intranuclear bacteria, <i>Candidatus Berkiella cookevillensis</i> and <i>Candidatus Berkiella aquae</i> . <i>PLoS ONE</i> , 2022, 17, e0278206.	2.5	0
6282	Genome-Wide Identification, Evolutionary and Functional Analyses of WRKY Family Members in <i>Ginkgo biloba</i> . <i>Genes</i> , 2023, 14, 343.	2.4	5

#	ARTICLE	IF	CITATIONS
6283	Identification and Functional Prediction of Long Non-Coding RNA in Longissimus Dorsi Muscle of Queshan Black and Large White Pigs. <i>Genes</i> , 2023, 14, 197.	2.4	3
6284	Snekmer: a scalable pipeline for protein sequence fingerprinting based on amino acid recoding. <i>Bioinformatics Advances</i> , 2023, 3, .	2.4	1
6285	Toward generalizable prediction of antibody thermostability using machine learning on sequence and structure features. <i>MABs</i> , 2023, 15, .	5.2	6
6286	The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3580.	4.1	1
6287	Rational Design of Profile HMMs for Sensitive and Specific Sequence Detection with Case Studies Applied to Viruses, Bacteriophages, and Casposons. <i>Viruses</i> , 2023, 15, 519.	3.3	1
6288	Genome-wide identification of the geranylgeranyl pyrophosphate synthase (GGPS) gene family involved in chlorophyll synthesis in cotton. <i>BMC Genomics</i> , 2023, 24, .	2.8	3
6289	An evolutionarily conserved bimodular domain anchors ZC3HC1 and its yeast homologue Pml39p to the nuclear basket. <i>Molecular Biology of the Cell</i> , 2023, 34, .	2.1	1
6291	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (<i>Juglans nigra</i>). <i>Horticulture Research</i> , 2023, 10, .	6.3	11
6292	Transcriptome sequencing of <i>Cocos nucifera</i> leaves in response to <i>Rhynchophorus ferrugineus</i> infestation. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
6293	Leaves of <i>Moringa oleifera</i> Are Potential Source of Bioactive Compound β -Carotene: Evidence from In Silico and Quantitative Gene Expression Analysis. <i>Molecules</i> , 2023, 28, 1578.	3.8	2
6294	The Bcl-2-associated athanogene gene family in tobacco (<i>Nicotiana tabacum</i>) and the function of NtBAG5 in leaf senescence. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	0
6295	HuCoPIA: An Atlas of Human vs. SARS-CoV-2 Interactome and the Comparative Analysis with Other Coronaviridae Family Viruses. <i>Viruses</i> , 2023, 15, 492.	3.3	1
6296	Distinguishing features of fold-switching proteins. <i>Protein Science</i> , 2023, 32, .	7.6	8
6297	Identification and Comparative Expression Profiles of Candidate Olfactory Receptors in the Transcriptomes of the Important Egg Parasitoid Wasp <i>Anastatus japonicus</i> Ashmead (Hymenoptera: Tj ETQq1 1 0.784314 r gBT /Overlo	3.3	0
6298	Insights into the Bioinformatics and Transcriptional Analysis of the Elongator Complexes (ELPs) Gene Family of Wheat: TaELPs Contribute to Wheat Abiotic Stress Tolerance and Leaf Senescence. <i>Plants</i> , 2023, 12, 952.	3.5	0
6299	Genome Size Changes by Duplication, Divergence, and Insertion in <i>Caenorhabditis</i> Worms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
6300	Genome-Wide Analysis of SIMILAR TO RCD ONE (SRO) Family Revealed Their Roles in Abiotic Stress in Poplar. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4146.	4.1	5
6301	Unraveling the Diverse Roles of Neglected Genes Containing Domains of Unknown Function (DUFs): Progress and Perspective. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4187.	4.1	8

#	ARTICLE	IF	CITATIONS
6302	Genome-Wide Identification, Classification, and Expression Analyses of the CsDGAT Gene Family in <i>Cannabis sativa</i> L. and Their Response to Cold Treatment. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4078.	4.1	1
6303	Functional Protein Dynamics Directly from Sequences. <i>Journal of Physical Chemistry B</i> , 2023, 127, 1914-1921.	2.6	5
6304	Genome-Wide Identification, Characterization and Experimental Expression Analysis of CNGC Gene Family in <i>Gossypium</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4617.	4.1	0
6305	Whole-genome sequencing and phylogenomic analyses of a novel zearalenone-degrading <i>Bacillus subtilis</i> B72. <i>3 Biotech</i> , 2023, 13, .	2.2	1
6306	Data-driven design of orthogonal protein-protein interactions. <i>Science Signaling</i> , 2023, 16, .	3.6	0
6307	Knockdown of Bmp1 and Pls1 Virulence Genes by Exogenous Application of RNAi-Inducing dsRNA in <i>Botrytis cinerea</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 4869.	4.1	1
6308	Metatranscriptomics and metabarcoding reveal spatiotemporal shifts in fungal communities and their activities in Chinese coastal waters. <i>Molecular Ecology</i> , 2023, 32, 2750-2765.	3.9	6
6309	Zinc/iron-regulated transporter-like protein gene family in <i>Theobroma cacao</i> L: Characteristics, evolution, function and 3D structure analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
6310	Transposon-derived transcription factors across metazoans. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	3.7	2
6311	Insights into the mechanisms of triptolide nephrotoxicity through network pharmacology-based analysis and RNA-seq. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	4
6312	Genomic Analysis, Evolution and Characterization of E3 Ubiquitin Protein Ligase (TRIM) Gene Family in Common Carp (<i>Cyprinus carpio</i>). <i>Genes</i> , 2023, 14, 667.	2.4	0
6313	Contrasting Metabolisms in Green and White Leaf Sectors of Variegated <i>Pelargonium zonale</i> —An Integrative Transcriptomic and Metabolomic Study. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5288.	4.1	2
6314	The first chromosome-level <i>Fallopia multiflora</i> genome assembly provides insights into stilbene biosynthesis. <i>Horticulture Research</i> , 2023, 10, .	6.3	1
6315	Whole-genome sequencing reveals putative underlying mechanisms of biocontrol capability of IBFCBF-5. <i>Acta Physiologiae Plantarum</i> , 2023, 45, .	2.1	1
6316	BysR, a LysR-Type Pleiotropic Regulator, Controls Production of Occidiofungin by Activating the LuxR-Type Transcriptional Regulator AmbR1 in <i>Burkholderia</i> sp. Strain JP2-270. <i>Microbiology Spectrum</i> , 2023, 11, .	3.0	0
6317	Parthenocarpy-related genes induced by naphthalene acetic acid in oil palm interspecific O ⁺ × C ⁻ [<i>Elaeis oleifera</i> (Kunth) Cort ⁺ × <i>Elaeis guineensis</i> Jacq.] hybrids. <i>Frontiers in Genetics</i> , 0, 14, .	2.3	0
6318	Functional and structural diversification of incomplete phosphotransferase system in cellulose-degrading clostridia. <i>ISME Journal</i> , 2023, 17, 823-835.	9.8	1
6319	Transcriptomics Reveals the Molecular Basis for Methyl Jasmonate to Promote the Synthesis of Monoterpenoids in <i>Schizonepeta tenuifolia</i> Briq.. <i>Current Issues in Molecular Biology</i> , 2023, 45, 2738-2756.	2.4	1

#	ARTICLE	IF	CITATIONS
6321	<i>Streptomonospora mangrovi</i> sp. nov., isolated from mangrove soil showing similar metabolic capabilities, but distinct secondary metabolites profiles. Archives of Microbiology, 2023, 205, .	2.2	0
6322	Modulation of long noncoding RNA (lncRNA) and messenger RNA (mRNA) expression in the liver of Beagle dogs by <i>Toxocara canis</i> infection. Parasites and Vectors, 2023, 16, .	2.5	1
6323	Novel Transcriptomic Interactomes of Noncoding RNAs in the Heart under Altered Thyroid Hormonal States. International Journal of Molecular Sciences, 2023, 24, 6560.	4.1	1
6324	Antibiotic resistance in <i>Neisseria gonorrhoeae</i> : broad-spectrum drug target identification using subtractive genomics. Genomics and Informatics, 2023, 21, e5.	0.8	1
6325	Molecular evolution, diversification, and expression assessment of MADS gene family in <i>Setaria italica</i> , <i>Setaria viridis</i> , and <i>Panicum virgatum</i> . Plant Cell Reports, 2023, 42, 1003-1024.	5.6	2
6327	Integrated Analysis of Transcriptome Expression Profiles Reveals miRNA-326â€“NKX3.2-Regulated Porcine Chondrocyte Differentiation. International Journal of Molecular Sciences, 2023, 24, 7257.	4.1	1
6328	Surface ID: A Geometry-aware System for Protein Molecular Surface Comparison. Bioinformatics, 0, , .	4.1	0
6329	Novel insights into chloroplast genome evolution in the green macroalgal genus <i>Ulva</i> (Ulvophyceae,) Tj ETQq1 1 0.784314 rgBT /Overlo	3.6	0
6330	Identification of <i>Aspergillus niger</i> Aquaporins Involved in Hydrogen Peroxide Signaling. Journal of Fungi (Basel, Switzerland), 2023, 9, 499.	3.5	3
6331	Integrated analysis of lncRNAs, mRNAs, and TFs to identify network modules underlying diterpenoid biosynthesis in <i>Salvia miltiorrhiza</i> . PeerJ, 0, 11, e15332.	2.0	0
6332	Identification of three capsule depolymerases in a bacteriophage infecting <i>Klebsiella pneumoniae</i> capsular types K7, K20, and K27 and therapeutic application. Journal of Biomedical Science, 2023, 30, .	7.0	4
6333	Mining Cyanobacterial Genomes for Drug-Like and Bioactive Natural Products. , 2012, , 159-197.		0
6338	Genetic and Transcriptional Regulatory Mechanisms of Lipase Activity in the Plant Pathogenic Fungus <i>Fusarium graminearum</i> . Microbiology Spectrum, 2023, 11, .	3.0	5
6339	GH20 and GH84 Î²-N-acetylglucosaminidases with different linkage specificities underpin mucin O-glycan breakdown capability of <i>Bifidobacterium bifidum</i> . Journal of Biological Chemistry, 2023, 299, 104781.	3.4	1
6342	High-quality chromosome-level scaffolds of the plant bug <i>Pachypeltis micranthus</i> provide insights into the availability of <i>Mikania micrantha</i> control. BMC Genomics, 2023, 24, .	2.8	0
6343	High and diurnally fluctuating carbon dioxide exposure produces lower mercury toxicity in a marine copepod. Marine Pollution Bulletin, 2023, 192, 115016.	5.0	0
6344	Transcriptome Screening of Long Noncoding RNAs and Their Target Protein-Coding Genes Unmasks a Dynamic Portrait of Seed Coat Coloration Associated with Anthocyanins in Tibetan Hulless Barley. International Journal of Molecular Sciences, 2023, 24, 10587.	4.1	2
6345	Genome-Wide Identification and Functional Analysis of the TIFY Family Genes in Response to Abiotic Stresses and Hormone Treatments in Tartary Buckwheat (<i>Fagopyrum tataricum</i>). International Journal of Molecular Sciences, 2023, 24, 10916.	4.1	1

#	ARTICLE	IF	CITATIONS
6346	The Transcriptomic Analysis of the Response of <i>Pinus massoniana</i> to Drought Stress and a Functional Study on the ERF1 Transcription Factor. <i>International Journal of Molecular Sciences</i> , 2023, 24, 11103.	4.1	1
6347	Human Factors in Manufacturing: A Systematic Literature Review. <i>Lecture Notes in Computer Science</i> , 2023, , 355-367.	1.3	0
6348	The Pitaya Flower Tissue's Gene Differential Expression Analysis between Self-Incompatible and Self-Compatible Varieties for the Identification of Genes Involved in Self-Incompatibility Regulation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 11406.	4.1	0
6349	SW16-7, a Novel Ackermannviridae Bacteriophage with Highly Effective Lytic Activity Targets <i>Salmonella enterica</i> Serovar Weltevreden. <i>Microorganisms</i> , 2023, 11, 2090.	3.6	1
6350	Antibiotic Resistance Mediated by <i>Escherichia coli</i> in Kuwait Marine Environment as Revealed through Genomic Analysis. <i>Antibiotics</i> , 2023, 12, 1366.	3.7	1
6351	Transcriptomic Analysis of Light-Induced Genes in <i>Nasonia vitripennis</i> : Possible Implications for Circadian Light Entrainment Pathways. <i>Biology</i> , 2023, 12, 1215.	2.8	0
6352	Pangenomic Analysis of Nucleo-Cytoplasmic Large DNA Viruses. I: The Phylogenetic Distribution of Conserved Oxygen-Dependent Enzymes Reveals a Capture-Genome Process. <i>Journal of Molecular Evolution</i> , 2023, 91, 647-668.	1.8	0
6353	Protein remote homology detection and structural alignment using deep learning. <i>Nature Biotechnology</i> , 0, , .	17.5	11
6354	Crystal structure of domain of unknown function 507 (DUF507) reveals a new protein fold. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
6355	Identification of <i>Dioscorea oppositifolia</i> Thunb. CDPK gene family reveals that DoCDPK20 is related to heat resistance. <i>PeerJ</i> , 0, 11, e16110.	2.0	0
6356	Characterization of a GH10 extremely thermophilic xylanase from the metagenome of hot spring for prebiotic production. <i>Scientific Reports</i> , 2023, 13, .	3.3	1
6357	VDR promotes testosterone synthesis in mouse Leydig cells via regulation of cholesterol side chain cleavage cytochrome P450 (Cyp11a1) expression. <i>Genes and Genomics</i> , 2023, 45, 1377-1387.	1.4	1
6358	Characterization of a Thermophilic and Inhibitor-Tolerant GH1 β -Glucosidase Present in a Hot Spring. <i>Water (Switzerland)</i> , 2023, 15, 3389.	2.7	1
6359	Systematic comparison of genome information processing and boundary recognition tools used for genomic island detection. <i>Computers in Biology and Medicine</i> , 2023, 166, 107550.	7.0	1
6360	Comparative analysis of KNOX genes and their expression patterns under various treatments in <i>Dendrobium huoshanense</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	1
6361	The transcriptome profile of the marine Calanoid copepod <i>Parvocalanus crassirostris</i> isolated from Kuwait territorial waters and generations cultured under different ocean acidification scenarios. <i>Regional Studies in Marine Science</i> , 2023, 67, 103231.	0.7	0
6362	Enzyme redesign and genetic code expansion. <i>Protein Engineering, Design and Selection</i> , 0, , .	2.1	1
6363	Genome-Level Investigation of WRKY Transcription Factors and Their Potential Roles in Fruit Peel Ripening and Coloration in the Common Fig (<i>Ficus carica</i> L.). <i>Journal of Plant Growth Regulation</i> , 0, , .	5.1	0

#	ARTICLE	IF	CITATIONS
6364	Unraveling the dataset transcriptomic response of Hydrangea macrophylla stem to mechanical stimulation: De novo assembly and functional annotation. Data in Brief, 2023, 51, 109784.	1.0	0
6366	Engineering serine hydroxymethyltransferases for efficient synthesis of L-serine in Escherichia coli. Bioresource Technology, 2024, 393, 130153.	9.6	1
6367	Polyploid Genome Assembly Provides Insights into Morphological Development and Ascorbic Acid Accumulation of Sauropus androgynus. International Journal of Molecular Sciences, 2024, 25, 300.	4.1	0
6368	Genome-Wide Identification of Trehalose-6-phosphate Synthase (TPS) Gene Family Reveals the Potential Role in Carbohydrate Metabolism in Peach. Genes, 2024, 15, 39.	2.4	0
6369	Verticillium dahliaeÂVdPBP1 Transcription Factor Is Required for Hyphal Growth, Virulence, and Microsclerotia Formation. Microorganisms, 2024, 12, 265.	3.6	0
6370	Genome-wide identification and expression analysis of <i>sucrose phosphate synthase</i> and <i>sucrose-6-phosphate phosphatase</i> family genes in <i>Camellia sinensis</i>. Beverage Plant Research, 2024, 4, 0-0.	1.9	0
6371	Transcriptome analysis of polyploid giant cancer cells and their progeny reveals a functional role for p21 in polyploidization and depolyploidization. Journal of Biological Chemistry, 2024, 300, 107136.	3.4	0
6372	Chromosome-level genome assembly of Platycarya strobilacea. Scientific Data, 2024, 11, .	5.3	0