The Pfam protein families database

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Citation Report

#	Article	IF	Citations
1	Protein Databases on the Internet. Current Protocols in Molecular Biology, 2004, 68, Unit 19.4.	2.9	11
2	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	6.5	6,372
3	Reuse or re-function?. Behavioral and Brain Sciences, 2010, 33, 266-267.	0.4	50
4	From the physical to the psychological: Mundane experiences influence social judgment and interpersonal behavior. Behavioral and Brain Sciences, 2010, 33, 267-268.	0.4	12
5	Neural reuse implies distributed coding. Behavioral and Brain Sciences, 2010, 33, 269-270.	0.4	0
6	The importance of ontogenetic change in typical and atypical development. Behavioral and Brain Sciences, 2010, 33, 271-272.	0.4	3
7	Reuse in the brain and elsewhere. Behavioral and Brain Sciences, 2010, 33, 282-283.	0.4	1
8	Neural reuse as a source of developmental homology. Behavioral and Brain Sciences, 2010, 33, 284-285.	0.4	4
9	Reuse of identified neurons in multiple neural circuits. Behavioral and Brain Sciences, 2010, 33, 285-285.	0.4	15
10	Neural reuse and human individual differences. Behavioral and Brain Sciences, 2010, 33, 287-288.	0.4	0
11	Massive modularity is consistent with most forms of neural reuse. Behavioral and Brain Sciences, 2010, 33, 289-290.	0.4	3
12	More than modularity and metaphor: The power of preadaptation and access. Behavioral and Brain Sciences, 2010, 33, 290-291.	0.4	0
13	Belling the cat: Why reuse theory is not enough. Behavioral and Brain Sciences, 2010, 33, 293-294.	0.4	0
14	Sensorimotor grounding and reused cognitive domains. Behavioral and Brain Sciences, 2010, 33, 270-271.	0.4	0
15	Sleep, neural reuse, and memory consolidation processes. Behavioral and Brain Sciences, 2010, 33, 273-273.	0.4	1
16	Reuse (neural, bodily, and environmental) as a fundamental organizational principle of human cognition. Behavioral and Brain Sciences, 2010, 33, 274-274.	0.4	0
17	Neural reuse: A polysemous and redundant biological system subserving niche-construction. Behavioral and Brain Sciences, 2010, 33, 276-277.	0.4	3
18	The Leabra architecture: Specialization without modularity. Behavioral and Brain Sciences, 2010, 33, 286-287.	0.4	5

#	Article	IF	Citations
19	Reuse of molecules and of neural circuits. Behavioral and Brain Sciences, 2010, 33, 288-289.	0.4	0
20	How and over what timescales does neural reuse actually occur?. Behavioral and Brain Sciences, 2010, 33, 272-273.	0.4	6
21	No bootstrapping without semantic inheritance. Behavioral and Brain Sciences, 2010, 33, 279-280.	0.4	0
22	Implications of neural reuse for brain injury therapy: Historical note on the work of Kurt Goldstein. Behavioral and Brain Sciences, 2010, 33, 281-282.	0.4	1
23	Optical holography as an analogue for a neural reuse mechanism. Behavioral and Brain Sciences, 2010, 33, 291-292.	0.4	1
24	Massive redeployment or distributed modularity?. Behavioral and Brain Sciences, 2010, 33, 292-293.	0.4	0
25	Understanding brain circuits and their dynamics. Behavioral and Brain Sciences, 2010, 33, 274-275.	0.4	2
26	Multi-use and constraints from original use. Behavioral and Brain Sciences, 2010, 33, 277-278.	0.4	9
27	Cortex in context: Response to commentaries on neural reuse. Behavioral and Brain Sciences, 2010, 33, 294-313.	0.4	1
28	Redeployed functions versus spreading activation: A potential confound. Behavioral and Brain Sciences, 2010, 33, 280-281.	0.4	3
29	Let us redeploy attention to sensorimotor experience. Behavioral and Brain Sciences, 2010, 33, 283-284.	0.4	45
30	Evolutionary Dynamics of Complete Campylobacter Pan-Genomes and the Bacterial Species Concept. Genome Biology and Evolution, 2010, 2, 646-655.	1.1	98
31	Neural reuse and cognitive homology. Behavioral and Brain Sciences, 2010, 33, 268-269.	0.4	6
32	Expression of Usherin in the Anthozoan <i>Nematostella vectensis</i>. Biological Bulletin, 2010, 218, 105-112.	0.7	7
33	Rrp47 and the function of the Sas10/C1D domain. Biochemical Society Transactions, 2010, 38, 1088-1092.	1.6	18
34	Comparison of protein phylogeny reconstruction methods using natural protein sequences. Moscow University Biological Sciences Bulletin, 2010, 65, 139-141.	0.1	1
35	Unicellular cyanobacteria with a new mode of life: the lack of photosynthetic oxygen evolution allows nitrogen fixation to proceed. Archives of Microbiology, 2010, 192, 783-790.	1.0	44
36	Comparative Genomics of Marine Mussels (Mytilus spp.) Gender Associated mtDNA: Rapidly Evolving atp8. Journal of Molecular Evolution, 2010, 71, 385-400.	0.8	64

#	ARTICLE	IF	CITATIONS
37	Genomic architecture of MHC-linked odorant receptor gene repertoires among 16 vertebrate species. Immunogenetics, 2010, 62, 569-584.	1.2	22
38	Flocculation protein structure and cellâ€“cell adhesion mechanism in Saccharomyces cerevisiae. Biotechnology Letters, 2010, 32, 1571-1585.	1.1	75
39	Protein annotation in the era of personal genomics. Current Opinion in Structural Biology, 2010, 20, 335-341.	2.6	1
40	From complete genome sequence to â€˜completeâ€™ understanding?. Trends in Biotechnology, 2010, 28, 398-406.	4.9	151
41	Lineage-specific expansion of DNA-binding transcription factor families. Trends in Genetics, 2010, 26, 388-393.	2.9	40
42	Predicting conserved protein motifs with Sub-HMMs. BMC Bioinformatics, 2010, 11, 205.	1.2	9
43	Intrinsically disordered domains deviate significantly from random sequences in mammalian proteins. BMC Bioinformatics, 2010, 11, S7.	1.2	9
44	Phylogenetic analysis of ferlin genes reveals ancient eukaryotic origins. BMC Evolutionary Biology, 2010, 10, 231.	3.2	49
45	Ancient origin of animal U-box ubiquitin ligases. BMC Evolutionary Biology, 2010, 10, 331.	3.2	23
46	Evolution of the Kdo2-lipid A biosynthesis in bacteria. BMC Evolutionary Biology, 2010, 10, 362.	3.2	37
47	Origin and fate of pseudogenes in Hemiascomycetes: a comparative analysis. BMC Genomics, 2010, 11, 260.	1.2	27
48	Proteome-wide survey of phosphorylation patterns affected by nuclear DNA polymorphisms in Arabidopsis thaliana. BMC Genomics, 2010, 11, 411.	1.2	21
49	Orthology confers intron position conservation. BMC Genomics, 2010, 11, 412.	1.2	29
50	Mobile genetic element proliferation and gene inactivation impact over the genome structure and metabolic capabilities of Sodalis glossinidius, the secondary endosymbiont of tsetse flies. BMC Genomics, 2010, 11, 449.	1.2	72
51	ProFITS of maize: a database of protein families involved in the transduction of signalling in the maize genome. BMC Genomics, 2010, 11, 580.	1.2	8
52	A widespread peroxiredoxin-like domain present in tumor suppression- and progression-implicated proteins. BMC Genomics, 2010, 11, 590.	1.2	26
53	Annotation and comparative analysis of the glycoside hydrolase genes in Brachypodium distachyon. BMC Genomics, 2010, 11, 600.	1.2	53
54	The complete genome sequence of Corynebacterium pseudotuberculosis FRC41 isolated from a 12-year-old girl with necrotizing lymphadenitis reveals insights into gene-regulatory networks contributing to virulence. BMC Genomics, 2010, 11, 728.	1.2	89

#	Article	IF	Citations
55	Involvement of EupR, a response regulator of the NarL/FixJ family, in the control of the uptake of the compatible solutes ectoines by the halophilic bacterium Chromohalobacter salexigens. BMC Microbiology, 2010, 10, 256.	1.3	26
56	Pseudomonas aeruginosa Î²-lactamase induction requires two permeases, AmpG and AmpP. BMC Microbiology, 2010, 10, 328.	1.3	41
57	Analysis of promoter activity of members of the PECTATE LYASE-LIKE (PLL) gene family in cell separation in Arabidopsis. BMC Plant Biology, 2010, 10, 152.	1.6	80
58	Whole genome co-expression analysis of soybean cytochrome P450 genes identifies nodulation-specific P450 monooxygenases. BMC Plant Biology, 2010, 10, 243.	1.6	106
59	Hydrophobins from Aspergillus species cannot be clearly divided into two classes. BMC Research Notes, 2010, 3, 344.	0.6	70
60	Screening and sequence analysis of the hemolysin gene of Fusobacterium necrophorum. Anaerobe, 2010, 16, 402-404.	1.0	8
61	Converging views of endocytosis in yeast and mammals. Current Opinion in Cell Biology, 2010, 22, 513-518.	2.6	40
62	Mining metagenomic data for novel domains: BACON, a new carbohydrateâ€binding module. FEBS Letters, 2010, 584, 2421-2426.	1.3	41
63	Genome (reâ€)annotation and openâ€source annotation pipelines. Microbial Biotechnology, 2010, 3, 362-369.	2.0	24
64	Unexpected allelic heterogeneity and spectrum of mutations in Fowler syndrome revealed by next-generation exome sequencing. Human Mutation, 2010, 31, 918-923.	1.1	116
65	Cloning and Characterization of the Biosynthetic Gene Cluster of 16â€Membered Macrolide Antibiotic FDâ€891: Involvement of a Dual Functional Cytochrome P450 Monooxygenase Catalyzing Epoxidation and Hydroxylation. ChemBioChem, 2010, 11, 1574-1582.	1.3	35
67	NMR Spectroscopic and Theoretical Analysis of a Spontaneously Formed Lysâ€"Asp Isopeptide Bond. Angewandte Chemie - International Edition, 2010, 49, 8421-8425.	7.2	88
68	Computational approaches for protein function prediction: A combined strategy from multiple sequence alignment to molecular docking-based virtual screening. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 1695-1712.	1.1	97
69	Structural analysis of<i>Bacillus pumilus</i>phenolic acid decarboxylase, a lipocalin-fold enzyme. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1407-1414.	0.7	26
70	The maize ALDH protein superfamily: linking structural features to functional specificities. BMC Structural Biology, 2010, 10, 43.	2.3	58
71	Proteomic analysis of the fish pathogen Flavobacterium columnare. Proteome Science, 2010, 8, 26.	0.7	28
72	A mixed community of actinomycetes produce multiple antibiotics for the fungus farming ant Acromyrmex octospinosus. BMC Biology, 2010, 8, 109.	1.7	211
73	Expansion of ribosomally produced natural products: a nitrile hydratase- and Nif11-related precursor family. BMC Biology, 2010, 8, 70.	1.7	134

#	ARTICLE	IF	CITATIONS
74	Computer aided selection of candidate vaccine antigens. Immunome Research, 2010, 6, S1.	0.1	93
75	EntrezAJAX: direct web browser access to the Entrez Programming Utilities. Source Code for Biology and Medicine, 2010, 5, 6.	1.7	2
76	Thioesterases: A new perspective based on their primary and tertiary structures. Protein Science, 2010, 19, 1281-1295.	3.1	121
77	Prediction of subcellular locations of proteins: Where to proceed?. Proteomics, 2010, 10, 3970-3983.	1.3	81
78	The unique set of putative membrane-associated anti-Ïƒ factors in Clostridium thermocellumâ€ƒsuggests a novel extracellular carbohydrate-sensing mechanism involved in gene regulation. FEMS Microbiology Letters, 2010, 308, 84-93.	0.7	73
79	Polypyrimidine tract-binding protein homologues from Arabidopsis underlie regulatory circuits based on alternative splicing and downstream control. Plant Journal, 2010, 64, 243-255.	2.8	64
80	Genome sequence of the model mushroom Schizophyllum commune. Nature Biotechnology, 2010, 28, 957-963.	9.4	490
81	The metavirome of a hypersaline environment. Environmental Microbiology, 2010, 12, 2965-2976.	1.8	78
82	Thiol Signalling Network with an Eye to Diabetes. Molecules, 2010, 15, 8890-8903.	1.7	79
83	AMPylation: something old is new again. Frontiers in Microbiology, 2010, 1, 113.	1.5	60
84	Systems Biology: The Next Frontier for Bioinformatics. Advances in Bioinformatics, 2010, 2010, 1-10.	5.7	51
85	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput â€œomicsâ€•Data. Advances in Bioinformatics, 2010, 2010, 1-19.	5.7	19
86	Of Bits and Bugs â€” On the Use of Bioinformatics and a Bacterial Crystal Structure to Solve a Eukaryotic Repeat-Protein Structure. PLoS ONE, 2010, 5, e13402.	1.1	21
87	Superpose3D: A Local Structural Comparison Program That Allows for User-Defined Structure Representations. PLoS ONE, 2010, 5, e11988.	1.1	14
88	In Silico Prediction of Human Pathogenicity in the Î³-Proteobacteria. PLoS ONE, 2010, 5, e13680.	1.1	14
89	Acyl-Protein Thioesterase 2 Catalizes the Deacylation of Peripheral Membrane-Associated GAP-43. PLoS ONE, 2010, 5, e15045.	1.1	104
90	A Dual Platform Approach to Transcript Discovery for the Planarian Schmidtea Mediterranea to Establish RNAseq for Stem Cell and Regeneration Biology. PLoS ONE, 2010, 5, e15617.	1.1	61
91	A Screen for RNA-Binding Proteins in Yeast Indicates Dual Functions for Many Enzymes. PLoS ONE, 2010, 5, e15499.	1.1	122

#	ARTICLE	IF	CITATIONS
92	FMN Binding and Photochemical Properties of Plant Putative Photoreceptors Containing Two LOV Domains, LOV/LOV Proteins. Journal of Biological Chemistry, 2010, 285, 34765-34772.	1.6	22
93	OsLEA1a, a New Em-Like Protein of Cereal Plants. Plant and Cell Physiology, 2010, 51, 2132-2144.	1.5	19
94	Conserved mechanism for sensor phosphatase control of two-component signaling revealed in the nitrate sensor NarX. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21140-21145.	3.3	91
95	Origin and evolution of peptide-modifying dioxygenases and identification of the wybutosine hydroxylase/hydroperoxidase. Nucleic Acids Research, 2010, 38, 5261-5279.	6.5	46
96	<i>Brochothrix thermosphacta</i>Bacteriophages Feature Heterogeneous and Highly Mosaic Genomes and Utilize Unique Prophage Insertion Sites. Journal of Bacteriology, 2010, 192, 5441-5453.	1.0	39
97	Selection of soluble protein expression constructs: the experimental determination of protein domain boundaries. Biochemical Society Transactions, 2010, 38, 908-913.	1.6	12
98	AlexSys: a knowledge-based expert system for multiple sequence alignment construction and analysis. Nucleic Acids Research, 2010, 38, 6338-6349.	6.5	12
99	Comparative Analysis of the Biochemical and Functional Properties of C-Terminal Domains of Autotransporters. Journal of Bacteriology, 2010, 192, 5588-5602.	1.0	23
100	The 2010 Nucleic Acids Research Database Issue and online Database Collection: a community of data resources. Nucleic Acids Research, 2010, 38, D1-D4.	6.5	86
101	Insecticide resistance through mutations in cholinesterases or carboxylesterases: data mining in the ESTHER database. Journal of Pesticide Sciences, 2010, 35, 315-320.	0.8	32
102	Deciphering the role of RNA-binding proteins in the post-transcriptional control of gene expression. Briefings in Functional Genomics, 2010, 9, 391-404.	1.3	143
103	WebPrInSeS: automated full-length clone sequence identification and verification using high-throughput sequencing data. Nucleic Acids Research, 2010, 38, W378-W384.	6.5	5
104	Genomic repertoires of DNA-binding transcription factors across the tree of life. Nucleic Acids Research, 2010, 38, 7364-7377.	6.5	140
105	RefProtDom: a protein database with improved domain boundaries and homology relationships. Bioinformatics, 2010, 26, 2361-2362.	1.8	13
106	Elective affinities: a Tudorâ€"Aubergine tale of germline partnership. Genes and Development, 2010, 24, 1963-1966.	2.7	8
107	Molecular Identification of N-Acetylaspartylglutamate Synthase and Î²-Citrylglutamate Synthase. Journal of Biological Chemistry, 2010, 285, 29826-29833.	1.6	45
108	Localization and Cellular Amounts of the WalRKJ (VicRKX) Two-Component Regulatory System Proteins in Serotype 2<i>Streptococcus pneumoniae</i>. Journal of Bacteriology, 2010, 192, 4388-4394.	1.0	46
109	Orthopoxvirus Genome Evolution: The Role of Gene Loss. Viruses, 2010, 2, 1933-1967.	1.5	160

#	ARTICLE	IF	CITATIONS
110	LOTUS, a new domain associated with small RNA pathways in the germline. Bioinformatics, 2010, 26, 1140-1144.	1.8	62
111	Issues in bioinformatics benchmarking: the case study of multiple sequence alignment. Nucleic Acids Research, 2010, 38, 7353-7363.	6.5	68
112	Highly Divergent Mitochondrial ATP Synthase Complexes in Tetrahymena thermophila. PLoS Biology, 2010, 8, e1000418.	2.6	72
113	Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. PLoS Computational Biology, 2010, 6, e1000798.	1.5	52
114	More Than 1,001 Problems with Protein Domain Databases: Transmembrane Regions, Signal Peptides and the Issue of Sequence Homology. PLoS Computational Biology, 2010, 6, e1000867.	1.5	56
115	Sequence Motifs in MADS Transcription Factors Responsible for Specificity and Diversification of Protein-Protein Interaction. PLoS Computational Biology, 2010, 6, e1001017.	1.5	61
116	Tight Regulation of the intS Gene of the KplE1 Prophage: A New Paradigm for Integrase Gene Regulation. PLoS Genetics, 2010, 6, e1001149.	1.5	17
117	The N-Terminal Domain of the Arenavirus L Protein Is an RNA Endonuclease Essential in mRNA Transcription. PLoS Pathogens, 2010, 6, e1001038.	2.1	145
118	Library of Disordered Patterns in 3D Protein Structures. PLoS Computational Biology, 2010, 6, e1000958.	1.5	60
119	Integrated functional networks of process, tissue, and developmental stage specific interactions in Arabidopsis thaliana. BMC Systems Biology, 2010, 4, 180.	3.0	21
120	Objective sequence-based subfamily classifications of mouse homeodomains reflect their in vitro DNA-binding preferences. Nucleic Acids Research, 2010, 38, 7927-7942.	6.5	2
121	The PpaA/AerR Regulators of Photosynthesis Gene Expression from Anoxygenic Phototrophic Proteobacteria Contain Heme-Binding SCHIC Domains. Journal of Bacteriology, 2010, 192, 5253-5256.	1.0	17
122	Patterns and processes in the evolution of the eukaryotic endomembrane system. Molecular Membrane Biology, 2010, 27, 469-489.	2.0	30
123	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-11.	3.0	7
124	The Impact of Gene Expression Regulation on Evolution of Extracellular Signaling Pathways. Molecular and Cellular Proteomics, 2010, 9, 2666-2677.	2.5	8
125	Molecular Mechanisms of Ligand-Mediated Attenuation of DNA Binding by MarR Family Transcriptional Regulators. Journal of Molecular Cell Biology, 2010, 2, 243-254.	1.5	163
126	Tandem BRCT Domains: DNA's Praetorian Guard. Genes and Cancer, 2010, 1, 1140-1146.	0.6	15
127	Characterization of the N-ATPase, a distinct, laterally transferred Na+-translocating form of the bacterial F-type membrane ATPase. Bioinformatics, 2010, 26, 1473-1476.	1.8	75

#	Article	IF	Citations
128	Novel sequence-based method for identifying transcription factor binding sites in prokaryotic genomes. Bioinformatics, 2010, 26, 2672-2677.	1.8	21
129	DNA end-processing enzyme polynucleotide kinase as a potential target in the treatment of cancer. Future Oncology, 2010, 6, 1031-1042.	1.1	47
130	Rapid calcium-dependent activation of Aurora-A kinase. Nature Communications, 2010, 1, 64.	5.8	74
131	Simple sequence-based kernels do not predict proteinâ€“protein interactions. Bioinformatics, 2010, 26, 2610-2614.	1.8	98
132	Identification of a Severe Acute Respiratory Syndrome Coronavirus-Like Virus in a Leaf-Nosed Bat in Nigeria. MBio, 2010, 1, .	1.8	141
133	General transcription factors and subunits of RNA polymerase III. Transcription, 2010, 1, 130-135.	1.7	16
134	Subdivision of the MDR superfamily of medium-chain dehydrogenases/reductases through iterative hidden Markov model refinement. BMC Bioinformatics, 2010, 11, 534.	1.2	35
135	Cloning of an ABC1-like Gene ZmABC1-10 and Its Responses to Cadmium and Other Abiotic Stresses in Maize (Zea mays L.). Acta Agronomica Sinica, 2010, 36, 2073-2083.	0.3	9
136	Identification of a Hemerythrin-like Domain in a P_{1B}-Type Transport ATPase. Biochemistry, 2010, 49, 7060-7068.	1.2	24
137	Crystal structures of glycinamide ribonucleotide synthetase, PurD, from thermophilic eubacteria. Journal of Biochemistry, 2010, 148, 429-438.	0.9	15
138	Cross-Talk between the Catalytic Core and the Regulatory Domain in Cystathionine Î²-Synthase: Study by Differential Covalent Labeling and Computational Modeling. Biochemistry, 2010, 49, 10526-10534.	1.2	15
139	Lipoic Acid Synthesis: A New Family of Octanoyltransferases Generally Annotated as Lipoate Protein Ligases. Biochemistry, 2010, 49, 10024-10036.	1.2	44
140	Diversity of structure and function of response regulator output domains. Current Opinion in Microbiology, 2010, 13, 150-159.	2.3	308
141	Structural and Biochemical Characterization of Yeast Monothiol Glutaredoxin Grx6. Journal of Molecular Biology, 2010, 398, 614-622.	2.0	45
142	Solution Structure of the Catalytic Domain of the Mitochondrial Protein ICT1 That Is Essential for Cell Vitality. Journal of Molecular Biology, 2010, 404, 260-273.	2.0	48
143	The Extended Conformation of the 2.9-Ã… Crystal Structure of the Three-PASTA Domain of a Ser/Thr Kinase from the Human Pathogen Staphylococcus aureus. Journal of Molecular Biology, 2010, 404, 847-858.	2.0	40
144	Identification of novel families and classification of the C2 domain superfamily elucidate the origin and evolution of membrane targeting activities in eukaryotes. Gene, 2010, 469, 18-30.	1.0	124
145	The Ferritin-like superfamily: Evolution of the biological iron storeman from a rubrerythrin-like ancestor. Biochimica Et Biophysica Acta - General Subjects, 2010, 1800, 691-705.	1.1	263

#	ARTICLE	IF	CITATIONS
146	The Protein Composition of Mitotic Chromosomes Determined Using Multiclassifier Combinatorial Proteomics. Cell, 2010, 142, 810-821.	13.5	266
147	The Systematic Functional Analysis of Plasmodium Protein Kinases Identifies Essential Regulators of Mosquito Transmission. Cell Host and Microbe, 2010, 8, 377-387.	5.1	267
148	The first complete genome sequence of a non-chicken aviadenovirus, proposed to be turkey adenovirus 1. Virus Research, 2010, 153, 226-233.	1.1	30
149	What lessons can be learned from studying the folding of homologous proteins?. Methods, 2010, 52, 38-50.	1.9	49
150	Identification and expression analysis of mical family genes in zebrafish. Journal of Genetics and Genomics, 2010, 37, 685-693.	1.7	14
151	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. Science, 2010, 328, 593-599.	6.0	465
152	agriGO: a GO analysis toolkit for the agricultural community. Nucleic Acids Research, 2010, 38, W64-W70.	6.5	2,289
153	Natural and Engineered Photoactivated Nucleotidyl Cyclases for Optogenetic Applications. Journal of Biological Chemistry, 2010, 285, 41501-41508.	1.6	194
154	Quantifying the mechanisms of domain gain in animal proteins. Genome Biology, 2010, 11, R74.	13.9	93
155	Rrp6, Rrp47 and Cofactors of the Nuclear Exosome. Advances in Experimental Medicine and Biology, 2010, 702, 91-104.	0.8	53
156	A Sequence Data Mining Protocol to Identify Best Representative Sequence for Protein Domain Families. , 2010, , .		1
157	Community- and Genome-Based Views of Plant-Associated Bacteria: Plantâ€"Bacterial Interactions in Soybean and Rice. Plant and Cell Physiology, 2010, 51, 1398-1410.	1.5	118
158	Cross-species identification of hydroxylation sites for ARD and FIH interaction. , 2011, , .		0
159	The <i>N</i> -Acylneuraminate Cytidyltransferase Gene, <i>neuA</i> , Is Heterogenous in Legionella pneumophila Strains but Can Be Used as a Marker for Epidemiological Typing in the Consensus Sequence-Based Typing Scheme. Journal of Clinical Microbiology, 2011, 49, 4052-4058.	1.8	27
160	DIPOS: database of interacting proteins in Oryza sativa. Molecular BioSystems, 2011, 7, 2615.	2.9	25
161	SCOP family fingerprints: An information theoretic approach to structural classification of protein domains. , 2011, , .		0
162	Guidelines for visualizing and annotating rule-based models. Molecular BioSystems, 2011, 7, 2779.	2.9	36
163	The roles of contact residue disorder and domain composition in characterizing proteinâ€"ligand binding specificity and promiscuity. Molecular BioSystems, 2011, 7, 3280.	2.9	1

#	ARTICLE	IF	CITATIONS
164	FACIL: Fast and Accurate Genetic Code Inference and Logo. Bioinformatics, 2011, 27, 1929-1933.	1.8	42
165	Evolution of biological interaction networks: from models to real data. Genome Biology, 2011, 12, 235.	13.9	37
166	antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. Nucleic Acids Research, 2011, 39, W339-W346.	6.5	1,622
167	Comparative genomics suggests differential deployment of linear and branched signaling across bacteria. Molecular BioSystems, 2011, 7, 3042.	2.9	3
168	Discriminative random field approach to prediction of protein residue contacts. , 2011, , .		5
169	The C2H2 zinc finger transcription factors are likely targets for Ni(ii) toxicity. Metallomics, 2011, 3, 1227.	1.0	18
170	Partial Genome Assembly for a Candidate Division OP11 Single Cell from an Anoxic Spring (Zodletone) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.4	73
171	HMMER web server: interactive sequence similarity searching. Nucleic Acids Research, 2011, 39, W29-W37.	6.5	4,492
172	ECF sigma factor-associated regulatory networks in Streptomyces colicolor A3(2). , 2011, , .		0
173	The Crystal Structure of <i>Escherichia coli</i> Group 4 Capsule Protein GfcC Reveals a Domain Organization Resembling That of Wza. Biochemistry, 2011, 50, 5465-5476.	1.2	31
174	Whole Genome Sequences of Four Brucella Strains. Journal of Bacteriology, 2011, 193, 3674-3675.	1.0	17
175	Analysis of the mitochondrial haplogroups of farm and wild-living raccoon dogs in Poland. Mitochondrial DNA, 2011, 22, 105-110.	0.6	14
176	DrugBank 3.0: a comprehensive resource for 'Omics' research on drugs. Nucleic Acids Research, 2011, 39, D1035-D1041.	6.5	1,566
177	Rational and Computational Design of Stabilized Variants of Cyanovirin-N That Retain Affinity and Specificity for Glycan Ligands. Biochemistry, 2011, 50, 10698-10712.	1.2	19
178	Characterization of the complete genomes of Camelus dromedarius papillomavirus types 1 and 2. Journal of General Virology, 2011, 92, 1769-1777.	1.3	22
179	Functional Proteomic Analysis of Rice Bran Esterases/Lipases and Characterization of a Novel Recombinant Esterase. Journal of Agricultural and Food Chemistry, 2011, 59, 2019-2025.	2.4	11
180	Improvements in Proteomic Metrics of Low Abundance Proteins through Proteome Equalization Using ProteoMiner Prior to MudPIT. Journal of Proteome Research, 2011, 10, 3690-3700.	1.8	86
181	The protein common interface database (ProtCID)--a comprehensive database of interactions of homologous proteins in multiple crystal forms. Nucleic Acids Research, 2011, 39, D761-D770.	6.5	79

#	Article	IF	Citations
182	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. Genes and Development, 2011, 25, 1915-1927.	2.7	3,208
183	Gene Re-annotation in Genome of the ExtremophilePyrobaculum Aerophilumby Using Bioinformatics Methods. Journal of Biomolecular Structure and Dynamics, 2011, 29, 391-401.	2.0	6
184	3did: identification and classification of domain-based interactions of known three-dimensional structure. Nucleic Acids Research, 2011, 39, D718-D723.	6.5	134
185	A Catalogue of Eukaryotic Transcription Factor Types, Their Evolutionary Origin, and Species Distribution. Sub-Cellular Biochemistry, 2011, 52, 25-73.	1.0	107
186	Emergence and Modular Evolution of a Novel Motility Machinery in Bacteria. PLoS Genetics, 2011, 7, e1002268.	1.5	77
187	Protein Structural Domains: Definition and Prediction. Current Protocols in Protein Science, 2011, 66, Unit2.14.	2.8	2
188	The Structure of Bacterial S-Layer Proteins. Progress in Molecular Biology and Translational Science, 2011, 103, 73-130.	0.9	58
189	A mass spectrometryâ€"guided genome mining approach for natural product peptidogenomics. Nature Chemical Biology, 2011, 7, 794-802.	3.9	329
190	Identification and characterization of a multidomain hyperthermophilic cellulase from an archaeal enrichment. Nature Communications, 2011, 2, 375.	5.8	163
191	Natural history of ABC systems: not only transporters. Essays in Biochemistry, 2011, 50, 19-42.	2.1	34
192	Construction and analysis of full-length cDNA library of Cryptosporidium parvum. Parasitology International, 2011, 60, 199-202.	0.6	18
193	Drosophila sbo regulates lifespan through its function in the synthesis of coenzyme Q in vivo. Journal of Genetics and Genomics, 2011, 38, 225-234.	1.7	29
194	Early cardiac morphogenesis defects caused by loss of embryonic macrophage function in Xenopus. Mechanisms of Development, 2011, 128, 303-315.	1.7	18
195	System-Wide Temporal Characterization of the Proteome and Phosphoproteome of Human Embryonic Stem Cell Differentiation. Science Signaling, 2011, 4, rs3.	1.6	389
196	Comparative genomics analysis of completely sequenced microbial genomes reveals the ubiquity of N-linked glycosylation in prokaryotes. Molecular BioSystems, 2011, 7, 1629.	2.9	9
197	Strategies for Pathway Analysis from GWAS Data. Current Protocols in Human Genetics, 2011, 71, Unit1.20.	3.5	13
198	Lafora disease E3-ubiquitin ligase malin is related to TRIM32 at both the phylogenetic and functional level. BMC Evolutionary Biology, 2011, 11, 225.	3.2	23
199	Identification of surface proteins in Enterococcus faecalis V583. BMC Genomics, 2011, 12, 135.	1.2	60

#	Article	IF	Citations
200	Synergistic use of plant-prokaryote comparative genomics for functional annotations. BMC Genomics, 2011, 12, S2.	1.2	43
201	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the Shewanella genus. BMC Genomics, 2011, 12, S3.	1.2	59
202	Transcriptome characterization of the South African abalone Haliotis midae using sequencing-by-synthesis. BMC Research Notes, 2011, 4, 59.	0.6	65
203	<i>Ab Initio</i> Modeling Led Annotation Suggests Nucleic Acid Binding Function for Many DUFs. OMICS A Journal of Integrative Biology, 2011, 15, 431-438.	1.0	25
204	Fast, scalable generation of highâ€quality protein multiple sequence alignments using Clustal Omega. Molecular Systems Biology, 2011, 7, 539.	3.2	12,778
205	The CBS Domain: A Protein Module with an Emerging Prominent Role in Regulation. ACS Chemical Biology, 2011, 6, 1156-1163.	1.6	129
206	A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. Nucleic Acids Research, 2011, 39, 4532-4552.	6.5	184
207	Taxonomic classification of metagenomic shotgun sequences with CARMA3. Nucleic Acids Research, 2011, 39, e91-e91.	6.5	99
208	CDD: a Conserved Domain Database for the functional annotation of proteins. Nucleic Acids Research, 2011, 39, D225-D229.	6.5	2,727
209	Evidence of cellulose metabolism by the giant panda gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17714-17719.	3.3	455
210	S4 Protein Sll1252 Is Necessary for Energy Balancing in Photosynthetic Electron Transport in <i>Synechocystis</i> sp. PCC 6803. Biochemistry, 2011, 50, 329-339.	1.2	5
211	Metagenomic Analyses: Past and Future Trends. Applied and Environmental Microbiology, 2011, 77, 1153-1161.	1.4	597
212	Protein Allostery at the Solidâ€“Liquid Interface: Endoglucanase Attachment to Cellulose Affects Glucan Clenching in the Binding Cleft. Journal of the American Chemical Society, 2011, 133, 16617-16624.	6.6	22
213	Functional Enrichment Analysis with Structural Variants: Pitfalls and Strategies. Cytogenetic and Genome Research, 2011, 135, 277-285.	0.6	24
214	Comparative genomics of the pathogenic ciliate Ichthyophthirius multifiliis, its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. Genome Biology, 2011, 12, R100.	13.9	102
215	Genome sequence of an Australian kangaroo, Macropus eugenii, provides insight into the evolution of mammalian reproduction and development. Genome Biology, 2011, 12, R81.	13.9	167
216	Coding potential of the products of alternative splicing in human. Genome Biology, 2011, 12, R9.	3.8	38
217	Strong functional patterns in the evolution of eukaryotic genomes revealed by the reconstruction of ancestral protein domain repertoires. Genome Biology, 2011, 12, R4.	13.9	84

#	Article	IF	Citations
218	Biosynthetic Gene Cluster of the Non-ribosomally Synthesized Cyclodepsipeptide Skyllamycin: Deciphering Unprecedented Ways of Unusual Hydroxylation Reactions. Journal of the American Chemical Society, 2011, 133, 6194-6205.	6.6	109
219	Solution Structure of LCI, a Novel Antimicrobial Peptide from <i>Bacillus subtilis</i>. Biochemistry, 2011, 50, 3621-3627.	1.2	47
220	Atomistic Structure of Monomolecular Surface Layer Self-Assemblies: Toward Functionalized Nanostructures. ACS Nano, 2011, 5, 2288-2297.	7.3	26
221	Peptidoglycan Remodeling and Conversion of an Inner Membrane into an Outer Membrane during Sporulation. Cell, 2011, 146, 799-812.	13.5	98
222	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. Cell Host and Microbe, 2011, 10, 260-272.	5.1	175
223	Unique sequences and predicted functions of myosins in Tetrahymena thermophila. Gene, 2011, 480, 10-20.	1.0	14
224	Global Identification of Modular Cullin-RING Ligase Substrates. Cell, 2011, 147, 459-474.	13.5	370
225	Association Between Seed Dormancy and Pericarp Color Is Controlled by a Pleiotropic Gene That Regulates Abscisic Acid and Flavonoid Synthesis in Weedy Red Rice. Genetics, 2011, 189, 1515-1524.	1.2	173
226	Ligand-Binding PAS Domains in a Genomic, Cellular, and Structural Context. Annual Review of Microbiology, 2011, 65, 261-286.	2.9	369
227	Construction, Structure and Dynamics of Post-Transcriptional Regulatory Network Directed by RNA-Binding Proteins. Advances in Experimental Medicine and Biology, 2011, 722, 103-117.	0.8	22
228	How old are RNA Networks?. Advances in Experimental Medicine and Biology, 2011, 722, 255-273.	0.8	4
229	The GRP1 PH Domain, Like the AKT1 PH Domain, Possesses a Sentry Glutamate Residue Essential for Specific Targeting to Plasma Membrane PI(3,4,5)P₃. Biochemistry, 2011, 50, 9845-9856.	1.2	25
230	ODV-Associated Proteins of the <i>Pieris rapae</i> Granulovirus. Journal of Proteome Research, 2011, 10, 2817-2827.	1.8	23
231	High-Resolution Crystal Structures of Trimeric and Rod Phycocyanin. Journal of Molecular Biology, 2011, 405, 201-213.	2.0	83
232	Multi-Scale Sequence Correlations Increase Proteome Structural Disorder and Promiscuity. Journal of Molecular Biology, 2011, 409, 439-449.	2.0	13
233	Conformational Changes in Adeno-Associated Virus Type 1 Induced by Genome Packaging. Journal of Molecular Biology, 2011, 409, 427-438.	2.0	19
234	The Extra-Membranous Domains of the Competence Protein HofQ Show DNA Binding, Flexibility and a Shared Fold with Type I KH Domains. Journal of Molecular Biology, 2011, 409, 642-653.	2.0	20
235	Expansion of Type II CAAX Proteases Reveals Evolutionary Origin of Î³-Secretase Subunit APH-1. Journal of Molecular Biology, 2011, 410, 18-26.	2.0	64

#	ARTICLE	IF	CITATIONS
236	Structural Basis for Electron and Methyl-Group Transfer in a Methyltransferase System Operating in the Reductive Acetyl-CoA Pathway. Journal of Molecular Biology, 2011, 411, 96-109.	2.0	33
237	The Molecular Basis of the Caskin1 and Mint1 Interaction with CASK. Journal of Molecular Biology, 2011, 412, 3-13.	2.0	36
238	Determinants of Homodimerization Specificity in Histidine Kinases. Journal of Molecular Biology, 2011, 413, 222-235.	2.0	38
239	Analyses of the Functional Regions of DEAD-Box RNA â€œHelicasesâ€•with Deletion and Chimera Constructs Tested In Vivo and In Vitro. Journal of Molecular Biology, 2011, 413, 451-472.	2.0	39
240	EGFR signaling regulates cell proliferation, differentiation and morphogenesis during planarian regeneration and homeostasis. Developmental Biology, 2011, 354, 87-101.	0.9	102
241	Genomic analysis of bacteriophage Ï•AB1, a Ï•KMV-like virus infecting multidrug-resistant Acinetobacter baumannii. Genomics, 2011, 97, 249-255.	1.3	27
242	A new disease-specific machine learning approach for the prediction of cancer-causing missense variants. Genomics, 2011, 98, 310-317.	1.3	68
243	High-throughput protein purification and quality assessment for crystallization. Methods, 2011, 55, 12-28.	1.9	138
244	Computational approaches to selecting and optimising targets for structural biology. Methods, 2011, 55, 3-11.	1.9	7
245	Light helps bacteria make important lifestyle decisions. Trends in Microbiology, 2011, 19, 441-448.	3.5	140
246	RNA-binding proteins and gene regulation in myogenesis. Trends in Pharmacological Sciences, 2011, 32, 652-658.	4.0	62
247	Comparative analysis of GT14/GT14-like gene family in Arabidopsis, Oryza, Populus, Sorghum and Vitis. Plant Science, 2011, 181, 688-695.	1.7	29
248	A non-canonical start codon in the Drosophila fragile X gene yields two functional isoforms. Neuroscience, 2011, 181, 48-66.	1.1	13
249	Identification of distant co-evolving residues in antigen 85C from Mycobacterium tuberculosis using statistical coupling analysis of the esterase family proteins. Journal of Biomedical Research, 2011, 25, 165-169.	0.7	8
250	Plant protein-coding gene families: emerging bioinformatics approaches. Trends in Plant Science, 2011, 16, 558-567.	4.3	31
251	Azospirillum Genomes Reveal Transition of Bacteria from Aquatic to Terrestrial Environments. PLoS Genetics, 2011, 7, e1002430.	1.5	191
252	Omics, Bioinformatics, and Infectious Disease Research. , 2011, , 523-539.		1
253	Proteome Databases and Other Online Resources for Chloroplast Research in Arabidopsis. Methods in Molecular Biology, 2011, 775, 93-115.	0.4	7

#	ARTICLE	IF	CITATIONS
254	Bacterial phytochromes: More than meets the light. Critical Reviews in Biochemistry and Molecular Biology, 2011, 46, 67-88.	2.3	192
255	Identification of a new lipase family in the Brazilian Atlantic Forest soil metagenome. Environmental Microbiology Reports, 2011, 3, 750-755.	1.0	18
256	Atg8: an autophagy-related ubiquitin-like protein family. Genome Biology, 2011, 12, 226.	13.9	434
257	Exome sequencing identifies a missense mutation in Isl1 associated with low penetrance otitis media in dearisch mice. Genome Biology, 2011, 12, R90.	13.9	22
258	Somatic<i>SF3B1</i>Mutation in Myelodysplasia with Ring Sideroblasts. New England Journal of Medicine, 2011, 365, 1384-1395.	13.9	1,094
259	Long evolutionary conservation and considerable tissue specificity of several atypical solute carrier transporters. Gene, 2011, 478, 11-18.	1.0	50
260	Abscisic acid-inducible 25 kDa xylem sap protein abundant in winter poplar. Plant Root, 2011, 5, 63-68.	0.3	2
261	Allergen Bioinformatics: Recent Trends and Developments. , 0, , .		4
262	Systematic and Phylogenetic Analysis of the Ole e 1 Pollen Protein Family Members in Plants. , 0, , .		3
263	Assessing Multiple Sequence Alignments Using Visual Tools. , 0, , .		0
264	A Pattern Search Method for Discovering Conserved Motifs in Bioactive Peptide Families. , 2011, , .		2
265	Reassessing the Lineage Fusion Hypothesis for the Origin of Double Membrane Bacteria. Nature Precedings, 2011, , .	0.1	0
266	Molecular evolution of RRM-containing proteins and glycine-rich RNA-binding proteins in plants. Nature Precedings, 2011, , .	0.1	0
267	ProDGe: investigating protein-protein interactions at the domain level. Nature Precedings, 2011, , .	0.1	0
268	Evolutionary histories of expanded peptidase families in Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2011, 106, 864-877.	0.8	12
269	Comparative analysis of human and bovine protein kinases reveals unique relationship and functional diversity. Genetics and Molecular Biology, 2011, 34, 587-591.	0.6	20
270	Adaptation of the AFLP technique as a new tool to detect genetic instability and transposition in interspecific hybrids. BioTechniques, 2011, 50, 247-250.	0.8	12
271	Partial Gene Duplication and the Formation of Novel Genes. , 2011, , .		4

#	ARTICLE	IF	CITATIONS
272	NovelSNPer: A Fast Tool for the Identification and Characterization of Novel SNPs and InDels. Advances in Bioinformatics, 2011, 2011, 1-11.	5.7	6
273	<i>Sulfolobus</i>Mutants, Generated via PCR Products, Which Lack Putative Enzymes of UV Photoproduct Repair. Archaea, 2011, 2011, 1-12.	2.3	23
274	Functional Diversity of the <i>Schistosoma mansoni</i> Tyrosine Kinases. Journal of Signal Transduction, 2011, 2011, 1-11.	2.0	19
275	Large-Scale Co-Expression Approach to Dissect Secondary Cell Wall Formation Across Plant Species. Frontiers in Plant Science, 2011, 2, 23.	1.7	127
276	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. Frontiers in Genetics, 2011, 2, 69.	1.1	12
277	Global Proteomic Analysis of Two Tick-Borne Emerging Zoonotic Agents: Anaplasma Phagocytophilum and Ehrlichia Chaffeensis. Frontiers in Microbiology, 2011, 2, 24.	1.5	65
278	Is the Genetic Landscape of the Deep Subsurface Biosphere Affected by Viruses?. Frontiers in Microbiology, 2011, 2, 219.	1.5	56
279	The Human Postsynaptic Density Shares Conserved Elements with Proteomes of Unicellular Eukaryotes and Prokaryotes. Frontiers in Neuroscience, 2011, 5, 44.	1.4	19
280	Lactobacillus Adhesion to Mucus. Nutrients, 2011, 3, 613-636.	1.7	249
281	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.	1.8	24
282	Reassessing Domain Architecture Evolution of Metazoan Proteins: Major Impact of Gene Prediction Errors. Genes, 2011, 2, 449-501.	1.0	20
283	The Evolution of Protein Structures and Structural Ensembles Under Functional Constraint. Genes, 2011, 2, 748-762.	1.0	50
285	Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont Piriformospora indica. PLoS Pathogens, 2011, 7, e1002290.	2.1	361
286	Disordered Patterns in Clustered Protein Data Bank and in Eukaryotic and Bacterial Proteomes. PLoS ONE, 2011, 6, e27142.	1.1	20
287	c-di-GMP Turn-Over in Clostridium difficile Is Controlled by a Plethora of Diguanylate Cyclases and Phosphodiesterases. PLoS Genetics, 2011, 7, e1002039.	1.5	128
288	Phylogenetic Comparison of F-Box (FBX) Gene Superfamily within the Plant Kingdom Reveals Divergent Evolutionary Histories Indicative of Genomic Drift. PLoS ONE, 2011, 6, e16219.	1.1	116
289	Novel Analysis of Oceanic Surface Water Metagenomes Suggests Importance of Polyphosphate Metabolism in Oligotrophic Environments. PLoS ONE, 2011, 6, e16499.	1.1	56
290	Diversity in Functional Organization of Class I and Class II Biotin Protein Ligase. PLoS ONE, 2011, 6, e16850.	1.1	5

#	ARTICLE	IF	CITATIONS
291	Elucidation of Functional Markers from Aspergillus nidulans Developmental Regulator FlbB and Their Phylogenetic Distribution. PLoS ONE, 2011, 6, e17505.	1.1	9
292	HMMerThread: Detecting Remote, Functional Conserved Domains in Entire Genomes by Combining Relaxed Sequence-Database Searches with Fold Recognition. PLoS ONE, 2011, 6, e17568.	1.1	2
293	Structure-Function Analysis of the HrpB2-HrcU Interaction in the Xanthomonas citri Type III Secretion System. PLoS ONE, 2011, 6, e17614.	1.1	13
294	Assembling a Protein-Protein Interaction Map of the SSU Processome from Existing Datasets. PLoS ONE, 2011, 6, e17701.	1.1	24
295	Computational Bacterial Genome-Wide Analysis of Phylogenetic Profiles Reveals Potential Virulence Genes of Streptococcus agalactiae. PLoS ONE, 2011, 6, e17964.	1.1	18
296	Domain Movement within a Gene: A Novel Evolutionary Mechanism for Protein Diversification. PLoS ONE, 2011, 6, e18819.	1.1	50
297	In Silico Survey of the Mitochondrial Protein Uptake and Maturation Systems in the Brown Alga Ectocarpus siliculosus. PLoS ONE, 2011, 6, e19540.	1.1	10
298	Common Peptides Study of Aminoacyl-tRNA Synthetases. PLoS ONE, 2011, 6, e20361.	1.1	4
299	Going Deeper: Metagenome of a Hadopelagic Microbial Community. PLoS ONE, 2011, 6, e20388.	1.1	95
300	Sequencing and Comparative Genome Analysis of Two Pathogenic Streptococcus gallolyticus Subspecies: Genome Plasticity, Adaptation and Virulence. PLoS ONE, 2011, 6, e20519.	1.1	41
301	A Novel Stress-Associated Protein â€˜AtSAP10â€™ from Arabidopsis thaliana Confers Tolerance to Nickel, Manganese, Zinc, and High Temperature Stress. PLoS ONE, 2011, 6, e20921.	1.1	79
302	LRR Conservation Mapping to Predict Functional Sites within Protein Leucine-Rich Repeat Domains. PLoS ONE, 2011, 6, e21614.	1.1	46
303	Exploiting Publicly Available Biological and Biochemical Information for the Discovery of Novel Short Linear Motifs. PLoS ONE, 2011, 6, e22270.	1.1	2
304	Alba-Domain Proteins of Trypanosoma brucei Are Cytoplasmic RNA-Binding Proteins That Interact with the Translation Machinery. PLoS ONE, 2011, 6, e22463.	1.1	101
305	The Fat Body Transcriptomes of the Yellow Fever Mosquito Aedes aegypti, Pre- and Post- Blood Meal. PLoS ONE, 2011, 6, e22573.	1.1	77
306	Global Analysis of Proline-Rich Tandem Repeat Proteins Reveals Broad Phylogenetic Diversity in Plant Secretomes. PLoS ONE, 2011, 6, e23167.	1.1	16
307	Reassessment of the Lineage Fusion Hypothesis for the Origin of Double Membrane Bacteria. PLoS ONE, 2011, 6, e23774.	1.1	6
308	One Carbon Metabolism in SAR11 Pelagic Marine Bacteria. PLoS ONE, 2011, 6, e23973.	1.1	173

#	Article	IF	Citations
309	Tm1: A Mutator/Foldback Transposable Element Family in Root-Knot Nematodes. PLoS ONE, 2011, 6, e24534.	1.1	24
310	Origins and Evolution of the HET-s Prion-Forming Protein: Searching for Other Amyloid-Forming Solenoids. PLoS ONE, 2011, 6, e27342.	1.1	8
311	Identification of Anaplasma marginale Type IV Secretion System Effector Proteins. PLoS ONE, 2011, 6, e27724.	1.1	53
312	The Discovery of Putative Urine Markers for the Specific Detection of Prostate Tumor by Integrative Mining of Public Genomic Profiles. PLoS ONE, 2011, 6, e28552.	1.1	16
313	ProKinO: An Ontology for Integrative Analysis of Protein Kinases in Cancer. PLoS ONE, 2011, 6, e28782.	1.1	34
314	LTR Retrotransposons in Fungi. PLoS ONE, 2011, 6, e29425.	1.1	94
316	Massive Genomic Decay in Serratia symbiotica, a Recently Evolved Symbiont of Aphids. Genome Biology and Evolution, 2011, 3, 195-208.	1.1	186
317	The InterPro BioMart: federated query and web service access to the InterPro Resource. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar033-bar033.	1.4	12
318	3DSwap: curated knowledgebase of proteins involved in 3D domain swapping. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar042-bar042.	1.4	28
319	TheViral MetaGenome Annotation Pipeline (VMGAP):an automated tool for the functional annotation of viral Metagenomic shotgun sequencing data. Standards in Genomic Sciences, 2011, 4, 418-429.	1.5	49
320	Gene prediction in metagenomic fragments based on the SVM algorithm. , 2011, , .		2
321	Complete Nucleomorph Genome Sequence of the Nonphotosynthetic Alga Cryptomonas paramecium Reveals a Core Nucleomorph Gene Set. Genome Biology and Evolution, 2011, 3, 44-54.	1.1	62
322	Mutational analysis of residues in the regulatory CBS domains of <i>Moorella thermoacetica</i> pyrophosphatase corresponding to disease-related residues of human proteins. Biochemical Journal, 2011, 433, 497-504.	1.7	8
323	Disease and Phenotype Data at Ensembl. Current Protocols in Human Genetics, 2011, 69, Unit 6.11.	3.5	3
324	The UCSC Genome Browser. Current Protocols in Human Genetics, 2011, 71, Unit18.6.	3.5	38
325	METADOMAIN: A PROFILE HMM-BASED PROTEIN DOMAIN CLASSIFICATION TOOL FOR SHORT SEQUENCES. , 2011, , .		5
326	Whole Genome Annotation: In Silico Analysis. , 0, , .		1
327	Update on the aldehyde dehydrogenase gene (ALDH) superfamily. Human Genomics, 2011, 5, 283.	1.4	276

#	ARTICLE	IF	CITATIONS
328	A Protocol for Computer-Based Protein Structure and Function Prediction. Journal of Visualized Experiments, 2011, , e3259.	0.2	54
329	Missense SLC25A38 variations play an important role in autosomal recessive inherited sideroblastic anemia. Haematologica, 2011, 96, 808-813.	1.7	57
330	A global census of nitrogenase diversity. Environmental Microbiology, 2011, 13, 1790-1799.	1.8	155
331	A systematic analysis of the early transcribed membrane protein family throughout the life cycle of Plasmodium yoelii. Cellular Microbiology, 2011, 13, 1755-1767.	1.1	25
332	Characterization of a thermally stable and organic solvent-adaptative NAD+-dependent formate dehydrogenase from Bacillus sp. F1. Journal of Applied Microbiology, 2011, 111, 1075-1085.	1.4	27
333	The transcriptome landscape of Arabidopsis male meiocytes from highâ€throughput sequencing: the complexity and evolution of the meiotic process. Plant Journal, 2011, 65, 503-516.	2.8	135
334	Evolutionary and comparative analysis of MYB and bHLH plant transcription factors. Plant Journal, 2011, 66, 94-116.	2.8	1,014
335	The DUF579 domain containing proteins IRX15 and IRX15â€L affect xylan synthesis in Arabidopsis. Plant Journal, 2011, 66, 387-400.	2.8	120
336	Arabidopsis genes <i>IRREGULAR XYLEM</i> (<i>IRX15</i>) and <i>IRX15L</i> encode DUF579â€containing proteins that are essential for normal xylan deposition in the secondary cell wall. Plant Journal, 2011, 66, 401-413.	2.8	134
337	Profiling of short RNAs during fleshy fruit development reveals stageâ€specific sRNAome expression patterns. Plant Journal, 2011, 67, 232-246.	2.8	138
338	The receptorâ€like kinase <i>SlSERK1</i> is required for <i>Miâ€1â€</i>mediated resistance to potato aphids in tomato. Plant Journal, 2011, 67, 459-471.	2.8	82
339	The RCC1 family protein RUG3 is required for splicing of <i>nad2</i> and complex I biogenesis in mitochondria of <i>Arabidopsis thaliana</i>. Plant Journal, 2011, 67, 1067-1080.	2.8	113
340	Differential sensitivity of coral larvae to natural levels of ultraviolet radiation during the onset of larval competence. Molecular Ecology, 2011, 20, 2955-2972.	2.0	47
341	A novel amidotransferase required for lipoic acid cofactor assembly in <i>Bacillus subtilis</i>. Molecular Microbiology, 2011, 80, 350-363.	1.2	51
342	An actinâ€based cytoskeleton in archaea. Molecular Microbiology, 2011, 80, 1052-1061.	1.2	142
343	TP0326, a <i>Treponema pallidum</i>Î²â€barrel assembly machinery A (BamA) orthologue and rare outer membrane protein. Molecular Microbiology, 2011, 80, 1496-1515.	1.2	61
344	The SLHâ€domain protein BslO is a determinant of Bacillus anthracis chain length. Molecular Microbiology, 2011, 81, 192-205.	1.2	32
345	Transcription factor genes of <i>Schizophyllum commune</i> involved in regulation of mushroom formation. Molecular Microbiology, 2011, 81, 1433-1445.	1.2	127

#	Article	IF	Citations
346	Negative control in two-component signal transduction by transmitter phosphatase activity. Molecular Microbiology, 2011, 82, 275-286.	1.2	99
347	Sortase enzymes in Gramâ€positive bacteria. Molecular Microbiology, 2011, 82, 1044-1059.	1.2	277
348	Rapid copy number expansion and recent recruitment of domains in Sâ€receptor kinaseâ€like genes contribute to the origin of selfâ€incompatibility. FEBS Journal, 2011, 278, 4323-4337.	2.2	20
349	Isolation of the fenoxaprop-ethyl (FE)-degrading bacterium Rhodococcus sp. T1, and cloning of FE hydrolase gene feh. FEMS Microbiology Letters, 2011, 323, 196-203.	0.7	34
350	Genetic analysis of the capsular polysaccharide synthesis locus in 15 Streptococcus suis serotypes. FEMS Microbiology Letters, 2011, 324, 117-124.	0.7	20
351	Tripartite ATP-independent periplasmic (TRAP) transporters in bacteria and archaea. FEMS Microbiology Reviews, 2011, 35, 68-86.	3.9	190
352	A differential proteome screening system for post-translational modificationâ€“dependent transcription factor interactions. Nature Protocols, 2011, 6, 359-364.	5.5	13
353	Hierarchical classification of glycoside hydrolases. Biochemistry (Moscow), 2011, 76, 622-635.	0.7	99
354	Nitrogen fixation and nitrogenase (<i>nifH</i>) expression in tropical waters of the eastern North Atlantic. ISME Journal, 2011, 5, 1201-1212.	4.4	111
355	Ecogenomics and genome landscapes of marine Pseudoalteromonas phage H105/1. ISME Journal, 2011, 5, 107-121.	4.4	62
356	Recognition of 2â€²-O-Methylated 3â€²-End of piRNA by the PAZ Domain of a Piwi Protein. Structure, 2011, 19, 172-180.	1.6	98
357	A Systematic Study of the Energetics Involved in Structural Changes upon Association and Connectivity in Protein Interaction Networks. Structure, 2011, 19, 881-889.	1.6	42
358	Atomic Resolution Insights into Curli Fiber Biogenesis. Structure, 2011, 19, 1307-1316.	1.6	82
359	Cellulases: ambiguous nonhomologous enzymes in a genomic perspective. Trends in Biotechnology, 2011, 29, 473-479.	4.9	78
360	MtbSDâ€“A comprehensive structural database for Mycobacterium tuberculosis. Tuberculosis, 2011, 91, 556-562.	0.8	5
361	A survey of schistosome protein domain types: Insights into unique biological properties. Molecular and Biochemical Parasitology, 2011, 177, 100-105.	0.5	2
362	Three-dimensional modeling of protein interactions and complexes is going â€˜omics. Current Opinion in Structural Biology, 2011, 21, 200-208.	2.6	86
363	Protein sequence comparison and fold recognition: progress and good-practice benchmarking. Current Opinion in Structural Biology, 2011, 21, 404-411.	2.6	73

#	Article	IF	Citations
364	Metagenomics and the protein universe. Current Opinion in Structural Biology, 2011, 21, 398-403.	2.6	62
365	The maternal genes Ci-p53/p73-a and Ci-p53/p73-b regulate zygotic ZicL expression and notochord differentiation in Ciona intestinalis embryos. Developmental Biology, 2011, 360, 216-229.	0.9	14
366	Domain architecture conservation in orthologs. BMC Bioinformatics, 2011, 12, 326.	1.2	54
367	Biophysical and structural considerations for protein sequence evolution. BMC Evolutionary Biology, 2011, 11, 361.	3.2	50
368	Ortho2ExpressMatrixâ€"a web server that interprets cross-species gene expression data by gene family information. BMC Genomics, 2011, 12, 483.	1.2	5
369	Production of a reference transcriptome and transcriptomic database (PocilloporaBase) for the cauliflower coral, Pocillopora damicornis. BMC Genomics, 2011, 12, 585.	1.2	75
370	Evolutionary traces decode molecular mechanism behind fast pace of myosin XI. BMC Structural Biology, 2011, 11, 35.	2.3	2
371	A Shigella boydii bacteriophage which resembles Salmonella phage ViI. Virology Journal, 2011, 8, 242.	1.4	62
372	Analysis of a viral metagenomic library from 200 m depth in Monterey Bay, California constructed by direct shotgun cloning. Virology Journal, 2011, 8, 287.	1.4	40
373	Spliceosomal intron size expansion in domesticated grapevine (Vitis vinifera). BMC Research Notes, 2011, 4, 52.	0.6	16
374	Disjunctive shared information between ontology concepts: application to Gene Ontology. Journal of Biomedical Semantics, 2011, 2, 5.	0.9	53
375	The Ras related GTPase Miro is not required for mitochondrial transport in Dictyostelium discoideum. European Journal of Cell Biology, 2011, 90, 342-355.	1.6	41
376	The retroviral proteinase active site and the N-terminus of Ddi1 are required for repression of protein secretion. FEBS Letters, 2011, 585, 139-142.	1.3	26
377	Identification and modelling of a PPM protein phosphatase fold in the <i>Legionella pneumophila</i> deAMPylase SidD. FEBS Letters, 2011, 585, 2749-2754.	1.3	12
378	Interaction of angio-associated migratory cell protein with the TPÎ± and TPÎ² isoforms of the human thromboxane A2 receptor. Cellular Signalling, 2011, 23, 700-717.	1.7	14
379	Selective Overproduction of the Proteasome Inhibitor Salinosporamide A via Precursor Pathway Regulation. Chemistry and Biology, 2011, 18, 1527-1536.	6.2	37
380	Rad23 escapes degradation because it lacks a proteasome initiation region. Nature Communications, 2011, 2, 192.	5.8	87
381	An Overview of Prokaryotic Transcription Factors. Sub-Cellular Biochemistry, 2011, 52, 7-23.	1.0	43

#	ARTICLE	IF	CITATIONS
382	Type VI secretion delivers bacteriolytic effectors to target cells. Nature, 2011, 475, 343-347.	13.7	643
383	Receptor domains of two-component signal transduction systems. Molecular BioSystems, 2011, 7, 1388.	2.9	28
384	Bell pepper endornavirus: molecular and biological properties, and occurrence in the genus Capsicum. Journal of General Virology, 2011, 92, 2664-2673.	1.3	92
385	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. Genetica, 2011, 139, 1543-1555.	0.5	23
386	Involvement of pore-forming molecules in immune defense and development of the Mediterranean mussel (Mytilus galloprovincialis). Developmental and Comparative Immunology, 2011, 35, 1017-1031.	1.0	33
387	Investigating Cancer-related Proteins Specific Domain Interactions and Differential Protein Interactions Caused by Alternative Splicing. , 2011, , .		1
388	Sequence-Structural Features and Evolutionary Relationships of Family GH57 Î±-Amylases and Their Putative Î±-Amylase-Like Homologues. Protein Journal, 2011, 30, 429-435.	0.7	37
389	TonB-dependent outer-membrane proteins and siderophore utilization in Pseudomonas fluorescens Pf-5. BioMetals, 2011, 24, 193-213.	1.8	45
390	Metalloproteins and the Pyrite-based Origin of Life: A Critical Assessment. Origins of Life and Evolution of Biospheres, 2011, 41, 347-356.	0.8	2
391	A functionally required unfoldome from the plant kingdom: intrinsically disordered N-terminal domains of GRAS proteins are involved in molecular recognition during plant development. Plant Molecular Biology, 2011, 77, 205-223.	2.0	135
392	A new approach to assess and predict the functional roles of proteins across all known structures. Journal of Structural and Functional Genomics, 2011, 12, 9-20.	1.2	4
393	The Structural Biology Knowledgebase: a portal to protein structures, sequences, functions, and methods. Journal of Structural and Functional Genomics, 2011, 12, 45-54.	1.2	65
394	Solution NMR structure of MED25(391â€“543) comprising the activator-interacting domain (ACID) of human mediator subunit 25. Journal of Structural and Functional Genomics, 2011, 12, 159-166.	1.2	18
395	A sample view of the pedunculate oak (Quercus robur) genome from the sequencing of hypomethylated and random genomic libraries. Tree Genetics and Genomes, 2011, 7, 1277-1285.	0.6	7
396	GmFtsH9 expression correlates with in vivo photosystem II function: chlorophyll a fluorescence transient analysis and eQTL mapping in soybean. Planta, 2011, 234, 815-827.	1.6	26
397	Identification and characterization of a serine protease inhibitor with two trypsin inhibitor-like domains from the human hookworm Ancylostoma duodenale. Parasitology Research, 2011, 108, 287-295.	0.6	24
398	Genome-enabled determination of amino acid biosynthesis in Xanthomonas campestris pv. campestris and identification of biosynthetic pathways for alanine, glycine, and isoleucine by 13C-isotopologue profiling. Molecular Genetics and Genomics, 2011, 286, 247-59.	1.0	19
399	Bacterial metallothioneins: past, present, and questions for the future. Journal of Biological Inorganic Chemistry, 2011, 16, 1011-1024.	1.1	138

#	ARTICLE	IF	CITATIONS
400	Computational study of the Na+/H+ antiporter from Vibrio parahaemolyticus. Journal of Molecular Modeling, 2011, 17, 1877-1890.	0.8	5
401	Symbiotic Streptomyces sp. TN119 GH 11 xylanase: a new pH-stable, protease- and SDS-resistant xylanase. Journal of Industrial Microbiology and Biotechnology, 2011, 38, 523-530.	1.4	34
402	New insights into the distribution of WXG100 protein secretion systems. Antonie Van Leeuwenhoek, 2011, 99, 127-131.	0.7	30
403	Positional cloning of ds1, the target leaf spot resistance gene against Bipolaris sorghicola in sorghum. Theoretical and Applied Genetics, 2011, 123, 131-142.	1.8	32
404	Characterization of a Glucose-, Xylose-, Sucrose-, and d-Galactose-Stimulated Î²-Glucosidase from the Alkalophilic Bacterium Bacillus halodurans C-125. Current Microbiology, 2011, 62, 833-839.	1.0	27
405	Unpredictability of metabolismâ€"the key role of metabolomics science in combination with next-generation genome sequencing. Analytical and Bioanalytical Chemistry, 2011, 400, 1967-1978.	1.9	87
406	Phylogenetic Distribution and Evolutionary History of Bacterial DEAD-Box Proteins. Journal of Molecular Evolution, 2011, 72, 413-431.	0.8	30
407	Fast Side Chain Replacement in Proteins Using a Coarse-Grained Approach for Evaluating the Effects of Mutation During Evolution. Journal of Molecular Evolution, 2011, 73, 23-33.	0.8	5
408	Lytic enzyme discovery through multigenomic sequence analysis in Clostridium perfringens. Applied Microbiology and Biotechnology, 2011, 89, 1783-1795.	1.7	33
409	The impact of plant biotechnology on food allergy. Current Opinion in Biotechnology, 2011, 22, 224-230.	3.3	22
410	Differential expression of cysteine desulfurases in soybean. BMC Plant Biology, 2011, 11, 166.	1.6	11
411	Conservation of ciliary proteins in plants with no cilia. BMC Plant Biology, 2011, 11, 185.	1.6	26
412	The impact of Ty3-gypsy group LTR retrotransposons Fatima on B-genome specificity of polyploid wheats. BMC Plant Biology, 2011, 11, 99.	1.6	26
413	1,000 structures and more from the MCSG. BMC Structural Biology, 2011, 11, 2.	2.3	14
414	Binary classification of protein molecules into intrinsically disordered and ordered segments. BMC Structural Biology, 2011, 11, 29.	2.3	69
415	CREST - a large and diverse superfamily of putative transmembrane hydrolases. Biology Direct, 2011, 6, 37.	1.9	74
416	Not all transmembrane helices are born equal: Towards the extension of the sequence homology concept to membrane proteins. Biology Direct, 2011, 6, 57.	1.9	28
417	Exploration of plant genomes in the FLAGdb++ environment. Plant Methods, 2011, 7, 8.	1.9	45

#	ARTICLE	IF	CITATIONS
418	DomainRBF: a Bayesian regression approach to the prioritization of candidate domains for complex diseases. BMC Systems Biology, 2011, 5, 55.	3.0	21
419	Unexpected complexity of the Reef-Building Coral Acropora millepora transcription factor network. BMC Systems Biology, 2011, 5, 58.	3.0	9
420	Conditional random field approach to prediction of protein-protein interactions using domain information. BMC Systems Biology, 2011, 5, S8.	3.0	24
421	Evolution of apoptosis-like programmed cell death in unicellular protozoan parasites. Parasites and Vectors, 2011, 4, 44.	1.0	122
422	The zinc-ribbon domain of Helicobacter pylori HP0958: requirement for RpoN accumulation and possible roles of homologs in other bacteria. Microbial Informatics and Experimentation, 2011, 1, 1-10.	7.6	11
423	Quantifying the effect of environment stability on the transcription factor repertoire of marine microbes. Microbial Informatics and Experimentation, 2011, 1, 9.	7.6	5
424	The Protein Data Bank in Europe (PDBe): bringing structure to biology. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 324-330.	2.5	27
425	Construct optimization for studying protein complexes: obtaining diffraction-quality crystals of the pseudosymmetric PSPC1â€“NONO heterodimer. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 981-987.	2.5	18
426	Purification, crystallization and preliminary crystallographic analysis of the CBS-domain protein MJ1004 fromMethanocaldococcus jannaschii. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 318-324.	0.7	5
427	Overexpression, crystallization and preliminary X-ray crystallographic analysis ofPyrococcus furiosusPF2050, a member of the DUF2666 protein family. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 930-932.	0.7	1
428	Crystallization and preliminary X-ray analysis of theEntamoeba histolyticaÎ±-actinin-2 rod domain. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1214-1217.	0.7	1
429	Purification and crystallization ofBacillus subtilisNrnA, a novel enzyme involved in nanoRNA degradation. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1235-1238.	0.7	4
430	Crystallization and X-ray data collection of HP0902 from <i>Helicobacter pylori</i> 26695. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1619-1622.	0.7	2
431	Ultra-fast sequence clustering from similarity networks with SiLiX. BMC Bioinformatics, 2011, 12, 116.	1.2	271
432	Binding Site Prediction for Protein-Protein Interactions and Novel Motif Discovery using Re-occurring Polypeptide Sequences. BMC Bioinformatics, 2011, 12, 225.	1.2	38
433	Algal Functional Annotation Tool: a web-based analysis suite to functionally interpret large gene lists using integrated annotation and expression data. BMC Bioinformatics, 2011, 12, 282.	1.2	84
434	Correlated mutations via regularized multinomial regression. BMC Bioinformatics, 2011, 12, 444.	1.2	9
435	A novel substitution matrix fitted to the compositional bias in Mollicutes improves the prediction of homologous relationships. BMC Bioinformatics, 2011, 12, 457.	1.2	10

#	ARTICLE	IF	CITATIONS
436	Dr. PIAS: an integrative system for assessing the druggability of protein-protein interactions. BMC Bioinformatics, 2011, 12, 50.	1.2	22
437	Using context to improve protein domain identification. BMC Bioinformatics, 2011, 12, 90.	1.2	44
438	Integrative analysis workflow for the structural and functional classification of C-type lectins. BMC Bioinformatics, 2011, 12, S5.	1.2	19
439	Functional specialization in nucleotide sugar transporters occurred through differentiation of the gene cluster EamA (DUF6) before the radiation of Viridiplantae. BMC Evolutionary Biology, 2011, 11, 123.	3.2	37
440	Protein coalitions in a core mammalian biochemical network linked by rapidly evolving proteins. BMC Evolutionary Biology, 2011, 11, 142.	3.2	3
441	Genetic mechanisms involved in the evolution of the cephalopod camera eye revealed by transcriptomic and developmental studies. BMC Evolutionary Biology, 2011, 11, 180.	3.2	17
442	Molecular evolution of the LNX gene family. BMC Evolutionary Biology, 2011, 11, 235.	3.2	30
443	A holistic phylogeny of the coronin gene family reveals an ancient origin of the tandem-coronin, defines a new subfamily, and predicts protein function. BMC Evolutionary Biology, 2011, 11, 268.	3.2	53
444	Evolutionary and functional insights into Leishmania META1: evidence for lateral gene transfer and a role for META1 in secretion. BMC Evolutionary Biology, 2011, 11, 334.	3.2	9
445	RSpred, a set of Hidden Markov Models to detect and classify the RIFIN and STEVOR proteins of Plasmodium falciparum. BMC Genomics, 2011, 12, 119.	1.2	9
446	Deep sequencing of the Camellia sinensis transcriptome revealed candidate genes for major metabolic pathways of tea-specific compounds. BMC Genomics, 2011, 12, 131.	1.2	374
447	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. BMC Genomics, 2011, 12, 146.	1.2	167
448	Eukaryotic Protein Kinases (ePKs) of the Helminth Parasite Schistosoma mansoni. BMC Genomics, 2011, 12, 215.	1.2	90
449	Blueprint for a minimal photoautotrophic cell: conserved and variable genes in Synechococcus elongatus PCC 7942. BMC Genomics, 2011, 12, 25.	1.2	8
450	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	1.2	49
451	The aspartic proteinase family of three Phytophthora species. BMC Genomics, 2011, 12, 254.	1.2	19
452	Transcriptome profiling of chemosensory appendages in the malaria vector Anopheles gambiae reveals tissue- and sex-specific signatures of odor coding. BMC Genomics, 2011, 12, 271.	1.2	181
453	Analysis of BAC end sequences in oak, a keystone forest tree species, providing insight into the composition of its genome. BMC Genomics, 2011, 12, 292.	1.2	33

#	ARTICLE	IF	CITATIONS
454	Characterization of transcriptome dynamics during watermelon fruit development: sequencing, assembly, annotation and gene expression profiles. BMC Genomics, 2011, 12, 454.	1.2	126
455	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. BMC Genomics, 2011, 12, 505.	1.2	57
456	Comparative Genomics of Helicobacter pylori and the human-derived Helicobacter bizzozeronii CIII-1 strain reveal the molecular basis of the zoonotic nature of non-pylori gastric Helicobacter infections in humans. BMC Genomics, 2011, 12, 534.	1.2	32
457	Complete genome sequence of Corynebacterium variabile DSM 44702 isolated from the surface of smear-ripened cheeses and insights into cheese ripening and flavor generation. BMC Genomics, 2011, 12, 545.	1.2	63
458	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	1.2	127
459	Genome-wide identification, classification and analysis of heat shock transcription factor family in maize. BMC Genomics, 2011, 12, 76.	1.2	189
460	Eukaryote-wide sequence analysis of mitochondrial Î²-barrel outer membrane proteins. BMC Genomics, 2011, 12, 79.	1.2	36
461	Interrogation of alternative splicing events in duplicated genes during evolution. BMC Genomics, 2011, 12, S16.	1.2	13
462	DetoxiProt: an integrated database for detoxification proteins. BMC Genomics, 2011, 12, S2.	1.2	10
463	Cutoff Scanning Matrix (CSM): structural classification and function prediction by protein inter-residue distance patterns. BMC Genomics, 2011, 12, S12.	1.2	58
464	Internal organization of large protein families: Relationship between the sequence, structure, and functionâ€based clustering. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2389-2402.	1.5	4
465	The evolution of function in strictosidine synthaseâ€like proteins. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3082-3098.	1.5	43
466	Structures of domains I and IV from YbbR are representative of a widely distributed protein family. Protein Science, 2011, 20, 396-405.	3.1	16
467	Fic domainâ€catalyzed adenylylation: Insight provided by the structural analysis of the type IV secretion system effector BepA. Protein Science, 2011, 20, 492-499.	3.1	50
468	NMR structure of the <i>Bordetella bronchiseptica</i> protein NP_888769.1 establishes a new phageâ€related protein family PF13554. Protein Science, 2011, 20, 1137-1144.	3.1	5
469	Structural classification and properties of ketoacyl synthases. Protein Science, 2011, 20, 1659-1667.	3.1	50
470	Largeâ€Scale Evaluation of CavBase for Analyzing the Polypharmacology of Kinase Inhibitors. Molecular Informatics, 2011, 30, 923-925.	1.4	5
471	Performance of mutation pathogenicity prediction methods on missense variants. Human Mutation, 2011, 32, 358-368.	1.1	468

#	Article	IF	Citations
472	Isolation and expression analysis of a homolog of the 14â€“3â€“3 epsilon gene in the diamondback moth, <i>Plutella xylostella</i>. Archives of Insect Biochemistry and Physiology, 2011, 76, 114-124.	0.6	2
473	Are viruses a source of new protein folds for organisms? â€“ Virosphere structure space and evolution. BioEssays, 2011, 33, 626-635.	1.2	37
474	Autotransporters with GDSL Passenger Domains: Molecular Physiology and Biotechnological Applications. ChemBioChem, 2011, 12, 1476-1485.	1.3	31
475	Discovery of a Metagenomeâ€Derived Enzyme that Produces Branchedâ€Chain Acylâ€(Acylâ€Carrierâ€Protein)s from Branchedâ€Chain Î±â€Keto Acids. ChemBioChem, 2011, 12, 1849-1853.	1.3	8
476	A family tree of vertebrate chemokine receptors for a unified nomenclature. Developmental and Comparative Immunology, 2011, 35, 705-715.	1.0	107
477	Progress in tracing the evolutionary paths of cytochrome P450. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 14-18.	1.1	198
478	RAPYD â€” Rapid Annotation Platform for Yeast Data. Journal of Biotechnology, 2011, 155, 118-126.	1.9	10
479	High-quality genome sequence of Pichia pastoris CBS7435. Journal of Biotechnology, 2011, 154, 312-320.	1.9	146
480	Programmed ribosomal frameshifting in the expression of the regulator of intestinal stem cell proliferation, adenomatous polyposis coli (APC). RNA Biology, 2011, 8, 637-647.	1.5	16
481	Nuclear import of a lipid-modified transcription factor. Cell Cycle, 2011, 10, 3897-3911.	1.3	40
482	Abundance and distribution of the highly iterated palindrome 1 (HIP1) among prokaryotes. Mobile Genetic Elements, 2011, 1, 159-168.	1.8	6
483	Genomics for Key Players in the N Cycle. Methods in Enzymology, 2011, 496, 289-318.	0.4	3
484	BioTRON. , 2011, , .		0
485	New Insights into the Evolution of Metazoan Cadherins. Molecular Biology and Evolution, 2011, 28, 647-657.	3.5	107
486	Genome-scale phylogenetic function annotation of large and diverse protein families. Genome Research, 2011, 21, 1969-1980.	2.4	54
487	Whole-Genome Sequences of Four Mycobacterium bovis BCG Vaccine Strains. Journal of Bacteriology, 2011, 193, 3152-3153.	1.0	28
488	Burkholderia cenocepacia ShvR-Regulated Genes That Influence Colony Morphology, Biofilm Formation, and Virulence. Infection and Immunity, 2011, 79, 2984-2997.	1.0	38
489	A Pilot Study of Bacterial Genes with Disrupted ORFs Reveals a Surprising Profusion of Protein Sequence Recoding Mediated by Ribosomal Frameshifting and Transcriptional Realignment. Molecular Biology and Evolution, 2011, 28, 3195-3211.	3.5	43

#	Article	IF	Citations
490	Characterization of Mutants Deficient in the l,d -Carboxypeptidase (DacB) and WalRK (VicRK) Regulon, Involved in Peptidoglycan Maturation of Streptococcus pneumoniae Serotype 2 Strain D39. Journal of Bacteriology, 2011, 193, 2290-2300.	1.0	57
491	Role of Sphingomonas sp. Strain Fr1 PhyR-NepR-Ïƒ ^{EcfG} Cascade in General Stress Response and Identification of a Negative Regulator of PhyR. Journal of Bacteriology, 2011, 193, 6629-6638.	1.0	60
492	Mutation Screening of the<i>GUCA1B</i>Gene in Patients with Autosomal Dominant Cone and Cone Rod Dystrophy. Ophthalmic Genetics, 2011, 32, 151-155.	0.5	12
493	KUPS: constructing datasets of interacting and non-interacting protein pairs with associated attributions. Nucleic Acids Research, 2011, 39, D750-D754.	6.5	32
494	RBPDB: a database of RNA-binding specificities. Nucleic Acids Research, 2011, 39, D301-D308.	6.5	477
495	The complete genome sequence of<i>Clostridium botulinum</i>F str. 230613, insertion sites, and recombination of BoNT gene clusters. Genome, 2011, 54, 546-554.	0.9	5
496	PredUs: a web server for predicting protein interfaces using structural neighbors. Nucleic Acids Research, 2011, 39, W283-W287.	6.5	101
497	Genomic Differentiation Between Temperate and Tropical Australian Populations of<i>Drosophila melanogaster</i>. Genetics, 2011, 187, 245-260.	1.2	217
498	Interaction of the human prostacyclin receptor with the PDZ adapter protein PDZK1: role in endothelial cell migration and angiogenesis. Molecular Biology of the Cell, 2011, 22, 2664-2679.	0.9	25
499	In Vivo, in Vitro, and X-ray Crystallographic Analyses Suggest the Involvement of an Uncharacterized Triose-phosphate Isomerase (TIM) Barrel Protein in Protection against Oxidative Stress. Journal of Biological Chemistry, 2011, 286, 41636-41646.	1.6	3
500	The Mediator Complex in Plants: Structure, Phylogeny, and Expression Profiling of Representative Genes in a Dicot (Arabidopsis) and a Monocot (Rice) during Reproduction and Abiotic Stress Â. Plant Physiology, 2011, 157, 1609-1627.	2.3	158
501	A comparative genome analysis of the RpoS sigmulon shows a high diversity of responses and origins. Microbiology (United Kingdom), 2011, 157, 1393-1401.	0.7	11
502	The YaaA Protein of the Escherichia coli OxyR Regulon Lessens Hydrogen Peroxide Toxicity by Diminishing the Amount of Intracellular Unincorporated Iron. Journal of Bacteriology, 2011, 193, 2186-2196.	1.0	61
503	DAnCER: Disease-Annotated Chromatin Epigenetics Resource. Nucleic Acids Research, 2011, 39, D889-D894.	6.5	19
504	Binding constraints on the evolution of enzymes and signalling proteins: the important role of negative pleiotropy. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1930-1935.	1.2	27
505	Augmented Annotation of the Schizosaccharomyces pombe Genome Reveals Additional Genes Required for Growth and Viability. Genetics, 2011, 187, 1207-1217.	1.2	26
506	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain Wigar10, Isolated from a Surface-Sterilized Garlic Bulb. Journal of Bacteriology, 2011, 193, 6999-7000.	1.0	5
507	Regulation of the Virulence Determinant OspC by <i>bbd18</i> on Linear Plasmid lp17 of Borrelia burgdorferi. Journal of Bacteriology, 2011, 193, 5365-5373.	1.0	25

#	ARTICLE	IF	CITATIONS
508	Crystal Structure of the Human N-Myc Downstream-regulated Gene 2 Protein Provides Insight into Its Role as a Tumor Suppressor. Journal of Biological Chemistry, 2011, 286, 12450-12460.	1.6	60
509	The RCSB Protein Data Bank: redesigned web site and web services. Nucleic Acids Research, 2011, 39, D392-D401.	6.5	549
510	eGOB: eukaryotic Gene Order Browser. Bioinformatics, 2011, 27, 1150-1151.	1.8	9
511	PRR7 Is a Transmembrane Adaptor Protein Expressed in Activated T Cells Involved in Regulation of T Cell Receptor Signaling and Apoptosis. Journal of Biological Chemistry, 2011, 286, 19617-19629.	1.6	11
512	Identification of a Chemoreceptor Zinc-Binding Domain Common to Cytoplasmic Bacterial Chemoreceptors. Journal of Bacteriology, 2011, 193, 4338-4345.	1.0	33
513	P2CS: a database of prokaryotic two-component systems. Nucleic Acids Research, 2011, 39, D771-D776.	6.5	84
514	The N-Terminal Domain of the Flo1 Flocculation Protein from Saccharomyces cerevisiae Binds Specifically to Mannose Carbohydrates. Eukaryotic Cell, 2011, 10, 110-117.	3.4	35
515	The eisosome core is composed of BAR domain proteins. Molecular Biology of the Cell, 2011, 22, 2360-2372.	0.9	91
516	Revisiting the Yeast PPR Proteinsâ€"Application of an Iterative Hidden Markov Model Algorithm Reveals New Members of the Rapidly Evolving Family. Molecular Biology and Evolution, 2011, 28, 2935-2948.	3.5	44
517	The walls have ears: the role of plant CrRLK1Ls in sensing and transducing extracellular signals. Journal of Experimental Botany, 2011, 62, 1581-1591.	2.4	133
518	ARTADE2DB: Improved Statistical Inferences for Arabidopsis Gene Functions and Structure Predictions by Dynamic Structure-Based Dynamic Expression (DSDE) Analyses. Plant and Cell Physiology, 2011, 52, 254-264.	1.5	15
519	Expression during Host Infection and Localization of Yersinia pestis Autotransporter Proteins. Journal of Bacteriology, 2011, 193, 5936-5949.	1.0	22
520	Complex Principal Component and Correlation Structure of 16 Yeast Genomic Variables. Molecular Biology and Evolution, 2011, 28, 2501-2512.	3.5	10
521	A GCN2-Like Eukaryotic Initiation Factor 2 Kinase Increases the Viability of Extracellular Toxoplasma gondii Parasites. Eukaryotic Cell, 2011, 10, 1403-1412.	3.4	44
522	Uncovering the Human Methyltransferasome. Molecular and Cellular Proteomics, 2011, 10, M110.000976.	2.5	234
523	A valid mouse model of AGRIN-associated congenital myasthenic syndrome. Human Molecular Genetics, 2011, 20, 4617-4633.	1.4	40
524	Specific expression of a TRIM-containing factor in ectoderm cells affects the skeletal morphogenetic program of the sea urchin embryo. Development (Cambridge), 2011, 138, 4279-4290.	1.2	20
525	Characterization of the Genome of the Polyvalent Lytic Bacteriophage GTE2, Which Has Potential for Biocontrol of Gordonia-, Rhodococcus-, and Nocardia-Stabilized Foams in Activated Sludge Plants. Applied and Environmental Microbiology, 2011, 77, 3923-3929.	1.4	69

#	Article	IF	Citations
526	Complete Genome Sequence of Gallibacterium anatis Strain UMN179, Isolated from a Laying Hen with Peritonitis. Journal of Bacteriology, 2011, 193, 3676-3677.	1.0	24
527	Characterization of the relationship between integrase, excisionase and antirepressor activities associated with a superinfecting Shiga toxin encoding bacteriophage. Nucleic Acids Research, 2011, 39, 2116-2129.	6.5	51
528	Genetic Response to Bacteriophage Infection in Lactococcus lactis Reveals a Four-Strand Approach Involving Induction of Membrane Stress Proteins, <scp>d</scp> -Alanylation of the Cell Wall, Maintenance of Proton Motive Force, and Energy Conservation. Journal of Virology, 2011, 85, 12032-12042.	1.5	56
529	Phosfinder: a web server for the identification of phosphate-binding sites on protein structures. Nucleic Acids Research, 2011, 39, W278-W282.	6.5	13
530	PlantTFDB 2.0: update and improvement of the comprehensive plant transcription factor database. Nucleic Acids Research, 2011, 39, D1114-D1117.	6.5	288
531	Complete characterization of the edited transcriptome of the mitochondrion of Physarum polycephalum using deep sequencing of RNA. Nucleic Acids Research, 2011, 39, 6044-6055.	6.5	105
532	ATP Synthase Complex of Plasmodium falciparum. Journal of Biological Chemistry, 2011, 286, 41312-41322.	1.6	69
533	The N-terminal Nucleophile Serine of Cephalosporin Acylase Executes the Second Autoproteolytic Cleavage and Acylpeptide Hydrolysis. Journal of Biological Chemistry, 2011, 286, 24476-24486.	1.6	11
534	The Gene3D Web Services: a platform for identifying, annotating and comparing structural domains in protein sequences. Nucleic Acids Research, 2011, 39, W546-W550.	6.5	16
535	PhEVER: a database for the global exploration of virusâ€"host evolutionary relationships. Nucleic Acids Research, 2011, 39, D569-D575.	6.5	10
536	GProX, a User-Friendly Platform for Bioinformatics Analysis and Visualization of Quantitative Proteomics Data. Molecular and Cellular Proteomics, 2011, 10, O110.007450.	2.5	150
537	CoMetâ€"a web server for comparative functional profiling of metagenomes. Nucleic Acids Research, 2011, 39, W518-W523.	6.5	50
538	A Complex Lipoate Utilization Pathway in Listeria monocytogenes. Journal of Biological Chemistry, 2011, 286, 31447-31456.	1.6	32
539	A novel three-unit tRNA splicing endonuclease found in ultrasmall Archaea possesses broad substrate specificity. Nucleic Acids Research, 2011, 39, 9695-9704.	6.5	32
540	Proteases/Antiproteases in Inflammatory Bowel Diseases. , 2011, , 173-215.		3
541	Complete Genome Sequence of Bifidobacterium bifidum S17. Journal of Bacteriology, 2011, 193, 301-302.	1.0	35
542	Polycystic kidney disease-like domains of clostridial collagenases and their role in collagen recruitment. Biological Chemistry, 2011, 392, 1039-1045.	1.2	16
543	CancerResource: a comprehensive database of cancer-relevant proteins and compound interactions supported by experimental knowledge. Nucleic Acids Research, 2011, 39, D960-D967.	6.5	70

#	ARTICLE	IF	CITATIONS
544	A reverse transcriptase-related protein mediates phage resistance and polymerizes untemplated DNA in vitro. Nucleic Acids Research, 2011, 39, 7620-7629.	6.5	49
545	Transcriptome dynamics through alternative polyadenylation in developmental and environmental responses in plants revealed by deep sequencing. Genome Research, 2011, 21, 1478-1486.	2.4	117
546	Identification of Drought-Responsive Universal Stress Proteins in Viridiplantae. Bioinformatics and Biology Insights, 2011, 5, BBI.S6061.	1.0	52
547	Prp8, the pivotal protein of the spliceosomal catalytic center, evolved from a retroelement-encoded reverse transcriptase. Rna, 2011, 17, 799-808.	1.6	78
548	Plasmids of Raw Milk Cheese Isolate Lactococcus lactis subsp. lactis Biovar diacetylactis DPC3901 Suggest a Plant-Based Origin for the Strain. Applied and Environmental Microbiology, 2011, 77, 6451-6462.	1.4	21
549	Extracellular Aldonolactonase from <i>Myceliophthora thermophila</i>. Applied and Environmental Microbiology, 2011, 77, 650-656.	1.4	50
550	Genome Sequence of the Spinosyns-Producing Bacterium Saccharopolyspora spinosa NRRL 18395. Journal of Bacteriology, 2011, 193, 3150-3151.	1.0	21
551	The Riboswitch Regulates a Thiamine Pyrophosphate ABC Transporter of the Oral Spirochete Treponema denticola. Journal of Bacteriology, 2011, 193, 3912-3922.	1.0	26
552	Genome Sequences of Salmonella enterica Serovar Typhimurium, Choleraesuis, Dublin, and Gallinarum Strains of Well- Defined Virulence in Food-Producing Animals. Journal of Bacteriology, 2011, 193, 3162-3163.	1.0	61
553	Mycoplasma gallisepticum and Mycoplasma synoviae express a cysteine protease CysP, which can cleave chicken IgG into Fab and Fc. Microbiology (United Kingdom), 2011, 157, 362-372.	0.7	41
554	The enigmatic genome of Chara australis virus. Journal of General Virology, 2011, 92, 2679-2690.	1.3	30
555	A Three-Step Validation Following Genome-Wide Data Mining for Myosin Family Members Improves Search Efficiency. , 2011, , .		1
556	PolyQ: a database describing the sequence and domain context of polyglutamine repeats in proteins. Nucleic Acids Research, 2011, 39, D272-D276.	6.5	18
557	The Protein Ontology: a structured representation of protein forms and complexes. Nucleic Acids Research, 2011, 39, D539-D545.	6.5	102
558	SLiMSearch 2.0: biological context for short linear motifs in proteins. Nucleic Acids Research, 2011, 39, W56-W60.	6.5	68
559	Niche of harmful alga <i>Aureococcus anophagefferens</i> revealed through ecogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4352-4357.	3.3	256
560	Bacterial Tubulin Distinct Loop Sequences and Primitive Assembly Properties Support Its Origin from a Eukaryotic Tubulin Ancestor. Journal of Biological Chemistry, 2011, 286, 19789-19803.	1.6	35
561	The Atypical Two-component Sensor Kinase Lpl0330 from Legionella pneumophila Controls the Bifunctional Diguanylate Cyclase-Phosphodiesterase Lpl0329 to Modulate Bis-(3â€²-5â€²)-cyclic Dimeric GMP Synthesis. Journal of Biological Chemistry, 2011, 286, 31136-31144.	1.6	36

#	ARTICLE	IF	CITATIONS
562	Topology of 1-Acyl-sn-glycerol-3-phosphate Acyltransferases SLC1 and ALE1 and Related Membrane-bound O-Acyltransferases (MBOATs) of Saccharomyces cerevisiae. Journal of Biological Chemistry, 2011, 286, 36438-36447.	1.6	49
563	A New Family of Carbohydrate Esterases Is Represented by a GDSL Hydrolase/Acetylxylan Esterase from Geobacillus stearothermophilus. Journal of Biological Chemistry, 2011, 286, 41993-42001.	1.6	52
564	Gypsy and the Birth of the SCAN Domain. Journal of Virology, 2011, 85, 12043-12052.	1.5	45
565	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. Nucleic Acids Research, 2011, 39, 4202-4219.	6.5	69
566	DIMA 3.0: Domain Interaction Map. Nucleic Acids Research, 2011, 39, D724-D729.	6.5	41
567	Laminin database: a tool to retrieve high-throughput and curated data for studies on laminins. Nucleic Acids Research, 2011, 39, D320-D323.	6.5	3
568	Recurrent Adaptation in RNA Interference Genes Across the Drosophila Phylogeny. Molecular Biology and Evolution, 2011, 28, 1033-1042.	3.5	76
569	An expanded binding model for Cys₂His₂zinc finger proteinâ€"DNA interfaces. Physical Biology, 2011, 8, 035010.	0.8	29
570	Identification and Sequencing of a Novel Rodent Gammaherpesvirus That Establishes Acute and Latent Infection in Laboratory Mice. Journal of Virology, 2011, 85, 2642-2656.	1.5	22
571	Role of RecJ-like Protein with 5â€²-3â€² Exonuclease Activity in Oligo(deoxy)nucleotide Degradation. Journal of Biological Chemistry, 2011, 286, 2807-2816.	1.6	32
572	Using the Acropora digitifera genome to understand coral responses to environmental change. Nature, 2011, 476, 320-323.	13.7	758
573	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1293-301.	3.3	1,231
574	A PLAC8-containing protein from an endomycorrhizal fungus confers cadmium resistance to yeast cells by interacting with Mlh3p. Nucleic Acids Research, 2011, 39, 7548-7563.	6.5	19
575	Autophagy in protists. Autophagy, 2011, 7, 127-158.	4.3	148
576	Flowering time variation in oilseed rape (Brassica napus L.) is associated with allelic variation in the FRIGIDA homologue BnaA.FRI.a. Journal of Experimental Botany, 2011, 62, 5641-5658.	2.4	114
577	Compensated pathogenic deviations. Biomolecular Concepts, 2011, 2, 281-292.	1.0	7
578	Identification of new homologs of PD-(D/E)XK nucleases by support vector machines trained on data derived from profileâ€"profile alignments. Nucleic Acids Research, 2011, 39, 1187-1196.	6.5	34
579	Identification of<i>Escherichia coli</i>ZapC (YcbW) as a Component of the Division Apparatus That Binds and Bundles FtsZ Polymers. Journal of Bacteriology, 2011, 193, 1393-1404.	1.0	97

#	Article	IF	Citations
580	Germline Fitness-Based Scoring of Cancer Mutations. Genetics, 2011, 188, 383-393.	1.2	15
581	The Steady-State Repertoire of Human SCF Ubiquitin Ligase Complexes Does Not Require Ongoing Nedd8 Conjugation. Molecular and Cellular Proteomics, 2011, 10, M110.006460.	2.5	54
582	Structure and Function of DsbA, a Key Bacterial Oxidative Folding Catalyst. Antioxidants and Redox Signaling, 2011, 14, 1729-1760.	2.5	96
583	AUXIN UP-REGULATED F-BOX PROTEIN1 Regulates the Cross Talk between Auxin Transport and Cytokinin Signaling during Plant Root Growth Â Â. Plant Physiology, 2011, 156, 1878-1893.	2.3	36
584	<i>HCF243</i> Encodes a Chloroplast-Localized Protein Involved in the D1 Protein Stability of the Arabidopsis Photosystem II Complex Â Â. Plant Physiology, 2011, 157, 608-619.	2.3	22
585	Structural and Functional Assays of AtTLP18.3 Identify Its Novel Acid Phosphatase Activity in Thylakoid Lumen Â Â. Plant Physiology, 2011, 157, 1015-1025.	2.3	39
586	A Three-Dimensional RNA Motif in<i>Potato spindle tuber viroid</i>Mediates Trafficking from Palisade Mesophyll to Spongy Mesophyll in<i>Nicotiana benthamiana</i>Â. Plant Cell, 2011, 23, 258-272.	3.1	69
587	Maize <i>opaque5</i> Encodes Monogalactosyldiacylglycerol Synthase and Specifically Affects Galactolipids Necessary for Amyloplast and Chloroplast Function Â Â. Plant Cell, 2011, 23, 2331-2347.	3.1	85
588	Structure and properties of the Ca2+-binding CUB domain, a widespread ligand-recognition unit involved in major biological functions. Biochemical Journal, 2011, 439, 185-193.	1.7	55
589	Fold and Function of the InlB B-repeat. Journal of Biological Chemistry, 2011, 286, 15496-15506.	1.6	38
590	The C-terminal Region of the Exosome-associated Protein Rrp47 Is Specifically Required for Box C/D Small Nucleolar RNA 3â€²-Maturation. Journal of Biological Chemistry, 2011, 286, 4535-4543.	1.6	36
591	ZF21 Protein, a Regulator of the Disassembly of Focal Adhesions and Cancer Metastasis, Contains a Novel Noncanonical Pleckstrin Homology Domain. Journal of Biological Chemistry, 2011, 286, 31598-31609.	1.6	14
592	A bacterial process for selenium nanosphere assembly. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13480-13485.	3.3	165
593	<i>In Vitro</i> Studies Indicate a High Resistance Potential for the Lantibiotic Nisin in Staphylococcus aureus and Define a Genetic Basis for Nisin Resistance. Antimicrobial Agents and Chemotherapy, 2011, 55, 2362-2368.	1.4	73
594	The<i>tib</i>Adherence Locus of Enterotoxigenic<i>Escherichia coli</i>Is Regulated by Cyclic AMP Receptor Protein. Journal of Bacteriology, 2011, 193, 1369-1376.	1.0	10
595	Full-Length De Novo Sequence of the Chlamydophila psittaci Type Strain, 6BC. Journal of Bacteriology, 2011, 193, 2662-2663.	1.0	21
596	Complex microbiome underlying secondary and primary metabolism in the tunicate- <i>Prochloron</i> symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1423-32.	3.3	146
597	Outer membrane adhesion factor multivalent adhesion molecule 7 initiates host cell binding during infection by Gram-negative pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11614-11619.	3.3	128

#	Article	IF	Citations
598	Identification of Nicotinamide Mononucleotide Deamidase of the Bacterial Pyridine Nucleotide Cycle Reveals a Novel Broadly Conserved Amidohydrolase Family. Journal of Biological Chemistry, 2011, 286, 40365-40375.	1.6	54
599	The GreenCut2 Resource, a Phylogenomically Derived Inventory of Proteins Specific to the Plant Lineage. Journal of Biological Chemistry, 2011, 286, 21427-21439.	1.6	113
600	Misannotations of rRNA can now generate 90% false positive protein matches in metatranscriptomic studies. Nucleic Acids Research, 2011, 39, 8792-8802.	6.5	57
601	Spatial clustering of protein binding sites for template based protein docking. Bioinformatics, 2011, 27, 2820-2827.	1.8	36
602	Evolutionary History and Functional Characterization of Three Large Genes Involved in Sporulation in Bacillus cereus Group Bacteria. Journal of Bacteriology, 2011, 193, 5420-5430.	1.0	5
603	Genome Sequence of the Ruminal Bacterium Megasphaera elsdenii. Journal of Bacteriology, 2011, 193, 5578-5579.	1.0	44
604	Chromatin-modifying Complex Component Nurf55/p55 Associates with Histones H3 and H4 and Polycomb Repressive Complex 2 Subunit Su(z)12 through Partially Overlapping Binding Sites. Journal of Biological Chemistry, 2011, 286, 23388-23396.	1.6	61
605	Protein Folding and Quality Control in the ER. Cold Spring Harbor Perspectives in Biology, 2011, 3, a007526-a007526.	2.3	290
606	2,3-Butanediol Production by Acetogenic Bacteria, an Alternative Route to Chemical Synthesis, Using Industrial Waste Gas. Applied and Environmental Microbiology, 2011, 77, 5467-5475.	1.4	362
607	LFR1 Ferric Iron Reductase of Leishmania amazonensis Is Essential for the Generation of Infective Parasite Forms. Journal of Biological Chemistry, 2011, 286, 23266-23279.	1.6	61
608	Multiple congenital anomalies-hypotonia-seizures syndrome is caused by a mutation in PIGN. Journal of Medical Genetics, 2011, 48, 383-389.	1.5	138
609	SEQUENCE-BASED ENZYME CATALYTIC DOMAIN PREDICTION USING CLUSTERING AND AGGREGATED MUTUAL INFORMATION CONTENT. Journal of Bioinformatics and Computational Biology, 2011, 09, 597-611.	0.3	7
610	Genome Sequence and Characterization of the <i>Tsukamurella</i> Bacteriophage TPA2. Applied and Environmental Microbiology, 2011, 77, 1389-1398.	1.4	59
611	Physical Mapping of Innate Immune Genes, Mucins and Lysozymes, and Other Non-Mucin Proteins in the Tammar Wallaby <i>(Macropus eugenii)</i>. Cytogenetic and Genome Research, 2011, 135, 118-125.	0.6	4
612	NRPSpredictor2â€"a web server for predicting NRPS adenylation domain specificity. Nucleic Acids Research, 2011, 39, W362-W367.	6.5	559
613	Automatic annotation of experimentally derived, evolutionarily conserved post-translational modifications onto multiple genomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar019-bar019.	1.4	3
614	Effective--a database of predicted secreted bacterial proteins. Nucleic Acids Research, 2011, 39, D591-D595.	6.5	102
615	The PIN-domain ribonucleases and the prokaryotic VapBC toxin-antitoxin array. Protein Engineering, Design and Selection, 2011, 24, 33-40.	1.0	148

#	ARTICLE	IF	CITATIONS
616	CorE from Myxococcus xanthus Is a Copper-Dependent RNA Polymerase Sigma Factor. PLoS Genetics, 2011, 7, e1002106.	1.5	49
617	ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. Nucleic Acids Research, 2011, 39, D80-D85.	6.5	38
618	Accelerated Profile HMM Searches. PLoS Computational Biology, 2011, 7, e1002195.	1.5	5,076
619	The FGGY Carbohydrate Kinase Family: Insights into the Evolution of Functional Specificities. PLoS Computational Biology, 2011, 7, e1002318.	1.5	48
620	Comparative Genomic Analysis of Human Fungal Pathogens Causing Paracoccidioidomycosis. PLoS Genetics, 2011, 7, e1002345.	1.5	164
621	Towards a Semen Proteome of the Dengue Vector Mosquito: Protein Identification and Potential Functions. PLoS Neglected Tropical Diseases, 2011, 5, e989.	1.3	110
622	Klebsiella pneumoniae yggG Gene Product: A Zinc-Dependent Metalloprotease. International Journal of Molecular Sciences, 2011, 12, 4441-4455.	1.8	4
623	Genome-Wide Identification, Classification, and Expression Analysis of Autophagy-Associated Gene Homologues in Rice (Oryza sativa L.). DNA Research, 2011, 18, 363-377.	1.5	133
624	Genome of Herbaspirillum seropedicae Strain SmR1, a Specialized Diazotrophic Endophyte of Tropical Grasses. PLoS Genetics, 2011, 7, e1002064.	1.5	188
625	Combinations of Protein-Chemical Complex Structures Reveal New Targets for Established Drugs. PLoS Computational Biology, 2011, 7, e1002043.	1.5	25
626	Genomic Insights into the Origin of Parasitism in the Emerging Plant Pathogen Bursaphelenchus xylophilus. PLoS Pathogens, 2011, 7, e1002219.	2.1	351
627	PDBpaint, a visualization webservice to tag protein structures with sequence annotations. Bioinformatics, 2011, 27, 2605-2606.	1.8	3
628	Independent Subtilases Expansions in Fungi Associated with Animals. Molecular Biology and Evolution, 2011, 28, 3395-3404.	3.5	51
629	Genetic Basis for Daptomycin Resistance in Enterococci. Antimicrobial Agents and Chemotherapy, 2011, 55, 3345-3356.	1.4	165
630	Differential Evolution of Voltage-Gated Sodium Channels in Tetrapods and Teleost Fishes. Molecular Biology and Evolution, 2011, 28, 859-871.	3.5	72
631	SUPERFAMILY 1.75 including a domain-centric gene ontology method. Nucleic Acids Research, 2011, 39, D427-D434.	6.5	147
632	OMPdb: a database of Â-barrel outer membrane proteins from Gram-negative bacteria. Nucleic Acids Research, 2011, 39, D324-D331.	6.5	60
633	A White Spruce Gene Catalog for Conifer Genome Analyses Â Â. Plant Physiology, 2011, 157, 14-28.	2.3	143

#	Article	IF	Citations
634	Modeling of multi domain contribution to protein interaction. , 2011, , .		0
635	Community cyberinfrastructure for Advanced Microbial Ecology Research and Analysis: the CAMERA resource. Nucleic Acids Research, 2011, 39, D546-D551.	6.5	291
636	Phosphate binding sites identification in protein structures. Nucleic Acids Research, 2011, 39, 1231-1242.	6.5	15
637	The Lymantria dispar IPLB-Ld652Y Cell Line Transcriptome Comprises Diverse Virus-Associated Transcripts. Viruses, 2011, 3, 2339-2350.	1.5	16
638	Crystal structures of an archaeal class II DNA photolyase and its complex with UV-damaged duplex DNA. EMBO Journal, 2011, 30, 4437-4449.	3.5	82
639	ThYme: a database for thioester-active enzymes. Nucleic Acids Research, 2011, 39, D342-D346.	6.5	55
640	Proteins with Complex Architecture as Potential Targets for Drug Design: A Case Study of Mycobacterium tuberculosis. PLoS Computational Biology, 2011, 7, e1002118.	1.5	21
641	FFAS server: novel features and applications. Nucleic Acids Research, 2011, 39, W38-W44.	6.5	130
642	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. Nucleic Acids Research, 2011, 39, 9473-9497.	6.5	154
643	Genomic Transition to Pathogenicity in Chytrid Fungi. PLoS Pathogens, 2011, 7, e1002338.	2.1	99
644	â€œFluctuogramsâ€•Reveal the Intermittent Intra-Protein Communication in Subtilisin Carlsberg and Correlate Mechanical Coupling with Co-Evolution. PLoS Computational Biology, 2011, 7, e1002023.	1.5	19
645	The Steroid Catabolic Pathway of the Intracellular Pathogen Rhodococcus equi Is Important for Pathogenesis and a Target for Vaccine Development. PLoS Pathogens, 2011, 7, e1002181.	2.1	73
646	Identification of a Putative Chaperone Involved in Stress Resistance and Virulence in Francisella tularensis. Infection and Immunity, 2011, 79, 1428-1439.	1.0	35
647	Accurate Quantification of Functional Analogy among Close Homologs. PLoS Computational Biology, 2011, 7, e1001074.	1.5	34
648	PAIR: the predicted Arabidopsis interactome resource. Nucleic Acids Research, 2011, 39, D1134-D1140.	6.5	57
649	Evidence of abundant stop codon readthrough in <i>Drosophila</i> and other metazoa. Genome Research, 2011, 21, 2096-2113.	2.4	196
650	Genome, Functional Gene Annotation, and Nuclear Transformation of the Heterokont Oleaginous Alga Nannochloropsis oceanica CCMP1779. PLoS Genetics, 2012, 8, e1003064.	1.5	376
651	The Genome of the Obligate Intracellular Parasite Trachipleistophora hominis: New Insights into Microsporidian Genome Dynamics and Reductive Evolution. PLoS Pathogens, 2012, 8, e1002979.	2.1	127

#	Article	IF	Citations
652	Co-expression of cell-wall related genes: new tools and insights. Frontiers in Plant Science, 2012, 3, 83.	1.7	55
653	Beyond the Binding Site: The Role of the Î²2 â€“ Î²3 Loop and Extra-Domain Structures in PDZ Domains. PLoS Computational Biology, 2012, 8, e1002429.	1.5	40
654	Intronic Cis-Regulatory Modules Mediate Tissue-Specific and Microbial Control of angptl4/fiaf Transcription. PLoS Genetics, 2012, 8, e1002585.	1.5	44
655	Genetic and Biochemical Dissection of a HisKA Domain Identifies Residues Required Exclusively for Kinase and Phosphatase Activities. PLoS Genetics, 2012, 8, e1003084.	1.5	88
656	The Chordate Proteome History Database. Evolutionary Bioinformatics, 2012, 8, EBO.S9186.	0.6	5
657	Deep Sequencing of Porphyromonas gingivalis and Comparative Transcriptome Analysis of a LuxS Mutant. Frontiers in Cellular and Infection Microbiology, 2012, 2, 79.	1.8	27
658	Interpretation of the Consequences of Mutations in Protein Kinases: Combined Use of Bioinformatics and Text Mining. Frontiers in Physiology, 2012, 3, 323.	1.3	9
659	Structural classification and properties of ketoacyl reductases, hydroxyacyl dehydratases and enoyl reductases. Protein Engineering, Design and Selection, 2012, 25, 803-811.	1.0	7
660	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	6.5	321
661	Molecular Characterization and Comparative Sequence Analysis of Defense-Related Gene, Oryza rufipogon Receptor-Like Protein Kinase 1. International Journal of Molecular Sciences, 2012, 13, 9343-9362.	1.8	5
662	A Transcriptomic Analysis of Echinococcus granulosus Larval Stages: Implications for Parasite Biology and Host Adaptation. PLoS Neglected Tropical Diseases, 2012, 6, e1897.	1.3	72
663	Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, â€œCandidatus Nitrosopumilus sediminisâ€• AR2, from Svalbard in the Arctic Circle. Journal of Bacteriology, 2012, 194, 6948-6949.	1.0	52
664	The HARE-HTH and associated domains. Cell Cycle, 2012, 11, 119-131.	1.3	81
665	Cellulose Degradation by Sulfolobus solfataricus Requires a Cell-Anchored Endo-Î²-1-4-Glucanase. Journal of Bacteriology, 2012, 194, 5091-5100.	1.0	42
666	A SEL1L Mutation Links a Canine Progressive Early-Onset Cerebellar Ataxia to the Endoplasmic Reticulumâ€“Associated Protein Degradation (ERAD) Machinery. PLoS Genetics, 2012, 8, e1002759.	1.5	52
667	Vasa-Like DEAD-Box RNA Helicases of Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2012, 6, e1686.	1.3	25
668	Genome Sequences and Characterization of the Related Gordonia Phages GTE5 and GRU1 and Their Use as Potential Biocontrol Agents. Applied and Environmental Microbiology, 2012, 78, 42-47.	1.4	34
669	Distinct functional roles of the two terminal halves of eukaryotic phosphofructokinase. Biochemical Journal, 2012, 445, 213-218.	1.7	3

#	Article	IF	Citations
670	This DÃ©jÃ Vu Feelingâ€"Analysis of Multidomain Protein Evolution in Eukaryotic Genomes. PLoS Computational Biology, 2012, 8, e1002701.	1.5	37
671	Production of Virus-Derived Ping-Pong-Dependent piRNA-like Small RNAs in the Mosquito Soma. PLoS Pathogens, 2012, 8, e1002470.	2.1	277
672	Discrete Cyclic di-GMP-Dependent Control of Bacterial Predation versus Axenic Growth in Bdellovibrio bacteriovorus. PLoS Pathogens, 2012, 8, e1002493.	2.1	80
673	Genome-Wide Identification and in Silico Analysis of Poplar Peptide Deformylases. International Journal of Molecular Sciences, 2012, 13, 5112-5124.	1.8	4
674	Characterization of Erysiphe necator-Responsive Genes in Chinese Wild Vitis quinquangularis. International Journal of Molecular Sciences, 2012, 13, 11497-11519.	1.8	16
675	DFVF: database of fungal virulence factors. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas032-bas032.	1.4	80
676	Network Evolution: Rewiring and Signatures of Conservation in Signaling. PLoS Computational Biology, 2012, 8, e1002411.	1.5	30
677	Characterization of Species-Specific Repeats in 613 Prokaryotic Species. DNA Research, 2012, 19, 219-230.	1.5	10
678	Independent Effects of Alternative Splicing and Structural Constraint on the Evolution of Mammalian Coding Exons. Molecular Biology and Evolution, 2012, 29, 187-193.	3.5	10
679	Whole Genome Analysis of Leptospira licerasiae Provides Insight into Leptospiral Evolution and Pathogenicity. PLoS Neglected Tropical Diseases, 2012, 6, e1853.	1.3	60
680	Viral Proteins Acquired from a Host Converge to Simplified Domain Architectures. PLoS Computational Biology, 2012, 8, e1002364.	1.5	33
681	Computer-Based Annotation of Putative AraC/XylS-Family Transcription Factors of Known Structure but Unknown Function. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-14.	3.0	14
682	Molecular Characterization of the EhaG and UpaG Trimeric Autotransporter Proteins from Pathogenic Escherichia coli. Applied and Environmental Microbiology, 2012, 78, 2179-2189.	1.4	65
683	ProtoNet 6.0: organizing 10 million protein sequences in a compact hierarchical family tree. Nucleic Acids Research, 2012, 40, D313-D320.	6.5	46
684	Long-Term and Short-Term Evolutionary Impacts of Transposable Elements on<i>Drosophila</i>. Genetics, 2012, 192, 1411-1432.	1.2	45
685	Comparative Genomics of Enterococci: Variation in Enterococcus faecalis, Clade Structure in E. faecium, and Defining Characteristics of <i>E</i> .Â <i>gallinarum</i> and <i>E</i> .Â <i>casseliflavus</i>. MBio, 2012, 3, e00318-11.	1.8	259
686	Genome Shrinkage and Loss of Nutrient-Providing Potential in the Obligate Symbiont of the Primitive Termite Mastotermes darwiniensis. Applied and Environmental Microbiology, 2012, 78, 204-210.	1.4	72
687	E3Net: A System for Exploring E3-mediated Regulatory Networks of Cellular Functions. Molecular and Cellular Proteomics, 2012, 11, O111.014076.	2.5	29

#	ARTICLE	IF	CITATIONS
688	A Novel Phage Element of Salmonella enterica Serovar Enteritidis P125109 Contributes to Accelerated Type III Secretion System 2-Dependent Early Inflammation Kinetics in a Mouse Colitis Model. Infection and Immunity, 2012, 80, 3236-3246.	1.0	26
689	The identification of short linear motif-mediated interfaces within the human interactome. Bioinformatics, 2012, 28, 976-982.	1.8	63
690	iELM--a web server to explore short linear motif-mediated interactions. Nucleic Acids Research, 2012, 40, W364-W369.	6.5	33
691	SitEx: a computer system for analysis of projections of protein functional sites on eukaryotic genes. Nucleic Acids Research, 2012, 40, D278-D283.	6.5	5
692	Complete Resequencing and Reannotation of the Lactobacillus plantarum WCFS1 Genome. Journal of Bacteriology, 2012, 194, 195-196.	1.0	109
693	A VapBC Toxin-Antitoxin Module Is a Posttranscriptional Regulator of Metabolic Flux in Mycobacteria. Journal of Bacteriology, 2012, 194, 2189-2204.	1.0	75
694	SdhE Is a Conserved Protein Required for Flavinylation of Succinate Dehydrogenase in Bacteria. Journal of Biological Chemistry, 2012, 287, 18418-18428.	1.6	58
695	Functional Cell Surface Display and Controlled Secretion of Diverse Agarolytic Enzymes by Escherichia coli with a Novel Ligation-Independent Cloning Vector Based on the Autotransporter YfaL. Applied and Environmental Microbiology, 2012, 78, 3051-3058.	1.4	16
696	MIPModDB: a central resource for the superfamily of major intrinsic proteins. Nucleic Acids Research, 2012, 40, D362-D369.	6.5	33
697	YeTFaSCo: a database of evaluated yeast transcription factor sequence specificities. Nucleic Acids Research, 2012, 40, D169-D179.	6.5	195
698	A conserved region in the prM protein is a critical determinant in the assembly of flavivirus particles. Journal of General Virology, 2012, 93, 27-38.	1.3	42
699	DNAtraffic--a new database for systems biology of DNA dynamics during the cell life. Nucleic Acids Research, 2012, 40, D1235-D1240.	6.5	4
700	A Genome-Wide RNAi Screen for Enhancers of <i>par</i> Mutants Reveals New Contributors to Early Embryonic Polarity in <i>Caenorhabditis elegans</i>. Genetics, 2012, 192, 929-942.	1.2	24
701	Evolutionary and genetic analyses of mitochondrial translation initiation factors identify the missing mitochondrial IF3 in S. cerevisiae. Nucleic Acids Research, 2012, 40, 6122-6134.	6.5	41
702	Heuristic Methods for Finding Pathogenic Variants in Gene Coding Sequences. Journal of the American Heart Association, 2012, 1, e002642.	1.6	12
703	Comparative Analysis of Benzoxazinoid Biosynthesis in Monocots and Dicots: Independent Recruitment of Stabilization and Activation Functions. Plant Cell, 2012, 24, 915-928.	3.1	58
704	Genome Sequences and Phylogenetic Analysis of K88- and F18-Positive Porcine Enterotoxigenic Escherichia coli. Journal of Bacteriology, 2012, 194, 395-405.	1.0	64
705	UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769.	6.5	83

#	ARTICLE	IF	CITATIONS
706	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	1.4	38
707	Small but Sufficient: the Rhodococcus Phage RRH1 Has the Smallest Known Siphoviridae Genome at 14.2 Kilobases. Journal of Virology, 2012, 86, 358-363.	1.5	36
708	An Efficient Markov Chain Monte Carlo Method for Mixture Models by Neighborhood Pruning. Journal of Computational and Graphical Statistics, 2012, 21, 197-216.	0.9	3
709	Tetrahymena genome database Wiki: a community-maintained model organism database. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas007-bas007.	1.4	38
710	Identification of two voltage-dependent anion channel-like protein sequences conserved in Kinetoplastida. Biology Letters, 2012, 8, 446-449.	1.0	17
711	Comparative Proteomics Reveals a Significant Bias Toward Alternative Protein Isoforms with Conserved Structure and Function. Molecular Biology and Evolution, 2012, 29, 2265-2283.	3.5	71
712	The Dynamics and Evolutionary Potential of Domain Loss and Emergence. Molecular Biology and Evolution, 2012, 29, 787-796.	3.5	68
713	GeneDB--an annotation database for pathogens. Nucleic Acids Research, 2012, 40, D98-D108.	6.5	217
714	Adaptive Immunity Restricts Replication of Novel Murine Astroviruses. Journal of Virology, 2012, 86, 12262-12270.	1.5	65
715	Nucleoid-Enriched Proteomes in Developing Plastids and Chloroplasts from Maize Leaves: A New Conceptual Framework for Nucleoid Functions Â Â Â. Plant Physiology, 2012, 158, 156-189.	2.3	216
716	Protein Databases on the Internet. Current Protocols in Molecular Biology, 2012, 97, Unit 19.4..	2.9	6
717	Profiling Lipidâ€"protein Interactions Using Nonquenched Fluorescent Liposomal Nanovesicles and Proteome Microarrays. Molecular and Cellular Proteomics, 2012, 11, 1177-1190.	2.5	36
718	The Dormancy Regulator DosR Controls Ribosome Stability in Hypoxic Mycobacteria. Journal of Biological Chemistry, 2012, 287, 24053-24063.	1.6	76
719	Structural bioinformatics of the human spliceosomal proteome. Nucleic Acids Research, 2012, 40, 7046-7065.	6.5	40
720	Pangenomic Study of Corynebacterium diphtheriae That Provides Insights into the Genomic Diversity of Pathogenic Isolates from Cases of Classical Diphtheria, Endocarditis, and Pneumonia. Journal of Bacteriology, 2012, 194, 3199-3215.	1.0	142
721	Involvement of Peptidylprolyl <i>cis</i> / <i>trans</i> Isomerases in Enterococcus faecalis Virulence. Infection and Immunity, 2012, 80, 1728-1735.	1.0	34
722	IDEAL: Intrinsically Disordered proteins with Extensive Annotations and Literature. Nucleic Acids Research, 2012, 40, D507-D511.	6.5	84
723	BnMs3 is required for tapetal differentiation and degradation, microspore separation, and pollen-wall biosynthesis in Brassica napus. Journal of Experimental Botany, 2012, 63, 2041-2058.	2.4	56

#	ARTICLE	IF	CITATIONS
724	Xanthusbase after five years expands to become Openmods. Nucleic Acids Research, 2012, 40, D1288-D1294.	6.5	1
725	AnimalTFDB: a comprehensive animal transcription factor database. Nucleic Acids Research, 2012, 40, D144-D149.	6.5	265
726	Recent Retrotransposon Insertions Are Methylated and Phylogenetically Clustered in Japonica Rice (Oryza sativa spp. japonica). Molecular Biology and Evolution, 2012, 29, 3193-3203.	3.5	22
727	Surface Display of N-Terminally Anchored Invasin by Lactobacillus plantarum Activates NF-Î°B in Monocytes. Applied and Environmental Microbiology, 2012, 78, 5864-5871.	1.4	53
728	FunTree: a resource for exploring the functional evolution of structurally defined enzyme superfamilies. Nucleic Acids Research, 2012, 40, D776-D782.	6.5	44
729	Assignment of protein sequences to existing domain and family classification systems: Pfam and the PDB. Bioinformatics, 2012, 28, 2763-2772.	1.8	56
730	Expression of PaNAC01, a Picea abies CUP-SHAPED COTYLEDON orthologue, is regulated by polar auxin transport and associated with differentiation of the shoot apical meristem and formation of separated cotyledons. Annals of Botany, 2012, 110, 923-934.	1.4	46
731	Analyzing large biological datasets with association networks. Nucleic Acids Research, 2012, 40, e131-e131.	6.5	40
732	A Rickettsia Genome Overrun by Mobile Genetic Elements Provides Insight into the Acquisition of Genes Characteristic of an Obligate Intracellular Lifestyle. Journal of Bacteriology, 2012, 194, 376-394.	1.0	152
733	The Novel Sigma Factor-Like Regulator RpoQ Controls Luminescence, Chitinase Activity, and Motility in Vibrio fischeri. MBio, 2012, 3, .	1.8	37
734	REvolver: Modeling Sequence Evolution under Domain Constraints. Molecular Biology and Evolution, 2012, 29, 2133-2145.	3.5	16
735	Towards Creating Complete Proteomic Structural Databases of Whole Organisms. Current Bioinformatics, 2012, 7, 424-435.	0.7	4
736	Fission yeast Lem2 and Man1 perform fundamental functions of the animal cell nuclear lamina. Nucleus, 2012, 3, 60-76.	0.6	94
737	canSAR: an integrated cancer public translational research and drug discovery resource. Nucleic Acids Research, 2012, 40, D947-D956.	6.5	62
738	High-quality sequence clustering guided by network topology and multiple alignment likelihood. Bioinformatics, 2012, 28, 1078-1085.	1.8	39
739	Lipid targeting domain with dual-membrane specificity that expands the diversity of intracellular targeting reactions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1816-1817.	3.3	4
740	MetaBase--the wiki-database of biological databases. Nucleic Acids Research, 2012, 40, D1250-D1254.	6.5	40
741	Transcriptional analysis of the Arabidopsis ovule by massively parallel signature sequencing. Journal of Experimental Botany, 2012, 63, 3829-3842.	2.4	31

#	Article	IF	Citations
742	C7orf30 is necessary for biogenesis of the large subunit of the mitochondrial ribosome. Nucleic Acids Research, 2012, 40, 4097-4109.	6.5	64
743	Bacteriophage cocktail significantly reduces Escherichia coli O157. Bacteriophage, 2012, 2, 178-185.	1.9	118
744	Diversity of integrating conjugative elements in actinobacteria. Mobile Genetic Elements, 2012, 2, 119-124.	1.8	35
745	A survey of sRNA families in Î±-proteobacteria. RNA Biology, 2012, 9, 119-129.	1.5	32
746	Modeling the Thermoproteaceae RNase P RNA. RNA Biology, 2012, 9, 1155-1160.	1.5	7
747	SPLOOCE. RNA Biology, 2012, 9, 1339-1343.	1.5	7
748	The<i>hok</i>mRNA family. RNA Biology, 2012, 9, 1399-1404.	1.5	13
749	Gene3D: a domain-based resource for comparative genomics, functional annotation and protein network analysis. Nucleic Acids Research, 2012, 40, D465-D471.	6.5	98
750	Screening of a Xylanase Clone from a Fosmid Library of Rumen Microbiota in Hu Sheep. Animal Biotechnology, 2012, 23, 156-173.	0.7	8
751	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. Nature Biotechnology, 2012, 30, 159-164.	9.4	378
752	Complete Genome Sequence of Pelagibacterium halotolerans B2T. Journal of Bacteriology, 2012, 194, 197-198.	1.0	20
753	in silico identification of novel cancer-related genes by comparative genomics of naked mole rat and rat. , 2012, , .		2
754	Evolution of a Large, Conserved, and Syntenic Gene Family in Insects. G3: Genes, Genomes, Genetics, 2012, 2, 313-319.	0.8	57
755	A Computational Model for Predicting Protein Interactions Based on Multidomain Collaboration. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1081-1090.	1.9	15
756	BEWARE OF MOVING TARGETS: REFERENCE PROTEOME CONTENT FLUCTUATES SUBSTANTIALLY OVER THE YEARS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250020.	0.3	12
757	Genome-wide identification and characterization of novel genes involved in terpenoid biosynthesis in Salvia miltiorrhiza. Journal of Experimental Botany, 2012, 63, 2809-2823.	2.4	239
758	Detecting differential usage of exons from RNA-seq data. Genome Research, 2012, 22, 2008-2017.	2.4	1,341
759	Bifidobacterium longum subsp. infantis uses two different Î²-galactosidases for selectively degrading type-1 and type-2 human milk oligosaccharides. Glycobiology, 2012, 22, 361-368.	1.3	120

#	Article	IF	Citations
760	HSPIR: a manually annotated heat shock protein information resource. Bioinformatics, 2012, 28, 2853-2855.	1.8	67
761	Draft Genome Sequence of an Ammonia-Oxidizing Archaeon, â€œCandidatus Nitrosopumilus koreensisâ€• AR1, from Marine Sediment. Journal of Bacteriology, 2012, 194, 6940-6941.	1.0	40
762	Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research, 2012, 40, D1178-D1186.	6.5	4,204
763	Molecular Structure and Function of the Novel BrnT/BrnA Toxin-Antitoxin System of Brucella abortus. Journal of Biological Chemistry, 2012, 287, 12098-12110.	1.6	75
764	Molecular Determinants of Modulation of CaV2.1 Channels by Visinin-like Protein 2*. Journal of Biological Chemistry, 2012, 287, 504-513.	1.6	10
765	Inference of Functional Properties from Large-scale Analysis of Enzyme Superfamilies. Journal of Biological Chemistry, 2012, 287, 35-42.	1.6	45
766	DAMPD: a manually curated antimicrobial peptide database. Nucleic Acids Research, 2012, 40, D1108-D1112.	6.5	93
767	The molecular basis of ubiquitin-like protein NEDD8 deamidation by the bacterial effector protein Cif. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1830-E1838.	3.3	28
768	Draft Genome Sequence of the Sulfur-Oxidizing Bacterium â€œCandidatus Sulfurovum sediminumâ€•AR, Which Belongs to the Epsilonproteobacteria. Journal of Bacteriology, 2012, 194, 4128-4129.	1.0	29
769	Evolutionary History and Genome Organization of DUF1220 Protein Domains. G3: Genes, Genomes, Genetics, 2012, 2, 977-986.	0.8	69
770	Structure of the surface layer of the methanogenic archaean <i>Methanosarcina acetivorans</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11812-11817.	3.3	67
771	Functional Characterization of Residues Required for the Herpes Simplex Virus 1 E3 Ubiquitin Ligase ICP0 To Interact with the Cellular E2 Ubiquitin-Conjugating Enzyme UBE2D1 (UbcH5a). Journal of Virology, 2012, 86, 6323-6333.	1.5	26
772	Genome-Based Reconstruction of the Protein Import Machinery in the Secondary Plastid of a Chlorarachniophyte Alga. Eukaryotic Cell, 2012, 11, 324-333.	3.4	33
773	FAMILY FINGERPRINTS: A GLOBAL APPROACH TO STRUCTURAL CLASSIFICATION. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242001.	0.3	0
774	Phylogenetic Analysis of Mitochondrial Outer Membrane Î²-Barrel Channels. Genome Biology and Evolution, 2012, 4, 110-125.	1.1	14
775	Genome Sequence of Blattabacterium sp. Strain BGIGA, Endosymbiont of the Blaberus giganteus Cockroach. Journal of Bacteriology, 2012, 194, 4450-4451.	1.0	23
776	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
777	DOMMINO: a database of macromolecular interactions. Nucleic Acids Research, 2012, 40, D501-D506.	6.5	27

#	ARTICLE	IF	CITATIONS
778	Metagenomic analysis: the challenge of the data bonanza. Briefings in Bioinformatics, 2012, 13, 743-746.	3.2	23
779	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2012, 40, D445-D452.	6.5	166
780	Deep Sequencing Identifies Viral and Wasp Genes with Potential Roles in Replication of Microplitis demolitor Bracovirus. Journal of Virology, 2012, 86, 3293-3306.	1.5	73
781	Divergence and Convergence in Enzyme Evolution. Journal of Biological Chemistry, 2012, 287, 21-28.	1.6	140
782	IMG/M: the integrated metagenome data management and comparative analysis system. Nucleic Acids Research, 2012, 40, D123-D129.	6.5	242
783	4- <i>O</i> -methylation of glucuronic acid in <i>Arabidopsis</i> glucuronoxylan is catalyzed by a domain of unknown function family 579 protein. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14253-14258.	3.3	164
784	An adaptation of Pfam profiles to predict protein sub-cellular localization in Gram positive bacteria. , 2012, 2012, 5554-7.		4
785	Techniques to cope with missing data in hostâ€"pathogen protein interaction prediction. Bioinformatics, 2012, 28, i466-i472.	1.8	36
786	Dynamics and Adaptive Benefits of Protein Domain Emergence and Arrangements during Plant Genome Evolution. Genome Biology and Evolution, 2012, 4, 316-329.	1.1	66
787	Sequence, Structure, and Evolution of Cellulases in Glycoside Hydrolase Family 48. Journal of Biological Chemistry, 2012, 287, 41068-41077.	1.6	32
788	Large-scale analysis of conserved rare codon clusters suggests an involvement in co-translational molecular recognition events. Bioinformatics, 2012, 28, 1438-1445.	1.8	45
789	EcoliWiki: a wiki-based community resource for Escherichia coli. Nucleic Acids Research, 2012, 40, D1270-D1277.	6.5	27
790	IMG: the integrated microbial genomes database and comparative analysis system. Nucleic Acids Research, 2012, 40, D115-D122.	6.5	1,210
791	CADRE: the Central Aspergillus Data REpository 2012. Nucleic Acids Research, 2012, 40, D660-D666.	6.5	55
792	Myosinome: A Database of Myosins from Select Eukaryotic Genomes to Facilitate Analysis of Sequence-Structure-Function Relationships. Bioinformatics and Biology Insights, 2012, 6, BBI.S9902.	1.0	7
793	EvoluCode: Evolutionary Barcodes as a Unifying Framework for Multilevel Evolutionary Data. Evolutionary Bioinformatics, 2012, 8, EBO.S8814.	0.6	4
794	Determinants of Exon-Level Evolutionary Rates in <i>Arabidopsis</i> Species. Evolutionary Bioinformatics, 2012, 8, EBO.S9743.	0.6	3
795	TnpPred: A Web Service for the Robust Prediction of Prokaryotic Transposases. Comparative and Functional Genomics, 2012, 2012, 1-5.	2.0	46

#	Article	IF	Citations
796	Mutations Derived from the Thermophilic Polyhydroxyalkanoate Synthase PhaC Enhance the Thermostability and Activity of PhaC from Cupriavidus necator H16. Journal of Bacteriology, 2012, 194, 2620-2629.	1.0	28
797	The Bic-C Family of Developmental Translational Regulators. Comparative and Functional Genomics, 2012, 2012, 1-23.	2.0	21
798	Structural and functional analysis of the archaeal endonuclease Nob1. Nucleic Acids Research, 2012, 40, 3259-3274.	6.5	64
799	Structural Disorder in Eukaryotes. PLoS ONE, 2012, 7, e34687.	1.1	157
800	Phosphoproteome of Pristionchus pacificus Provides Insights into Architecture of Signaling Networks in Nematode Models. Molecular and Cellular Proteomics, 2012, 11, 1631-1639.	2.5	30
801	SMART 7: recent updates to the protein domain annotation resource. Nucleic Acids Research, 2012, 40, D302-D305.	6.5	1,462
802	Recognition models to predict DNA-binding specificities of homeodomain proteins. Bioinformatics, 2012, 28, i84-i89.	1.8	36
803	The Helicobacter pylori Autotransporter ImaA (HP0289) Modulates the Immune Response and Contributes to Host Colonization. Infection and Immunity, 2012, 80, 2286-2296.	1.0	26
804	Two surfaces on the histone chaperone Rtt106 mediate histone binding, replication, and silencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E144-53.	3.3	43
805	Output Targets and Transcriptional Regulation by a Cyclic Dimeric GMP-Responsive Circuit in the Vibrio parahaemolyticus Scr Network. Journal of Bacteriology, 2012, 194, 914-924.	1.0	65
806	The Human Cytomegalovirus-Specific <i>UL1</i> Gene Encodes a Late-Phase Glycoprotein Incorporated in the Virion Envelope. Journal of Virology, 2012, 86, 4091-4101.	1.5	26
807	ProOpDB: Prokaryotic Operon DataBase. Nucleic Acids Research, 2012, 40, D627-D631.	6.5	178
808	Comparative interactomics with Funcoup 2.0. Nucleic Acids Research, 2012, 40, D821-D828.	6.5	49
809	PhosphoSitePlus: a comprehensive resource for investigating the structure and function of experimentally determined post-translational modifications in man and mouse. Nucleic Acids Research, 2012, 40, D261-D270.	6.5	1,388
810	InterEvol database: exploring the structure and evolution of protein complex interfaces. Nucleic Acids Research, 2012, 40, D847-D856.	6.5	47
811	VFDB 2012 update: toward the genetic diversity and molecular evolution of bacterial virulence factors. Nucleic Acids Research, 2012, 40, D641-D645.	6.5	457
812	Linear motifs confer functional diversity onto splice variants. Nucleic Acids Research, 2012, 40, 7123-7131.	6.5	65
813	Positive-unlabeled learning for disease gene identification. Bioinformatics, 2012, 28, 2640-2647.	1.8	150

#	ARTICLE	IF	CITATIONS
814	Cyclic Di-GMP Phosphodiesterases RmdA and RmdB Are Involved in Regulating Colony Morphology and Development in Streptomyces coelicolor. Journal of Bacteriology, 2012, 194, 4642-4651.	1.0	39
815	Structural Variants in the Soybean Genome Localize to Clusters of Biotic Stress-Response Genes Â Â. Plant Physiology, 2012, 159, 1295-1308.	2.3	175
816	InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Research, 2012, 40, D306-D312.	6.5	921
817	Identification of Two Novel Endoplasmic Reticulum Body-Specific Integral Membrane Proteins Â Â. Plant Physiology, 2012, 161, 108-120.	2.3	51
818	Computational Modelling of Linear Motif-Mediated Protein Interactions. Current Topics in Medicinal Chemistry, 2012, 12, 1553-1561.	1.0	11
819	SVM-based prediction of protein-protein interactions of Glucosinolate biosynthesis. , 2012, , .		1
820	MSV3d: database of human MisSense variants mapped to 3D protein structure. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas018-bas018.	1.4	24
821	A Single Ancient Origin for Prototypical Serine/Arginine-Rich Splicing Factors Â Â. Plant Physiology, 2012, 158, 546-560.	2.3	28
822	Human Retinoblastoma Binding Protein 9, a Serine Hydrolase Implicated in Pancreatic Cancers. Protein and Peptide Letters, 2012, 19, 194-197.	0.4	13
823	A function to every gene: royal blood and order in the sequence universe. , 0, , 150-163.		0
824	Meta-analysis of the expression of the mitosis-related gene Fam83D. Oncology Letters, 2012, 4, 1335-1340.	0.8	18
825	FxkR Provides the Missing Link in the <i>fixL-fixK</i> Signal Transduction Cascade in <i>Rhizobium etli</i> CFN42. Molecular Plant-Microbe Interactions, 2012, 25, 1506-1517.	1.4	26
826	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. Molecular Systems Biology, 2012, 8, 581.	3.2	29
827	Amylases without known homologues discovered in an acid mine drainage: significance and impact. Scientific Reports, 2012, 2, 354.	1.6	21
828	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.	1.9	4
829	Identification of Unknown Protein Function Using Metabolite Cocktail Screening. Structure, 2012, 20, 1715-1725.	1.6	45
830	Transthyretin is a metallopeptidase with an inducible active site. Biochemical Journal, 2012, 443, 769-778.	1.7	40
831	Insect Genomics. , 2012, , 1-29.		0

#	ARTICLE	IF	CITATIONS
832	Novel conjugative plasmids from the natural isolate Lactococcus lactis subspecies cremoris DPC3758: A repository of genes for the potential improvement of dairy starters. Journal of Dairy Science, 2012, 95, 3593-3608.	1.4	19
833	Roadmap for Annotating Transposable Elements in Eukaryote Genomes. Methods in Molecular Biology, 2012, 859, 53-68.	0.4	15
834	Protein structure prediction from sequence variation. Nature Biotechnology, 2012, 30, 1072-1080.	9.4	569
835	The sunflower (<i>Helianthus annuus</i> L.) genome reflects a recent history of biased accumulation of transposable elements. Plant Journal, 2012, 72, 142-153.	2.8	88
836	The genome of flax (<i>Linum usitatissimum</i>) assembled <i>de novo</i> from short shotgun sequence reads. Plant Journal, 2012, 72, 461-473.	2.8	415
837	Largeâ€scale transcriptome characterization and mass discovery of SNPs in globe artichoke and its related taxa. Plant Biotechnology Journal, 2012, 10, 956-969.	4.1	33
838	Insights from the architecture of the bacterial transcription apparatus. Journal of Structural Biology, 2012, 179, 299-319.	1.3	46
839	Indexing Uncertain Data in General Metric Spaces. IEEE Transactions on Knowledge and Data Engineering, 2012, 24, 1640-1657.	4.0	22
840	Genome-Wide Identification, Functional Analysis and Expression Profiling of the Aux/IAA Gene Family in Tomato. Plant and Cell Physiology, 2012, 53, 659-672.	1.5	138
841	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10456-10461.	3.3	39
842	In Silico Identification and Characterization of Effector Catalogs. Methods in Molecular Biology, 2012, 835, 415-425.	0.4	11
843	Unusual roles of host metabolic enzymes and housekeeping proteins in plant virus replication. Current Opinion in Virology, 2012, 2, 676-682.	2.6	24
844	Molecular Identification of Hydroxylysine Kinase and of Ammoniophospholyases Acting on 5-Phosphohydroxy-l-lysine and Phosphoethanolamine. Journal of Biological Chemistry, 2012, 287, 7246-7255.	1.6	46
845	Homology Modeling: Generating Structural Models to Understand Protein Function and Mechanism. Biological and Medical Physics Series, 2012, , 97-116.	0.3	9
846	Diversity and Analysis of Bacterial Terpene Synthases. Methods in Enzymology, 2012, 515, 123-162.	0.4	39
847	Use of Structural Phylogenetic Networks for Classification of the Ferritin-like Superfamily. Journal of Biological Chemistry, 2012, 287, 20565-20575.	1.6	66
848	Chlapsin, a chloroplastidial aspartic proteinase from the green algae Chlamydomonas reinhardtii. Planta, 2012, 236, 283-296.	1.6	8
849	Prioritization of pathogenic mutations in the protein kinase superfamily. BMC Genomics, 2012, 13, S3.	1.2	21

#	ARTICLE	IF	CITATIONS
850	Genome-wide identification and characterization of replication origins by deep sequencing. Genome Biology, 2012, 13, R27.	13.9	85
851	The crystal structure of the Rv0301â€Rv0300 VapBCâ€3 toxinâ€"antitoxin complex from <i>M. tuberculosis</i> reveals a Mg²⁺ ion in the active site and a putative RNAâ€binding site. Protein Science, 2012, 21, 1754-1767.	3.1	54
852	MotViz: A Tool for Sequence Motif Prediction in Parallel to Structural Visualization and Analyses. Genomics, Proteomics and Bioinformatics, 2012, 10, 35-43.	3.0	1
853	Additive multiple k-mer transcriptome of the keelworm Pomatoceros lamarckii (Annelida; Serpulidae) reveals annelid trochophore transcription factor cassette. Development Genes and Evolution, 2012, 222, 325-339.	0.4	11
854	Three structural representatives of the PF06855 protein domain family from Staphyloccocus aureus and Bacillus subtilis have SAM domain-like folds and different functions. Journal of Structural and Functional Genomics, 2012, 13, 163-170.	1.2	3
855	Solution NMR structure of Alr2454 from Nostoc sp. PCC 7120, the first structural representative of Pfam domain family PF11267. Journal of Structural and Functional Genomics, 2012, 13, 171-176.	1.2	3
856	Crystal structure of a catalytically active GG(D/E)EF diguanylate cyclase domain from Marinobacter aquaeolei with bound c-di-GMP product. Journal of Structural and Functional Genomics, 2012, 13, 177-183.	1.2	12
857	Cloning and Characterization of the Wx Gene Encoding a Granule-Bound Starch Synthase in Lotus (Nelumbo nucifera Gaertn). Plant Molecular Biology Reporter, 2012, 30, 1210-1217.	1.0	9
858	Advances in the methods for studying gut microbiota and their relevance to the research of dietary fiber functions. Food Research International, 2012, 48, 916-929.	2.9	49
859	Evolutionary analysis of Antarctic teleost Toll-like receptor 2. Fish and Shellfish Immunology, 2012, 33, 1076-1085.	1.6	11
860	The transcriptional regulatory network of Corynebacterium jeikeium K411 and its interaction with metabolic routes contributing to human body odor formation. Journal of Biotechnology, 2012, 159, 235-248.	1.9	17
861	A transcriptional study of acidogenic chemostat cells of Clostridium acetobutylicum â€" Cellular behavior in adaptation to n-butanol. Journal of Biotechnology, 2012, 161, 366-377.	1.9	45
862	Functional characterization of SlscADH1, a fruit-ripening-associated short-chain alcohol dehydrogenase of tomato. Journal of Plant Physiology, 2012, 169, 1435-1444.	1.6	35
863	The overlapping host responses to bacterial cyclic dinucleotides. Microbes and Infection, 2012, 14, 188-197.	1.0	26
864	Selection and characterisation of guanidine-resistant mutants of human enterovirus 71. Virus Research, 2012, 169, 72-79.	1.1	22
865	VIP DB â€" A viral protein domain usage and distribution database. Genomics, 2012, 100, 149-156.	1.3	0
866	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4+ T cells. Genomics, 2012, 100, 303-313.	1.3	12
867	Protein domain repetition is enriched in Streptococcal cell-surface proteins. Genomics, 2012, 100, 370-379.	1.3	12

#	Article	IF	Citations
868	Identification of novel oxygen sensors using a combined approach in Xanthomonas campestris pv. campestris. Annals of Microbiology, 2012, 62, 957-964.	1.1	0
869	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	2.4	586
870	Multifunctional proteins revealed by overlapping clustering in protein interaction network. Bioinformatics, 2012, 28, 84-90.	1.8	150
871	Genome-wide Analysis of Ovate Family Proteins in Arabidopsis. The Journal of Northeast Agricultural University, 2012, 19, 49-59.	0.1	2
872	The Ras protein superfamily: Evolutionary tree and role of conserved amino acids. Journal of Cell Biology, 2012, 196, 189-201.	2.3	321
873	Manifold learning reveals nonlinear structure in metagenomic profiles. , 2012, , .		6
874	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
875	RGRank: Ranking Semantically Related Genes. , 2012, , .		3
876	Occurrence of disordered patterns and homorepeats in eukaryotic and bacterial proteomes. Molecular BioSystems, 2012, 8, 327-337.	2.9	31
877	Identifying protein binding functionality of protein family sequences by Aligned Pattern clusters. , 2012, , .		1
878	Rewiring the dynamic interactome. Molecular BioSystems, 2012, 8, 2054.	2.9	26
879	Identification and Characterization of an RTX Toxinâ€"Like Gene and Its Operon from Avibacterium paragallinarum. Avian Diseases, 2012, 56, 537-544.	0.4	9
880	Characterization of the Interactions of Mammalian RNA Polymerase I Associated Proteins PAF53 and PAF49. Biochemistry, 2012, 51, 6519-6526.	1.2	12
881	Promiscuous domains: facilitating stability of the yeast proteinâ€"protein interaction network. Molecular BioSystems, 2012, 8, 766-771.	2.9	10
882	Solution NMR Structure of Yeast Succinate Dehydrogenase Flavinylation Factor Sdh5 Reveals a Putative Sdh1 Binding Site. Biochemistry, 2012, 51, 8475-8477.	1.2	29
883	Using structural domains to predict obligate and non-obligate protein-protein interactions. , 2012, , .		4
884	Drug-target network in myocardial infarction: A structural analysis. , 2012, , .		1
885	SLiMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. Nucleic Acids Research, 2012, 40, 10628-10641.	6.5	92

#	Article	IF	Citations
886	SNPeffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. Nucleic Acids Research, 2012, 40, D935-D939.	6.5	235
887	A genome-wide view of transcription factor gene diversity in chordate evolution: less gene loss in amphioxus?. Briefings in Functional Genomics, 2012, 11, 177-186.	1.3	36
888	Differences in the Substrate Specificities and Active-Site Structures of Two Î±-<scp>L</scp>-Fucosidases (Glycoside Hydrolase Family 29) from<i>Bacteroides thetaiotaomicron</i>. Bioscience, Biotechnology and Biochemistry, 2012, 76, 1022-1024.	0.6	75
889	Attributes of short linear motifs. Molecular BioSystems, 2012, 8, 268-281.	2.9	502
890	Order and disorder in large multi-site docking proteins of the Gab familyâ€”implications for signalling complex formation and inhibitor design strategies. Molecular BioSystems, 2012, 8, 33-46.	2.9	47
891	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
892	Evolution and Virulence Contributions of the Autotransporter Proteins YapJ and YapK of Yersinia pestis CO92 and Their Homologs in Y. pseudotuberculosis IP32953. Infection and Immunity, 2012, 80, 3693-3705.	1.0	8
893	Characterization of the [2Fe-2S] Cluster of <i>Escherichia coli</i> Transcription Factor IscR. Biochemistry, 2012, 51, 4453-4462.	1.2	85
894	Sequential Enzymatic Epoxidation Involved in Polyether Lasalocid Biosynthesis. Journal of the American Chemical Society, 2012, 134, 7246-7249.	6.6	59
895	Metal Affinity Enrichment Increases the Range and Depth of Proteome Identification for Extracellular Microbial Proteins. Journal of Proteome Research, 2012, 11, 861-870.	1.8	1
896	Evolution and function of CAG/polyglutamine repeats in proteinâ€“protein interaction networks. Nucleic Acids Research, 2012, 40, 4273-4287.	6.5	166
897	Alternative routes of acetyl-CoA synthesis identified by comparative genomic analysis: involvement in the lipid production of oleaginous yeast and fungi. Microbiology (United Kingdom), 2012, 158, 217-228.	0.7	106
898	GRAS proteins: the versatile roles of intrinsically disordered proteins in plant signalling. Biochemical Journal, 2012, 442, 1-12.	1.7	136
899	Ultrafast clustering algorithms for metagenomic sequence analysis. Briefings in Bioinformatics, 2012, 13, 656-668.	3.2	403
900	Characterization of <i>Arabidopsis</i> calcium-dependent protein kinases: activated or not by calcium?. Biochemical Journal, 2012, 447, 291-299.	1.7	102
901	Analysis of conditions affecting auto-phosphorylation of human kinases during expression in bacteria. Protein Expression and Purification, 2012, 81, 136-143.	0.6	35
902	Hox genes from the parasitic flatworm Schistosoma japonicum. Genomics, 2012, 99, 59-65.	1.3	5
903	Functional genomics based prioritization of potential nsSNPs in EPHX1, GSTT1, GSTM1 and GSTP1 genes for breast cancer susceptibility studies. Genomics, 2012, 99, 330-339.	1.3	17

#	ARTICLE	IF	CITATIONS
904	Subclassification and Biochemical Analysis of Plant Papain-Like Cysteine Proteases Displays Subfamily-Specific Characteristics Â Â. Plant Physiology, 2012, 158, 1583-1599.	2.3	166
905	Structural, Functional, and Evolutionary Analysis of the Unusually Large Stilbene Synthase Gene Family in Grapevine Â. Plant Physiology, 2012, 160, 1407-1419.	2.3	138
906	Subversion of Cell Signaling by Pathogens. Cold Spring Harbor Perspectives in Biology, 2012, 4, a006114-a006114.	2.3	101
907	Functional equivalence and evolutionary convergence in complex communities of microbial sponge symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1878-87.	3.3	361
908	Widespread Genetic Switches and Toxicity Resistance Proteins for Fluoride. Science, 2012, 335, 233-235.	6.0	356
909	Charting the Landscape of Tandem BRCT Domainâ€“Mediated Protein Interactions. Science Signaling, 2012, 5, rs6.	1.6	88
910	Diversity, classification and function of the plant protein kinase superfamily. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2619-2639.	1.8	277
911	Discovery of <i>Pyrobaculum</i> small RNA families with atypical pseudouridine guide RNA features. Rna, 2012, 18, 402-411.	1.6	25
912	Ter-dependent stress response systems: novel pathways related to metal sensing, production of a nucleoside-like metabolite, and DNA-processing. Molecular BioSystems, 2012, 8, 3142.	2.9	88
913	Dinoflagellate tandem array gene transcripts are highly conserved and not polycistronic. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15793-15798.	3.3	73
914	Structural and functional characterization of Î±-isopropylmalate synthase and citramalate synthase, members of the LeuA dimer superfamily. Archives of Biochemistry and Biophysics, 2012, 519, 202-209.	1.4	18
915	A Phylogenetic Analysis of Normal Modes Evolution in Enzymes and Its Relationship to Enzyme Function. Journal of Molecular Biology, 2012, 422, 442-459.	2.0	22
916	Calcium-Independent Inhibition of PCSK9 by Affinity-Improved Variants of the LDL Receptor EGF(A) Domain. Journal of Molecular Biology, 2012, 422, 685-696.	2.0	30
917	Structural basis of specificity in tetrameric Kluyveromyces lactis Î²-galactosidase. Journal of Structural Biology, 2012, 177, 392-401.	1.3	88
918	C-terminal acidic domain of ubiquitin-conjugating enzymes: A multi-functional conserved intrinsically disordered domain in family 3 of E2 enzymes. Journal of Structural Biology, 2012, 178, 245-259.	1.3	17
919	Hydroxysteroid dehydrogenases (HSDs) in bacteria â€“ A bioinformatic perspective. Journal of Steroid Biochemistry and Molecular Biology, 2012, 129, 31-46.	1.2	94
920	Identification and classification of conopeptides using profile Hidden Markov Models. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 488-492.	1.1	18
921	The genome of the xerotolerant mold Wallemia sebi reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. Fungal Genetics and Biology, 2012, 49, 217-226.	0.9	103

#	ARTICLE	IF	CITATIONS
922	Identification, mRNA expression and genomic structure of TLR22 and its association with GCRV susceptibility/resistance in grass carp (Ctenopharyngodon idella). Developmental and Comparative Immunology, 2012, 36, 450-462.	1.0	111
923	Distribution and characteristics of ABFs, cecropins, nemapores, and lysozymes in nematodes. Developmental and Comparative Immunology, 2012, 36, 502-520.	1.0	35
924	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. Cell, 2012, 149, 214-231.	13.5	1,368
925	Molecular characterization of toll-like receptor 2 (TLR2), analysis of its inductive expression and associated down-stream signaling molecules following ligands exposure and bacterial infection in the Indian major carp, rohu (Labeo rohita). Fish and Shellfish Immunology, 2012, 32, 411-425.	1.6	79
926	Molecular cloning and characterization of nucleotide binding and oligomerization domain-1 (NOD1) receptor in the Indian Major Carp, rohu (Labeo rohita), and analysis of its inductive expression and down-stream signalling molecules following ligands exposure and Gram-negative bacterial infections. Fish and Shellfish Immunology, 2012, 32, 899-908.	1.6	60
927	Self/nonself recognition in Tuber melanosporum is not mediated by a heterokaryon incompatibility system. Fungal Biology, 2012, 116, 261-275.	1.1	34
928	Evolution of prokaryotic homologues of the eukaryotic SEFIR protein domain. Gene, 2012, 492, 160-166.	1.0	12
929	Identification of a novel isoform of DHRS4 protein with a nuclear localization signal. Gene, 2012, 494, 161-167.	1.0	7
930	The soybean aldehyde dehydrogenase (ALDH) protein superfamily. Gene, 2012, 495, 128-133.	1.0	35
931	In silico analysis of DosR regulon proteins of Mycobacterium tuberculosis. Gene, 2012, 506, 233-241.	1.0	20
932	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. Journal of Bacteriology, 2012, 194, 1216-1225.	1.0	90
933	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
934	Computational Analysis of Cysteine and Methionine Metabolism and Its Regulation in Dairy Starter and Related Bacteria. Journal of Bacteriology, 2012, 194, 3522-3533.	1.0	29
935	GFam: a platform for automatic annotation of gene families. Nucleic Acids Research, 2012, 40, e152-e152.	6.5	3
936	Computational tools for the synthetic design of biochemical pathways. Nature Reviews Microbiology, 2012, 10, 191-202.	13.6	206
937	Bioinformatical Detection of Recognition Factors for Ubiquitin and SUMO. Methods in Molecular Biology, 2012, 832, 249-261.	0.4	30
938	Posttraumatic regeneration involves differential expression of long terminal repeat (LTR) retrotransposons. Developmental Dynamics, 2012, 241, 1625-1636.	0.8	21
939	Convergent evolution in structural elements of proteins investigated using cross profile analysis. BMC Bioinformatics, 2012, 13, 11.	1.2	33

#	ARTICLE	IF	CITATIONS
940	MergeAlign: improving multiple sequence alignment performance by dynamic reconstruction of consensus multiple sequence alignments. BMC Bioinformatics, 2012, 13, 117.	1.2	64
941	Genes2FANs: connecting genes through functional association networks. BMC Bioinformatics, 2012, 13, 156.	1.2	28
942	Disentangling evolutionary signals: conservation, specificity determining positions and coevolution. Implication for catalytic residue prediction. BMC Bioinformatics, 2012, 13, 235.	1.2	35
943	BLANNOTATOR: enhanced homology-based function prediction of bacterial proteins. BMC Bioinformatics, 2012, 13, 33.	1.2	12
944	Fitting hidden Markov models of protein domains to a target species: application to Plasmodium falciparum. BMC Bioinformatics, 2012, 13, 67.	1.2	14
945	Protein docking prediction using predicted protein-protein interface. BMC Bioinformatics, 2012, 13, 7.	1.2	60
946	A comparative evaluation of sequence classification programs. BMC Bioinformatics, 2012, 13, 92.	1.2	99
947	Scalable global alignment for multiple biological networks. BMC Bioinformatics, 2012, 13, S11.	1.2	27
948	Argot2: a large scale function prediction tool relying on semantic similarity of weighted Gene Ontology terms. BMC Bioinformatics, 2012, 13, S14.	1.2	137
949	Molecular evolution of a-kinase anchoring protein (AKAP)-7: implications in comparative PKA compartmentalization. BMC Evolutionary Biology, 2012, 12, 125.	3.2	19
950	Functional divergence of gene duplicates â€“ a domain-centric view. BMC Evolutionary Biology, 2012, 12, 126.	3.2	5
951	The independent prokaryotic origins of eukaryotic fructose-1, 6-bisphosphatase and sedoheptulose-1, 7-bisphosphatase and the implications of their origins for the evolution of eukaryotic Calvin cycle. BMC Evolutionary Biology, 2012, 12, 208.	3.2	16
952	Ancient gene transfer from algae to animals: Mechanisms and evolutionary significance. BMC Evolutionary Biology, 2012, 12, 83.	3.2	33
953	Variation of presence/absence genes among Arabidopsis populations. BMC Evolutionary Biology, 2012, 12, 86.	3.2	47
954	Characterization and gene expression analysis of the cir multi-gene family of plasmodium chabaudi chabaudi (AS). BMC Genomics, 2012, 13, 125.	1.2	26
955	A genome-wide study of two-component signal transduction systems in eight newly sequenced mutans streptococci strains. BMC Genomics, 2012, 13, 128.	1.2	31
956	Divergent gene expression in the conserved dauer stage of the nematodes Pristionchus pacificus and Caenorhabditis elegans. BMC Genomics, 2012, 13, 254.	1.2	38
957	Comparative transcriptome analysis between planarian Dugesia japonica and other platyhelminth species. BMC Genomics, 2012, 13, 289.	1.2	34

#	ARTICLE	IF	CITATIONS
958	A survey of putative secreted and transmembrane proteins encoded in the C. elegans genome. BMC Genomics, 2012, 13, 333.	1.2	28
959	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	1.2	84
960	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (Petaurista alborufus lena). BMC Genomics, 2012, 13, 466.	1.2	27
961	Controversies in modern evolutionary biology: the imperative for error detection and quality control. BMC Genomics, 2012, 13, 5.	1.2	40
962	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, Botryococcus braunii race B (Showa)*. BMC Genomics, 2012, 13, 576.	1.2	52
963	The Schistosoma mansoni phylome: using evolutionary genomics to gain insight into a parasiteâ€™s biology. BMC Genomics, 2012, 13, 617.	1.2	28
964	Dynamics of domain coverage of the protein sequence universe. BMC Genomics, 2012, 13, 634.	1.2	10
965	Is chemically dispersed oil more toxic to Atlantic cod (Gadus morhua) larvae than mechanically dispersed oil? A transcriptional evaluation. BMC Genomics, 2012, 13, 702.	1.2	40
966	Identification and localisation of the NB-LRR gene family within the potato genome. BMC Genomics, 2012, 13, 75.	1.2	290
967	Complete genome sequence of Enterococcus faecium strain TX16 and comparative genomic analysis of Enterococcus faecium genomes. BMC Microbiology, 2012, 12, 135.	1.3	126
968	Comparative analysis of diguanylate cyclase and phosphodiesterase genes in Klebsiella pneumoniae. BMC Microbiology, 2012, 12, 139.	1.3	16
969	Comparative genome analysis of 19 Ureaplasma urealyticum and Ureaplasma parvumstrains. BMC Microbiology, 2012, 12, 88.	1.3	91
970	Genome-wide mapping of NBS-LRR genes and their association with disease resistance in soybean. BMC Plant Biology, 2012, 12, 139.	1.6	143
971	Identification of the dehydrin gene family from grapevine species and analysis of their responsiveness to various forms of abiotic and biotic stress. BMC Plant Biology, 2012, 12, 140.	1.6	153
972	The study of two barley Type I-like MADS-boxgenes as potential targets of epigenetic regulation during seed development. BMC Plant Biology, 2012, 12, 166.	1.6	24
973	The Plant Short-Chain Dehydrogenase (SDR) superfamily: genome-wide inventory and diversification patterns. BMC Plant Biology, 2012, 12, 219.	1.6	115
974	Evolutionarily consistent families in SCOP: sequence, structure and function. BMC Structural Biology, 2012, 12, 27.	2.3	14
975	Genome and proteome analysis of 7-7-1, a flagellotropic phage infecting Agrobacterium sp H13-3. Virology Journal, 2012, 9, 102.	1.4	23

#	ARTICLE	IF	CITATIONS
976	Whole genome sequencing of phage resistant Bacillus anthracismutants reveals an essential role for cell surface anchoring protein CsaB in phage AP50c adsorption. Virology Journal, 2012, 9, 246.	1.4	28
977	A novel virus genome discovered in an extreme environment suggests recombination between unrelated groups of RNA and DNA viruses. Biology Direct, 2012, 7, 13.	1.9	141
978	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. Biology Direct, 2012, 7, 18.	1.9	440
979	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. Biology Direct, 2012, 7, 32.	1.9	19
980	ALOG domains: provenance of plant homeotic and developmental regulators from the DNA-binding domain of a novel class of DIRS1-type retroposons. Biology Direct, 2012, 7, 39.	1.9	41
981	Assessment of the structural and functional impact of in-frame mutations of the DMD gene, using the tools included in the eDystrophin online database. Orphanet Journal of Rare Diseases, 2012, 7, 45.	1.2	45
982	Specification, annotation, visualization and simulation of a large rule-based model for ERBB receptor signaling. BMC Systems Biology, 2012, 6, 107.	3.0	31
983	i AK692: A genome-scale metabolic model of Spirulina platensis C1. BMC Systems Biology, 2012, 6, 71.	3.0	36
984	Novel enzymes for the degradation of cellulose. Biotechnology for Biofuels, 2012, 5, 45.	6.2	803
985	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC Research Notes, 2012, 5, 574.	0.6	42
986	A minimal ligand binding pocket within a network of correlated mutations identified by multiple sequence and structural analysis of G protein coupled receptors. BMC Biophysics, 2012, 5, 13.	4.4	7
988	Protein Databases on the Internet. Current Protocols in Protein Science, 2012, 70, Unit2.6.	2.8	11
989	Two intercellular signals required for fruiting body formation in <i>Myxococcus xanthus</i> act sequentially but nonâ€hierarchically. Molecular Microbiology, 2012, 86, 65-81.	1.2	24
990	MobiDB: a comprehensive database of intrinsic protein disorder annotations. Bioinformatics, 2012, 28, 2080-2081.	1.8	142
991	Mycobacteriophage Endolysins: Diverse and Modular Enzymes with Multiple Catalytic Activities. PLoS ONE, 2012, 7, e34052.	1.1	112
992	Transcriptome sequencing in SÃ©zary syndrome identifies SÃ©zary cell and mycosis fungoides-associated lncRNAs and novel transcripts. Blood, 2012, 120, 3288-3297.	0.6	85
993	SAPIN: A framework for the structural analysis of protein interaction networks. Bioinformatics, 2012, 28, 2998-2999.	1.8	10
994	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	5.5	1,474

#	ARTICLE	IF	CITATIONS
995	On-Line Resources for Xenopus. Methods in Molecular Biology, 2012, 917, 541-562.	0.4	0
996	A Global Characterization and Identification of Multifunctional Enzymes. PLoS ONE, 2012, 7, e38979.	1.1	53
997	Protein intrinsic disorder and induced pluripotent stem cells. Molecular BioSystems, 2012, 8, 134-150.	2.9	45
998	Alternative Splicing as a Source of Phenotypic Differences Between Species: Protein-Level Mechanisms. , 2012, , 343-356.		1
999	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. Topics in Current Genetics, 2012, , 17-39.	0.7	16
1000	HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. Nature Methods, 2012, 9, 173-175.	9.0	1,878
1001	Cloning, purification and preliminary X-ray data analysis of the human ID2 homodimer. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1354-1358.	0.7	3
1002	Structure of the recombinant BPTI/Kunitz-type inhibitor<i>r</i>ShPI-1A from the marine invertebrate<i>Stichodactyla helianthus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1289-1293.	0.7	10
1003	Plasmodium falciparum Prp16 homologue and its role in splicing. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2012, 1819, 1186-1199.	0.9	11
1004	Interaction of the human prostacyclin receptor and the NHERF4 family member intestinal and kidney enriched PDZ protein (IKEPP). Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 1998-2012.	1.9	4
1005	Expression of complement receptors 1 (CR1/CD35) and 2 (CR2/CD21), and co-signaling molecule CD19 in cattle. Developmental and Comparative Immunology, 2012, 38, 487-494.	1.0	2
1006	Identification of potential drug targets in Yersinia pestis using metabolic pathway analysis: MurE ligase as a case study. European Journal of Medicinal Chemistry, 2012, 57, 185-195.	2.6	29
1007	Expressional and functional variation of horizontally acquired cellulases in the nematode Pristionchus pacificus. Gene, 2012, 506, 274-282.	1.0	27
1008	What is needed for next-generation ecological and evolutionary genomics?. Trends in Ecology and Evolution, 2012, 27, 673-678.	4.2	77
1009	Cloning, expression, and characterization of a novel Opisthorchis viverrini calcium-binding EF-hand protein. Parasitology International, 2012, 61, 94-100.	0.6	26
1010	Epitopic hexapeptide sequences from Baltic cod parvalbumin beta (allergen Gad c 1) are common in the universal proteome. Peptides, 2012, 38, 105-109.	1.2	6
1011	Identification of genes differentially expressed in grapevine associated with resistance to Elsinoe ampelina through suppressive subtraction hybridization. Plant Physiology and Biochemistry, 2012, 58, 253-268.	2.8	30
1012	Targeting essential cell wall lipase Rv3802c for potential therapeutics against tuberculosis. Journal of Molecular Graphics and Modelling, 2012, 38, 235-242.	1.3	8

#	Article	IF	Citations
1013	Identification of a tubulin-Î± gene specifically expressed in testis and adductor muscle during stable reference gene selection in the hermaphrodite gonad of the lion's paw scallop Nodipecten subnodosus. Marine Genomics, 2012, 6, 33-44.	0.4	19
1014	Revelation of a Catalytic Calcium-Binding Site Elucidates Unusual Metal Dependence of a Human Apyrase. Journal of the American Chemical Society, 2012, 134, 15595-15603.	6.6	23
1015	Structure of a Novel Winged-Helix Like Domain from Human NFRKB Protein. PLoS ONE, 2012, 7, e43761.	1.1	5
1017	Up, Down, and Around: Identifying Recurrent Interactions Within and Between Super-secondary Structures in Î²-Propellers. Methods in Molecular Biology, 2012, 932, 35-50.	0.4	2
1018	Discovery of Dynein and its Properties. , 2012, , 2-87.		3
1019	Is there a biological cost of protein disorder? Analysis of cancer-associated mutations. Molecular BioSystems, 2012, 8, 296-307.	2.9	43
1020	Interactome-wide prediction of short, disordered protein interaction motifs in humans. Molecular BioSystems, 2012, 8, 282-295.	2.9	30
1021	Overexpression of Rice CBS Domain Containing Protein Improves Salinity, Oxidative, and Heavy Metal Tolerance in Transgenic Tobacco. Molecular Biotechnology, 2012, 52, 205-216.	1.3	90
1022	Computational approaches, databases and tools for in silico motif discovery. Interdisciplinary Sciences, Computational Life Sciences, 2012, 4, 239-255.	2.2	1
1023	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
1024	Homology modeling and functional annotation of bubaline pregnancy associated glycoprotein 2. Journal of Animal Science and Biotechnology, 2012, 3, 13.	2.1	8
1025	Genomic Approaches for Interrogating the Biochemistry of Medicinal Plant Species. Methods in Enzymology, 2012, 517, 139-159.	0.4	46
1026	How Do You Find Transcription Factors? Computational Approaches to Compile and Annotate Repertoires of Regulators for Any Genome. Methods in Molecular Biology, 2012, 786, 3-19.	0.4	11
1027	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. Molecular BioSystems, 2012, 8, 1661.	2.9	63
1028	Bacteriophages with the Ability to Degrade Uropathogenic Escherichia Coli Biofilms. Viruses, 2012, 4, 471-487.	1.5	94
1029	1.8 Structure Validation and Analysis. , 2012, , 116-135.		3
1030	Inferences from structural comparison: flexibility, secondary structure wobble and sequence alignment optimization. BMC Bioinformatics, 2012, 13, S12.	1.2	5
1031	Massive expansion of the calpain gene family in unicellular eukaryotes. BMC Evolutionary Biology, 2012, 12, 193.	3.2	34

#	Article	IF	Citations
1032	Unusual domain architecture of aminoacyl tRNA synthetases and their paralogs from Leishmania major. BMC Genomics, 2012, 13, 621.	1.2	37
1033	The protein interaction network of a taxis signal transduction system in a Halophilic Archaeon. BMC Microbiology, 2012, 12, 272.	1.3	37
1034	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. ISME Journal, 2012, 6, 1186-1199.	4.4	511
1035	Organellar proteomics reveals hundreds of novel nuclear proteins in the malaria parasite Plasmodium falciparum. Genome Biology, 2012, 13, R108.	13.9	139
1036	Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation. Genome Medicine, 2012, 4, 89.	3.6	91
1037	Functional repertoire, molecular pathways and diseases associated with 3D domain swapping in the human proteome. Journal of Clinical Bioinformatics, 2012, 2, 8.	1.2	12
1038	Global Analysis of Small Molecule Binding to Related Protein Targets. PLoS Computational Biology, 2012, 8, e1002333.	1.5	41
1039	Intrinsic Disorder in the Human Spliceosomal Proteome. PLoS Computational Biology, 2012, 8, e1002641.	1.5	73
1040	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.	1.5	11
1041	Using Hierarchical Clustering of Secreted Protein Families to Classify and Rank Candidate Effectors of Rust Fungi. PLoS ONE, 2012, 7, e29847.	1.1	235
1042	A Novel Extracellular Metallopeptidase Domain Shared by Animal Host-Associated Mutualistic and Pathogenic Microbes. PLoS ONE, 2012, 7, e30287.	1.1	96
1043	PIPS: Pathogenicity Island Prediction Software. PLoS ONE, 2012, 7, e30848.	1.1	70
1044	Cystinosin, MPDU1, SWEETs and KDELR Belong to a Well-Defined Protein Family with Putative Function of Cargo Receptors Involved in Vesicle Trafficking. PLoS ONE, 2012, 7, e30876.	1.1	46
1045	The Dispanins: A Novel Gene Family of Ancient Origin That Contains 14 Human Members. PLoS ONE, 2012, 7, e31961.	1.1	74
1046	Core Site-Moiety Maps Reveal Inhibitors and Binding Mechanisms of Orthologous Proteins by Screening Compound Libraries. PLoS ONE, 2012, 7, e32142.	1.1	20
1047	Analysis of the Peptidoglycan Hydrolase Complement of Lactobacillus casei and Characterization of the Major Î³-D-Glutamyl-L-Lysyl-Endopeptidase. PLoS ONE, 2012, 7, e32301.	1.1	54
1048	The Diversification of the LIM Superclass at the Base of the Metazoa Increased Subcellular Complexity and Promoted Multicellular Specialization. PLoS ONE, 2012, 7, e33261.	1.1	50
1049	Identification and Characterization of Microcin S, a New Antibacterial Peptide Produced by Probiotic Escherichia coli G3/10. PLoS ONE, 2012, 7, e33351.	1.1	65

#	ARTICLE	IF	CITATIONS
1050	Membrane Docking Geometry of GRP1 PH Domain Bound to a Target Lipid Bilayer: An EPR Site-Directed Spin-Labeling and Relaxation Study. PLoS ONE, 2012, 7, e33640.	1.1	18
1051	High Through-Put Sequencing of the Parhyale hawaiensis mRNAs and microRNAs to Aid Comparative Developmental Studies. PLoS ONE, 2012, 7, e33784.	1.1	35
1052	Reduced Polymorphism in Domains Involved in Protein-Protein Interactions. PLoS ONE, 2012, 7, e34503.	1.1	2
1053	The YARHG Domain: An Extracellular Domain in Search of a Function. PLoS ONE, 2012, 7, e35575.	1.1	3
1054	GHOSTM: A GPU-Accelerated Homology Search Tool for Metagenomics. PLoS ONE, 2012, 7, e36060.	1.1	22
1055	Comparative Analysis of the 5S rRNA and Its Associated Proteins Reveals Unique Primitive Rather Than Parasitic Features in Giardia lamblia. PLoS ONE, 2012, 7, e36878.	1.1	6
1056	Phylogenetic Analysis of a Spontaneous Cocoa Bean Fermentation Metagenome Reveals New Insights into Its Bacterial and Fungal Community Diversity. PLoS ONE, 2012, 7, e38040.	1.1	112
1057	How Many Protein-Protein Interactions Types Exist in Nature?. PLoS ONE, 2012, 7, e38913.	1.1	27
1058	IMG/M-HMP: A Metagenome Comparative Analysis System for the Human Microbiome Project. PLoS ONE, 2012, 7, e40151.	1.1	43
1059	The Dengue Vector Aedes aegypti Contains a Functional High Mobility Group Box 1 (HMGB1) Protein with a Unique Regulatory C-Terminus. PLoS ONE, 2012, 7, e40192.	1.1	14
1060	Large-Scale Transcriptome Analysis of Retroelements in the Migratory Locust, Locusta migratoria. PLoS ONE, 2012, 7, e40532.	1.1	30
1061	Identification of Potential Small Molecule Binding Pockets on Rho Family GTPases. PLoS ONE, 2012, 7, e40809.	1.1	15
1062	Predictive Sequence Analysis of the Candidatus Liberibacter asiaticus Proteome. PLoS ONE, 2012, 7, e41071.	1.1	22
1063	Prediction and Analysis of the Protein Interactome in Pseudomonas aeruginosa to Enable Network-Based Drug Target Selection. PLoS ONE, 2012, 7, e41202.	1.1	33
1064	Structures of Human DPP7 Reveal the Molecular Basis of Specific Inhibition and the Architectural Diversity of Proline-Specific Peptidases. PLoS ONE, 2012, 7, e43019.	1.1	23
1065	A Bioinformatic Strategy for the Detection, Classification and Analysis of Bacterial Autotransporters. PLoS ONE, 2012, 7, e43245.	1.1	65
1066	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. PLoS ONE, 2012, 7, e43866.	1.1	60
1067	System Wide Analysis of the Evolution of Innate Immunity in the Nematode Model Species Caenorhabditis elegans and Pristionchus pacificus. PLoS ONE, 2012, 7, e44255.	1.1	52

#	Article	IF	Citations
1068	Genome-Wide Identification and Analysis of the TIFY Gene Family in Grape. PLoS ONE, 2012, 7, e44465.	1.1	104
1069	Genome Dynamics Explain the Evolution of Flowering Time CCT Domain Gene Families in the Poaceae. PLoS ONE, 2012, 7, e45307.	1.1	93
1070	Detailed Transcriptome Description of the Neglected Cestode Taenia multiceps. PLoS ONE, 2012, 7, e45830.	1.1	27
1071	A Walk into the LuxR Regulators of Actinobacteria: Phylogenomic Distribution and Functional Diversity. PLoS ONE, 2012, 7, e46758.	1.1	61
1072	In Vitro Site Selection of a Consensus Binding Site for the Drosophila melanogaster Tbx20 Homolog Midline. PLoS ONE, 2012, 7, e48176.	1.1	7
1073	Putative Monofunctional Type I Polyketide Synthase Units: A Dinoflagellate-Specific Feature?. PLoS ONE, 2012, 7, e48624.	1.1	36
1074	Remarkable Diversity in the Enzymes Catalyzing the Last Step in Synthesis of the Pimelate Moiety of Biotin. PLoS ONE, 2012, 7, e49440.	1.1	34
1075	Interactogeneous: Disease Gene Prioritization Using Heterogeneous Networks and Full Topology Scores. PLoS ONE, 2012, 7, e49634.	1.1	32
1076	Computational Prediction of Protein-Protein Interactions in Leishmania Predicted Proteomes. PLoS ONE, 2012, 7, e51304.	1.1	32
1077	Protein Phylogenetic Analysis of Ca2+/cation Antiporters and Insights into their Evolution in Plants. Frontiers in Plant Science, 2012, 3, 1.	1.7	490
1078	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. Frontiers in Plant Science, 2012, 3, 5.	1.7	73
1079	Plant Glycosyltransferases Beyond CAZy: A Perspective on DUF Families. Frontiers in Plant Science, 2012, 3, 59.	1.7	84
1080	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. Frontiers in Genetics, 2012, 3, 283.	1.1	220
1081	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. Frontiers in Cellular and Infection Microbiology, 2012, 2, 89.	1.8	67
1082	Detecting differential usage of exons from RNA-Seq data. Nature Precedings, 0, , .	0.1	21
1083	Abiotic Stress Responses in Plants: A Focus on the SRO Family. , 2012, , .		3
1084	Subtractive libraries for prospecting differentially expressed genes in the soybean under water deficit. Genetics and Molecular Biology, 2012, 35, 304-314.	0.6	29
1085	The REACT Suite: A Software Toolkit for Microbial REgulon Annotation and Comparative Transcriptomics. , 0, , .		0

#	ARTICLE	IF	CITATIONS
1086	Evolution, expansion and expression of the Kunitz/BPTI gene family associated with long-term blood feeding in Ixodes Scapularis. BMC Evolutionary Biology, 2012, 12, 4.	3.2	62
1087	Transaminases for the synthesis of enantiopure beta-amino acids. AMB Express, 2012, 2, 11.	1.4	85
1088	Modulation of the multistate folding of designed TPR proteins through intrinsic and extrinsic factors. Protein Science, 2012, 21, 327-338.	3.1	26
1089	Camps 2.0: Exploring the sequence and structure space of prokaryotic, eukaryotic, and viral membrane proteins. Proteins: Structure, Function and Bioinformatics, 2012, 80, 839-857.	1.5	13
1090	Identification of RNAâ€"protein interaction networks using PARâ€CLIP. Wiley Interdisciplinary Reviews RNA, 2012, 3, 159-177.	3.2	192
1091	Mass spectrometryâ€based proteomics strategies for protease cleavage site identification. Proteomics, 2012, 12, 516-529.	1.3	35
1092	Twoâ€dimensional gelâ€based alkaline proteome of the probiotic bacterium <i><scp>L</scp>actobacillus acidophilus</i><scp>NCFM</scp>. Proteomics, 2012, 12, 1006-1014.	1.3	7
1093	<scp>PRDB</scp>: <scp>P</scp>rotein <scp>R</scp>epeat <scp>D</scp>ata<scp>B</scp>ase. Proteomics, 2012, 12, 1333-1336.	1.3	12
1094	Cysteineâ€rich domains related to Frizzled receptors and Hedgehogâ€interacting proteins. Protein Science, 2012, 21, 1172-1184.	3.1	32
1095	Toward a systems level view of the ECM and related proteins: A framework for the systematic definition and analysis of biological systems. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1522-1544.	1.5	26
1096	Solution structures of the doubleâ€stranded RNAâ€binding domains from rna helicase A. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1699-1706.	1.5	7
1097	Solution NMR structure of the ribosomal protein RPâ€L35Ae from <i>Pyrococcus furiosus</i>. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1901-1906.	1.5	3
1098	Computational design, construction, and characterization of a set of specificity determining residues in proteinâ€"protein interactions. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2426-2436.	1.5	4
1099	The ABC transporters in <i>Candidatus</i> Liberibacter asiaticus. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2614-2628.	1.5	36
1100	required to maintain repression2 Is a Novel Protein That Facilitates Locus-Specific Paramutation in Maize. Plant Cell, 2012, 24, 1761-1775.	3.1	33
1101	Determination of ribonuclease sequence-specificity using Pentaprobes and mass spectrometry. Rna, 2012, 18, 1267-1278.	1.6	39
1102	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2012, 856, 187-216.	0.4	47
1103	Developmental Milestones Punctuate Gene Expression in the Caenorhabditis Embryo. Developmental Cell, 2012, 22, 1101-1108.	3.1	207

#	ARTICLE	IF	CITATIONS
1104	Metaproteogenomic analysis of a community of sponge symbionts. ISME Journal, 2012, 6, 1515-1525.	4.4	131
1105	A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342.	7.7	553
1106	Long Noncontractile Tail Machines of Bacteriophages. Advances in Experimental Medicine and Biology, 2012, 726, 115-142.	0.8	101
1107	Nprl3 is required for normal development of the cardiovascular system. Mammalian Genome, 2012, 23, 404-415.	1.0	38
1108	Chapter 12. Expanding the Target Space: Druggability Assessments. RSC Drug Discovery Series, 2012, , 302-318.	0.2	0
1109	Horizontal gene transfers as metagenomic gene duplications. Molecular BioSystems, 2012, 8, 790.	2.9	11
1110	Origin of metazoan cadherin diversity and the antiquity of the classical cadherin/Î²-catenin complex. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13046-13051.	3.3	169
1111	Transcriptome Analysis in Tardigrade Species Reveals Specific Molecular Pathways for Stress Adaptations. Bioinformatics and Biology Insights, 2012, 6, BBI.S9150.	1.0	39
1112	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. Journal of Pathology, 2012, 227, 286-297.	2.1	161
1113	Modular regulatory principles of large non-coding RNAs. Nature, 2012, 482, 339-346.	13.7	2,036
1114	Biosynthesis of Teichoic Acids in<i>Streptococcus pneumoniae</i>and Closely Related Species: Lessons from Genomes. Microbial Drug Resistance, 2012, 18, 344-358.	0.9	123
1115	CENP-T proteins are conserved centromere receptors of the Ndc80 complex. Nature Cell Biology, 2012, 14, 604-613.	4.6	168
1116	A practical guide for the computational selection of residues to be experimentally characterized in protein families. Briefings in Bioinformatics, 2012, 13, 329-336.	3.2	10
1117	Structural basis of histidine kinase autophosphorylation deduced by integrating genomics, molecular dynamics, and mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1733-42.	3.3	140
1118	Cloning and Expression Analysis of Genes Encoding Lytic Endopeptidases L1 and L5 from Lysobacter sp. Strain XL1. Applied and Environmental Microbiology, 2012, 78, 7082-7089.	1.4	21
1119	Exploration and Mining of the Bacterial Terpenome. Accounts of Chemical Research, 2012, 45, 463-472.	7.6	150
1120	Prediction and Comparison of <i>Salmonella</i>ï£¿Human and <i>Salmonella</i>ï£¿<i>Arabidopsis</i> Interactomes. Chemistry and Biodiversity, 2012, 9, 991-1018.	1.0	41
1121	Biosynthesis of Xyrrolin, a New Cytotoxic Hybrid Polyketide/Nonâ€ribosomal Peptide Pyrroline with Anticancer Potential, in <i>Xylaria</i> sp. BCC 1067. ChemBioChem, 2012, 13, 895-903.	1.3	18

#	Article	IF	Citations
1122	Accurate de novo structure prediction of large transmembrane protein domains using fragment-assembly and correlated mutation analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1540-7.	3.3	176
1123	Sharing Programming Resources Between Bio* Projects Through Remote Procedure Call and Native Call Stack Strategies. Methods in Molecular Biology, 2012, 856, 513-527.	0.4	1
1124	Independent evolution of striated muscles in cnidarians and bilaterians. Nature, 2012, 487, 231-234.	13.7	221
1125	Identification and characterization of two novel genomic RNA segments of fig mosaic virus, RNA5 and RNA6. Journal of General Virology, 2012, 93, 1612-1619.	1.3	40
1126	Evolution of Synapse Complexity and Diversity. Annual Review of Neuroscience, 2012, 35, 111-131.	5.0	131
1127	The UCSC Archaeal Genome Browser: 2012 update. Nucleic Acids Research, 2012, 40, D646-D652.	6.5	89
1128	Avirulence Proteins AvrBs7 from Xanthomonas gardneri and AvrBs1.1 from Xanthomonas euvesicatoria Contribute to a Novel Gene-for-Gene Interaction in Pepper. Molecular Plant-Microbe Interactions, 2012, 25, 307-320.	1.4	35
1129	PSICOV: precise structural contact prediction using sparse inverse covariance estimation on large multiple sequence alignments. Bioinformatics, 2012, 28, 184-190.	1.8	686
1130	Genomic organization and comparative chromosome mapping of the U1 snRNA gene in cichlid fish, with an emphasis in Oreochromis niloticus. Chromosome Research, 2012, 20, 279-292.	1.0	49
1131	Solution NMR structures reveal unique homodimer formation by a winged helix-turn-helix motif and provide first structures for protein domain family PF10771. Journal of Structural and Functional Genomics, 2012, 13, 1-7.	1.2	2
1132	KB-Rank: efficient protein structure and functional annotation identification via text query. Journal of Structural and Functional Genomics, 2012, 13, 101-110.	1.2	4
1133	Structure- and sequence-based function prediction for non-homologous proteins. Journal of Structural and Functional Genomics, 2012, 13, 111-123.	1.2	27
1134	Target selection for structural genomics based on combining fold recognition and crystallisation prediction methods: application to the human proteome. Journal of Structural and Functional Genomics, 2012, 13, 37-46.	1.2	7
1135	Characterization and expression of attacin, an antibacterial protein-encoding gene, from the beet armyworm, Spodoptera exigua (HÃ¼bner) (Insecta: Lepidoptera: Noctuidae). Molecular Biology Reports, 2012, 39, 5151-5159.	1.0	45
1136	Systematic analysis of plant-specific B3 domain-containing proteins based on the genome resources of 11 sequenced species. Molecular Biology Reports, 2012, 39, 6267-6282.	1.0	38
1137	Large-scale collection and annotation of gene models for date palm (Phoenix dactylifera, L.). Plant Molecular Biology, 2012, 79, 521-536.	2.0	26
1138	Genome-wide Identification and Characterization of a Dehydrin Gene Family in Poplar (Populus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 10	1.0	34
1139	The biosynthesis of the polyether antibiotic nanchangmycin is controlled by two pathway-specific transcriptional activators. Archives of Microbiology, 2012, 194, 415-426.	1.0	26

#	Article	IF	Citations
1140	Genetic basis of destruxin production in the entomopathogen Metarhizium robertsii. Current Genetics, 2012, 58, 105-116.	0.8	43
1141	Genome-wide analysis of WRKY transcription factors in Solanum lycopersicum. Molecular Genetics and Genomics, 2012, 287, 495-513.	1.0	330
1142	Plasmid pP62BP1 isolated from an Arctic Psychrobacter sp. strain carries two highly homologous type II restriction-modification systems and a putative organic sulfate metabolism operon. Extremophiles, 2012, 16, 363-376.	0.9	8
1143	Full-length structural model of RET3 and SEC21 in COPI: identification of binding sites on the appendage for accessory protein recruitment motifs. Journal of Molecular Modeling, 2012, 18, 3199-3212.	0.8	5
1144	Transient Infantile Hypertriglyceridemia, Fatty Liver, and Hepatic Fibrosis Caused by Mutated GPD1, Encoding Glycerol-3-Phosphate Dehydrogenase 1. American Journal of Human Genetics, 2012, 90, 49-60.	2.6	74
1145	Metagenomeâ€based Screening Reveals Worldwide Distribution of LOVâ€Domain Proteins. Photochemistry and Photobiology, 2012, 88, 107-118.	1.3	24
1146	Tracing the origin and evolutionary history of plant nucleotideâ€binding siteâ€“leucineâ€rich repeat (<i>NBSâ€LRR</i>) genes. New Phytologist, 2012, 193, 1049-1063.	3.5	198
1147	Iron transporters in marine prokaryotic genomes and metagenomes. Environmental Microbiology, 2012, 14, 114-128.	1.8	93
1148	Deciphering cell wall integrity signalling in <i>Aspergillus fumigatus</i>: identification and functional characterization of cell wall stress sensors and relevant Rho GTPases. Molecular Microbiology, 2012, 83, 506-519.	1.2	106
1149	Identification and expression analysis of <i>fabp2</i> gene from common carp <i>Cyprinus carpio</i>. Journal of Fish Biology, 2012, 80, 679-691.	0.7	13
1150	The N-terminal domain of the Flo11 protein from Saccharomyces cerevisiae is an adhesin without mannose-binding activity. FEMS Yeast Research, 2012, 12, 78-87.	1.1	28
1151	Phenotypic variation in Acidovorax radicisN35 influences plant growth promotion. FEMS Microbiology Ecology, 2012, 79, 751-762.	1.3	22
1152	Genomic comparison of the endophyte Herbaspirillum seropedicaeSmR1 and the phytopathogen Herbaspirillum rubrisubalbicansM1 by suppressive subtractive hybridization and partial genome sequencing. FEMS Microbiology Ecology, 2012, 80, 441-451.	1.3	44
1153	Reactive oxygen and oxidative stress tolerance in plant pathogenic Pseudomonas. FEMS Microbiology Letters, 2012, 327, 1-8.	0.7	94
1154	Choosing the right lifestyle: adhesion and development in<i>Saccharomyces cerevisiae</i>. FEMS Microbiology Reviews, 2012, 36, 25-58.	3.9	149
1155	Microalgae in the postgenomic era: a blooming reservoir for new natural products. FEMS Microbiology Reviews, 2012, 36, 761-785.	3.9	131
1156	Ferlins: Regulators of Vesicle Fusion for Auditory Neurotransmission, Receptor Trafficking and Membrane Repair. Traffic, 2012, 13, 185-194.	1.3	119
1157	Unexpected diversity in Shisa-like proteins suggests the importance of their roles as transmembrane adaptors. Cellular Signalling, 2012, 24, 758-769.	1.7	54

#	Article	IF	Citations
1158	Characterization of chicken melanoma differentiation-associated gene 5 (MDA5) from alternative translation initiation. Comparative Immunology, Microbiology and Infectious Diseases, 2012, 35, 335-343.	0.7	24
1159	Crystal structure of <i>Pyrococcus furiosus</i> PF2050, a member of the DUF2666 protein family. FEBS Letters, 2012, 586, 1384-1388.	1.3	0
1160	Bioinformatics predicts diverse Aspergillus hydrophobins with novel properties. Food Hydrocolloids, 2012, 27, 503-516.	5.6	44
1161	Expression of Wnt9, TCTP, and Bmp1/Tll in sea cucumber visceral regeneration. Gene Expression Patterns, 2012, 12, 24-35.	0.3	62
1162	Comparative analysis of the molecular mechanisms controlling the initiation of chromosomal DNA replication in yeast and in mammalian cells. Biotechnology Advances, 2012, 30, 73-98.	6.0	22
1163	Fluoride enhances the activity of fungicides that destabilize cell membranes. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 3317-3322.	1.0	31
1164	Phaseâ€dependent generation and transmission of time information by the KaiABC circadian clock oscillator through SasAâ€KaiC interaction in cyanobacteria. Genes To Cells, 2012, 17, 398-419.	0.5	25
1165	Shortâ€chain dehydrogenases/reductases in cyanobacteria. FEBS Journal, 2012, 279, 1030-1043.	2.2	23
1166	Systematic analysis and comparison of nucleotideâ€binding site disease resistance genes in maize. FEBS Journal, 2012, 279, 2431-2443.	2.2	86
1167	The use of information theory in evolutionary biology. Annals of the New York Academy of Sciences, 2012, 1256, 49-65.	1.8	72
1168	Genomic resources for the brown planthopper, <i>Nilaparvata lugens</i>: Transcriptome pyrosequencing and microarray design. Insect Science, 2012, 19, 1-12.	1.5	23
1169	Mpg2 interacts and cooperates with Mpg1 to maintain yeast glycosylation. FEMS Yeast Research, 2012, 12, 511-520.	1.1	2
1170	A novel family of bacterial dioxygenases that catalyse the hydroxylation of free l-amino acids. FEMS Microbiology Letters, 2012, 331, 97-104.	0.7	30
1171	Functional bias of positively selected genes in Streptococcus genomes. Infection, Genetics and Evolution, 2012, 12, 274-277.	1.0	3
1172	Genes under positive selection in a model plant pathogenic fungus, Botrytis. Infection, Genetics and Evolution, 2012, 12, 987-996.	1.0	40
1173	Modular Evolution and the Origins of Symmetry: Reconstruction of a Three-Fold Symmetric Globular Protein. Structure, 2012, 20, 161-171.	1.6	97
1174	Contribution of buried aspartic acid to the stability of the PDZ2 protein. Journal of Chemical Thermodynamics, 2012, 52, 64-68.	1.0	2
1175	Identification of type VI secretion systems in Moritella viscosa. Veterinary Microbiology, 2012, 158, 436-442.	0.8	9

#	Article	IF	Citations
1176	The Î±2 helix in the DNA ligase IV BRCT-1 domain is required for targeted degradation of ligase IV during adenovirus infection. Virology, 2012, 428, 128-135.	1.1	5
1177	Quantitative proteomics in teleost fish: Insights and challenges for neuroendocrine and neurotoxicology research. General and Comparative Endocrinology, 2012, 176, 314-320.	0.8	28
1178	Effector identification in the lettuce downy mildew <i>Bremia lactucae</i> by massively parallel transcriptome sequencing. Molecular Plant Pathology, 2012, 13, 719-731.	2.0	52
1179	Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from <i>Corynebacterium glutamicum</i>. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 391-403.	2.5	26
1180	Crystallization of a novel metal-containing cupin from<i>Acidobacterium</i>sp. and preliminary diffraction data analysis. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 451-454.	0.7	3
1181	Cactin is essential for G1 progression in <i>Toxoplasma gondii</i>. Molecular Microbiology, 2012, 84, 566-577.	1.2	26
1182	The NsrR regulon in nitrosative stress resistance of <i>Salmonella enterica</i> serovar Typhimurium. Molecular Microbiology, 2012, 85, 1179-1193.	1.2	80
1183	Bioinformatics meets parasitology. Parasite Immunology, 2012, 34, 265-275.	0.7	23
1184	Comparative coâ€expression analysis in plant biology. Plant, Cell and Environment, 2012, 35, 1787-1798.	2.8	83
1185	Phylloquinone (vitamin K₁) biosynthesis in plants: two peroxisomal thioesterases of lactobacillales origin hydrolyze 1,4â€dihydroxyâ€2â€naphthoylâ€coa. Plant Journal, 2012, 71, 205-215.	2.8	77
1186	Seasonal change in the abundance of <i>Synechococcus</i> and multiple distinct phylotypes in Monterey Bay determined by <i>rbcL</i> and <i>narB</i> quantitative PCR. Environmental Microbiology, 2012, 14, 580-593.	1.8	28
1187	The components of the putative iron transport system in the cyanobacterium <i>Anabaena</i> sp. PCC 7120. Environmental Microbiology, 2012, 14, 1655-1670.	1.8	44
1188	Molecular evolution of key genes for type II secretion in <i>Legionella pneumophila</i>. Environmental Microbiology, 2012, 14, 2017-2033.	1.8	17
1189	Genomic and functional analysis of <i>Vibrio</i> phage SIOâ€2 reveals novel insights into ecology and evolution of marine siphoviruses. Environmental Microbiology, 2012, 14, 2071-2086.	1.8	42
1190	Verification of the PREFAB alignment database. Biophysics (Russian Federation), 2012, 57, 133-137.	0.2	0
1191	Occurrence of six-amino-acid motifs in three eukaryotic proteomes. Molecular Biology, 2012, 46, 168-173.	0.4	5
1192	The evolutionary history of protein fold families and proteomes confirms that the archaeal ancestor is more ancient than the ancestors of other superkingdoms. BMC Evolutionary Biology, 2012, 12, 13.	3.2	57
1193	Comparative genomic analysis of the genus Staphylococcus including Staphylococcus aureus and its newly described sister species Staphylococcus simiae. BMC Genomics, 2012, 13, 38.	1.2	51

#	Article	IF	Citations
1194	Predict impact of single amino acid change upon protein structure. BMC Genomics, 2012, 13, S4.	1.2	48
1195	The Caenorhabditis elegans D2-like dopamine receptor DOP-2 physically interacts with GPA-14, a GÎ±<sub>i</sub> subunit. Journal of Molecular Signaling, 2012, 7, 3.	0.5	20
1196	Metagenomics - a guide from sampling to data analysis. Microbial Informatics and Experimentation, 2012, 2, 3.	7.6	680
1197	UMD-DYSF, a novel locus specific database for the compilation and interactive analysis of mutations in the dysferlin gene. Human Mutation, 2012, 33, E2317-E2331.	1.1	35
1198	Molecular model of human heparanase with proposed binding mode of a heparan sulfate oligosaccharide and catalytic amino acids. Biopolymers, 2012, 97, 21-34.	1.2	19
1199	Inactivation of the positive LuxR-type oligomycin biosynthesis regulators OlmRI and OlmRII increases avermectin production in Streptomyces avermitilis. Science Bulletin, 2012, 57, 869-876.	1.7	18
1200	Molecular characterization and expression analysis of the putative interleukin 6 receptor (IL-6RÎ± and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf N-terminal Ig domain with variable numbers of two repeats. Immunogenetics, 2012, 64, 229-244.	1.2	14
1201	Diversification, phylogeny and evolution of auxin response factor (ARF) family: insights gained from analyzing maize ARF genes. Molecular Biology Reports, 2012, 39, 2401-2415.	1.0	70
1202	Insight from the draft genome of Dietzia cinnamea P4 reveals mechanisms of survival in complex tropical soil habitats and biotechnology potential. Antonie Van Leeuwenhoek, 2012, 101, 289-302.	0.7	29
1203	Homology modeling, molecular dynamics and QM/MM study of the regulatory protein PhoP from Corynebacterium pseudotuberculosis. Journal of Molecular Modeling, 2012, 18, 1219-1227.	0.8	7
1204	Downregulation of OsPK1, a cytosolic pyruvate kinase, by T-DNA insertion causes dwarfism and panicle enclosure in rice. Planta, 2012, 235, 25-38.	1.6	49
1205	CcpA and three newly identified proteins are involved in biofilm development in <i>Lactobacillus plantarum</i>. Journal of Basic Microbiology, 2013, 53, 62-71.	1.8	27
1206	Genomicsâ€informed design of loopâ€mediated isothermal amplification for detection of phytopathogenic <i>Xanthomonas arboricola</i> pv.Â<i>pruni</i> at the intraspecific level. Plant Pathology, 2013, 62, 475-484.	1.2	38
1207	Genome sequence and analysis of a broad-host range lytic bacteriophage that infects the Bacillus cereus group. Virology Journal, 2013, 10, 48.	1.4	44
1208	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. Biology Direct, 2013, 8, 15.	1.9	221
1209	Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. Biology Direct, 2013, 8, 13.	1.9	45
1210	Carbohydrate-binding modules (CBMs) revisited: reduced amount of water counterbalances the need for CBMs. Biotechnology for Biofuels, 2013, 6, 30.	6.2	123
1211	Identification of novel arthropod vector G protein-coupled receptors. Parasites and Vectors, 2013, 6, 150.	1.0	9

#	Article	IF	Citations
1212	Domain analysis of symbionts and hosts (DASH) in a genome-wide survey of pathogenic human viruses. BMC Research Notes, 2013, 6, 209.	0.6	0
1213	Computational analysis of physico-chemical properties and homology modeling of carbonic anhydrase from Cordyceps militaris. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 209-212.	1.2	6
1214	Isolation of Sporothrix schenckii GDA1 and functional characterization of the encoded guanosine diphosphatase activity. Archives of Microbiology, 2013, 195, 499-506.	1.0	11
1215	Genome-wide identification and analysis of late embryogenesis abundant (LEA) genes in Prunus mume. Molecular Biology Reports, 2013, 40, 1937-1946.	1.0	88
1216	Identification, Phylogeny, and Expression Analysis of Pto-like Genes in Pepper. Plant Molecular Biology Reporter, 2013, 31, 901-916.	1.0	2
1217	Genome-Wide Analysis of the AP2/ERF Gene Family in Prunus mume. Plant Molecular Biology Reporter, 2013, 31, 741-750.	1.0	77
1218	Taxonomic Profiling and Metagenome Analysis of a Microbial Community from a Habitat Contaminated with Industrial Discharges. Microbial Ecology, 2013, 66, 533-550.	1.4	39
1220	The nutrient supplying capabilities of <i><scp>U</scp>zinura</i>, an endosymbiont of armoured scale insects. Environmental Microbiology, 2013, 15, 1988-1999.	1.8	51
1221	Effects of phosphorus starvation versus limitation on the marine cyanobacterium <i><scp>P</scp>rochlorococcus</i>â€…<scp>MED4 II</scp>: gene expression. Environmental Microbiology, 2013, 15, 2129-2143.	1.8	31
1222	Structural representative of the protein family PF14466 has a new fold and establishes links with the C2 and PLAT domains from the widely distant Pfams PF00168 and PF01477. Protein Science, 2013, 22, 1000-1007.	3.1	5
1223	Molecular Mechanism of Membrane Binding of the GRP1 PH Domain. Journal of Molecular Biology, 2013, 425, 3073-3090.	2.0	56
1224	Proteolytic processing of the Yersinia pestis YapG autotransporter by the omptin protease Pla and the contribution of YapG to murine plague pathogenesis. Journal of Medical Microbiology, 2013, 62, 1124-1134.	0.7	10
1225	Tam41 Is a CDP-Diacylglycerol Synthase Required for Cardiolipin Biosynthesis in Mitochondria. Cell Metabolism, 2013, 17, 709-718.	7.2	135
1226	PAAR-repeat proteins sharpen and diversify the type VI secretion system spike. Nature, 2013, 500, 350-353.	13.7	466
1227	How to inherit statistically validated annotation within BAR+ protein clusters. BMC Bioinformatics, 2013, 14, S4.	1.2	8
1228	Functional inference by ProtoNet family tree: the uncharacterized proteome of Daphnia pulex. BMC Bioinformatics, 2013, 14, S11.	1.2	1
1229	Function prediction from networks of local evolutionary similarity in protein structure. BMC Bioinformatics, 2013, 14, S6.	1.2	9
1230	Reconstituting protein interaction networks using parameter-dependent domain-domain interactions. BMC Bioinformatics, 2013, 14, 154.	1.2	17

#	ARTICLE	IF	CITATIONS
1231	FANTOM: Functional and taxonomic analysis of metagenomes. BMC Bioinformatics, 2013, 14, 38.	1.2	35
1232	Variant surface antigens of malaria parasites: functional and evolutionary insights from comparative gene family classification and analysis. BMC Genomics, 2013, 14, 427.	1.2	65
1233	Global transcriptome profiles of Camellia sinensis during cold acclimation. BMC Genomics, 2013, 14, 415.	1.2	268
1234	Transcriptome sequencing and de novo annotation of the critically endangered Adriatic sturgeon. BMC Genomics, 2013, 14, 407.	1.2	71
1235	Reductive evolution in Streptococcus agalactiae and the emergence of a host adapted lineage. BMC Genomics, 2013, 14, 252.	1.2	81
1236	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. BMC Genomics, 2013, 14, 204.	1.2	61
1237	Intron retention and transcript chimerism conserved across mammals: Ly6g5b and Csnk2b-Ly6g5b as examples. BMC Genomics, 2013, 14, 199.	1.2	10
1238	The protein translocation systems in plants â€“ composition and variability on the example of Solanum lycopersicum. BMC Genomics, 2013, 14, 189.	1.2	23
1239	Genomic analysis of the regulatory elements and links with intrinsic DNA structural properties in the shrunken genome of Buchnera. BMC Genomics, 2013, 14, 73.	1.2	20
1240	Members of the Sinorhizobium meliloti ChvI regulon identified by a DNA binding screen. BMC Microbiology, 2013, 13, 132.	1.3	16
1241	Common bean (Phaseolus vulgarisL.) PvTIFY orchestrates global changes in transcript profile response to jasmonate and phosphorus deficiency. BMC Plant Biology, 2013, 13, 26.	1.6	48
1242	Identification of ovarian cancer associated genes using an integrated approach in a Boolean framework. BMC Systems Biology, 2013, 7, 12.	3.0	15
1243	Specific In Planta Recognition of Two GKLR Proteins of the Downy Mildew <i>Bremia lactucae</i> Revealed in a Large Effector Screen in Lettuce. Molecular Plant-Microbe Interactions, 2013, 26, 1259-1270.	1.4	52
1244	Identification of MDP (muramyl dipeptide)-binding key domains in NOD2 (nucleotide-binding and) Tj ETQq1 1 0.784314 rgBT /Overlock 1007-1023.	0.9	20
1245	A predicted functional gene network for the plant pathogen Phytophthora infestans as a framework for genomic biology. BMC Genomics, 2013, 14, 483.	1.2	20
1246	Segmental duplications in the silkworm genome. BMC Genomics, 2013, 14, 521.	1.2	18
1247	Application of Genome-Scale Metabolic Models in Metabolic Engineering. Industrial Biotechnology, 2013, 9, 203-214.	0.5	26
1248	Sarm1-Mediated Axon Degeneration Requires Both SAM and TIR Interactions. Journal of Neuroscience, 2013, 33, 13569-13580.	1.7	302

#	ARTICLE	IF	CITATIONS
1249	Serine/threonine kinases and E2-ubiquitin conjugating enzymes in Planctomycetes: unexpected findings. Antonie Van Leeuwenhoek, 2013, 104, 509-520.	0.7	12
1250	The PmNAC1 gene is induced by auxin and expressed in differentiating vascular cells in callus cultures of Passiflora. Plant Cell, Tissue and Organ Culture, 2013, 115, 275-283.	1.2	8
1251	A Passiflora homolog of a D-type cyclin gene is differentially expressed in response to sucrose, auxin, and cytokinin. Plant Cell, Tissue and Organ Culture, 2013, 115, 233-242.	1.2	12
1253	Extrapolating the effect of deleterious nsSNPs in the binding adaptability of flavopiridol with CDK7 protein: a molecular dynamics approach. Human Genomics, 2013, 7, 10.	1.4	47
1254	Drug Discovery and Development via Synthetic Biology. , 2013, , 183-206.		9
1255	The impact of temperature on marine phytoplankton resource allocation and metabolism. Nature Climate Change, 2013, 3, 979-984.	8.1	358
1256	Draft Assembly of the Symbiodinium minutum Nuclear Genome Reveals Dinoflagellate Gene Structure. Current Biology, 2013, 23, 1399-1408.	1.8	488
1257	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	9.4	341
1258	Vivaldi: Visualization and validation of biomacromolecular NMR structures from the PDB. Proteins: Structure, Function and Bioinformatics, 2013, 81, 583-591.	1.5	13
1259	Genome-wide Mapping of DNA Methylation in the Human Malaria Parasite Plasmodium falciparum. Cell Host and Microbe, 2013, 14, 696-706.	5.1	79
1260	Microcephaly Thin Corpus Callosum Intellectual Disability Syndrome Caused by Mutated TAF2. Pediatric Neurology, 2013, 49, 411-416.e1.	1.0	36
1261	Comparative genomic analysis of twelve Streptococcus suis (pro)phages. Genomics, 2013, 101, 336-344.	1.3	41
1262	Charge asymmetry in the proteins of the outer membrane. Bioinformatics, 2013, 29, 2122-2128.	1.8	50
1263	Teaching the bioinformatics of signaling networks: an integrated approach to facilitate multi-disciplinary learning. Briefings in Bioinformatics, 2013, 14, 618-632.	3.2	15
1264	The chitinolytic machinery of <i><scp>S</scp>erratiaÂmarcescens</i> â€“ a model system for enzymatic degradation of recalcitrant polysaccharides. FEBS Journal, 2013, 280, 3028-3049.	2.2	244
1265	Reduction and Expansion in Microsporidian Genome Evolution: New Insights from Comparative Genomics. Genome Biology and Evolution, 2013, 5, 2285-2303.	1.1	114
1266	High-Resolution Structural Analysis Shows How Tah1 Tethers Hsp90 to the R2TP Complex. Structure, 2013, 21, 1834-1847.	1.6	42
1267	Isolation and characterization of a carrot nucleolar protein with structural and sequence similarity to the vertebrate PESCADILLO protein. Plant Science, 2013, 208, 83-92.	1.7	0

#	ARTICLE	IF	CITATIONS
1268	Analysis of the regulation of the Ustilago maydis proteome by dimorphism, pH or MAPK and GCN5 genes. Journal of Proteomics, 2013, 79, 251-262.	1.2	14
1269	Computational determination of the orientation of a heat repeat-like domain of DNA-PKcs. Computational Biology and Chemistry, 2013, 42, 1-4.	1.1	1
1270	Computational modeling and experimental validation of the <i>Legionella</i> and <i>Coxiella</i> virulence-related type-IVB secretion signal. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E707-15.	3.3	166
1271	MetaSAMSâ€"A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. Journal of Biotechnology, 2013, 167, 156-165.	1.9	17
1272	Adaptation of the Osmotolerant Yeast <i>Zygosaccharomyces rouxii</i> to an Osmotic Environment Through Copy Number Amplification of <i>FLO11D</i>. Genetics, 2013, 195, 393-405.	1.2	21
1273	Comparative analysis of Leishmania exoproteomes: Implication for hostâ€"pathogen interactions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2653-2662.	1.1	8
1274	Phycobilisome: architecture of a light-harvesting supercomplex. Photosynthesis Research, 2013, 116, 265-276.	1.6	196
1275	Progesterone regulates the expression and activity of two mouse isoforms of the glycoprotein folding sensor UDP-Glc: Glycoprotein glucosyltransferase (UGGT). Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 3368-3374.	1.9	11
1276	Protein docking using caseâ€based reasoning. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2150-2158.	1.5	98
1277	Sequence determination and analysis of three plasmids of Pseudomonas sp. GLE121, a psychrophile isolated from surface ice of Ecology Glacier (Antarctica). Plasmid, 2013, 70, 254-262.	0.4	24
1278	Evolutionary origin of amino acid transporter families SLC32, SLC36 and SLC38 and physiological, pathological and therapeutic aspects. Molecular Aspects of Medicine, 2013, 34, 571-585.	2.7	125
1280	GET_HOMOLOGUES, a Versatile Software Package for Scalable and Robust Microbial Pangenome Analysis. Applied and Environmental Microbiology, 2013, 79, 7696-7701.	1.4	902
1281	CBS domains: Ligand binding sites and conformational variability. Archives of Biochemistry and Biophysics, 2013, 540, 70-81.	1.4	105
1282	The Evolution of Small Insertions and Deletions in the Coding Genes of Drosophila melanogaster. Molecular Biology and Evolution, 2013, 30, 2699-2708.	3.5	6
1283	Insights into polypharmacology from drug-domain associations. Bioinformatics, 2013, 29, 1934-1937.	1.8	18
1284	Phylogenetic relationship and virulence inference of Streptococcus Anginosus Group: curated annotation and whole-genome comparative analysis support distinct species designation. BMC Genomics, 2013, 14, 895.	1.2	51
1285	Cloning of new acylamidase gene from Rhodococcus erythropolis and its expression in Escherichia coli. Russian Journal of Genetics, 2013, 49, 1078-1081.	0.2	5
1286	Genomic and expression analysis of a solute carrier protein (CcSLC25a5) gene from Cyprinus carpio Linnaeus. SpringerPlus, 2013, 2, 458.	1.2	1

#	Article	IF	Citations
1287	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. BMC Evolutionary Biology, 2013, 13, 202.	3.2	51
1288	kClust: fast and sensitive clustering of large protein sequence databases. BMC Bioinformatics, 2013, 14, 248.	1.2	83
1289	Novel autoproteolytic and DNA-damage sensing components in the bacterial SOS response and oxidized methylcytosine-induced eukaryotic DNA demethylation systems. Biology Direct, 2013, 8, 20.	1.9	59
1290	The root transcriptome for North American ginseng assembled and profiled across seasonal development. BMC Genomics, 2013, 14, 564.	1.2	35
1291	PFClust: a novel parameter free clustering algorithm. BMC Bioinformatics, 2013, 14, 213.	1.2	15
1292	Reductive evolution and the loss of PDC/PAS domains from the genus Staphylococcus. BMC Genomics, 2013, 14, 524.	1.2	12
1293	Comparative analysis of genome sequences from four strains of the Buchnera aphidicola Mp endosymbion of the green peach aphid, Myzus persicae. BMC Genomics, 2013, 14, 917.	1.2	31
1294	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in Phytophthora sojae. BMC Genomics, 2013, 14, 839.	1.2	30
1295	Transcriptome profiling of fruit development and maturation in Chinese white pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td	1.2	50
1296	Solution NMR structure of CD1104B from pathogenic Clostridium difficile reveals a distinct Î±-helical architecture and provides first structural representative of protein domain family PF14203. Journal of Structural and Functional Genomics, 2013, 14, 155-160.	1.2	2
1297	Using desolvation energies of structural domains to predict stability of protein complexes. Network Modeling Analysis in Health Informatics and Bioinformatics, 2013, 2, 267-275.	1.2	5
1298	SHARP: genome-scale identification of geneâ€"proteinâ€"reaction associations in cyanobacteria. Photosynthesis Research, 2013, 118, 181-190.	1.6	6
1299	Agrigenomics for Microalgal Biofuel Production: An Overview of Various Bioinformatics Resources and Recent Studies to Link OMICS to Bioenergy and Bioeconomy. OMICS A Journal of Integrative Biology, 2013, 17, 537-549.	1.0	41
1300	Molecular Phylogeny, Homology Modeling, and Molecular Dynamics Simulation of Race-Specific Bacterial Blight Disease Resistance Protein (xa5) of Rice: A Comparative Agriproteomics Approach. OMICS A Journal of Integrative Biology, 2013, 17, 423-438.	1.0	9
1301	Dynamic protein phosphorylation during the growth of Xanthomonas campestris pv. campestris B100 revealed by a gel-based proteomics approach. Journal of Biotechnology, 2013, 167, 111-122.	1.9	16
1302	A matrix based algorithm for proteinâ€"protein interaction prediction using domainâ€"domain associations. Journal of Theoretical Biology, 2013, 326, 36-42.	0.8	16
1303	Drug-Domain Interaction Networks in Myocardial Infarction. IEEE Transactions on Nanobioscience, 2013, 12, 182-188.	2.2	2
1304	Multiple biological sequence alignment in heterogeneous multicore clusters with user-selectable task allocation policies. Journal of Supercomputing, 2013, 63, 740-756.	2.4	4

#	ARTICLE	IF	CITATIONS
1305	Protein interactions in the murine cytomegalovirus capsid revealed by cryoEM. Protein and Cell, 2013, 4, 833-845.	4.8	7
1306	Flavoprotein oxidases: classification and applications. Applied Microbiology and Biotechnology, 2013, 97, 5177-5188.	1.7	123
1307	Learning the language of post-transcriptional gene regulation. Genome Biology, 2013, 14, 130.	3.8	18
1308	Modulation of protein stability and aggregation properties by surface charge engineering. Molecular BioSystems, 2013, 9, 2379.	2.9	32
1309	Comparison of Dimensional Reduction Methods for Detecting and Visualizing Novel Patterns in Human and Marine Microbiome. IEEE Transactions on Nanobioscience, 2013, 12, 199-205.	2.2	5
1310	Reproduction-Related Genes in the Pearl Oyster Genome. Zoological Science, 2013, 30, 826.	0.3	26
1311	A Novel Type of Peptidoglycan-binding Domain Highly Specific for Amidated d-Asp Cross-bridge, Identified in Lactobacillus casei Bacteriophage Endolysins. Journal of Biological Chemistry, 2013, 288, 20416-20426.	1.6	24
1312	Accelerating gene context analysis using bitmaps. , 2013, , .		11
1313	Identifying essential proteins based on protein domains in protein-protein interaction networks. , 2013, , .		3
1314	Biosynthetic Multitasking Facilitates Thalassospiramide Structural Diversity in Marine Bacteria. Journal of the American Chemical Society, 2013, 135, 1155-1162.	6.6	55
1315	Identification and structural characterization of serobactins, a suite of lipopeptide siderophores produced by the grass endophyte <i><scp>H</scp>erbaspirillum seropedicae</i>. Environmental Microbiology, 2013, 15, 916-927.	1.8	66
1316	LepChorionDB, a database of Lepidopteran chorion proteins and a set of tools useful for the identification of chorion proteins in Lepidopteran proteomes. Insect Biochemistry and Molecular Biology, 2013, 43, 189-196.	1.2	8
1317	Two <i>Sinorhizobium meliloti</i> glutaredoxins regulate iron metabolism and symbiotic bacteroid differentiation. Environmental Microbiology, 2013, 15, 795-810.	1.8	46
1318	Rubus canadensis virus 1, a novel betaflexivirus identified in blackberry. Archives of Virology, 2013, 158, 445-449.	0.9	10
1319	A neural network algorithm for semi-supervised node label learning from unbalanced data. Neural Networks, 2013, 43, 84-98.	3.3	43
1320	Predicting permanent and transient proteinâ€"protein interfaces. Proteins: Structure, Function and Bioinformatics, 2013, 81, 805-818.	1.5	48
1321	Importance of Different Types of Prior Knowledge in Selecting Genomeâ€Wide Findings for Followâ€Up. Genetic Epidemiology, 2013, 37, 205-213.	0.6	14
1322	Characterization of human NLZ1/ZNF703 identifies conserved domains essential for proper subcellular localization and transcriptional repression. Journal of Cellular Biochemistry, 2013, 114, 120-133.	1.2	18

#	ARTICLE	IF	CITATIONS
1323	Staphylococcus aureus TMPK and TK showing distinct structural differences with human TMPK and TK â€“ A probable explanation in the pathogenesis. Journal of Pharmacy Research, 2013, 7, 89-95.	0.4	0
1324	Identification of a Ninein (NIN) mutation in a family with spondyloepimetaphyseal dysplasia with joint laxity (leptodactylic type)-like phenotype. Matrix Biology, 2013, 32, 387-392.	1.5	15
1325	Origin and evolution of medium chain alcohol dehydrogenases. Chemico-Biological Interactions, 2013, 202, 91-96.	1.7	30
1326	N-Terminal Domains in Two-Domain Proteins Are Biased to Be Shorter and Predicted to Fold Faster Than Their C-Terminal Counterparts. Cell Reports, 2013, 3, 1051-1056.	2.9	8
1327	Modelling knowledge strategy for solving the DNA sequence annotation problem through CommonKADS methodology. Expert Systems With Applications, 2013, 40, 3943-3952.	4.4	7
1328	Topological Plasticity of Enzymes Involved in Disulfide Bond Formation Allows Catalysis in Either the Periplasm Or the Cytoplasm. Journal of Molecular Biology, 2013, 425, 3268-3276.	2.0	26
1329	Tracing the evolution of the Î±-amylase subfamily GH13_36 covering the amylolytic enzymes intermediate between oligo-1,6-glucosidases and neopullulanases. Carbohydrate Research, 2013, 367, 48-57.	1.1	61
1330	Characterization of the AtsR Hybrid Sensor Kinase Phosphorelay Pathway and Identification of Its Response Regulator in Burkholderia cenocepacia. Journal of Biological Chemistry, 2013, 288, 30473-30484.	1.6	14
1331	An abundant LEA protein in the anhydrobiotic midge, PvLEA4, acts as a molecular shield by limiting growth of aggregating protein particles. Insect Biochemistry and Molecular Biology, 2013, 43, 1055-1067.	1.2	65
1332	Genome-wide analysis of endosperm-specific genes in rice. Gene, 2013, 530, 236-247.	1.0	46
1333	Large plasmids of Escherichia coli and Salmonella encode highly diverse arrays of accessory genes on common replicon families. Plasmid, 2013, 69, 36-48.	0.4	31
1334	Rhipicephalus microplus lipocalins (LRMs): Genomic identification and analysis of the bovine immune response using in silico predicted B and T cell epitopes. International Journal for Parasitology, 2013, 43, 739-752.	1.3	24
1335	Evolutionary variation and adaptation in a conserved protein kinase allosteric network: Implications for inhibitor design. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1322-1329.	1.1	9
1336	The crystal structure of a novel phosphopantothenate synthetase from the hyperthermophilic archaea, Thermococcus onnurineus NA1. Biochemical and Biophysical Research Communications, 2013, 439, 533-538.	1.0	4
1337	Functional characterization of the polyketide synthase gene required for ochratoxin A biosynthesis in Penicillium verrucosum. International Journal of Food Microbiology, 2013, 161, 172-181.	2.1	31
1338	Robust cuticular penetration resistance in the common bed bug (Cimex lectularius L.) correlates with increased steady-state transcript levels of CPR-type cuticle protein genes. Pesticide Biochemistry and Physiology, 2013, 106, 190-197.	1.6	99
1339	Differential regulation of MHCII genes by PRMT6, via an AT-hook motif of RFX5. Molecular Immunology, 2013, 56, 390-398.	1.0	9
1340	Rho participates in chemoreceptor-induced changes in morphology to hair bundle mechanoreceptors of the sea anemone, Nematostella vectensis. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2013, 165, 139-148.	0.8	5

#	Article	IF	Citations
1341	Cloning of the Lentinula edodes B mating-type locus and identification of the genetic structure controlling B mating. Gene, 2013, 531, 270-278.	1.0	26
1342	Evolution of the tissue factor pathway inhibitor-like Kunitz domain-containing protein family in Rhipicephalus microplus. International Journal for Parasitology, 2013, 43, 81-94.	1.3	19
1343	Identification of susceptibility modules for coronary artery disease using a genome wide integrated network analysis. Gene, 2013, 531, 347-354.	1.0	17
1344	A Conserved Spiral Structure for Highly Diverged Phage Tail Assembly Chaperones. Journal of Molecular Biology, 2013, 425, 2436-2449.	2.0	20
1345	Structure and Signaling Mechanism of a Zinc-Sensory Diguanylate Cyclase. Structure, 2013, 21, 1149-1157.	1.6	95
1346	Type II Toxin-Antitoxins: Structural and Functional Aspects of Type II Loci in Mycobacteria. , 2013, , 137-156.		0
1347	Expression of sulfatases in Rhodopirellula baltica and the diversity of sulfatases in the genus Rhodopirellula. Marine Genomics, 2013, 9, 51-61.	0.4	145
1348	Structure and Intrinsic Disorder in Protein Autoinhibition. Structure, 2013, 21, 332-341.	1.6	83
1349	Identification of an additional protein involved in mannan biosynthesis. Plant Journal, 2013, 73, 105-117.	2.8	45
1350	Selecting age-related functional characteristics in the human gut microbiome. Microbiome, 2013, 1, 2.	4.9	45
1352	Bioinformatics methods for the comparative analysis of metazoan mitochondrial genome sequences. Molecular Phylogenetics and Evolution, 2013, 69, 320-327.	1.2	31
1353	Modeling the zing finger protein SmZF1 from Schistosoma mansoni: Insights into DNA binding and gene regulation. Journal of Molecular Graphics and Modelling, 2013, 39, 29-38.	1.3	4
1354	Localization Prediction and Structure-Based In Silico Analysis of Bacterial Proteins: With Emphasis on Outer Membrane Proteins. Methods in Molecular Biology, 2013, 939, 115-140.	0.4	3
1355	Nitric oxide generated by the rice blast fungus <i>Magnaporthe oryzae</i> drives plant infection. New Phytologist, 2013, 197, 207-222.	3.5	75
1356	Raw starch-degrading Î±-amylase from<i>Bacillus aquimaris</i>MKSC 6.2: isolation and expression of the gene, bioinformatics and biochemical characterization of the recombinant enzyme. Journal of Applied Microbiology, 2013, 114, 108-120.	1.4	56
1357	Regulon controlled by the <scp>G</scp>pp<scp>X</scp> hybrid two component system in <i><scp>P</scp>orphyromonas gingivalis</i>. Molecular Oral Microbiology, 2013, 28, 70-81.	1.3	16
1358	The xylan utilization system of the plant pathogen <i><scp>X</scp>anthomonas campestris</i> pv <i>campestris</i> controls epiphytic life and reveals common features with oligotrophic bacteria and animal gut symbionts. New Phytologist, 2013, 198, 899-915.	3.5	59
1359	The Genetic Architecture of Biofilm Formation in a Clinical Isolate of <i>Saccharomyces cerevisiae</i>. Genetics, 2013, 193, 587-600.	1.2	37

#	Article	IF	Citations
1360	Saccharinae Bioinformatics Resources. , 2013, , 303-330.		0
1361	Proteomic Analysis of Clathrin Interactions in Trypanosomes Reveals Dynamic Evolution of Endocytosis. Traffic, 2013, 14, 440-457.	1.3	37
1362	Druggability predictions: methods, limitations, and applications. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2013, 3, 327-338.	6.2	30
1363	Genome-wide identification, molecular evolution and expression analyses of the phospholipase D gene family in three Rosaceae species. Scientia Horticulturae, 2013, 153, 13-21.	1.7	20
1364	Fig mosaic emaravirus p4 protein is involved in cell-to-cell movement. Journal of General Virology, 2013, 94, 682-686.	1.3	42
1365	Searching for protein signatures using a multilevel alphabet. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1058-1068.	1.5	1
1366	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. Science, 2013, 339, 1207-1210.	6.0	439
1367	MOTIF DISCOVERY WITH DATA MINING IN 3D PROTEIN STRUCTURE DATABASES: DISCOVERY, VALIDATION AND PREDICTION OF THE U-SHAPE ZINC BINDING ("HUF-ZINC") MOTIF. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340008.	0.3	3
1368	Marine microbial symbiosis heats up: the phylogenetic and functional response of a sponge holobiont to thermal stress. ISME Journal, 2013, 7, 991-1002.	4.4	266
1369	A quantum model of exaptation: Incorporating potentiality into evolutionary theory. Progress in Biophysics and Molecular Biology, 2013, 113, 108-116.	1.4	23
1370	The Orphan Protein Bis-Î³-glutamylcystine Reductase Joins the Pyridine Nucleotide Disulfide Reductase Family. Biochemistry, 2013, 52, 2905-2913.	1.2	8
1371	Structure of a complete four-domain chitinase from<i>Moritella marina</i>, a marine psychrophilic bacterium. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 821-829.	2.5	37
1372	Chromosome 10 in the tomato plant carries clusters of genes responsible for field resistance/defence to Phytophthora infestans. Genomics, 2013, 101, 249-255.	1.3	7
1373	A modified pathway for the production of acetone in Escherichia coli. Metabolic Engineering, 2013, 15, 218-225.	3.6	24
1374	The discovery of Foxl2 paralogs in chondrichthyan, coelacanth and tetrapod genomes reveals an ancient duplication in vertebrates. Heredity, 2013, 111, 57-65.	1.2	22
1375	Genome mining for methanobactins. BMC Biology, 2013, 11, 17.	1.7	64
1376	Features of evolutionarily conserved alternative splicing events between B rassica and A rabidopsis. New Phytologist, 2013, 199, 252-263.	3.5	36
1377	Evolutionary and mechanistic insights into substrate and product accommodation of <scp>CTP</scp>:phosphocholine cytidylyltransferase from <i><scp>P</scp>lasmodiumÂfalciparum</i>. FEBS Journal, 2013, 280, 3132-3148.	2.2	16

#	ARTICLE	IF	CITATIONS
1378	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.	1.6	11,344
1379	Gene invasion in distant eukaryotic lineages: discovery of mutually exclusive genetic elements reveals marine biodiversity. ISME Journal, 2013, 7, 1764-1774.	4.4	27
1380	Deep sequencing of non-ribosomal peptide synthetases and polyketide synthases from the microbiomes of Australian marine sponges. ISME Journal, 2013, 7, 1842-1851.	4.4	53
1381	Predicting the Impact of Single-Nucleotide Polymorphisms in CDK2â€"Flavopiridol Complex by Molecular Dynamics Analysis. Cell Biochemistry and Biophysics, 2013, 66, 681-695.	0.9	14
1382	Comparative Genomics of a Plant-Pathogenic Fungus,<i>Pyrenophora tritici-repentis</i>, Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. G3: Genes, Genomes, Genetics, 2013, 3, 41-63.	0.8	167
1383	Partial venom gland transcriptome of a Drosophila parasitoid wasp, Leptopilina heterotoma, reveals novel and shared bioactive profiles with stinging Hymenoptera. Gene, 2013, 526, 195-204.	1.0	54
1384	Apple gene function and gene family database: an integrated bioinformatics database for apple research. Plant Growth Regulation, 2013, 70, 199-206.	1.8	15
1385	The <scp>RNAi</scp> machinery regulates growth and development in the filamentous fungus <i><scp>T</scp>richoderma atroviride</i>. Molecular Microbiology, 2013, 89, 96-112.	1.2	88
1386	Identification of Legionella Effectors Using Bioinformatic Approaches. Methods in Molecular Biology, 2013, 954, 595-602.	0.4	18
1387	Metagenome and metaproteome analyses of microbial communities in mesophilic biogas-producing anaerobic batch fermentations indicate concerted plant carbohydrate degradation. Systematic and Applied Microbiology, 2013, 36, 330-338.	1.2	182
1388	Emerging role of rhomboid family proteins in mammalian biology and disease. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2840-2848.	1.4	51
1389	A Practical Approach to Reconstruct Evolutionary History of Animal Sialyltransferases and Gain Insights into the Sequenceâ€"Function Relationships of Golgi-Glycosyltransferases. Methods in Molecular Biology, 2013, 1022, 73-97.	0.4	9
1390	Specificity through cooperation: BATFâ€"IRF interactions control immune-regulatory networks. Nature Reviews Immunology, 2013, 13, 499-509.	10.6	319
1391	Protein Engineering and Stabilization from Sequence Statistics. Methods in Enzymology, 2013, 523, 237-256.	0.4	25
1392	Tools for Protein Posttranslational Modifications Analysis: FAK, a Case Study. Methods in Molecular Biology, 2013, 1007, 335-358.	0.4	1
1393	The Herbaspirillum seropedicae SmR1 Fnr orthologs controls the cytochrome composition of the electron transport chain. Scientific Reports, 2013, 3, 2544.	1.6	17
1394	Proteins of novel lactic acid bacteria from Apis mellifera mellifera: an insight into the production of known extra-cellular proteins during microbial stress. BMC Microbiology, 2013, 13, 235.	1.3	78
1395	A population-based evolutionary search approach to the multiple minima problem in de novo protein structure prediction. BMC Structural Biology, 2013, 13, S4.	2.3	18

#	Article	IF	Citations
1396	Ranking and compacting binding segments of protein families using aligned pattern clusters. Proteome Science, 2013, 11, S8.	0.7	15
1397	Zinc Biochemistry: From a Single Zinc Enzyme to a Key Element of Life. Advances in Nutrition, 2013, 4, 82-91.	2.9	550
1398	Structural analysis and molecular dynamics simulations of novel Î´-endotoxin Cry1Id from Bacillus thuringiensis to pave the way for development of novel fusion proteins against insect pests of crops. Journal of Molecular Modeling, 2013, 19, 5301-5316.	0.8	12
1399	Structure-Function Analysis of the Human Ferroportin Iron Exporter (SLC40A1): Effect of Hemochromatosis Type 4 Disease Mutations and Identification of Critical Residues. Human Mutation, 2013, 34, 1371-1380.	1.1	48
1400	Structure of the Flavoprotein Tryptophan 2-Monooxygenase, a Key Enzyme in the Formation of Galls in Plants. Biochemistry, 2013, 52, 2620-2626.	1.2	26
1406	The <i>Apl</i>I Restriction-Modification System in an Edible Cyanobacterium, <i>Arthrospira</i> (<i>Spirulina</i>) <i>platensis</i> NIES-39, Recognizes the Nucleotide Sequence 5â€²-CTGCAG-3â€². Bioscience, Biotechnology and Biochemistry, 2013, 77, 782-788.	0.6	11
1407	Nuclear Magnetic Resonance Solution Structure of the Peptidoglycan-Binding SPOR Domain from <i>Escherichia coli</i> DamX: Insights into Septal Localization. Biochemistry, 2013, 52, 627-639.	1.2	16
1408	Characterizing the Range of Extracellular Protein Post-Translational Modifications in a Cellulose-Degrading Bacteria Using a Multiple Proteolyic Digestion/Peptide Fragmentation Approach. Analytical Chemistry, 2013, 85, 3144-3151.	3.2	7
1409	Desmosterol and DHCR24: Unexpected new directions for a terminal step in cholesterol synthesis. Progress in Lipid Research, 2013, 52, 666-680.	5.3	101
1410	Transcriptome Analysis of Developing Ovules in Rice Isolated by Laser Microdissection. Plant and Cell Physiology, 2013, 54, 750-765.	1.5	60
1411	The automatic annotation of bacterial genomes. Briefings in Bioinformatics, 2013, 14, 1-12.	3.2	122
1412	Structure of EvaA: A Paradigm for Sugar 2,3-Dehydratases. Biochemistry, 2013, 52, 2078-2088.	1.2	3
1413	Dirigent domain-containing protein is part of the machinery required for formation of the lignin-based Casparian strip in the root. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14498-14503.	3.3	269
1414	Solution NMR structures provide first structural coverage of the large protein domain family PF08369 and complementary structural coverage of dark operative protochlorophyllide oxidoreductase complexes. Journal of Structural and Functional Genomics, 2013, 14, 119-126.	1.2	0
1415	The Structural Model of <i>Salmonella typhimurium</i> Ethanolamine Ammonia-Lyase Directs a Rational Approach to the Assembly of the Functional [(EutBâ€"EutC)₂]₃ Oligomer from Isolated Subunits. Biochemistry, 2013, 52, 1419-1428.	1.2	18
1416	Distribution and cluster analysis of predicted intrinsically disordered protein Pfam domains. Intrinsically Disordered Proteins, 2013, 1, e25724.	1.9	12
1417	Elucidating Human Phosphatase-Substrate Networks. Science Signaling, 2013, 6, rs10.	1.6	145
1418	Growth Temperature and Genome Size in Bacteria Are Negatively Correlated, Suggesting Genomic Streamlining During Thermal Adaptation. Genome Biology and Evolution, 2013, 5, 966-977.	1.1	179

#	ARTICLE	IF	CITATIONS
1419	Hydrogenosomes in the diplomonad Spironucleus salmonicida. Nature Communications, 2013, 4, 2493.	5.8	48
1420	A Sensitive and Accurate protein domain cLassification Tool (SALT) for short reads. Bioinformatics, 2013, 29, 2103-2111.	1.8	10
1421	A SAS-6-Like Protein Suggests that the Toxoplasma Conoid Complex Evolved from Flagellar Components. Eukaryotic Cell, 2013, 12, 1009-1019.	3.4	70
1422	Complete Genome Sequence of the Sugar Beet Endophyte Pseudomonas poae RE*1-1-14, a Disease-Suppressive Bacterium. Genome Announcements, 2013, 1, e0002013.	0.8	20
1423	Genome Sequence of Serratia plymuthica Strain S13, an Endophyte with Germination- and Plant-Growth-Promoting Activity from the Flower of Styrian Oil Pumpkin. Genome Announcements, 2013, 1, .	0.8	13
1424	Integration of the Second Messenger c-di-GMP into the Chemotactic Signaling Pathway. MBio, 2013, 4, e00001-13.	1.8	59
1425	Clustering under approximation stability. Journal of the ACM, 2013, 60, 1-34.	1.8	46
1426	Revealing Protein Structures by Co-Occurrence Clustering of Aligned Pattern Clusters. , 2013, , .		0
1427	Protein signature-based estimation of metagenomic abundances including all domains of life and viruses. Bioinformatics, 2013, 29, 973-980.	1.8	36
1428	Missense mutation in the ATPase, aminophospholipid transporter protein ATP8A2 is associated with cerebellar atrophy and quadrupedal locomotion. European Journal of Human Genetics, 2013, 21, 281-285.	1.4	110
1429	Identification of the YfgF MASE1 domain as a modulator of bacterial responses to aspartate. Open Biology, 2013, 3, 130046.	1.5	9
1430	Analysis of Complete Genomes of<i>Propionibacterium acnes</i>Reveals a Novel Plasmid and Increased Pseudogenes in an Acne Associated Strain. BioMed Research International, 2013, 2013, 1-11.	0.9	58
1431	Chapter 15: Disease Gene Prioritization. PLoS Computational Biology, 2013, 9, e1002902.	1.5	65
1432	Defining the Core Proteome of the Chloroplast Envelope Membranes. Frontiers in Plant Science, 2013, 4, 11.	1.7	75
1433	A comparison of the molecular organization of genomic regions associated with resistance to common bacterial blight in two Phaseolus vulgaris genotypes. Frontiers in Plant Science, 2013, 4, 318.	1.7	14
1434	Modeling the Effect of APC Truncation on Destruction Complex Function in Colorectal Cancer Cells. PLoS Computational Biology, 2013, 9, e1003217.	1.5	23
1435	Genomic Mechanisms Accounting for the Adaptation to Parasitism in Nematode-Trapping Fungi. PLoS Genetics, 2013, 9, e1003909.	1.5	97
1436	Immune response of the Caribbean sea fan, Gorgonia ventalina, exposed to an Aplanochytrium parasite as revealed by transcriptome sequencing. Frontiers in Physiology, 2013, 4, 180.	1.3	58

#	ARTICLE	IF	CITATIONS
1437	Dynamic Evolution of Endogenous Retrovirus-Derived Genes Expressed in Bovine Conceptuses during the Period of Placentation. Genome Biology and Evolution, 2013, 5, 296-306.	1.1	30
1438	eFG: an electronic resource for Fusarium graminearum. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat042-bat042.	1.4	5
1439	Large Linear Plasmids of Borrelia Species That Cause Relapsing Fever. Journal of Bacteriology, 2013, 195, 3629-3639.	1.0	38
1440	Proteome of the Nematode-Trapping Cells of the Fungus Monacrosporium haptotylum. Applied and Environmental Microbiology, 2013, 79, 4993-5004.	1.4	35
1441	A Versatile Class of Cell Surface Directional Motors Gives Rise to Gliding Motility and Sporulation in Myxococcus xanthus. PLoS Biology, 2013, 11, e1001728.	2.6	41
1442	A High Molecular-Mass Anoxybacillus sp. SK3-4 Amylopullulanase: Characterization and Its Relationship in Carbohydrate Utilization. International Journal of Molecular Sciences, 2013, 14, 11302-11318.	1.8	31
1443	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. International Journal of Molecular Sciences, 2013, 14, 11444-11483.	1.8	8
1444	Amino Acid Changes in Disease-Associated Variants Differ Radically from Variants Observed in the 1000 Genomes Project Dataset. PLoS Computational Biology, 2013, 9, e1003382.	1.5	54
1445	Construction of a rice glycoside hydrolase phylogenomic database and identification of targets for biofuel research. Frontiers in Plant Science, 2013, 4, 330.	1.7	35
1446	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. Molecular and Cellular Proteomics, 2013, 12, 1689-1700.	2.5	31
1447	Predicting the accuracy of multiple sequence alignment algorithms by using computational intelligent techniques. Nucleic Acids Research, 2013, 41, e26-e26.	6.5	13
1448	Comparative Genomics of Odorant Binding Proteins in Anopheles gambiae, Aedes aegypti, and Culex quinquefasciatus. Genome Biology and Evolution, 2013, 5, 163-180.	1.1	112
1449	Beyond BLASTing: Tertiary and Quaternary Structure Analysis Helps Identify Major Vault Proteins. Genome Biology and Evolution, 2013, 5, 217-232.	1.1	6
1450	Structures and reaction mechanisms of the two related enzymes, PurN and PurU. Journal of Biochemistry, 2013, 154, 569-579.	0.9	5
1451	Atypical Glycolysis in Clostridium thermocellum. Applied and Environmental Microbiology, 2013, 79, 3000-3008.	1.4	92
1452	Yeast PPR proteins, watchdogs of mitochondrial gene expression. RNA Biology, 2013, 10, 1477-1494.	1.5	39
1453	Structural and Biochemical Analyses of Mycobacterium tuberculosis N-Acetylmuramyl-l-alanine Amidase Rv3717 Point to a Role in Peptidoglycan Fragment Recycling. Journal of Biological Chemistry, 2013, 288, 31549-31555.	1.6	36
1454	Caffeate Respiration in the Acetogenic Bacterium Acetobacterium woodii: a Coenzyme A Loop Saves Energy for Caffeate Activation. Applied and Environmental Microbiology, 2013, 79, 1942-1947.	1.4	30

#	ARTICLE	IF	CITATIONS
1455	Transcriptome and Proteome Data Reveal Candidate Genes for Pollinator Attraction in Sexually Deceptive Orchids. PLoS ONE, 2013, 8, e64621.	1.1	46
1456	Functional Analysis of Sporophytic Transcripts Repressed by the Female Gametophyte in the Ovule of Arabidopsis thaliana. PLoS ONE, 2013, 8, e76977.	1.1	6
1457	DLocalMotif: a discriminative approach for discovering local motifs in protein sequences. Bioinformatics, 2013, 29, 39-46.	1.8	16
1458	Profiling Protein Kinases and Other ATP Binding Proteins in Arabidopsis Using Acyl-ATP Probes. Molecular and Cellular Proteomics, 2013, 12, 2481-2496.	2.5	31
1459	SpoIVA and SipL Are Clostridium difficile Spore Morphogenetic Proteins. Journal of Bacteriology, 2013, 195, 1214-1225.	1.0	129
1460	Identification and prioritization of novel uncharacterized peptidases for biochemical characterization. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat022.	1.4	6
1461	<i>cat</i>RAPID <i>omics</i>: a web server for large-scale prediction of proteinâ€“RNA interactions. Bioinformatics, 2013, 29, 2928-2930.	1.8	247
1462	Genome-wide survey of DNA-binding proteins in Arabidopsis thaliana : analysis of distribution and functions. Nucleic Acids Research, 2013, 41, 7212-7219.	6.5	14
1463	The crystal structure of the DNA-binding domain of vIRF-1 from the oncogenic KSHV reveals a conserved fold for DNA binding and reinforces its role as a transcription factor. Nucleic Acids Research, 2013, 41, 4295-4306.	6.5	19
1464	CMCompare webserver: comparing RNA families via covariance models. Nucleic Acids Research, 2013, 41, W499-W503.	6.5	10
1465	Crystallization and preliminary crystallographic analysis of Axe2, an acetylxylan esterase from<i>Geobacillus stearothermophilus</i>. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 430-434.	0.7	17
1466	Evolutionary history of the TBP-domain superfamily. Nucleic Acids Research, 2013, 41, 2832-2845.	6.5	27
1467	Strategies and molecular tools to fight antimicrobial resistance: resistome, transcriptome, and antimicrobial peptides. Frontiers in Microbiology, 2013, 4, 412.	1.5	51
1468	Comparative Genomics Analysis of the Metallomes. Metal Ions in Life Sciences, 2013, 12, 529-580.	2.8	14
1469	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in Enterococcus faecium. Genome Biology and Evolution, 2013, 5, 1524-1535.	1.1	87
1470	Genomic and Secretomic Analyses Reveal Unique Features of the Lignocellulolytic Enzyme System of Penicillium decumbens. PLoS ONE, 2013, 8, e55185.	1.1	159
1471	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. Science Signaling, 2013, 6, ra38.	1.6	47
1472	The Online Protein Processing Resource (TOPPR): a database and analysis platform for protein processing events. Nucleic Acids Research, 2013, 41, D333-D337.	6.5	17

#	Article	IF	Citations
1473	Cyclic Di-GMP Modulates the Disease Progression of Erwinia amylovora. Journal of Bacteriology, 2013, 195, 2155-2165.	1.0	77
1474	Separating homeologs by phasing in the tetraploid wheat transcriptome. Genome Biology, 2013, 14, R66.	3.8	126
1475	Origins and diversity of eukaryotic CO2-concentrating mechanisms: lessons for the future. Journal of Experimental Botany, 2013, 64, 769-786.	2.4	144
1476	IruO Is a Reductase for Heme Degradation by IsdI and IsdG Proteins in Staphylococcus aureus. Journal of Biological Chemistry, 2013, 288, 25749-25759.	1.6	23
1477	LigSearch: a knowledge-based web server to identify likely ligands for a protein target. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2395-2402.	2.5	2
1478	Structural characterization of the ribonuclease H-like type ASKHA superfamily kinase MK0840 fromMethanopyrus kandleri. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2440-2450.	2.5	4
1479	The twilight zone of cis element alignments. Nucleic Acids Research, 2013, 41, 1438-1449.	6.5	11
1480	The challenge of increasing Pfam coverage of the human proteome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat023.	1.4	22
1481	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat065-bat065.	1.4	4
1482	Cloud Prediction of Protein Structure and Function with PredictProtein for Debian. BioMed Research International, 2013, 2013, 1-6.	0.9	16
1483	Turning gold into â€˜junkâ€™: transposable elements utilize central proteins of cellular networks. Nucleic Acids Research, 2013, 41, 3190-3200.	6.5	22
1484	An estimated 5% of new protein structures solved today represent a new Pfam family. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2186-2193.	2.5	12
1485	Crystallization and preliminary diffraction analysis of the catalytic domain of major extracellular endoglucanase fromXanthomonas campestrispv.campestris. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 137-140.	0.7	2
1486	YgfX (CptA) is a multimeric membrane protein that interacts with the succinate dehydrogenase assembly factor SdhE (YgfY). Microbiology (United Kingdom), 2013, 159, 1352-1365.	0.7	8
1487	ThreaDom: extracting protein domain boundary information from multiple threading alignments. Bioinformatics, 2013, 29, i247-i256.	1.8	79
1488	Prediction of contact matrix for proteinâ€“protein interaction. Bioinformatics, 2013, 29, 1018-1025.	1.8	15
1489	Molecular function prediction for a family exhibiting evolutionary tendencies toward substrate specificity swapping: Recurrence of tyrosine aminotransferase activity in the Iî± subfamily. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1593-1609.	1.5	6
1490	Analysis of periplasmic sensor domains from <i>Anaeromyxobacter dehalogenans</i> 2<scp>CP</scp>â€C: Structure of one sensor domain from a histidine kinase and another from a chemotaxis protein. MicrobiologyOpen, 2013, 2, 766-777.	1.2	7

#	Article	IF	Citations
1491	An <scp>ER</scp>â€directed transcriptional response to unfolded protein stress in the absence of conserved sensorâ€transducer proteins in <i><scp>G</scp>iardia lamblia</i>. Molecular Microbiology, 2013, 88, 754-771.	1.2	11
1492	ESPRESSO: A system for estimating protein expression and solubility in protein expression systems. Proteomics, 2013, 13, 1444-1456.	1.3	40
1493	Regulation of <scp>V</scp>â€nitrogenase genes in <i><scp>A</scp>nabaena variabilis</i> by <scp>RNA</scp> processing and by dual repressors. Molecular Microbiology, 2013, 88, 413-424.	1.2	30
1494	Structure and Function of Carbohydrate-Binding Module Families 13 and 42 of Glycoside Hydrolases, Comprising a Î²-Trefoil Fold. Bioscience, Biotechnology and Biochemistry, 2013, 77, 1363-1371.	0.6	46
1495	A homology/<i>ab initio</i> hybrid algorithm for sampling nearâ€native protein conformations. Journal of Computational Chemistry, 2013, 34, 1925-1936.	1.5	14
1496	Probing the Key Interactions between Human Atg5 and Atg16 Proteins: A Prospective Application of Molecular Modeling. ChemMedChem, 2013, 8, 1270-1275.	1.6	8
1497	The Cleavage Domain of the Amyloid Precursor Protein Transmembrane Helix Does Not Exhibit Aboveâ€Average Backbone Dynamics. ChemBioChem, 2013, 14, 1943-1948.	1.3	22
1498	Orchidstra: An Integrated Orchid Functional Genomics Database. Plant and Cell Physiology, 2013, 54, e11-e11.	1.5	41
1499	Role of the Guanine Nucleotide Exchange Factor Rom2 in Cell Wall Integrity Maintenance of Aspergillus fumigatus. Eukaryotic Cell, 2013, 12, 288-298.	3.4	37
1500	The Nucleic Acid-binding Domain and Translational Repression Activity of a Xenopus Terminal Uridylyl Transferase. Journal of Biological Chemistry, 2013, 288, 20723-20733.	1.6	21
1501	Coevolutionary signals across protein lineages help capture multiple protein conformations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20533-20538.	3.3	163
1502	Fly cryptochrome and the visual system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6163-6168.	3.3	103
1503	Assembly of the Yeast Exoribonuclease Rrp6 with Its Associated Cofactor Rrp47 Occurs in the Nucleus and Is Critical for the Controlled Expression of Rrp47. Journal of Biological Chemistry, 2013, 288, 15959-15970.	1.6	25
1504	Bioinformatics and Systems Biology: bridging the gap between heterogeneous student backgrounds. Briefings in Bioinformatics, 2013, 14, 589-598.	3.2	12
1505	Role of the CipA Scaffoldin Protein in Cellulose Solubilization, as Determined by Targeted Gene Deletion and Complementation in Clostridium thermocellum. Journal of Bacteriology, 2013, 195, 733-739.	1.0	34
1506	Cooperative Degradation of Chitin by Extracellular and Cell Surface-Expressed Chitinases from Paenibacillus sp. Strain FPU-7. Applied and Environmental Microbiology, 2013, 79, 7482-7490.	1.4	66
1507	Glycyrrhiza uralensis Transcriptome Landscape and Study of Phytochemicals. Plant and Cell Physiology, 2013, 54, 697-710.	1.5	80
1508	The nuclear F-actin interactome of Xenopus oocytes reveals an actin-bundling kinesin that is essential for meiotic cytokinesis. EMBO Journal, 2013, 32, 1886-1902.	3.5	62

#	ARTICLE	IF	CITATIONS
1509	Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. Bioinformatics, 2013, 29, 695-703.	1.8	74
1510	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants Â Â. Plant Physiology, 2013, 162, 769-778.	2.3	44
1511	Biochemical Properties and Crystal Structure of a Î²-Phenylalanine Aminotransferase from Variovorax paradoxus. Applied and Environmental Microbiology, 2013, 79, 185-195.	1.4	29
1512	Relapsed Classic E-Cadherin (<i>CDH1</i>)â€"Mutated Invasive Lobular Breast Cancer Shows a High Frequency of <i>HER2</i> (<i>ERBB2</i>) Gene Mutations. Clinical Cancer Research, 2013, 19, 2668-2676.	3.2	122
1513	Complete Genome of Lactococcus lactis subsp. cremoris UC509.9, Host for a Model Lactococcal P335 Bacteriophage. Genome Announcements, 2013, 1, .	0.8	39
1514	A Novel <i>dnaJ</i> Family Gene, <i>sflA</i> , Encodes an Inhibitor of Flagellation in Marine Vibrio Species. Journal of Bacteriology, 2013, 195, 816-822.	1.0	31
1515	RNA pentaloop structures as effective targets of regulators belonging to the RsmA/CsrA protein family. RNA Biology, 2013, 10, 1030-1041.	1.5	37
1516	Primary mediastinal large B-cell lymphoma segregating in a family: exome sequencing identifies MLL as a candidate predisposition gene. Blood, 2013, 121, 3428-3430.	0.6	21
1517	Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. BioData Mining, 2013, 6, 25.	2.2	50
1518	Genome sequence of the moderately halophilic bacterium Salinicoccus carnicancri type strain CrmT (= DSM 23852T). Standards in Genomic Sciences, 2013, 8, 255-263.	1.5	11
1519	Re-annotation of the Saccharopolyspora erythraea genome using a systems biology approach. BMC Genomics, 2013, 14, 699.	1.2	21
1520	Genome sequence of the chromate-resistant bacterium Leucobacter salsicius type strain M1-8T. Standards in Genomic Sciences, 2013, 9, 495-504.	1.5	9
1521	Bacterial genomes: what they teach us about cellulose degradation. Biofuels, 2013, 4, 669-681.	1.4	34
1522	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. ELife, 2013, 2, e00675.	2.8	379
1523	Identification and In-vivo Characterization of a Novel OhrR Transcriptional Regulator in Burkholderia xenovorans LB400. Journal of Molecular Biology Research, 2013, 3, .	0.1	3
1524	The Distribution of Polyhedral Bacterial Microcompartments Suggests Frequent Horizontal Transfer and Operon Reassembly. Journal of Phylogenetics & Evolutionary Biology, 2013, 01, .	0.2	22
1525	Cathelicidins Revisited. International Journal of Systems Biology and Biomedical Technologies, 2013, 2, 8-32.	0.2	1
1526	N-Acetylmuramoyl-l-alanine Amidase. , 2013, , 1401-1407.		1

#	ARTICLE	IF	CITATIONS
1527	Ecogenomic Perspectives on Domains of Unknown Function: Correlation-Based Exploration of Marine Metagenomes. PLoS ONE, 2013, 8, e50869.	1.1	11
1528	The Genome Sequences of Cellulomonas fimi and â€œCellvibrio gilvusâ€• Reveal the Cellulolytic Strategies of Two Facultative Anaerobes, Transfer of â€œCellvibrio gilvusâ€• to the Genus Cellulomonas, and Proposal of Cellulomonas gilvus sp. nov. PLoS ONE, 2013, 8, e53954.	1.1	56
1529	Impact of Whole-Genome and Tandem Duplications in the Expansion and Functional Diversification of the F-Box Family in Legumes (Fabaceae). PLoS ONE, 2013, 8, e55127.	1.1	30
1530	Evolution of the Ferric Reductase Domain (FRD) Superfamily: Modularity, Functional Diversification, and Signature Motifs. PLoS ONE, 2013, 8, e58126.	1.1	68
1531	Genome Sequence of Lactobacillus pentosus KCA1: Vaginal Isolate from a Healthy Premenopausal Woman. PLoS ONE, 2013, 8, e59239.	1.1	50
1532	Genomic Organization, Phylogenetic Comparison and Differential Expression of the SBP-Box Family Genes in Grape. PLoS ONE, 2013, 8, e59358.	1.1	102
1533	Genomic Evaluation of Thermoanaerobacter spp. for the Construction of Designer Co-Cultures to Improve Lignocellulosic Biofuel Production. PLoS ONE, 2013, 8, e59362.	1.1	39
1534	Exploration of Noncoding Sequences in Metagenomes. PLoS ONE, 2013, 8, e59488.	1.1	4
1535	Simultaneous Transcriptome Analysis of Sorghum and Bipolaris sorghicola by Using RNA-seq in Combination with De Novo Transcriptome Assembly. PLoS ONE, 2013, 8, e62460.	1.1	79
1536	Structural and Population-Based Evaluations of TBC1D1 p.Arg125Trp. PLoS ONE, 2013, 8, e63897.	1.1	8
1537	Plasmidome-Analysis of ESBL-Producing Escherichia coli Using Conventional Typing and High-Throughput Sequencing. PLoS ONE, 2013, 8, e65793.	1.1	44
1538	A DNA-Based Registry for All Animal Species: The Barcode Index Number (BIN) System. PLoS ONE, 2013, 8, e66213.	1.1	1,562
1539	Comparative Genomics Reveal That Host-Innate Immune Responses Influence the Clinical Prevalence of Legionella pneumophila Serogroups. PLoS ONE, 2013, 8, e67298.	1.1	33
1540	Giant Hydrogen Sulfide Plume in the Oxygen Minimum Zone off Peru Supports Chemolithoautotrophy. PLoS ONE, 2013, 8, e68661.	1.1	158
1541	Are Cellulosome Scaffolding Protein CipC and CBM3-Containing Protein HycP, Involved in Adherence of Clostridium cellulolyticum to Cellulose?. PLoS ONE, 2013, 8, e69360.	1.1	16
1542	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. PLoS ONE, 2013, 8, e72439.	1.1	46
1543	Carbohydrate-Active Enzymes in Pythium and Their Role in Plant Cell Wall and Storage Polysaccharide Degradation. PLoS ONE, 2013, 8, e72572.	1.1	106
1544	OptZyme: Computational Enzyme Redesign Using Transition State Analogues. PLoS ONE, 2013, 8, e75358.	1.1	22

#	Article	IF	Citations
1545	Characterization of the yehUT Two-Component Regulatory System of Salmonella enterica Serovar Typhi and Typhimurium. PLoS ONE, 2013, 8, e84567.	1.1	16
1546	Characterization and Phylogenetic Analysis of the Mitochondrial Genome of Glarea lozoyensis Indicates High Diversity within the Order Helotiales. PLoS ONE, 2013, 8, e74792.	1.1	9
1547	Inferring the Brassica rapa Interactome Using Proteinâ€“Protein Interaction Data from Arabidopsis thaliana. Frontiers in Plant Science, 2012, 3, 297.	1.7	25
1548	Examining marginal sequence similarities between bacterial type III secretion system components and Trypanosoma cruzi surface proteins: horizontal gene transfer or convergent evolution?. Frontiers in Genetics, 2013, 4, 143.	1.1	6
1549	Annotation extension through protein family annotation coherence metrics. Frontiers in Genetics, 2013, 4, 201.	1.1	5
1550	The Genome of Nitrospina gracilis Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. Frontiers in Microbiology, 2013, 4, 27.	1.5	243
1551	Uses of Phage Display in Agriculture: Sequence Analysis and Comparative Modeling of Late Embryogenesis Abundant Client Proteins Suggest Protein-Nucleic Acid Binding Functionality. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-11.	0.7	6
1552	Genetic Covariance. , 2013, , 242-245.		0
1553	Mitochondrial Genome of Phlebia radiata Is the Second Largest (156 kbp) among Fungi and Features Signs of Genome Flexibility and Recent Recombination Events. PLoS ONE, 2014, 9, e97141.	1.1	80
1554	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. PLoS ONE, 2014, 9, e85568.	1.1	57
1555	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476.	1.1	19
1556	Phylogeny and Molecular Evolution Analysis of PIN-FORMED 1 in Angiosperm. PLoS ONE, 2014, 9, e89289.	1.1	6
1557	De Novo Structure Prediction of Globular Proteins Aided by Sequence Variation-Derived Contacts. PLoS ONE, 2014, 9, e92197.	1.1	98
1558	Expression of the Pupal Determinant broad during Metamorphic and Neotenic Development of the Strepsipteran Xenos vesparum Rossi. PLoS ONE, 2014, 9, e93614.	1.1	15
1559	The Complexity of Vesicle Transport Factors in Plants Examined by Orthology Search. PLoS ONE, 2014, 9, e97745.	1.1	34
1560	Comparative Transcriptome Analysis of Four Prymnesiophyte Algae. PLoS ONE, 2014, 9, e97801.	1.1	34
1561	A Pseudomonas aeruginosa EF-Hand Protein, EfhP (PA4107), Modulates Stress Responses and Virulence at High Calcium Concentration. PLoS ONE, 2014, 9, e98985.	1.1	39
1562	Structural Diversity in the Dandelion (Taraxacum officinale) Polyphenol Oxidase Family Results in Different Responses to Model Substrates. PLoS ONE, 2014, 9, e99759.	1.1	28

#	ARTICLE	IF	CITATIONS
1563	Conserved Prosegment Residues Stabilize a Late-Stage Folding Transition State of Pepsin Independently of Ground States. PLoS ONE, 2014, 9, e101339.	1.1	6
1564	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. PLoS ONE, 2014, 9, e104794.	1.1	43
1565	Transcriptome of American Oysters, Crassostrea virginica, in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance. PLoS ONE, 2014, 9, e105097.	1.1	74
1566	Inferring Meaningful Communities from Topology-Constrained Correlation Networks. PLoS ONE, 2014, 9, e113438.	1.1	0
1567	Prediction of Protein-Protein Interaction Strength Using Domain Features with Supervised Regression. Scientific World Journal, The, 2014, 2014, 1-7.	0.8	10
1568	High frequency of phylogenetically diverse reductive dehalogenase-homologous genes in deep subseafloor sedimentary metagenomes. Frontiers in Microbiology, 2014, 5, 80.	1.5	61
1569	Functional Analysis of Hypothetical Proteins of Chlamydia Trachomatis: A Bioinformatics Based Approach for Prioritizing the Targets. Journal of Computer Science and Systems Biology, 2014, 7, .	0.0	2
1570	Genetic characterisation of Langerin gene in human immunodeficiency virus-1-infected women from Bahia, Brazil. Memorias Do Instituto Oswaldo Cruz, 2014, 109, 250-255.	0.8	0
1571	Environmental Risk Assessment of Replication Competent Viral Vectors Applied in Clinical Trials: Potential Effects of Inserted Sequences. Current Gene Therapy, 2014, 13, 395-412.	0.9	7
1572	A Nodule-Specific Lipid Transfer Protein AsE246 Participates in Transport of Plant-Synthesized Lipids to Symbiosome Membrane and Is Essential for Nodule Organogenesis in Chinese Milk Vetch Â Â Â. Plant Physiology, 2014, 164, 1045-1058.	2.3	74
1573	Putative osmosensor â€“ OsHK3b â€“ a histidine kinase protein from rice shows high structural conservation with its ortholog AtHK1 from<i>Arabidopsis</i>. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1318-1332.	2.0	14
1574	A Consensus Algorithm for Simple Motifs Finding. , 2014, , .		0
1575	Mycobacterium Tuberculosis Proteome Microarray for Global Studies of Protein Function and Immunogenicity. Cell Reports, 2014, 9, 2317-2329.	2.9	77
1576	Biological process annotation of proteins across the plant kingdom. Current Plant Biology, 2014, 1, 73-82.	2.3	7
1577	Discovering protein-DNA binding cores by aligned pattern clustering. , 2014, , .		4
1578	Quantitative analysis of race-specific resistance to Colletotrichum lindemuthianum in common bean. Molecular Breeding, 2014, 34, 1313-1329.	1.0	35
1579	Identification of glycoproteins secreted by wild-type Botrytis cinerea and by protein O-mannosyltransferase mutants. BMC Microbiology, 2014, 14, 254.	1.3	20
1580	Adaptive genomic structural variation in the grape powdery mildew pathogen, Erysiphe necator. BMC Genomics, 2014, 15, 1081.	1.2	162

#	ARTICLE	IF	CITATIONS
1581	Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1676-1683.	3.3	51
1582	Genome-wide analysis of the R2R3-MYB transcription factor gene family in sweet orange (Citrus) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	52
1583	Alfalfa snakin-1 prevents fungal colonization and probably coevolved with rhizobia. BMC Plant Biology, 2014, 14, 248.	1.6	51
1584	Kinase domain-targeted isolation of defense-related receptor-like kinases (RLK/Pelle) in Platanusâ€‰Ã—â€‰acerifolia: phylogenetic and structural analysis. BMC Research Notes, 2014, 7, 884.	0.6	7
1585	Overexpression of p49/STRAP alters cellular cytoskeletal structure and gross anatomy in mice. BMC Cell Biology, 2014, 15, 32.	3.0	20
1586	Functional Analysis of Light-harvesting-like Protein 3 (LIL3) and Its Light-harvesting Chlorophyll-binding Motif in Arabidopsis. Journal of Biological Chemistry, 2014, 289, 987-999.	1.6	38
1587	Metagenomics reveals that detoxification systems are underrepresented in marine bacterial communities. BMC Genomics, 2014, 15, 749.	1.2	35
1588	Low frequency of paleoviral infiltration across the avian phylogeny. Genome Biology, 2014, 15, 539.	3.8	60
1589	The genome of Paenibacillus sabinae T27 provides insight into evolution, organization and functional elucidation of nif and nif-like genes. BMC Genomics, 2014, 15, 723.	1.2	27
1590	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. Nucleic Acids Research, 2014, 42, e145-e145.	6.5	90
1591	Lectin Structures: Classification Based on the 3-D Structures. Methods in Molecular Biology, 2014, 1200, 579-606.	0.4	45
1592	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. ISME Journal, 2014, 8, 1904-1919.	4.4	150
1593	Gene Duplication, Lineage-Specific Expansion, and Subfunctionalization in the MADF-BESS Family Patterns the <i>Drosophila</i> Wing Hinge. Genetics, 2014, 196, 481-496.	1.2	32
1594	Metabolic analysis of <i>Chlorobium chlorochromatii</i> CaD3 reveals clues of the symbiosis in â€˜<i>Chlorochromatium aggregatum</i>â€™. ISME Journal, 2014, 8, 991-998.	4.4	13
1595	Alternatives to vitamin B1 uptake revealed with discovery of riboswitches in multiple marine eukaryotic lineages. ISME Journal, 2014, 8, 2517-2529.	4.4	69
1596	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. Genome Biology and Evolution, 2014, 6, 3122-3136.	1.1	24
1597	Functional features and protein network of human sperm-egg interaction. Systems Biology in Reproductive Medicine, 2014, 60, 329-337.	1.0	18
1598	Analysis of the Protein Domain and Domain Architecture Content in Fungi and Its Application in the Search of New Antifungal Targets. PLoS Computational Biology, 2014, 10, e1003733.	1.5	25

#	Article	IF	Citations
1599	DHCR24 associates strongly with the endoplasmic reticulum beyond predicted membrane domains: implications for the activities of this multi-functional enzyme. Bioscience Reports, 2014, 34, .	1.1	19
1600	Histidine Degradation via an Aminotransferase Increases the Nutritional Flexibility of Candida glabrata. Eukaryotic Cell, 2014, 13, 758-765.	3.4	26
1601	Ball Python Nidovirus: a Candidate Etiologic Agent for Severe Respiratory Disease in <i>Python regius</i>. MBio, 2014, 5, e01484-14.	1.8	82
1602	The stability region of the Streptomyces lividans plasmid pIJ101 encodes a DNA-binding protein recognizing a highly conserved short palindromic sequence motif. Frontiers in Microbiology, 2014, 5, 499.	1.5	8
1603	PLIC: proteinâ€"ligand interaction clusters. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau029.	1.4	37
1604	AromaDeg, a novel database for phylogenomics of aerobic bacterial degradation of aromatics. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau118.	1.4	57
1605	Phenotypic profiling of ABC transporter coding genes in Myxococcus xanthus. Frontiers in Microbiology, 2014, 5, 352.	1.5	8
1606	A Scalable and Accurate Targeted Gene Assembly Tool (SAT-Assembler) for Next-Generation Sequencing Data. PLoS Computational Biology, 2014, 10, e1003737.	1.5	31
1607	TXNDC5, a Newly Discovered Disulfide Isomerase with a Key Role in Cell Physiology and Pathology. International Journal of Molecular Sciences, 2014, 15, 23501-23518.	1.8	59
1608	The Genome of Spironucleus salmonicida Highlights a Fish Pathogen Adapted to Fluctuating Environments. PLoS Genetics, 2014, 10, e1004053.	1.5	63
1609	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. Frontiers in Physiology, 2013, 4, 315.	1.3	17
1610	The Structure and Dynamics of BmR1 Protein from Brugia malayi: In Silico Approaches. International Journal of Molecular Sciences, 2014, 15, 11082-11099.	1.8	16
1611	Ancient Origins of Vertebrate-Specific Innate Antiviral Immunity. Molecular Biology and Evolution, 2014, 31, 140-153.	3.5	55
1612	High Potential Source for Biomass Degradation Enzyme Discovery and Environmental Aspects Revealed through Metagenomics of Indian Buffalo Rumen. BioMed Research International, 2014, 2014, 1-10.	0.9	35
1613	The Domain Landscape of Virus-Host Interactomes. BioMed Research International, 2014, 2014, 1-13.	0.9	30
1614	A comprehensive aligned nifH gene database: a multipurpose tool for studies of nitrogen-fixing bacteria. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau001.	1.4	173
1615	Widespread Genome Reorganization of an Obligate Virus Mutualist. PLoS Genetics, 2014, 10, e1004660.	1.5	83
1616	Quantitative Analysis of the Mitochondrial and Plastid Proteomes of the Moss <i>Physcomitrella patens</i> Reveals Protein Macrocompartmentation and Microcompartmentation. Plant Physiology, 2014, 164, 2081-2095.	2.3	61

#	Article	IF	Citations
1617	Crystal Structure of the Human, FIC-Domain Containing Protein HYPE and Implications for Its Functions. Structure, 2014, 22, 1831-1843.	1.6	48
1618	Draft Genome Sequence of Kitasatospora cheerisanensis KCTC 2395, Which Produces Plecomacrolide against Phytopathogenic Fungi. Genome Announcements, 2014, 2, .	0.8	6
1619	Immunoproteomics: current approach for subunit vaccine design. International Journal of Immunological Studies, 2014, 2, 16.	0.2	0
1620	In-silico analysis of Aspergillus niger beta-glucosidases. , 2014, , .		1
1621	Deciphering kinaseâ€"substrate relationships by analysis of domain-specific phosphorylation network. Bioinformatics, 2014, 30, 1730-1738.	1.8	17
1622	Distribution, classification, domain architectures and evolution of prolyl oligopeptidases in prokaryotic lineages. BMC Genomics, 2014, 15, 985.	1.2	15
1623	Promiscuous and Adaptable Enzymes Fill â€œHolesâ€• in the Tetrahydrofolate Pathway in <i>Chlamydia</i> Species. MBio, 2014, 5, e01378-14.	1.8	47
1624	Molecular architecture and the structural basis for anion interaction in prestin and SLC26 transporters. Nature Communications, 2014, 5, 3622.	5.8	74
1625	Evolution of Bacterial Protein-Tyrosine Kinases and Their Relaxed Specificity Toward Substrates. Genome Biology and Evolution, 2014, 6, 800-817.	1.1	35
1626	Evolutionary Insights into Premetazoan Functions of the Neuronal Protein Homer. Molecular Biology and Evolution, 2014, 31, 2342-2355.	3.5	46
1627	Decelerated genome evolution in modern vertebrates revealed by analysis of multiple lancelet genomes. Nature Communications, 2014, 5, 5896.	5.8	136
1628	Functional evaluation of the role of C-type lectin domain family 16A at the chromosome 16p13 locus. Clinical and Experimental Immunology, 2014, 175, 485-497.	1.1	16
1629	The paradox of marine heterotrophic nitrogen fixation: abundances of heterotrophic diazotrophs do not account for nitrogen fixation rates in the <scp>E</scp>astern <scp>T</scp>ropical <scp>S</scp>outh <scp>P</scp>acific. Environmental Microbiology, 2014, 16, 3095-3114.	1.8	99
1630	An application of ontology-based filtering method in discovery of saliva biomarkers for gastric cancer. , 2014, , .		1
1631	Expression patterns and protein structure of a lipid transfer protein END1 from Arabidopsis. Planta, 2014, 240, 1319-1334.	1.6	6
1632	Direct Coupling Analysis for Protein Contact Prediction. Methods in Molecular Biology, 2014, 1137, 55-70.	0.4	52
1634	The Plasmid Complement of Lactococcus lactis UC509.9 Encodes Multiple Bacteriophage Resistance Systems. Applied and Environmental Microbiology, 2014, 80, 4341-4349.	1.4	18
1635	3PFDB+: improved search protocol and update for the identification of representatives of protein sequence domain families. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau026.	1.4	5

#	ARTICLE	IF	CITATIONS
1636	A unique octameric structure of Axe2, an intracellular acetyl-xylooligosaccharide esterase from<i>Geobacillus stearothermophilus</i>. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 261-278.	2.5	30
1637	A Roadmap for Functional Structural Variants in the Soybean Genome. G3: Genes, Genomes, Genetics, 2014, 4, 1307-1318.	0.8	42
1638	A 2,4-dichlorophenoxyacetic acid degradation plasmid pM7012 discloses distribution of an unclassified megaplasmid group across bacterial species. Microbiology (United Kingdom), 2014, 160, 525-536.	0.7	11
1639	Evolution of the Cytosolic Iron-Sulfur Cluster Assembly Machinery in Blastocystis Species and Other Microbial Eukaryotes. Eukaryotic Cell, 2014, 13, 143-153.	3.4	47
1640	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. BMC Genomics, 2014, 15, 1159.	1.2	10
1641	A Subfamily of Putative Cytokinin Receptors Is Revealed by an Analysis of the Evolution of the Two-Component Signaling System of Plants Â Â. Plant Physiology, 2014, 165, 227-237.	2.3	37
1642	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. Nucleic Acids Research, 2014, 42, D389-D395.	6.5	31
1643	Understanding and identifying amino acid repeats. Briefings in Bioinformatics, 2014, 15, 582-591.	3.2	60
1644	Prediction of domain boundaries in protein sequences using predicted secondary structure and physicochemical properties of amino acids. , 2014, , .		0
1645	A Systematic Computational Analysis of Biosynthetic Gene Cluster Evolution: Lessons for Engineering Biosynthesis. PLoS Computational Biology, 2014, 10, e1004016.	1.5	164
1646	Evolutionary Conservation and Expression of Human RNA-Binding Proteins and Their Role in Human Genetic Disease. Advances in Experimental Medicine and Biology, 2014, 825, 1-55.	0.8	119
1647	Profile Hidden Markov Models for the Detection of Viruses within Metagenomic Sequence Data. PLoS ONE, 2014, 9, e105067.	1.1	153
1648	Signaling regulates activity of DHCR24, the final enzyme in cholesterol synthesis. Journal of Lipid Research, 2014, 55, 410-420.	2.0	52
1649	Nutrigenomics. , 2014, , 501-515.		0
1650	Massive Gene Transfer and Extensive RNA Editing of a Symbiotic Dinoflagellate Plastid Genome. Genome Biology and Evolution, 2014, 6, 1408-1422.	1.1	68
1651	Edc3 Function in Yeast and Mammals Is Modulated by Interaction with NAD-Related Compounds. G3: Genes, Genomes, Genetics, 2014, 4, 613-622.	0.8	10
1652	An Assembly of Proteins and Lipid Domains Regulates Transport of Phosphatidylserine to Phosphatidylserine Decarboxylase 2 in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2014, 289, 5809-5819.	1.6	31
1653	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	6.5	5,425

#	Article	IF	Citations
1654	Molecular cloning of Ra-sHSPI, a novel member of the HSP20 family from Rhipicephalus annulatus salivary glands. International Journal of Biological Macromolecules, 2014, 67, 7-15.	3.6	9
1655	Deep-sequencing analysis of an apricot tree with vein clearing symptoms reveals the presence of a novel betaflexivirus. Virus Research, 2014, 181, 1-5.	1.1	27
1656	Genetic characterization of 4-cresol catabolism in Corynebacterium glutamicum. Journal of Biotechnology, 2014, 192, 355-365.	1.9	15
1657	Tracing the origin and evolution of plant TIR-encoding genes. Gene, 2014, 546, 408-416.	1.0	11
1658	Distribution, expression and expansion of Aspergillus fumigatus LINE-like retrotransposon populations in clinical and environmental isolates. Fungal Genetics and Biology, 2014, 64, 36-44.	0.9	4
1659	Genomics and bioinformatics resources for translational science in Rosaceae. Plant Biotechnology Reports, 2014, 8, 49-64.	0.9	18
1660	A new cytochrome P450 system from Bacillus megaterium DSM319 for the hydroxylation of 11-keto-Î²-boswellic acid (KBA). Applied Microbiology and Biotechnology, 2014, 98, 1703-1717.	1.7	34
1661	Development of novel EST-derived resistance gene markers in hop (Humulus lupulus L.). Molecular Breeding, 2014, 33, 61-74.	1.0	6
1662	Î²-Glucuronidase from Lactobacillus brevis useful for baicalin hydrolysis belongs to glycoside hydrolase family 30. Applied Microbiology and Biotechnology, 2014, 98, 4021-4032.	1.7	42
1663	Metagenomics Using Next-Generation Sequencing. Methods in Molecular Biology, 2014, 1096, 183-201.	0.4	77
1664	Bioinformatics tools for genome mining of polyketide and non-ribosomal peptides. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 443-450.	1.4	72
1665	PmTCP1 encodes a putative TCP transcription factor and is differentially expressed during in vitro organogenesis in Passiflora. In Vitro Cellular and Developmental Biology - Plant, 2014, 50, 36-44.	0.9	3
1666	The complete genome sequence of Piper yellow mottle virus (PYMoV). Archives of Virology, 2014, 159, 385-388.	0.9	40
1667	Genome-wide single nucleotide polymorphism discovery and validation in adzuki bean. Molecular Breeding, 2014, 33, 497-501.	1.0	22
1668	Lipoteichoic Acids, Phosphate-Containing Polymers in the Envelope of Gram-Positive Bacteria. Journal of Bacteriology, 2014, 196, 1133-1142.	1.0	115
1669	Structural insights into the MDP binding and CARD-CARD interaction in zebrafish (<i>Danio rerio</i>) NOD2: a molecular dynamics approach. Journal of Molecular Recognition, 2014, 27, 260-275.	1.1	38
1670	Transcriptome resources for the frogs <i><scp>L</scp>ithobates clamitans</i> and <i><scp>P</scp>seudacris regilla</i>, emphasizing antimicrobial peptides and conserved loci for phylogenetics. Molecular Ecology Resources, 2014, 14, 178-183.	2.2	24
1671	High-resolution analysis of gene activity during the <i>Xenopus</i> mid-blastula transition. Development (Cambridge), 2014, 141, 1927-1939.	1.2	87

#	Article	IF	Citations
1672	EARLY EVOLUTION OF THE GENETIC BASIS FOR SOMA IN THE VOLVOCACEAE. Evolution; International Journal of Organic Evolution, 2014, 68, 2014-2025.	1.1	20
1673	Characterization of the pyrophosphate-dependent 6-phosphofructokinase from Xanthomonas campestris pv. campestris. Archives of Biochemistry and Biophysics, 2014, 546, 53-63.	1.4	14
1674	Linker mutations reveal the complexity of synaptotagmin 1 action during synaptic transmission. Nature Neuroscience, 2014, 17, 670-677.	7.1	50
1675	Modeling the Met Form of Human Tyrosinase: A Refined and Hydrated Pocket for Antagonist Design. Chemical Biology and Drug Design, 2014, 84, 206-215.	1.5	23
1676	Computational Identification of Pathogenic Associated nsSNPs and its Structural Impact in UROD Gene: A Molecular Dynamics Approach. Cell Biochemistry and Biophysics, 2014, 70, 735-746.	0.9	3
1677	Genomic adaptations of the halophilic Dead Sea filamentous fungus Eurotium rubrum. Nature Communications, 2014, 5, 3745.	5.8	62
1678	A comparative analysis of trypanosomatid SNARE proteins. Parasitology International, 2014, 63, 341-348.	0.6	17
1679	Immune Evasion by Pathogenic Leptospira Strains: The Secretion of Proteases that Directly Cleave Complement Proteins. Journal of Infectious Diseases, 2014, 209, 876-886.	1.9	82
1680	Genome-Wide Fractionation and Identification of WRKY Transcription Factors in Chinese Cabbage (Brassica rapa ssp. pekinensis) Reveals Collinearity and Their Expression Patterns Under Abiotic and Biotic Stresses. Plant Molecular Biology Reporter, 2014, 32, 781-795.	1.0	69
1681	Identification and functional characterization of a new IL-1 family member, IL-1Fm2, in most evolutionarily advanced fish. Innate Immunity, 2014, 20, 487-500.	1.1	28
1682	Structural insights from GRP78â€"NF-Î°B binding interactions: A computational approach to understand a possible neuroprotective pathway in brain injuries. Journal of Theoretical Biology, 2014, 345, 43-51.	0.8	8
1683	Revealing the hidden functional diversity of an enzyme family. Nature Chemical Biology, 2014, 10, 42-49.	3.9	113
1684	Comparative expression profiling reveals gene functions in female meiosis and gametophyte development in Arabidopsis. Plant Journal, 2014, 80, 615-628.	2.8	40
1685	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978.	5.8	532
1686	The Ubiquitous Distribution of Late Embryogenesis Abundant Proteins across Cell Compartments in <i>Arabidopsis</i> Offers Tailored Protection against Abiotic Stress. Plant Cell, 2014, 26, 3148-3166.	3.1	179
1687	Expression of acylamidase gene in Rhodococcus erythropolis strains. Russian Journal of Genetics, 2014, 50, 1003-1007.	0.2	8
1688	A census of human RNA-binding proteins. Nature Reviews Genetics, 2014, 15, 829-845.	7.7	1,671
1689	The Tomato Kinome and the Tomato Kinase Library ORFeome: Novel Resources for the Study of Kinases and Signal Transduction in Tomato and <i>Solanaceae</i> Species. Molecular Plant-Microbe Interactions, 2014, 27, 7-17.	1.4	30

#	ARTICLE	IF	CITATIONS
1690	Lactococcus lactis TrxD represents a subgroup of thioredoxins prevalent in Gram-positive bacteria containing WCXDC active site motifs. Archives of Biochemistry and Biophysics, 2014, 564, 164-172.	1.4	7
1691	NMR Solution Structure of the Terminal Immunoglobulin-like Domain from the Leptospira Host-Interacting Outer Membrane Protein, LigB. Biochemistry, 2014, 53, 5249-5260.	1.2	20
1692	Exploring mechanisms of human disease through structurally resolved protein interactome networks. Molecular BioSystems, 2014, 10, 9-17.	2.9	27
1693	A Root-Expressed <scp>l</scp>-Phenylalanine:4-Hydroxyphenylpyruvate Aminotransferase Is Required for Tropane Alkaloid Biosynthesis in <i>Atropa belladonna</i> Â Â. Plant Cell, 2014, 26, 3745-3762.	3.1	69
1694	From structure to function: the convergence of structure based models and co-evolutionary information. Physical Chemistry Chemical Physics, 2014, 16, 6496-6507.	1.3	47
1695	Cloning, expression and characterization of a novel aldehyde dehydrogenase gene from Flammeovirga pacifica. Applied Biochemistry and Microbiology, 2014, 50, 571-579.	0.3	1
1696	A Novel Chloroplast-Localized Pentatricopeptide Repeat Protein Involved in Splicing Affects Chloroplast Development and Abiotic Stress Response in Rice. Molecular Plant, 2014, 7, 1329-1349.	3.9	114
1697	Structural and functional investigation of zebrafish (Danio rerio) NOD1 leucine rich repeat domain and its interaction with iE-DAP. Molecular BioSystems, 2014, 10, 2942-2953.	2.9	23
1698	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. Nature Communications, 2014, 5, 4471.	5.8	133
1699	The Wall-associated Kinase gene family in rice genomes. Plant Science, 2014, 229, 181-192.	1.7	59
1700	Population Structure and Domestication Revealed by High-Depth Resequencing of Korean Cultivated and Wild Soybean Genomes. DNA Research, 2014, 21, 153-167.	1.5	92
1701	Lipochitin Oligosaccharides Immobilized through Oximes in Glycan Microarrays Bind LysM Proteins. ChemBioChem, 2014, 15, 425-434.	1.3	10
1702	A homolog of lariat-debranching enzyme modulates turnover of branched RNA. Rna, 2014, 20, 1337-1348.	1.6	34
1703	Genetic structure and biological properties of the first ancient multiresistance plasmid pKLH80 isolated from a permafrost bacterium. Microbiology (United Kingdom), 2014, 160, 2253-2263.	0.7	30
1704	The complete plasmid sequences of Salmonella enterica serovar Typhimurium U288. Plasmid, 2014, 76, 32-39.	0.4	21
1705	Diversity and activity of marine bacterioplankton during a diatom bloom in the North Sea assessed by total RNA and pyrotag sequencing. Marine Genomics, 2014, 18, 185-192.	0.4	84
1706	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. Nature Communications, 2014, 5, 4498.	5.8	617
1707	The Natural History of ADP-Ribosyltransferases and the ADP-Ribosylation System. Current Topics in Microbiology and Immunology, 2014, 384, 3-32.	0.7	99

#	Article	IF	Citations
1708	Plant, Animal, and Fungal Micronutrient Queuosine Is Salvaged by Members of the DUF2419 Protein Family. ACS Chemical Biology, 2014, 9, 1812-1825.	1.6	48
1709	Coevolutionary information, protein folding landscapes, and the thermodynamics of natural selection. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12408-12413.	3.3	126
1710	Genome-wide screening of pathogenicity islands in Mycobacterium tuberculosis based on the genomic barcode visualization. Molecular Biology Reports, 2014, 41, 5883-5889.	1.0	6
1711	Computational integration of genomic traits into 16S rDNA microbiota sequencing studies. Gene, 2014, 549, 186-191.	1.0	19
1712	NAC transcription factor genes: genome-wide identification, phylogenetic, motif andÂcis-regulatory element analysis in pigeonpea (Cajanus cajan (L.) Millsp.). Molecular Biology Reports, 2014, 41, 7763-7773.	1.0	24
1713	Algorithms for global proteinâ€“protein interaction network alignment. Network Modeling Analysis in Health Informatics and Bioinformatics, 2014, 3, 1.	1.2	3
1714	Comparative genomics of Bradyrhizobium japonicum CPAC 15 and Bradyrhizobium diazoefficiens CPAC 7: elite model strains for understanding symbiotic performance with soybean. BMC Genomics, 2014, 15, 420.	1.2	71
1715	Genome-wide analysis of regulatory proteases sequences identified through bioinformatics data mining in Taenia solium. BMC Genomics, 2014, 15, 428.	1.2	6
1716	Characterization of the kidney transcriptome of the South American olive mouse Abrothrix olivacea. BMC Genomics, 2014, 15, 446.	1.2	15
1717	Stenotrophomonas comparative genomics reveals genes and functions that differentiate beneficial and pathogenic bacteria. BMC Genomics, 2014, 15, 482.	1.2	90
1718	The reduced kinome of Ostreococcus tauri: core eukaryotic signalling components in a tractable model species. BMC Genomics, 2014, 15, 640.	1.2	18
1719	Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3) is predicted to interact with its partner through an ARM-type Î±-helical structure. BMC Research Notes, 2014, 7, 435.	0.6	9
1720	Modular organization and reticulate evolution of the ORF1 of Jockey superfamily transposable elements. Mobile DNA, 2014, 5, 19.	1.3	11
1721	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. Cell, 2014, 158, 1431-1443.	13.5	1,515
1722	Albino midrib 1, encoding a putative potassium efflux antiporter, affects chloroplast development and drought tolerance in rice. Plant Cell Reports, 2014, 33, 1581-1594.	2.8	58
1723	Conformational landscapes for KMSKS loop in tyrosyl-tRNA synthetases. Journal of Structural and Functional Genomics, 2014, 15, 45-61.	1.2	14
1724	Solution NMR structures of homeodomains from human proteins ALX4, ZHX1, and CASP8AP2 contribute to the structural coverage of the Human Cancer Protein Interaction Network. Journal of Structural and Functional Genomics, 2014, 15, 201-207.	1.2	1
1725	Molecular cloning and characterization of a lysozyme cDNA from the mole cricket Gryllotalpa orientalis (Orthoptera: Gryllotalpidae). Molecular Biology Reports, 2014, 41, 5745-5754.	1.0	12

#	ARTICLE	IF	CITATIONS
1726	Sequence comparison and phylogenetic analysis by the Maximum Likelihood method of ribosome-inactivating proteins from angiosperms. Plant Molecular Biology, 2014, 85, 575-588.	2.0	76
1727	Antibodies against CKI1RD, a receiver domain of the sensor histidine kinase in Arabidopsis thaliana: From antigen preparation to in planta immunolocalization. Phytochemistry, 2014, 100, 6-15.	1.4	2
1728	Gene expression regulation of the PF00480 or PF14340 domain proteins suggests their involvement in sulfur metabolism. Computational Biology and Chemistry, 2014, 49, 7-13.	1.1	3
1729	Solution NMR structures of immunoglobulin-like domains 7 and 12 from obscurin-like protein 1 contribute to the structural coverage of the human cancer protein interaction network. Journal of Structural and Functional Genomics, 2014, 15, 209-214.	1.2	0
1730	Exploration of the binding modes of buffalo PGRP1 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.	1.7	8
1731	Virus proteins similar to human proteins as possible disturbance on human pathways. Systems and Synthetic Biology, 2014, 8, 283-295.	1.0	2
1732	Cloning and in silico analysis of a cinnamyl alcohol dehydrogenase gene in Pennisetum purpureum. Journal of Genetics, 2014, 93, 145-158.	0.4	17
1733	On the necessity of dissecting sequence similarity scores into segment-specific contributions for inferring protein homology, function prediction and annotation. BMC Bioinformatics, 2014, 15, 166.	1.2	10
1734	An evolutionary ratchet leading to loss of elongation factors in eukaryotes. BMC Evolutionary Biology, 2014, 14, 35.	3.2	6
1735	A multicopy Y-chromosomal SGNH hydrolase gene expressed in the testis of the platyfish has been captured and mobilized by a Helitron transposon. BMC Genetics, 2014, 15, 44.	2.7	13
1736	Genomic characteristics and comparative genomics analysis of Penicillium chrysogenum KF-25. BMC Genomics, 2014, 15, 144.	1.2	14
1737	A pangenomic analysis of the Nannochloropsis organellar genomes reveals novel genetic variations in key metabolic genes. BMC Genomics, 2014, 15, 212.	1.2	41
1738	Prevalence of transcription factors in ascomycete and basidiomycete fungi. BMC Genomics, 2014, 15, 214.	1.2	114
1739	Copy number variations among silkworms. BMC Genomics, 2014, 15, 251.	1.2	10
1740	Genome sequence and transcriptome analyses of the thermophilic zygomycete fungus Rhizomucor miehei. BMC Genomics, 2014, 15, 294.	1.2	39
1741	A customized Web portal for the genome of the ctenophore Mnemiopsis leidyi. BMC Genomics, 2014, 15, 316.	1.2	28
1742	A network-based approach to identify substrate classes of bacterial glycosyltransferases. BMC Genomics, 2014, 15, 349.	1.2	337
1743	The nuclear receptor gene family in the Pacific oyster, Crassostrea gigas, contains a novel subfamily group. BMC Genomics, 2014, 15, 369.	1.2	75

#	Article	IF	Citations
1744	Genome analysis and CRISPR typing of Salmonella enterica serovar Virchow. BMC Genomics, 2014, 15, 389.	1.2	25
1745	Evolution and expression analysis of the grape (Vitis vinifera L.) WRKY gene family. Journal of Experimental Botany, 2014, 65, 1513-1528.	2.4	246
1746	EttA regulates translation by binding the ribosomal E site and restricting ribosome-tRNA dynamics. Nature Structural and Molecular Biology, 2014, 21, 152-159.	3.6	80
1747	The Solution Structure of the Regulatory Domain of Tyrosine Hydroxylase. Journal of Molecular Biology, 2014, 426, 1483-1497.	2.0	47
1748	Vaccinia virus F5 is required for normal plaque morphology in multiple cell lines but not replication in culture or virulence in mice. Virology, 2014, 456-457, 145-156.	1.1	7
1749	Exploring the Biological and Chemical Complexity of the Ligases. Journal of Molecular Biology, 2014, 426, 2098-2111.	2.0	11
1750	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	9.4	1,159
1751	Mobile elements and mitochondrial genome expansion in the soil fungus and potato pathogen<i>Rhizoctonia solani</i>AG-3. FEMS Microbiology Letters, 2014, 352, 165-173.	0.7	143
1752	Supersize me: Cronobacter sakazakii phage GAP32. Virology, 2014, 460-461, 138-146.	1.1	46
1753	Replacement of a terminal cytochrome c oxidase by ubiquinol oxidase during the evolution of acetic acid bacteria. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1810-1820.	0.5	27
1754	Identifying Pathogenicity Islands in Bacterial Pathogenomics Using Computational Approaches. Pathogens, 2014, 3, 36-56.	1.2	78
1755	Structural Annotation of the Mycobacterium tuberculosis Proteome. Microbiology Spectrum, 2014, 2, .	1.2	2
1756	Bhageerath-H: A homology/ab initio hybrid server for predicting tertiary structures of monomeric soluble proteins. BMC Bioinformatics, 2014, 15, S7.	1.2	45
1757	The Periplasmic PDZ Domainâ€"Containing Protein Prc Modulates Full Virulence, Envelops Stress Responses, and Directly Interacts with Dipeptidyl Peptidase of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>. Molecular Plant-Microbe Interactions, 2014, 27, 101-112.	1.4	25
1758	Novel mitochondrial mutations in the ATP6 and ATP8 genes in patients with breast cancer. Molecular Medicine Reports, 2014, 10, 1772-1778.	1.1	38
1759	Parallel algorithms for clustering biological graphs on distributed and shared memory architectures. International Journal of High Performance Computing and Networking, 2014, 7, 241.	0.4	21
1760	Discovering co-occurring patterns and their biological significance in protein families. BMC Bioinformatics, 2014, 15, S2.	1.2	5
1761	Robustness of birth-death and gain models for inferring evolutionary events. BMC Genomics, 2014, 15, S9.	1.2	2

#	ARTICLE	IF	CITATIONS
1762	Explore protein-protein interaction network involved in glucosinolate biosynthesis. , 2014, , .		0
1763	Coq7p relevant residues for protein activity and stability. Biochimie, 2015, 119, 92-102.	1.3	13
1764	Most partial domains in proteins are alignment and annotation artifacts. Genome Biology, 2015, 16, 99.	3.8	27
1766	Regulation of transcription factors on sexual dimorphism of fig wasps. Scientific Reports, 2015, 5, 10696.	1.6	2
1767	Phylotranscriptomic analysis uncovers a wealth of tissue inhibitor of metalloproteinases variants in echinoderms. Royal Society Open Science, 2015, 2, 150377.	1.1	21
1768	Genome-wide Identification of WRKY Genes in the Desert Poplar Populus euphratica and Adaptive Evolution of the Genes in Response to Salt Stress. Evolutionary Bioinformatics, 2015, 11s1, EBO.S22067.	0.6	20
1769	Overview of the Cancer Genetics and Pathway Curation tasks of BioNLP Shared Task 2013. BMC Bioinformatics, 2015, 16, S2.	1.2	44
1770	Event inference in multidomain families with phylogenetic reconciliation. BMC Bioinformatics, 2015, 16, S8.	1.2	32
1771	Dimeric interactions and complex formation using direct coevolutionary couplings. Scientific Reports, 2015, 5, 13652.	1.6	75
1772	dissectHMMER: a HMMER-based score dissection framework that statistically evaluates fold-critical sequence segments for domain fold similarity. Biology Direct, 2015, 10, 39.	1.9	18
1773	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
1774	Complete genome sequence of Salinicoccus halodurans H3B36, isolated from the Qaidam Basin in China. Standards in Genomic Sciences, 2015, 10, 116.	1.5	7
1775	Pinpointing disease genes through phenomic and genomic data fusion. BMC Genomics, 2015, 16, S3.	1.2	14
1776	The first draft genome of the aquatic model plant Lemna minor opens the route for future stress physiology research and biotechnological applications. Biotechnology for Biofuels, 2015, 8, 188.	6.2	112
1777	Characterization of the dextran-binding domain in the glucan-binding protein C of<i>Streptococcus mutans</i>. Journal of Applied Microbiology, 2015, 119, 1148-1157.	1.4	12
1778	Random mutagenesis of the nucleotideâ€binding domain of <scp>NRC</scp>1 (<scp>NB</scp>â€<scp>LRR</scp> Required for Hypersensitive Responseâ€Associated Cell Deathâ€1), a downstream signalling nucleotideâ€binding, leucineâ€rich repeat (<scp>NB</scp>â€<scp>LRR</scp>) protein, identifies gainâ€ofâ€function mutations in the nucleotideâ€binding pocket. New Phytologist, 2015, 208, 210-223.	3.5	37
1779	Microarray hybridization analysis of light-dependent gene expression inPenicillium chrysogenumidentifies bZIP transcription factor PcAtfA. Journal of Basic Microbiology, 2015, 55, 480-489.	1.8	8
1780	ProtoBug: functional families from the complete proteomes of insects. Database: the Journal of Biological Databases and Curation, 2015, 2015, bau122.	1.4	1

#	ARTICLE	IF	CITATIONS
1781	A Structure-Based Classification and Analysis of Protein Domain Family Binding Sites and Their Interactions. Biology, 2015, 4, 327-343.	1.3	5
1782	How Common Is Disorder? Occurrence of Disordered Residues in Four Domains of Life. International Journal of Molecular Sciences, 2015, 16, 19490-19507.	1.8	24
1783	Discovery of new protein families and functions: new challenges in functional metagenomics for biotechnologies and microbial ecology. Frontiers in Microbiology, 2015, 6, 563.	1.5	52
1784	Changes in gene expression of Prymnesium parvum induced by nitrogen and phosphorus limitation. Frontiers in Microbiology, 2015, 6, 631.	1.5	46
1785	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. Frontiers in Microbiology, 2015, 6, 1192.	1.5	49
1786	The Semantics of the Modular Architecture of Protein Structures. Current Protein and Peptide Science, 2015, 17, 62-71.	0.7	8
1787	Genome-Wide Transcriptome and Expression Profile Analysis of Phalaenopsis during Explant Browning. PLoS ONE, 2015, 10, e0123356.	1.1	16
1788	The Orphan Nuclear Receptor TLX Is an Enhancer of STAT1-Mediated Transcription and Immunity to Toxoplasma gondii. PLoS Biology, 2015, 13, e1002200.	2.6	25
1789	Nmf9 Encodes a Highly Conserved Protein Important to Neurological Function in Mice and Flies. PLoS Genetics, 2015, 11, e1005344.	1.5	11
1790	Discovery of Chemosensory Genes in the Oriental Fruit Fly, Bactrocera dorsalis. PLoS ONE, 2015, 10, e0129794.	1.1	42
1791	Genome-Wide Identification and Expression of Xenopus F-Box Family of Proteins. PLoS ONE, 2015, 10, e0136929.	1.1	3
1792	De Novo Assembly and Characterization of the Invasive Northern Pacific Seastar Transcriptome. PLoS ONE, 2015, 10, e0142003.	1.1	16
1793	Role of Bioinformatic Tools and Databases in Cotton Research. Agronomy, 2015, , 303-337.	0.2	2
1794	Developing of the Computer Method for Annotation of Bacterial Genes. Advances in Bioinformatics, 2015, 2015, 1-9.	5.7	15
1796	RNA helicase A activity is inhibited by oncogenic transcription factor EWS-FLI1. Nucleic Acids Research, 2015, 43, 1069-1080.	6.5	30
1797	Comparative analysis of metagenomes from three methanogenic hydrocarbon-degrading enrichment cultures with 41 environmental samples. ISME Journal, 2015, 9, 2028-2045.	4.4	87
1798	Expression of extra-cellular levansucrase in Pseudomonas syringae is controlled by the in planta fitness-promoting metabolic repressor HexR. BMC Microbiology, 2015, 15, 48.	1.3	14
1799	It's more than stamp collecting: how genome sequencing can unify biological research. Trends in Genetics, 2015, 31, 411-421.	2.9	37

#	ARTICLE	IF	CITATIONS
1800	Reinforcing the Egg-Timer: Recruitment of Novel Lophotrochozoa Homeobox Genes to Early and Late Development in the Pacific Oyster. Genome Biology and Evolution, 2015, 7, 677-688.	1.1	42
1801	The plant parasite Pratylenchus coffeae carriesÂaÂminimalÂnematode genome. Nematology, 2015, 17, 621-637.	0.2	43
1802	Comparative analysis of the L, M, and S RNA segments of Crimean-Congo haemorrhagic fever virus isolates from southern Africa. Journal of Medical Virology, 2015, 87, 717-724.	2.5	7
1803	A genetic map of cassava (Manihot esculenta Crantz) with integrated physical mapping of immunity-related genes. BMC Genomics, 2015, 16, 190.	1.2	65
1804	Influence of in situ progressive N-terminal is still controversial truncation of glycogen branching enzyme in Escherichia coli DH5Î± on glycogen structure, accumulation, and bacterial viability. BMC Microbiology, 2015, 15, 96.	1.3	26
1805	A novel essential domain perspective for exploring gene essentiality. Bioinformatics, 2015, 31, 2921-2929.	1.8	7
1806	Complete genome and gene expression analyses ofAsaia bogorensisreveal unique responses to culture with mammalian cells as a potential opportunistic human pathogen. DNA Research, 2015, 22, 357-366.	1.5	14
1807	Scrutinizing the immune defence inventory of Camponotus floridanus applying total transcriptome sequencing. BMC Genomics, 2015, 16, 540.	1.2	33
1808	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>. Journal of Experimental Botany, 2015, 66, 5867-5880.	2.4	24
1809	EvoTol: a protein-sequence based evolutionary intolerance framework for disease-gene prioritization. Nucleic Acids Research, 2015, 43, e33-e33.	6.5	33
1810	Biochemical and Kinetic Characterization of the Eukaryotic Phosphotransacetylase Class IIa Enzyme from Phytophthora ramorum. Eukaryotic Cell, 2015, 14, 652-660.	3.4	2
1811	The language of the protein universe. Current Opinion in Genetics and Development, 2015, 35, 50-56.	1.5	27
1812	SpirPro: A Spirulina proteome database and web-based tools for the analysis of protein-protein interactions at the metabolic level in Spirulina (Arthrospira) platensis C1. BMC Bioinformatics, 2015, 16, 233.	1.2	14
1813	Proteins involved in more domain types tend to be more essential. International Journal of Bioinformatics Research and Applications, 2015, 11, 91.	0.1	3
1814	ModelOMatic: Fast and Automated Model Selection between RY, Nucleotide, Amino Acid, and Codon Substitution Models. Systematic Biology, 2015, 64, 42-55.	2.7	68
1815	Metatranscriptome of marine bacterioplankton during winter time in the North Sea assessed by total RNA sequencing. Marine Genomics, 2015, 19, 45-46.	0.4	14
1816	Genome-wide analysis of the GRAS gene family in Prunus mume. Molecular Genetics and Genomics, 2015, 290, 303-317.	1.0	74
1817	The long intergenic noncoding RNA landscape of human lymphocytes highlights the regulation of T cell differentiation by linc-MAF-4. Nature Immunology, 2015, 16, 318-325.	7.0	300

#	Article	IF	Citations
1818	The Origin of CDR H3 Structural Diversity. Structure, 2015, 23, 302-311.	1.6	78
1819	Genome-wide identification and analysis of the apple (Malus Ã— domestica Borkh.) TIFY gene family. Tree Genetics and Genomes, 2015, 11, 1.	0.6	51
1820	Comprehensive Genome-Wide Analysis of the Aux/IAA Gene Family in Eucalyptus: Evidence for the Role of EgrIAA4 in Wood Formation. Plant and Cell Physiology, 2015, 56, 700-714.	1.5	37
1821	Differential evolution of members of the <i>rhomboid</i> gene family with conservative and divergent patterns. New Phytologist, 2015, 206, 368-380.	3.5	23
1822	UProC: tools for ultra-fast protein domain classification. Bioinformatics, 2015, 31, 1382-1388.	1.8	85
1823	The phage growth limitation system in Streptomyces coelicolor A(3)2 is a toxin/antitoxin system, comprising enzymes with DNA methyltransferase, protein kinase and ATPase activity. Virology, 2015, 477, 100-109.	1.1	47
1824	Discovery of Novel Genes Derived from Transposable Elements Using Integrative Genomic Analysis. Molecular Biology and Evolution, 2015, 32, 1487-1506.	3.5	49
1825	A GntR-type transcriptional repressor controls sialic acid utilization in Bifidobacterium breve UCC2003. FEMS Microbiology Letters, 2015, 362, 1-9.	0.7	17
1826	The Origin and Evolution of Ribonucleotide Reduction. Life, 2015, 5, 604-636.	1.1	74
1827	C-S bond cleavage by a polyketide synthase domain. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10359-10364.	3.3	39
1828	A novel Na+(K+)/H+ antiporter plays an important role in the growth of Acetobacter tropicalis SKU1100 at high temperatures via regulation of cation and pH homeostasis. Journal of Biotechnology, 2015, 211, 46-55.	1.9	6
1829	Characterization of Epidemic IncI1-Iγ Plasmids Harboring Ambler Class A and C Genes in Escherichia coli and Salmonella enterica from Animals and Humans. Antimicrobial Agents and Chemotherapy, 2015, 59, 5357-5365.	1.4	62
1830	Comparing different machine learning and mathematical regression models to evaluate multiple sequence alignments. Neurocomputing, 2015, 164, 123-136.	3.5	12
1831	Genome sequence of a white rot fungus Schizopora paradoxa KUC8140 for wood decay and mycoremediation. Journal of Biotechnology, 2015, 211, 42-43.	1.9	21
1832	Collation and analyses of DNA-binding protein domain families from sequence and structural databanks. Molecular BioSystems, 2015, 11, 1110-1118.	2.9	5
1833	Protein Domain-Level Landscape of Cancer-Type-Specific Somatic Mutations. PLoS Computational Biology, 2015, 11, e1004147.	1.5	59
1834	Soybean kinome: functional classification and gene expression patterns. Journal of Experimental Botany, 2015, 66, 1919-1934.	2.4	43
1835	Protein Topology Determines Cysteine Oxidation Fate: The Case of Sulfenyl Amide Formation among Protein Families. PLoS Computational Biology, 2015, 11, e1004051.	1.5	39

#	ARTICLE	IF	CITATIONS
1836	Predicting Peptide-Mediated Interactions on a Genome-Wide Scale. PLoS Computational Biology, 2015, 11, e1004248.	1.5	16
1837	The Aspartate-Less Receiver (ALR) Domains: Distribution, Structure and Function. PLoS Pathogens, 2015, 11, e1004795.	2.1	25
1838	Batf3 deficiency is not critical for the generation of CD8Î±+ dendritic cells. Immunobiology, 2015, 220, 518-524.	0.8	18
1839	Proteasome stress responses in Schistosoma mansoni. Parasitology Research, 2015, 114, 1747-1760.	0.6	8
1840	Diversity of the expression profiles of late embryogenesis abundant (LEA) protein encoding genes in the anhydrobiotic midge Polypedilum vanderplanki. Planta, 2015, 242, 451-459.	1.6	30
1841	Rapid turnover of antimicrobial-type cysteine-rich protein genes in closely related Oryza genomes. Molecular Genetics and Genomics, 2015, 290, 1753-1770.	1.0	6
1842	Genome-wide Classification, Identification and Expression Profile of the C3HC4-type RING Finger Gene Family in Poplar (Populus trichocarpa). Plant Molecular Biology Reporter, 2015, 33, 1740-1754.	1.0	11
1843	micropan: an R-package for microbial pan-genomics. BMC Bioinformatics, 2015, 16, 79.	1.2	165
1844	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.	1.2	48
1845	Genome-wide survey and expression analysis of F-box genes in chickpea. BMC Genomics, 2015, 16, 67.	1.2	68
1846	Identification of three extra-chromosomal replicons in Leptospira pathogenic strain and development of new shuttle vectors. BMC Genomics, 2015, 16, 90.	1.2	17
1847	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	1.2	49
1848	Retained duplicate genes in green alga Chlamydomonas reinhardtii tend to be stress responsive and experience frequent response gains. BMC Genomics, 2015, 16, 149.	1.2	12
1849	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.	1.6	138
1850	Structural Features of the Receptor Tyrosine Kinase Ectodomains. , 2015, , 163-193.		6
1851	Convergent evolution toward an improved growth rate and a reduced resistance range in <i>Prochlorococcus</i> strains resistant to phage. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2191-200.	3.3	54
1852	MPIC: A Mitochondrial Protein Import Components Database for Plant and Non-Plant Species. Plant and Cell Physiology, 2015, 56, e10-e10.	1.5	24
1853	Faster sequence homology searches by clustering subsequences. Bioinformatics, 2015, 31, 1183-1190.	1.8	64

#	Article	IF	Citations
1854	Sequence and expression analysis of the AMT gene family in poplar. Frontiers in Plant Science, 2015, 6, 337.	1.7	43
1855	A functional role of Rv1738 in <i>Mycobacterium tuberculosis</i> persistence suggested by racemic protein crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4310-4315.	3.3	43
1856	HAlign: Fast multiple similar DNA/RNA sequence alignment based on the centre star strategy. Bioinformatics, 2015, 31, 2475-2481.	1.8	136
1857	Novel substrate specificities of two lacto-N-biosidases towards Î²-linked galacto-N-biose-containing oligosaccharides of globo H, Gb5,Âand GA1. Carbohydrate Research, 2015, 408, 18-24.	1.1	15
1858	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. Nucleic Acids Research, 2015, 43, D76-D81.	6.5	287
1859	Amino- and Carboxyl-Terminal CCR5 Mutations in Brazilian HIV-1-Infected Women and Homology Model of p.L55Q CCR5 Mutant. AIDS Research and Human Retroviruses, 2015, 31, 685-691.	0.5	0
1860	Biomarker Panels and Multiple Readouts. , 2015, , 159-166.		0
1861	Characterizing activity sequences using profile Hidden Markov Models. Expert Systems With Applications, 2015, 42, 5705-5722.	4.4	49
1862	Computational study of a bifunctionalent-kaurene synthase fromPhyscomitrella patens(Hedw.) Bruch & Schimp.: an insight into the origin of terpenoid biosynthesis in plants. Acta Botanica Gallica, 2015, 162, 139-152.	0.9	2
1863	Computational tools for epitope vaccine design and evaluation. Current Opinion in Virology, 2015, 11, 103-112.	2.6	60
1864	AnABlast: a new<i>in silico</i>strategy for the genome-wide search of novel genes and fossil regions. DNA Research, 2015, 22, 439-449.	1.5	11
1865	Computational analysis of a cys-loop ligand gated ion channel from the green alga Chlamydomonas reinhardtii. Molecular Biology, 2015, 49, 742-754.	0.4	2
1866	Structure of the Bacillus anthracis Sortase A Enzyme Bound to Its Sorting Signal. Journal of Biological Chemistry, 2015, 290, 25461-25474.	1.6	21
1867	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science, 2015, 350, 434-438.	6.0	677
1868	The Plant Genome Integrative Explorer Resource: PlantGen<scp>IE</scp>.org. New Phytologist, 2015, 208, 1149-1156.	3.5	282
1869	The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. Genome Biology and Evolution, 2015, 7, 2321-2332.	1.1	70
1870	Exploring the rice dispensable genome using a metagenome-like assembly strategy. Genome Biology, 2015, 16, 187.	3.8	90
1871	Computing the origin and evolution of the ribosome from its structure â€" Uncovering processes of macromolecular accretion benefiting synthetic biology. Computational and Structural Biotechnology Journal, 2015, 13, 427-447.	1.9	26

#	Article	IF	Citations
1872	Insights into the evolution of enzyme substrate promiscuity after the discovery of (Î²Î±)8 isomerase evolutionary intermediates from a diverse metagenome. BMC Evolutionary Biology, 2015, 15, 107.	3.2	16
1873	Trends in genome dynamics among major orders of insects revealed through variations in protein families. BMC Genomics, 2015, 16, 583.	1.2	5
1874	Light-assisted small-molecule screening against protein kinases. Nature Chemical Biology, 2015, 11, 952-954.	3.9	42
1875	Identification and characterization of TIFY family genes in Brachypodium distachyon. Journal of Plant Research, 2015, 128, 995-1005.	1.2	39
1876	Evolution and Diversity of the Ras Superfamily of Small GTPases in Prokaryotes. Genome Biology and Evolution, 2015, 7, 57-70.	1.1	51
1877	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.	6.5	26
1878	Homology modeling, functional annotation and comparative genomics of outer membrane protein H of Pasteurella multocida. Journal of Theoretical Biology, 2015, 386, 18-24.	0.8	4
1879	The Enterobacterium Trabulsiella odontotermitis Presents Novel Adaptations Related to Its Association with Fungus-Growing Termites. Applied and Environmental Microbiology, 2015, 81, 6577-6588.	1.4	18
1880	Methods of processing mass spectrometry data to identify peptides and proteins. Moscow University Chemistry Bulletin, 2015, 70, 211-222.	0.2	0
1881	Terpene synthases are widely distributed in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 857-862.	3.3	441
1882	Understanding the distinguishable structural and functional features in zebrafish TLR3 and TLR22, and their binding modes with fish dsRNA viruses: an exploratory structural model analysis. Amino Acids, 2015, 47, 381-400.	1.2	27
1883	Genome-wide identification and comparative expression analysis reveal a rapid expansion and functional divergence of duplicated genes in the WRKY gene family of cabbage, Brassica oleracea var. capitata. Gene, 2015, 557, 35-42.	1.0	51
1884	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus Eucalyptus. New Phytologist, 2015, 206, 1328-1336.	3.5	19
1885	In-silico characterization of Formin Binding Protein 4 Family of proteins. Interdisciplinary Sciences, Computational Life Sciences, 2015, 7, 43-64.	2.2	4
1886	Mitochondrial DNA polymorphism in genes encoding ND1, COI and CYTB in canine malignant cancers. Mitochondrial DNA, 2015, 26, 452-458.	0.6	14
1887	A novel methyltransferase from the intracellular pathogen <i><scp>P</scp>lasmodiophora brassicae</i> methylates salicylic acid. Molecular Plant Pathology, 2015, 16, 349-364.	2.0	88
1888	Genome-wide identification of transcription factors and transcription-factor binding sites in oleaginous microalgae Nannochloropsis. Scientific Reports, 2014, 4, 5454.	1.6	75
1889	Lactic acid bacterial symbionts in honeybees â€“ an unknown key to honey's antimicrobial and therapeutic activities. International Wound Journal, 2016, 13, 668-679.	1.3	111

#	ARTICLE	IF	CITATIONS
1890	RGAugury: a pipeline for genome-wide prediction of resistance gene analogs (RGAs) in plants. BMC Genomics, 2016, 17, 852.	1.2	162
1891	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted byLucilia sericataMedical Maggots. BioMed Research International, 2016, 2016, 1-27.	0.9	24
1892	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.	0.9	42
1893	Red Algal Mitochondrial Genomes are More Complete than Previously Reported. Genome Biology and Evolution, 2017, 9, evw267.	1.1	19
1894	Sister Dehalobacter Genomes Reveal Specialization in Organohalide Respiration and Recent Strain Differentiation Likely Driven by Chlorinated Substrates. Frontiers in Microbiology, 2016, 7, 100.	1.5	18
1895	Diazotroph Diversity in the Sea Ice, Melt Ponds, and Surface Waters of the Eurasian Basin of the Central Arctic Ocean. Frontiers in Microbiology, 2016, 7, 1884.	1.5	39
1896	Identification of a Non-Pentapeptide Region Associated with Rapid Mycobacterial Evolution. PLoS ONE, 2016, 11, e0154059.	1.1	1
1897	GPU-Acceleration of Sequence Homology Searches with Database Subsequence Clustering. PLoS ONE, 2016, 11, e0157338.	1.1	8
1898	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea (Cajanus cajan L.). Frontiers in Plant Science, 2015, 6, 1065.	1.7	39
1899	Diverse Evolutionary Trajectories for Small RNA Biogenesis Genes in the Oomycete Genus Phytophthora. Frontiers in Plant Science, 2016, 7, 284.	1.7	27
1900	Systematic Investigation of FLOWERING LOCUS T-Like Poaceae Gene Families Identifies the Short-Day Expressed Flowering Pathway Gene, TaFT3 in Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2016, 7, 857.	1.7	37
1901	A Primary Sequence Analysis of the ARGONAUTE Protein Family in Plants. Frontiers in Plant Science, 2016, 7, 1347.	1.7	24
1902	In Silico Analysis: Annotations about Structural and Functional Features of DUF 2726 Family Member Proteins. Bangladesh Journal of Microbiology, 2016, , 53-58.	0.2	0
1903	A novel <scp>l</scp>â€arabinoseâ€responsive regulator discovered in the riceâ€blast fungus <i>Pyricularia oryzae</i> (<i>Magnaporthe oryzae</i>). FEBS Letters, 2016, 590, 550-558.	1.3	22
1904	Serobactinsâ€mediated iron acquisition systems optimize competitive fitness of <scp><i>H</i></scp><i>erbaspirillum seropedicae</i> inside rice plants. Environmental Microbiology, 2016, 18, 2523-2533.	1.8	17
1905	xHMMER3x2: Utilizing HMMER3â€™s speed and HMMER2â€™s sensitivity and specificity in the glocal alignment mode for improved large-scale protein domain annotation. Biology Direct, 2016, 11, 63.	1.9	4
1906	Identification and characterization of histone lysine methylation modifiers in Fragaria vesca. Scientific Reports, 2016, 6, 23581.	1.6	28
1907	Comparative phylogenetic analysis and transcriptional profiling of MADS-box gene family identified DAM and FLC-like genes in apple (Malusx domestica). Scientific Reports, 2016, 6, 20695.	1.6	80

#	ARTICLE	IF	CITATIONS
1908	Synbiological systems for complex natural products biosynthesis. Synthetic and Systems Biotechnology, 2016, 1, 221-229.	1.8	3
1909	RBPPred: predicting RNA-binding proteins from sequence using SVM. Bioinformatics, 2017, 33, 854-862.	1.8	75
1910	Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. Genome Biology and Evolution, 2016, 8, 3323-3339.	1.1	42
1911	Global transcriptional analysis suggests Lasiodiplodia theobromae pathogenicity factors involved in modulation of grapevine defensive response. BMC Genomics, 2016, 17, 615.	1.2	51
1912	MET-activating Residues in the B-repeat of the Listeria monocytogenes Invasion Protein InlB. Journal of Biological Chemistry, 2016, 291, 25567-25577.	1.6	8
1913	The mechanism of the effect of U18666a on blocking the activity of 3Î²-hydroxysterol Î”-24-reductase (DHCR24): molecular dynamics simulation study and free energy analysis. Journal of Molecular Modeling, 2016, 22, 46.	0.8	12
1914	A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1979-1986.	2.0	5
1915	Identification of WD40 repeats by secondary structure-aided profileâ€“profile alignment. Journal of Theoretical Biology, 2016, 398, 122-129.	0.8	7
1916	Phosphorylation of spore coat proteins by a family of atypical protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3482-91.	3.3	56
1917	Evolutionary Ancestry of Eukaryotic Protein Kinases and Choline Kinases. Journal of Biological Chemistry, 2016, 291, 5199-5205.	1.6	11
1918	Crystal Structure of the GRAS Domain of SCARECROW-LIKE7 in<i>Oryza sativa</i>. Plant Cell, 2016, 28, 1025-1034.	3.1	53
1919	The ancient small mobilizable plasmid pALWED1.8 harboring a new variant of the non-cassette streptomycin/spectinomycin resistance gene aadA27. Plasmid, 2016, 84-85, 36-43.	0.4	28
1920	On the Entropy of Protein Families. Journal of Statistical Physics, 2016, 162, 1267-1293.	0.5	22
1921	Complex Formed between Intramembrane Metalloprotease SpoIVFB and Its Substrate, Pro-ÏƒK. Journal of Biological Chemistry, 2016, 291, 10347-10362.	1.6	6
1922	Classification and Exploration of 3D Protein Domain Interactions Using Kbdock. Methods in Molecular Biology, 2016, 1415, 91-105.	0.4	4
1923	A Variable Active Site Residue Influences the Kinetics of Response Regulator Phosphorylation and Dephosphorylation. Biochemistry, 2016, 55, 5595-5609.	1.2	16
1924	bcgTree: automatized phylogenetic tree building from bacterial core genomes. Genome, 2016, 59, 783-791.	0.9	151
1925	Polysaccharide utilisation loci of <i>Bacteroidetes</i> from two contrasting open ocean sites in the North Atlantic. Environmental Microbiology, 2016, 18, 4456-4470.	1.8	56

#	ARTICLE	IF	CITATIONS
1926	The Gearbox of the Bacterial Flagellar Motor Switch. Structure, 2016, 24, 1209-1220.	1.6	30
1927	High rates of microbial dinitrogen fixation and sulfate reduction associated with the Mediterranean seagrass Posidonia oceanica. Systematic and Applied Microbiology, 2016, 39, 476-483.	1.2	56
1928	Repeated Duplication of Argonaute2 Is Associated with Strong Selection and Testis Specialization in <i>Drosophila</i>. Genetics, 2016, 204, 757-769.	1.2	20
1929	GExplore 1.4: An expanded web interface for queries on<i>Caenorhabditis elegans</i>protein and gene function. Worm, 2016, 5, e1234659.	1.0	34
1930	Complete Genome Sequence of <i>Bacillus velezensis</i> CBMB205, a Phosphate-Solubilizing Bacterium Isolated from the Rhizoplane of Rice in the Republic of Korea. Genome Announcements, 2016, 4, .	0.8	13
1931	Characterization of OsLEA1a and its inhibitory effect on the resistance of E. coli to diverse abiotic stresses. International Journal of Biological Macromolecules, 2016, 91, 1010-1017.	3.6	17
1932	LINEs between Species: Evolutionary Dynamics of LINE-1 Retrotransposons across the Eukaryotic Tree of Life. Genome Biology and Evolution, 2016, 8, 3301-3322.	1.1	66
1934	Mitochondrial metabolites extend lifespan. Aging Cell, 2016, 15, 336-348.	3.0	52
1935	Transcriptome analysis reveals rod/cone photoreceptor specific signatures across mammalian retinas. Human Molecular Genetics, 2016, 25, ddw268.	1.4	36
1936	Counting animal species with DNA barcodes: Canadian insects. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150333.	1.8	267
1937	Sequence analyses and chromosomal distribution of the Tc1/Mariner element in Parodontidae fish (Teleostei: Characiformes). Gene, 2016, 593, 308-314.	1.0	26
1938	NRL-Regulated Transcriptome Dynamics of Developing Rod Photoreceptors. Cell Reports, 2016, 17, 2460-2473.	2.9	104
1939	Anaerobes in Biotechnology. Advances in Biochemical Engineering/Biotechnology, 2016, , .	0.6	9
1940	The complexity of the translation ability of circRNAs. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1245-1251.	0.9	163
1941	A Combined Computational and Genetic Approach Uncovers Network Interactions of the Cyanobacterial Circadian Clock. Journal of Bacteriology, 2016, 198, 2439-2447.	1.0	16
1942	Structural Determinants of Sleeping Beauty Transposase Activity. Molecular Therapy, 2016, 24, 1369-1377.	3.7	7
1943	Genome-wide identification, structural analysis and new insights into late embryogenesis abundant (LEA) gene family formation pattern in Brassica napus. Scientific Reports, 2016, 6, 24265.	1.6	91
1944	Evolution of Protein Domain Repeats in Metazoa. Molecular Biology and Evolution, 2016, 33, 3170-3182.	3.5	41

#	Article	IF	Citations
1945	The Gonium pectorale genome demonstrates co-option of cell cycle regulation during the evolution of multicellularity. Nature Communications, 2016, 7, 11370.	5.8	125
1947	Rsite2: an efficient computational method to predict the functional sites of noncoding RNAs. Scientific Reports, 2016, 6, 19016.	1.6	15
1948	Biochemical pathways supporting beta-lactam biosynthesis in the springtail <i>Folsomia candida</i>. Biology Open, 2016, 5, 1784-1789.	0.6	13
1949	The complete genome sequences of sulfur-oxidizing Gammaproteobacteria Sulfurifustis variabilis skN76T and Sulfuricaulis limicola HA5T. Standards in Genomic Sciences, 2016, 11, 71.	1.5	37
1950	Three DUF1996 Proteins Localize in Vacuoles and Function in Fungal Responses to Multiple Stresses and Metal Ions. Scientific Reports, 2016, 6, 20566.	1.6	14
1951	DOMMINO 2.0: integrating structurally resolved protein-, RNA-, and DNA-mediated macromolecular interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	1.4	34
1952	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.	1.0	20
1953	Systems biology of the structural proteome. BMC Systems Biology, 2016, 10, 26.	3.0	46
1954	Prediction of residue-residue contact matrix for protein-protein interaction with Fisher score features and deep learning. Methods, 2016, 110, 97-105.	1.9	41
1955	Duplication and Diversification of Dipteran Argonaute Genes, and the Evolutionary Divergence of Piwi and Aubergine. Genome Biology and Evolution, 2016, 8, 507-518.	1.1	98
1956	Emergence and Evolution of Hominidae-Specific Coding and Noncoding Genomic Sequences. Genome Biology and Evolution, 2016, 8, 2076-2092.	1.1	12
1957	Cloning, molecular characterization, and expression analysis of the unc45 myosin chaperone b(unc45b)gene of grass carp (Ctenopharyngodon idellus). Journal of Muscle Research and Cell Motility, 2016, 37, 71-81.	0.9	1
1958	Capture of endogenously biotinylated proteins from Pseudomonas aeruginosa displays unexpected downregulation of LiuD upon iron nutrition. Bioorganic and Medicinal Chemistry, 2016, 24, 3330-3335.	1.4	1
1959	Cell mediated immune response of the Mediterranean sea urchin Paracentrotus lividus after PAMPs stimulation. Developmental and Comparative Immunology, 2016, 62, 29-38.	1.0	19
1960	Biochemical properties and crystal structure of the flavin reductase FerA from Paracoccus denitrificans. Microbiological Research, 2016, 188-189, 9-22.	2.5	14
1961	Environmental Breviatea harbour mutualistic Arcobacter epibionts. Nature, 2016, 534, 254-258.	13.7	68
1962	Characterization of multiple sequence alignment errors using complete-likelihood score and position-shift map. BMC Bioinformatics, 2016, 17, 133.	1.2	7
1963	Hologenome analysis of two marine sponges with different microbiomes. BMC Genomics, 2016, 17, 158.	1.2	60

#	ARTICLE	IF	CITATIONS
1964	DUF3380 Domain from a Salmonella Phage Endolysin Shows Potent <i>N</i> -Acetylmuramidase Activity. Applied and Environmental Microbiology, 2016, 82, 4975-4981.	1.4	49
1965	Fragment-based modelling of single stranded RNA bound to RNA recognition motif containing proteins. Nucleic Acids Research, 2016, 44, 4565-4580.	6.5	20
1966	Species-Level Para- and Polyphyly in DNA Barcode Gene Trees: Strong Operational Bias in European Lepidoptera. Systematic Biology, 2016, 65, 1024-1040.	2.7	160
1967	Long noncoding RNAs: Central to nervous system development. International Journal of Developmental Neuroscience, 2016, 55, 109-116.	0.7	34
1968	Comparative Phylogenomics of Pathogenic and Nonpathogenic Species. G3: Genes, Genomes, Genetics, 2016, 6, 235-244.	0.8	38
1969	Host specialization of the blast fungus Magnaporthe oryzae is associated with dynamic gain and loss of genes linked to transposable elements. BMC Genomics, 2016, 17, 370.	1.2	157
1970	Complete Genome Sequence of Dyella thiooxydans ATSB10, a Thiosulfate-Oxidizing Bacterium Isolated from Sunflower Fields in South Korea. Genome Announcements, 2016, 4, .	0.8	1
1971	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. Environmental Microbiology, 2016, 18, 2825-2842.	1.8	72
1972	SeqTools: visual tools for manual analysis of sequence alignments. BMC Research Notes, 2016, 9, 39.	0.6	26
1973	Identification of catalytically important residues of the carotenoid 1,2-hydratases from Rubrivivax gelatinosus and Thiocapsa roseopersicina. Applied Microbiology and Biotechnology, 2016, 100, 1275-1284.	1.7	21
1974	The CopC Family: Structural and Bioinformatic Insights into a Diverse Group of Periplasmic Copper Binding Proteins. Biochemistry, 2016, 55, 2278-2290.	1.2	78
1975	Genome Sequence and Analysis of<i>Escherichia coli</i>MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. Genome Biology and Evolution, 2016, 8, 742-752.	1.1	35
1976	A multi-objective optimization approach accurately resolves protein domain architectures. Bioinformatics, 2016, 32, 345-353.	1.8	45
1977	Genome-wide analysis of CrRLK1L gene family in Gossypium and identification of candidate CrRLK1L genes related to fiber development. Molecular Genetics and Genomics, 2016, 291, 1137-1154.	1.0	27
1978	A passion fruit putative ortholog of the SOMATIC EMBRYOGENESIS RECEPTOR KINASE1 gene is expressed throughout the in vitro de novo shoot organogenesis developmental program. Plant Cell, Tissue and Organ Culture, 2016, 125, 107-117.	1.2	15
1979	Comparative Genomics of Core Metabolism Genes of Cellulolytic and Non-cellulolytic Clostridium Species. Advances in Biochemical Engineering/Biotechnology, 2016, 156, 79-112.	0.6	2
1980	Characterization of DNA methyltransferase and demethylase genes in Fragaria vesca. Molecular Genetics and Genomics, 2016, 291, 1333-1345.	1.0	37
1981	The Pfam protein families database: towards a more sustainable future. Nucleic Acids Research, 2016, 44, D279-D285.	6.5	5,391

#	Article	IF	Citations
1982	Two MYB transcription factors regulate flavonoid biosynthesis in pear fruit (<i>Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 742 Td (bret	2.4	137
1983	Algorithms for modeling global and context-specific functional relationship networks. Briefings in Bioinformatics, 2016, 17, 686-695.	3.2	3
1984	A Computational Approach for the Discovery of Proteinâ€“RNA Networks. Methods in Molecular Biology, 2016, 1358, 29-39.	0.4	3
1985	PPIXpress: construction of condition-specific protein interaction networks based on transcript expression. Bioinformatics, 2016, 32, 571-578.	1.8	21
1986	Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 3-15.	0.9	178
1987	GIPSy: Genomic island prediction software. Journal of Biotechnology, 2016, 232, 2-11.	1.9	128
1988	Late Embryogenesis Abundant (LEA) Gene Family in Maize: Identification, Evolution, and Expression Profiles. Plant Molecular Biology Reporter, 2016, 34, 15-28.	1.0	42
1989	Computational Analysis of Missense Variants of G Protein-Coupled Receptors Involved in the Neuroendocrine Regulation of Reproduction. Neuroendocrinology, 2016, 103, 230-239.	1.2	16
1990	Construction and evaluation of a chimeric protein made fromFasciola hepaticaleucine aminopeptidase and cathepsin L1. Journal of Helminthology, 2016, 90, 7-13.	0.4	6
1991	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 81, 336-346.	0.7	32
1992	De novo assembly of a tadpole shrimp (<i>Triops newberryi</i>) transcriptome and preliminary differential gene expression analysis. Molecular Ecology Resources, 2017, 17, 161-171.	2.2	28
1993	Exploring the genomic diversity of black yeasts and relatives (<i>Chaetothyriales</i>,<i>Ascomycota</i>). Studies in Mycology, 2017, 86, 1-28.	4.5	144
1994	Elevated temperature increases in planta expression levels of virulence related genes in Magnaporthe oryzae and compromises resistance in Oryza sativa cv. Nipponbare. Functional Plant Biology, 2017, 44, 358.	1.1	15
1995	Genome-wide identification of the TIFY gene family in three cultivated Gossypium species and the expression of JAZ genes. Scientific Reports, 2017, 7, 42418.	1.6	46
1996	Isolation and characterization of a virulent bacteriophage infecting Acinetobacter johnsonii from activated sludge. Research in Microbiology, 2017, 168, 472-481.	1.0	19
1997	Origins and challenges of viral dark matter. Virus Research, 2017, 239, 136-142.	1.1	167
1998	Domain prediction with probabilistic directional context. Bioinformatics, 2017, 33, 2471-2478.	1.8	4
1999	Identification and expression analyses of the alanine aminotransferase (AlaAT) gene family in poplar seedlings. Scientific Reports, 2017, 7, 45933.	1.6	20

#	ARTICLE	IF	CITATIONS
2000	The Nucleoporin Nup2 Contains a Meiotic-Autonomous Region that Promotes the Dynamic Chromosome Events of Meiosis. Genetics, 2017, 206, 1319-1337.	1.2	18
2001	Bioinformatic and expression analyses on carotenoid dioxygenase genes in fruit development and abiotic stress responses in Fragaria vesca. Molecular Genetics and Genomics, 2017, 292, 895-907.	1.0	27
2002	Comparative genomic analysis of SET domain family reveals the origin, expansion, and putative function of the arthropod-specific SmydA genes as histone modifiers in insects. GigaScience, 2017, 6, 1-16.	3.3	19
2003	Shotgun Metagenomic Sequencing Analysis of Soft-Rot Enterobacteriaceae in Polymicrobial Communities. Methods in Molecular Biology, 2017, 1539, 85-97.	0.4	2
2004	Structural conservation of the PIN domain active site across all domains of life. Protein Science, 2017, 26, 1474-1492.	3.1	33
2005	Genome-wide identification and expression profiling of EIL gene family in woody plant representative poplar (Populus trichocarpa). Archives of Biochemistry and Biophysics, 2017, 627, 30-45.	1.4	13
2006	The Human CCHC-type Zinc Finger Nucleic Acid-Binding Protein Binds G-Rich Elements in Target mRNA Coding Sequences and Promotes Translation. Cell Reports, 2017, 18, 2979-2990.	2.9	106
2007	A Two-component NADPH Oxidase (NOX)-like System in Bacteria Is Involved in the Electron Transfer Chain to the Methionine Sulfoxide Reductase MsrP. Journal of Biological Chemistry, 2017, 292, 2485-2494.	1.6	35
2008	Trypanosome outer kinetochore proteins suggest conservation of chromosome segregation machinery across eukaryotes. Journal of Cell Biology, 2017, 216, 379-391.	2.3	87
2009	Genomic and physiological analyses of â€˜<i>Reinekea forsetii</i>â€™ reveal a versatile opportunistic lifestyle during spring algae blooms. Environmental Microbiology, 2017, 19, 1209-1221.	1.8	13
2010	Analyses of long non-coding RNAs and mRNA profiling through RNA sequencing of MDBK cells at different stages of bovine viral diarrhea virus infection. Research in Veterinary Science, 2017, 115, 508-516.	0.9	34
2012	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.	1.6	27
2013	Expression of membrane-bound dehydrogenases from a mother of vinegar metagenome in Gluconobacter oxydans. Applied Microbiology and Biotechnology, 2017, 101, 7901-7912.	1.7	17
2014	Metagenome Assembly and Functional Annotation. , 2017, , 151-159.		0
2015	The Conserved RNA Exonuclease Rexo5 Is Required for 3â€² End Maturation of 28S rRNA, 5S rRNA, and snoRNAs. Cell Reports, 2017, 21, 758-772.	2.9	15
2016	Long Non Coding RNA Biology. Advances in Experimental Medicine and Biology, 2017, , .	0.8	18
2017	A novel lipoate attachment enzyme is shared by Plasmodium and Chlamydia species. Molecular Microbiology, 2017, 106, 439-451.	1.2	11
2018	Molecular characterization of transport lectin vesicular integral membrane protein 36ÂkDa (VIP36) in the life cycle of Schistosoma mansoni. Parasitology Research, 2017, 116, 2765-2773.	0.6	3

#	ARTICLE	IF	CITATIONS
2019	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of Drosophila. Current Biology, 2017, 27, 2869-2877.e6.	1.8	37
2020	The phylogeny of extant starfish (Asteroidea: Echinodermata) including Xyloplax, based on comparative transcriptomics. Molecular Phylogenetics and Evolution, 2017, 115, 161-170.	1.2	40
2021	The hnRNP Q-like gene is retroinserted into the B chromosomes of the cichlid fish Astatotilapia latifasciata. Chromosome Research, 2017, 25, 277-290.	1.0	12
2022	Technological Developments in lncRNA Biology. Advances in Experimental Medicine and Biology, 2017, 1008, 283-323.	0.8	296
2023	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. Journal of the American Heart Association, 2017, 6, .	1.6	36
2024	Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.		1
2025	Genomic data reveal high conservation but divergent evolutionary pattern of Polycomb/Trithorax group genes in arthropods. Insect Science, 2019, 26, 20-34.	1.5	11
2026	Core features of triacylglyceride production in Ettlia oleoabundans revealed by lipidomic and gene expression profiling under distinct induction conditions. Algal Research, 2017, 26, 453-462.	2.4	3
2027	Identification and expression analysis of the apple (Malus Ã— domestica) basic helix-loop-helix transcription factor family. Scientific Reports, 2017, 7, 28.	1.6	43
2028	Across-proteome modeling of dimer structures for the bottom-up assembly of protein-protein interaction networks. BMC Bioinformatics, 2017, 18, 257.	1.2	9
2029	Analysis of the grape (Vitis vinifera L.) thaumatin-like protein (TLP) gene family and demonstration that TLP29 contributes to disease resistance. Scientific Reports, 2017, 7, 4269.	1.6	75
2030	A differentially regulated <scp>AP</scp>2/<scp>ERF</scp> transcription factor gene cluster acts downstream of a <scp>MAP</scp> kinase cascade to modulate terpenoid indole alkaloid biosynthesis in <i>Catharanthus roseus</i>. New Phytologist, 2017, 213, 1107-1123.	3.5	157
2031	A Novel highly thermostable branched-chain amino acid aminotransferase from the crenarchaeon Vulcanisaeta moutnovskia. Enzyme and Microbial Technology, 2017, 96, 127-134.	1.6	22
2032	Metazoan evolution of the armadillo repeat superfamily. Cellular and Molecular Life Sciences, 2017, 74, 525-541.	2.4	37
2034	Genome Wide Mapping of Peptidases in Rhodnius prolixus: 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.	1.3	19
2035	Identification of a Novel Alternative Splicing Variant of VvPMA1 in Grape Root under Salinity. Frontiers in Plant Science, 2017, 8, 605.	1.7	8
2036	Whole-Genome Identification and Expression Pattern of the Vicinal Oxygen Chelate Family in Rapeseed (Brassica napus L.). Frontiers in Plant Science, 2017, 8, 745.	1.7	16
2037	YSK2 Type Dehydrin (SbDhn1) from Sorghum bicolor Showed Improved Protection under High Temperature and Osmotic Stress Condition. Frontiers in Plant Science, 2017, 8, 918.	1.7	45

#	ARTICLE	IF	CITATIONS
2038	WHITE STRIPE LEAF4 Encodes a Novel P-Type PPR Protein Required for Chloroplast Biogenesis during Early Leaf Development. Frontiers in Plant Science, 2017, 8, 1116.	1.7	71
2039	De novo Assembly of the Camellia nitidissima Transcriptome Reveals Key Genes of Flower Pigment Biosynthesis. Frontiers in Plant Science, 2017, 8, 1545.	1.7	43
2040	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. Frontiers in Immunology, 2017, 8, 1382.	2.2	25
2041	Comparative Omics and Trait Analyses of Marine Pseudoalteromonas Phages Advance the Phage OTU Concept. Frontiers in Microbiology, 2017, 8, 1241.	1.5	34
2042	Conserved Transcriptional Responses to Nutrient Stress in Bloom-Forming Algae. Frontiers in Microbiology, 2017, 8, 1279.	1.5	31
2043	The Sit-and-Wait Hypothesis in Bacterial Pathogens: A Theoretical Study of Durability and Virulence. Frontiers in Microbiology, 2017, 8, 2167.	1.5	24
2044	Bioactive Nutrients and Nutrigenomics in Age-Related Diseases. Molecules, 2017, 22, 105.	1.7	61
2045	Relating protein functional diversity to cell type number identifies genes that determine dynamic aspects of chromatin organisation as potential contributors to organismal complexity. PLoS ONE, 2017, 12, e0185409.	1.1	4
2046	Identifying pathogenicity of human variants via paralog-based yeast complementation. PLoS Genetics, 2017, 13, e1006779.	1.5	30
2047	The Biomphalaria glabrata DNA methylation machinery displays spatial tissue expression, is differentially active in distinct snail populations and is modulated by interactions with Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2017, 11, e0005246.	1.3	39
2048	Segmental duplications: evolution and impact among the current Lepidoptera genomes. BMC Evolutionary Biology, 2017, 17, 161.	3.2	13
2049	Draft genome sequences of two opportunistic pathogenic strains of Staphylococcus cohnii isolated from human patients. Standards in Genomic Sciences, 2017, 12, 49.	1.5	11
2050	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
2051	Decoding Complex Soil Microbial Communities through New Age "Omics". Journal of Microbial & Biochemical Technology, 2017, 09, .	0.2	3
2052	Characterization of Cytosine Methylation and the DNA Methyltransferases of <i>Toxoplasma gondii</i>. International Journal of Biological Sciences, 2017, 13, 458-470.	2.6	13
2053	RNA-binding proteins and their role in the regulation of gene expression in Trypanosoma cruzi and Saccharomyces cerevisiae. Genetics and Molecular Biology, 2017, 40, 22-30.	0.6	38
2054	Studying AMPK in an Evolutionary Context. Methods in Molecular Biology, 2018, 1732, 111-142.	0.4	3
2055	Cancer-Associated Long Noncoding RNA SMRT-2 Controls Epidermal Differentiation. Journal of Investigative Dermatology, 2018, 138, 1445-1449.	0.3	13

#	Article	IF	Citations
2056	PpHB22, a member of HD-Zip proteins, activates PpDAM1 to regulate bud dormancy transition in â€˜Suliâ€™ pear (Pyrus pyrifolia White Pear Group). Plant Physiology and Biochemistry, 2018, 127, 355-365.	2.8	30
2057	Reconstruction of the sialylation pathway in the ancestor of eukaryotes. Scientific Reports, 2018, 8, 2946.	1.6	20
2058	Cell-type-resolved alternative splicing patterns in mouse liver. DNA Research, 2018, 25, 265-275.	1.5	14
2059	Enzymatic asymmetric synthesis of chiral amino acids. Chemical Society Reviews, 2018, 47, 1516-1561.	18.7	269
2060	Discovery of dynein and its properties. , 2018, , 3-87.		4
2061	The evolutionary biology of dyneins. , 2018, , 100-138.		5
2062	Effect of SrtA on Interspecies Adherence of Oral Bacteria. Current Medical Science, 2018, 38, 160-166.	0.7	4
2063	Hostâ€“parasite interactions and ecology of the malaria parasiteâ€”a bioinformatics approach. Briefings in Functional Genomics, 2018, 17, 451-457.	1.3	4
2064	In silico comparative analysis of GGDEF and EAL domain signaling proteins from the Azospirillum genomes. BMC Microbiology, 2018, 18, 20.	1.3	18
2065	Genome-Wide Identification, Classification, and Expression Analysis of SNARE Genes in Chinese Cabbage (Brassica rapa ssp. pekinensis) Infected by Turnip mosaic virus. Plant Molecular Biology Reporter, 2018, 36, 210-224.	1.0	5
2066	Next-generation sequencing of Dreissena polymorpha transcriptome sheds light on its mitochondrial DNA. Hydrobiologia, 2018, 810, 255-263.	1.0	8
2067	Transcriptome and toxin family analysis of the paralysis tick, Ixodes holocyclus. International Journal for Parasitology, 2018, 48, 71-82.	1.3	33
2068	Databases and Associated Bioinformatic Tools in Studies of Food Allergens, Epitopes and Haptens â€“ a Review. Polish Journal of Food and Nutrition Sciences, 2018, 68, 103-113.	0.6	3
2069	Immunohistochemical null-phenotype for mismatch repair proteins in colonic carcinoma associated with concurrent MLH1 hypermethylation and MSH2 somatic mutations. Familial Cancer, 2018, 17, 225-228.	0.9	17
2070	Clinical and molecular characterization of <i>KCNT1</i> -related severe early-onset epilepsy. Neurology, 2018, 90, e55-e66.	1.5	89
2071	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensorâ€domain protein. Protein Science, 2018, 27, 568-572.	3.1	1
2072	Bacteriophages. Methods in Molecular Biology, 2018, , .	0.4	21
2073	Essential Steps in Characterizing Bacteriophages: Biology, Taxonomy, and Genome Analysis. Methods in Molecular Biology, 2018, 1681, 197-215.	0.4	20

#	ARTICLE	IF	CITATIONS
2074	A Phylogenetic Study of Monalysin Family of Proteobacterial Pore-Forming Toxins. , 2018, , .		0
2075	Comparative Analysis of Genomic Island Prediction Tools. Frontiers in Genetics, 2018, 9, 619.	1.1	29
2076	Mining Late Embryogenesis Abundant (LEA) Family Genes in Cleistogenes songorica, a Xerophyte Perennial Desert Plant. International Journal of Molecular Sciences, 2018, 19, 3430.	1.8	28
2077	Complete genome sequence of the halophile bacterium Kushneria konosiri X49T, isolated from salt-fermented Konosirus punctatus. Standards in Genomic Sciences, 2018, 13, 19.	1.5	8
2078	Expansion and Divergence of Argonaute Genes in the Oomycete Genus Phytophthora. Frontiers in Microbiology, 2018, 9, 2841.	1.5	14
2079	Rice <i>TCM1</i> Encoding a Component of the TAC Complex is Required for Chloroplast Development under Cold Stress. Plant Genome, 2018, 11, 160065.	1.6	9
2080	Accumulation of Transposable Elements in Autosomes and Giant Sex Chromosomes of Omophoita (Chrysomelidae: Alticinae). Cytogenetic and Genome Research, 2018, 156, 215-222.	0.6	10
2081	TCP Transcription Factors in Moso Bamboo (Phyllostachys edulis): Genome-Wide Identification and Expression Analysis. Frontiers in Plant Science, 2018, 9, 1263.	1.7	60
2082	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. Frontiers in Plant Science, 2018, 9, 1376.	1.7	10
2083	Deciphering the structure of the condensin protein complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11911-11916.	3.3	15
2084	Venom gland transcriptomics and microRNA profiling of juvenile and adult yellow-bellied sea snake, Hydrophis platurus, from Playa del Coco (Guanacaste, Costa Rica). Toxicon, 2018, 153, 96-105.	0.8	14
2085	Computational Tools and Databases of Microbes and Its Bioprospecting for Sustainable Development. , 2018, , 385-397.		0
2086	The crystal structure of an essential high-temperature requirement protein HtrA1 (Rv1223) from Mycobacterium tuberculosis reveals its unique features. Acta Crystallographica Section D: Structural Biology, 2018, 74, 906-921.	1.1	3
2087	Computational Approaches to Understand the Genome and Protein Sequences of Fungi. , 2018, , 635-649.		0
2088	Phylogenomics Reveal the Dynamic Evolution of Fungal Nitric Oxide Reductases and Their Relationship to Secondary Metabolism. Genome Biology and Evolution, 2018, 10, 2474-2489.	1.1	44
2089	The floral transcriptome of Machilus yunnanensis, a tree in the magnoliid family Lauraceae. Computational Biology and Chemistry, 2018, 77, 456-465.	1.1	1
2090	Transcriptome Analysis Reveals Dynamic Gene Expression Profiles in Porcine Alveolar Macrophages in Response to the Chinese Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus. BioMed Research International, 2018, 2018, 1-23.	0.9	24
2091	How is structural divergence related to evolutionary information?. Molecular Phylogenetics and Evolution, 2018, 127, 859-866.	1.2	13

#	ARTICLE	IF	CITATIONS
2092	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. International Journal of Genomics, 2018, 2018, 1-10.	0.8	8
2093	Genome-Wide analysis of aluminum-activated malate transporter family genes in six rosaceae species, and expression analysis and functional characterization on malate accumulation in Chinese white pear. Plant Science, 2018, 274, 451-465.	1.7	26
2094	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. ELife, 2018, 7, .	2.8	40
2095	Mutational analysis of the proâ€peptide of a marine intracellular subtilisin protease supports its role in inhibition. Proteins: Structure, Function and Bioinformatics, 2018, 86, 965-977.	1.5	5
2097	Studying the Evolution of Histone Variants Using Phylogeny. Methods in Molecular Biology, 2018, 1832, 273-291.	0.4	6
2098	Identification of WRKY Gene Family from Dimocarpus longan and Its Expression Analysis during Flower Induction and Abiotic Stress Responses. International Journal of Molecular Sciences, 2018, 19, 2169.	1.8	38
2099	Two divergent Symbiodinium genomes reveal conservation of a gene cluster for sunscreen biosynthesis and recently lost genes. BMC Genomics, 2018, 19, 458.	1.2	114
2100	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.	1.5	11
2101	Environmental Stress Responses and Experimental Handling Artifacts of a Model Organism, the Copepod Acartia tonsa (Dana). Frontiers in Marine Science, 2018, 5, .	1.2	13
2102	Membrane Topology and Heme Binding of the Histidine Kinases HrrS and ChrS in Corynebacterium glutamicum. Frontiers in Microbiology, 2018, 9, 183.	1.5	14
2103	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.	1.5	79
2104	Distribution Patterns of Polyphosphate Metabolism Pathway and Its Relationships With Bacterial Durability and Virulence. Frontiers in Microbiology, 2018, 9, 782.	1.5	34
2105	Bacillales Members from the Olive Rhizosphere Are Effective Biological Control Agents against the Defoliating Pathotype of Verticillium dahliae. Agriculture (Switzerland), 2018, 8, 90.	1.4	39
2106	A Possible Trifunctional Î²-Carotene Synthase Gene Identified in the Draft Genome of Aurantiochytrium sp. Strain KH105. Genes, 2018, 9, 200.	1.0	32
2107	Protein moonlighting elucidates the essential human pathway catalyzing lipoic acid assembly on its cognate enzymes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7063-E7072.	3.3	33
2108	Development of Versatile Vectors for Heterologous Expression in Bacillus. Microorganisms, 2018, 6, 51.	1.6	8
2109	Current trends in Bioinformatics: An Insight. , 2018, , .		1
2110	Modelling Polyketide Synthases and Similar Macromolecular Complexes. , 2018, , 121-144.		0

#	ARTICLE	IF	CITATIONS
2111	Structural insights into a novel functional dimer of Staphylococcus aureus RNase HII. Biochemical and Biophysical Research Communications, 2018, 503, 1207-1213.	1.0	1
2112	Eukaryote specific folds: Part of the whole. Proteins: Structure, Function and Bioinformatics, 2018, 86, 868-881.	1.5	7
2113	Improved strategy for the curation and classification of kinases, with broad applicability to other eukaryotic protein groups. Scientific Reports, 2018, 8, 6808.	1.6	10
2114	Whole-genome de novo sequencing reveals unique genes that contributed to the adaptive evolution of the Mikado pheasant. GigaScience, 2018, 7, .	3.3	21
2115	Genome-wide identification and characterization of cysteine-rich polycomb-like protein (CPP) family genes in cucumber (Cucumis sativus) and their roles in stress responses. Biologia (Poland), 2018, 73, 425-435.	0.8	16
2116	Identification and analysis of odorant-binding protein genes from the wolf spider Pardosa pseudoannulata (Araneae: Lycosidae) based on its transcriptome. Chemoecology, 2018, 28, 123-130.	0.6	5
2117	Assessment of an Organ-Specific <i>de Novo</i> Transcriptome of the Nematode Trap-Crop, <i>Solanum sisymbriifolium</i>. G3: Genes, Genomes, Genetics, 2018, 8, 2135-2143.	0.8	4
2118	Dissecting metabolic flux in C4 plants: experimental and theoretical approaches. Phytochemistry Reviews, 2018, 17, 1253-1274.	3.1	6
2119	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 422 Td	1.3	10
2120	Genome sequence and genetic transformation of a widely distributed and cultivated poplar. Plant Biotechnology Journal, 2019, 17, 451-460.	4.1	89
2121	Regulation of phosphoribosyl ubiquitination by a calmodulin-dependent glutamylase. Nature, 2019, 572, 387-391.	13.7	91
2122	The DUF1996 and WSC domainâ€containing protein Wsc1I acts as a novel sensor of multiple stress cues in <i>Beauveria bassiana</i>. Cellular Microbiology, 2019, 21, e13100.	1.1	18
2123	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2019, 1910, 469-504.	0.4	30
2124	Identification of candidate genes involved in steroidal alkaloids biosynthesis in organ-specific transcriptomes of Veratrum nigrum L.. Gene, 2019, 712, 143962.	1.0	6
2125	Sharing Programming Resources Between Bio* Projects. Methods in Molecular Biology, 2019, 1910, 747-766.	0.4	6
2126	Gains and losses of metabolic function inferred from a phylotranscriptomic analysis of algae. Scientific Reports, 2019, 9, 10482.	1.6	7
2127	A GntR-Like Transcription Factor HypR Regulates Expression of Genes Associated With L-Hydroxyproline Utilization in Streptomyces coelicolor A3(2). Frontiers in Microbiology, 2019, 10, 1451.	1.5	7
2128	Adaptive dif Modules in Permafrost Strains of Acinetobacter lwoffii and Their Distribution and Abundance Among Present Day Acinetobacter Strains. Frontiers in Microbiology, 2019, 10, 632.	1.5	22

#	ARTICLE	IF	CITATIONS
2129	Genome-wide identification and functional analysis of oleosin genes in Brassica napus L.. BMC Plant Biology, 2019, 19, 294.	1.6	30
2130	Genome-wide characterization and evolutionary analysis of heat shock transcription factors (HSFs) to reveal their potential role under abiotic stresses in radish (Raphanus sativus L.). BMC Genomics, 2019, 20, 772.	1.2	23
2131	in silico screening and molecular dynamics simulations study to identify novel potent inhibitors against Mycobacterium tuberculosis DnaG primase. Acta Tropica, 2019, 199, 105154.	0.9	2
2132	Large-scale identification and functional analysis of <i>NLR</i> genes in blast resistance in the Tetep rice genome sequence. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18479-18487.	3.3	63
2133	Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. BMC Genomics, 2019, 20, 661.	1.2	18
2134	Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. Genome Biology, 2019, 20, 187.	3.8	71
2135	Genome-wide identification of and functional insights into the late embryogenesis abundant (LEA) gene family in bread wheat (Triticum aestivum). Scientific Reports, 2019, 9, 13375.	1.6	42
2136	Identification of RING-H2 Gene Candidates Related to Wood Formation in Poplar. Forests, 2019, 10, 698.	0.9	1
2137	Transcription analysis of the response of the porcine adrenal cortex to a single subclinical dose of lipopolysaccharide from Salmonella Enteritidis. International Journal of Biological Macromolecules, 2019, 141, 1228-1245.	3.6	5
2138	FGB1 and WSC3 are <i>in plantaâ€</i>induced <i>Î²</i>â€glucanâ€binding fungal lectins with different functions. New Phytologist, 2019, 222, 1493-1506.	3.5	43
2139	Comparative transcriptomics in <i>Leishmania braziliensis</i>: disclosing differential gene expression of coding and putative noncoding RNAs across developmental stages. RNA Biology, 2019, 16, 639-660.	1.5	20
2140	Secretome analysis of Strongyloides venezuelensis parasitic stages reveals that soluble and insoluble proteins are involved in its parasitism. Parasites and Vectors, 2019, 12, 21.	1.0	23
2141	Similarity regression predicts evolution of transcription factor sequence specificity. Nature Genetics, 2019, 51, 981-989.	9.4	105
2142	Heterologous Microcompartment Assembly in <i>Bacillaceae</i>: Establishing the Components Necessary for Scaffold Formation. ACS Synthetic Biology, 2019, 8, 1642-1654.	1.9	9
2143	Prediction and validation of DREB transcription factors for salt tolerance in Solanum lycopersicum L.: An integrated experimental and computational approach. Environmental and Experimental Botany, 2019, 165, 1-18.	2.0	6
2144	Cyberinfrastructure to Improve Forest Health and Productivity: The Role of Tree Databases in Connecting Genomes, Phenomes, and the Environment. Frontiers in Plant Science, 2019, 10, 813.	1.7	24
2145	Genome-Wide Identification and Expression Analyses of the bZIP Transcription Factor Genes in moso bamboo (Phyllostachys edulis). International Journal of Molecular Sciences, 2019, 20, 2203.	1.8	26
2146	Non-photochemical quenching in the cells of the carotenogenic chlorophyte Haematococcus lacustris under favorable conditions and under stress. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1429-1442.	1.1	20

#	Article	IF	Citations
2147	Identification of the LEA family members from Caragana korshinskii (Fabaceae) and functional characterization of CkLEA2-3 in response to abiotic stress in Arabidopsis. Revista Brasileira De Botanica, 2019, 42, 227-238.	0.5	9
2148	Structural bioinformatics insights into the CARDâ€CARD interaction mediated by the mitochondrial antiviralâ€signaling protein of black carp. Journal of Cellular Biochemistry, 2019, 120, 12534-12543.	1.2	8
2149	Temporal variability of diazotroph community composition in the upwelling region off NW Iberia. Scientific Reports, 2019, 9, 3737.	1.6	18
2150	Selection pressure causes differentiation of the SPL gene family in the Juglandaceae. Molecular Genetics and Genomics, 2019, 294, 1037-1048.	1.0	6
2151	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	3.8	114
2152	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.	1.0	1
2153	Comparative transcriptome analysis reveals new molecular pathways for cucumber genes related to sex determination. Plant Reproduction, 2019, 32, 193-216.	1.3	25
2154	Grammar of protein domain architectures. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3636-3645.	3.3	46
2155	Isolation and Genomic Characterization of an Acinetobacter johnsonii Bacteriophage AJO2 From Bulking Activated Sludge. Frontiers in Microbiology, 2019, 10, 266.	1.5	7
2156	Drift and Directional Selection Are the Evolutionary Forces Driving Gene Expression Divergence in Eye and Brain Tissue of<i>Heliconius</i>Butterflies. Genetics, 2019, 213, 581-594.	1.2	29
2157	iRBP-Motif-PSSM: Identification of RNA-Binding Proteins Based on Collaborative Learning. IEEE Access, 2019, 7, 168956-168962.	2.6	8
2158	A large self-transmissible resistance plasmid from Nigeria contains genes that ameliorate a carrying cost. Scientific Reports, 2019, 9, 19624.	1.6	8
2159	Single-molecule real-time sequencing facilitates the analysis of transcripts and splice isoforms of anthers in Chinese cabbage (Brassica rapa L. ssp. pekinensis). BMC Plant Biology, 2019, 19, 517.	1.6	16
2160	Coevolutionary Analysis of Protein Subfamilies by Sequence Reweighting. Entropy, 2019, 21, 1127.	1.1	13
2161	Comparative Analysis of the YABBY Gene Family of Bienertia sinuspersici, a Single-Cell C4 Plant. Plants, 2019, 8, 536.	1.6	12
2162	A systems biology approach uncovers a gene co-expression network associated with cell wall degradability in maize. PLoS ONE, 2019, 14, e0227011.	1.1	2
2163	Comparative transcriptome analysis of TUCPs in Gossypium hirsutum Ligon-lintless-1 mutant and their proposed functions in cotton fiber development. Molecular Genetics and Genomics, 2019, 294, 23-34.	1.0	5
2164	Comparative genomics of the major parasitic worms. Nature Genetics, 2019, 51, 163-174.	9.4	377

#	ARTICLE	IF	CITATIONS
2165	Isolation of Cellulase Genes From Thermophilies. , 2019, , 151-169.		2
2166	Transcriptome and Comparative Genomics Analyses Reveal New Functional Insights on Key Determinants of Pathogenesis and Interbacterial Competition in <i>Pectobacterium</i> and <i>Dickeya</i> spp. Applied and Environmental Microbiology, 2019, 85, .	1.4	61
2167	The methionine biosynthesis regulator AaMetR contributes to oxidative stress tolerance and virulence in Alternaria alternata. Microbiological Research, 2019, 219, 94-109.	2.5	33
2168	Complete Genome Sequence of Lactococcus lactis subsp. cremoris 3107, Host for the Model Lactococcal P335 Bacteriophage TP901-1. Microbiology Resource Announcements, 2019, 8, .	0.3	4
2169	Genome-scale identification, classification, and tissue specific expression analysis of late embryogenesis abundant (LEA) genes under abiotic stress conditions in Sorghum bicolor L.. PLoS ONE, 2019, 14, e0209980.	1.1	59
2170	Genetic basis for the establishment of endosymbiosis in <i>Paramecium</i>. ISME Journal, 2019, 13, 1360-1369.	4.4	30
2171	Long non-coding RNAs in banana: prediction, mapping and their comparative studies using Musa balbisiana and Musa acuminata transcriptome. Trees - Structure and Function, 2019, 33, 359-369.	0.9	3
2172	Strategies for Pathway Analysis Using GWAS and WGS Data. Current Protocols in Human Genetics, 2019, 100, e79.	3.5	26
2173	The RES domain toxins of RESâ€Xre toxinâ€antitoxin modules induce cell stasis by degrading NAD⁺. Molecular Microbiology, 2019, 111, 221-236.	1.2	46
2174	A map of constrained coding regions in the human genome. Nature Genetics, 2019, 51, 88-95.	9.4	201
2175	The draft genomes of five agriculturally important African orphan crops. GigaScience, 2019, 8, .	3.3	108
2176	Molecular phylogenetics supports a clade of red algal parasites retaining native plastids: taxonomy and terminology revised. Journal of Phycology, 2019, 55, 279-288.	1.0	8
2177	Phylogenetic spread of sequence data affects fitness of consensus enzymes: Insights from triosephosphate isomerase. Proteins: Structure, Function and Bioinformatics, 2020, 88, 274-283.	1.5	2
2178	Genome-wide functional association networks: background, data & state-of-the-art resources. Briefings in Bioinformatics, 2020, 21, 1224-1237.	3.2	20
2179	Comparative quantitative proteomics of osmotic signal transduction mutants in Botrytis cinerea explain mutant phenotypes and highlight interaction with cAMP and Ca2+ signalling pathways. Journal of Proteomics, 2020, 212, 103580.	1.2	5
2180	In-silico and in-vitro analysis of endocan interaction with statins. International Journal of Biological Macromolecules, 2020, 146, 1087-1099.	3.6	13
2181	Junction Location Identifier (JuLI). Journal of Molecular Diagnostics, 2020, 22, 304-318.	1.2	6
2182	Into the bloom: Molecular response of pelagic tunicates to fluctuating food availability. Molecular Ecology, 2020, 29, 292-307.	2.0	6

#	Article	IF	Citations
2184	A Depletion of Stop Codons in lincRNA is Owing to Transfer of Selective Constraint from Coding Sequences. Molecular Biology and Evolution, 2020, 37, 1148-1164.	3.5	1
2185	Draft Genomes of Two Artocarpus Plants, Jackfruit (A. heterophyllus) and Breadfruit (A. altilis). Genes, 2020, 11, 27.	1.0	30
2186	Positive Selection and Gene Expression Analyses from Salivary Glands Reveal Discrete Adaptations within the Ecologically Diverse Bat Family Phyllostomidae. Genome Biology and Evolution, 2020, 12, 1419-1428.	1.1	7
2187	Expansion of Adhesion Genes Drives Pathogenic Adaptation of Nematode-Trapping Fungi. IScience, 2020, 23, 101057.	1.9	31
2188	The multipurpose family of flavoprotein oxidases. The Enzymes, 2020, 47, 63-86.	0.7	12
2189	Leaf shape in Populus tremula is a complex, omnigenic trait. Ecology and Evolution, 2020, 10, 11922-11940.	0.8	19
2190	An Educational Bioinformatics Project to Improve Genome Annotation. Frontiers in Microbiology, 2020, 11, 577497.	1.5	6
2191	Acinetobacter Plasmids: Diversity and Development of Classification Strategies. Frontiers in Microbiology, 2020, 11, 588410.	1.5	11
2192	A high-quality sponge gourd (Luffa cylindrica) genome. Horticulture Research, 2020, 7, 128.	2.9	35
2193	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. Communications Biology, 2020, 3, 424.	2.0	26
2194	Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont, <i>Basidiobolus</i>. G3: Genes, Genomes, Genetics, 2020, 10, 3417-3433.	0.8	27
2195	Comprehensive Identification and Characterization of Long Non-coding RNAs Associated With Rice Black-Streaked Dwarf Virus Infection in Laodelphax striatellus (FallÃ©n) Midgut. Frontiers in Physiology, 2020, 11, 1011.	1.3	6
2196	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	1.7	54
2197	Structural Characterization of the Essential Cell Division Protein FtsE and Its Interaction with FtsX in Streptococcus pneumoniae. MBio, 2020, 11, .	1.8	11
2198	Comparative transcriptome analysis of defense response of rice to Nilaparvata lugens and Chilo suppressalis infestation. International Journal of Biological Macromolecules, 2020, 163, 2270-2285.	3.6	16
2199	Bioinformatics approach to understand natureâ€™s unified mechanism of stereo-divergent synthesis of isoprenoid skeletons. World Journal of Microbiology and Biotechnology, 2020, 36, 142.	1.7	2
2200	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.	1.1	9
2201	PINCER: improved CRISPR/Cas9 screening by efficient cleavage at conserved residues. Nucleic Acids Research, 2020, 48, 9462-9477.	6.5	6

#	Article	IF	Citations
2202	Origins and Stepwise Expansion of R2R3-MYB Transcription Factors for the Terrestrial Adaptation of Plants. Frontiers in Plant Science, 2020, 11, 575360.	1.7	11
2203	Genome-Wide Analysis of the Cyclin Gene Family and Their Expression Profile in Medicago truncatula. International Journal of Molecular Sciences, 2020, 21, 9430.	1.8	13
2204	The AP2/ERF Gene Family in Triticum durum: Genome-Wide Identification and Expression Analysis under Drought and Salinity Stresses. Genes, 2020, 11, 1464.	1.0	79
2205	HpeNet: Co-expression Network Database for de novo Transcriptome Assembly of Paeonia lactiflora Pall. Frontiers in Genetics, 2020, 11, 570138.	1.1	6
2206	Horizontally Acquired Quorum-Sensing Regulators Recruited by the PhoP Regulatory Network Expand the Host Adaptation Repertoire in the Phytopathogen <i>Pectobacterium brasiliense</i>. MSystems, 2020, 5, .	1.7	11
2207	Analyses of chemosensory genes provide insight into the evolution of behavioral differences to phytochemicals in Bactrocera species. Molecular Phylogenetics and Evolution, 2020, 151, 106858.	1.2	12
2208	Genetic and Clinical Heterogeneity in Thirteen New Cases with Aceruloplasminemia. Atypical Anemia as a Clue for an Early Diagnosis. International Journal of Molecular Sciences, 2020, 21, 2374.	1.8	25
2209	Genome Sequence Resource of <i>Coniella vitis</i>, a Fungal Pathogen Causing Grape White Rot Disease. Molecular Plant-Microbe Interactions, 2020, 33, 787-789.	1.4	4
2210	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (Pyrus bretschneideri) and other Rosaceae species. Genomics, 2020, 112, 3484-3496.	1.3	20
2211	Identification of a novel phage targeting methicillin-resistant Staphylococcus aureus In vitro and In vivo. Microbial Pathogenesis, 2020, 149, 104317.	1.3	17
2212	Transcriptome, Spliceosome and Editome Expression Patterns of the Porcine Endometrium in Response to a Single Subclinical Dose of Salmonella Enteritidis Lipopolysaccharide. International Journal of Molecular Sciences, 2020, 21, 4217.	1.8	9
2213	Adjustment of photosynthetic activity to drought and fluctuating light in wheat. Plant, Cell and Environment, 2020, 43, 1484-1500.	2.8	45
2214	Hybrid histidine kinase activation by cyclic di-GMPâ€"mediated domain liberation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1000-1008.	3.3	28
2215	Phenotypic and Transcriptomic Analysis of Two Pinellia ternata Varieties T2 line and T2Plus line. Scientific Reports, 2020, 10, 4614.	1.6	6
2216	Aurora A regulation by reversible cysteine oxidation reveals evolutionarily conserved redox control of Ser/Thr protein kinase activity. Science Signaling, 2020, 13, .	1.6	65
2217	A redox-active switch in fructosamine-3-kinases expands the regulatory repertoire of the protein kinase superfamily. Science Signaling, 2020, 13, .	1.6	12
2218	Genome-wide identification and transcript profiles of walnut heat stress transcription factor involved in abiotic stress. BMC Genomics, 2020, 21, 474.	1.2	21
2219	Genome-wide analysis of WRKY transcription factors in Aquilaria sinensis (Lour.) Gilg. Scientific Reports, 2020, 10, 3018.	1.6	20

#	ARTICLE	IF	CITATIONS
2220	Crystal structure of Alr1298, a pentapeptide repeat protein from the cyanobacterium <i>Nostoc</i> sp. PCC 7120, determined at 2.1 Ã… resolution. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1143-1153.	1.5	7
2221	Bioactive compounds of Streptomyces: Biosynthesis to applications. Studies in Natural Products Chemistry, 2020, , 467-491.	0.8	13
2222	Comparative analysis of the P-type ATPase gene family in seven Rosaceae species and an expression analysis in pear (Pyrus bretschneideri Rehd.). Genomics, 2020, 112, 2550-2563.	1.3	14
2223	The round goby genome provides insights into mechanisms that may facilitate biological invasions. BMC Biology, 2020, 18, 11.	1.7	32
2224	Evolutionary relationships between the transcriptional repressors of the polyhydroxyalkanoate reserve storage system in prokaryotes: Conserved but phylogenetically heterogeneous. Gene, 2020, 735, 144397.	1.0	2
2225	A novel pattern matching algorithm for genomic patterns related to protein motifs. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050011.	0.3	0
2226	Genome-wide identification and expression analysis of the VQ gene family in sunflower (Helianthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	6
2227	Quantitative analysis of proteins secreted by Leishmania (Viannia) braziliensis strains associated to distinct clinical manifestations of American Tegumentary Leishmaniasis. Journal of Proteomics, 2021, 232, 104077.	1.2	10
2228	Genomic Insights Into the Lifestyles of Thaumarchaeota Inside Sponges. Frontiers in Microbiology, 2020, 11, 622824.	1.5	16
2229	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nature Biotechnology, 2021, 39, 578-585.	9.4	569
2230	Expansin Engineering Database: A navigation and classification tool for expansins and homologues. Proteins: Structure, Function and Bioinformatics, 2021, 89, 149-162.	1.5	9
2231	Genome-wide identification, evolution, expression, and alternative splicing profiles of peroxiredoxin genes in cotton. PeerJ, 2021, 9, e10685.	0.9	4
2232	Transcriptome characterization and generation of marker resource for Himalayan vulnerable species, Ulmus wallichiana. Molecular Biology Reports, 2021, 48, 721-729.	1.0	3
2233	Insights into structure and dynamics of extracellular domain of Toll-like receptor 5 in Cirrhinus mrigala (mrigala): A molecular dynamics simulation approach. PLoS ONE, 2021, 16, e0245358.	1.1	10
2234	The Nuclear Genome of Lingzhi Mushroom. Compendium of Plant Genomes, 2021, , 47-71.	0.3	0
2235	Conserved paradoxical relationships among the evolutionary, structural and expressional features of KRAB zinc-finger proteins reveal their special functional characteristics. BMC Molecular and Cell Biology, 2021, 22, 7.	1.0	7
2236	Bulinus truncatus transcriptome â€" a resource to enable molecular studies of snail and schistosome biology. Current Research in Parasitology and Vector-borne Diseases, 2021, 1, 100015.	0.7	5
2237	Complete Genome Sequencing of Acinetobacter baumannii AC1633 and Acinetobacter nosocomialis AC1530 Unveils a Large Multidrug-Resistant Plasmid Encoding the NDM-1 and OXA-58 Carbapenemases. MSphere, 2021, 6, .	1.3	14

#	ARTICLE	IF	CITATIONS
2239	Genome sequences of Tropheus moorii and Petrochromis trewavasae, two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. Scientific Reports, 2021, 11, 4309.	1.6	4
2240	Novel Two-Component System-Like Elements Reveal Functional Domains Associated with Restrictionâ€“Modification Systems and paraMORC ATPases in Bacteria. Genome Biology and Evolution, 2021, 13, .	1.1	4
2241	A de novo Transcriptome Assembly of the European Flounder (Platichthys flesus): The Preselection of Transcripts Encoding Active Forms of Enzymes. Frontiers in Marine Science, 2021, 8, .	1.2	5
2242	Genome-wide comparative analysis of Mg transporter gene family between Triticum turgidum and Camelina sativa. BioMetals, 2021, 34, 639-660.	1.8	20
2243	Use of Mathematical Methods for the Biosafety Assessment of Agricultural Crops. Applied Biochemistry and Microbiology, 2021, 57, 271-279.	0.3	2
2246	Genera specific distribution of DEAD-box RNA helicases in cyanobacteria. Microbial Genomics, 2021, 7, .	1.0	4
2247	Gene expression for secondary metabolite biosynthesis in hop (Humulus lupulus L.) leaf lupulin glands exposed to heat and low-water stress. Scientific Reports, 2021, 11, 5138.	1.6	16
2248	Transcriptomic Analysis of Seasonal Gene Expression and Regulation during Xylem Development in â€œShanxinâ€•Hybrid Poplar (Populus davidiana Ã— Populus bolleana). Forests, 2021, 12, 451.	0.9	5
2249	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
2250	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, .	3.3	18
2251	Activation mechanism of a small prototypic Rec-GGDEF diguanylate cyclase. Nature Communications, 2021, 12, 2162.	5.8	14
2252	Identification of biophysical interaction patterns in direct coupling analysis. Physical Review E, 2021, 103, 042418.	0.8	0
2253	The first inâ€depth exploration of the genome of the engineered bacterium, Gluconobacter thailandicus. Biotechnology and Applied Biochemistry, 2021, , .	1.4	1
2254	The cytochrome P450 (CYP) superfamily in cnidarians. Scientific Reports, 2021, 11, 9834.	1.6	7
2255	Genome-Wide Analysis of Potassium Channel Genes in Rice: Expression of the OsAKT and OsKAT Genes under Salt Stress. Genes, 2021, 12, 784.	1.0	49
2256	The Sugar Transporter family in wheat (<i>Triticum aestivum</i>. L): genome-wide identification, classification, and expression profiling during stress in seedlings. PeerJ, 2021, 9, e11371.	0.9	6
2257	New Insights Into Structure and Function of TIFY Genes in Zea mays and Solanum lycopersicum: A Genome-Wide Comprehensive Analysis. Frontiers in Genetics, 2021, 12, 657970.	1.1	31
2259	<i>cat</i>RAPID<i>omics v2.0</i>: going deeper and wider in the prediction of proteinâ€“RNA interactions. Nucleic Acids Research, 2021, 49, W72-W79.	6.5	79

#	Article	IF	Citations
2260	Identification and function analysis of fasciclin-like arabinogalactan protein family genes in pear (Pyrus bretschneideri). Plant Systematics and Evolution, 2021, 307, 1.	0.3	3
2261	Evaluation of Indigenous Olive Biocontrol Rhizobacteria as Protectants against Drought and Salt Stress. Microorganisms, 2021, 9, 1209.	1.6	8
2262	Characterization of expansin genes and their transcriptional regulation by histone modifications in strawberry. Planta, 2021, 254, 21.	1.6	8
2263	First Evidence of Function for Schistosoma japonicumriok-1 and RIOK-1. Pathogens, 2021, 10, 862.	1.2	3
2264	Using machine learning approaches for multi-omics data analysis: A review. Biotechnology Advances, 2021, 49, 107739.	6.0	277
2265	A fast protein binding site comparison algorithm for proteomeâ€wide protein function prediction and drug repurposing. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1541-1556.	1.5	9
2266	Dynamics of Baltic Sea phages driven by environmental changes. Environmental Microbiology, 2021, 23, 4576-4594.	1.8	5
2267	Genome-wide identification of alcohol dehydrogenase (ADH) gene family under waterlogging stress in wheat (<i>Triticum aestivum</i>). PeerJ, 2021, 9, e11861.	0.9	11
2268	AtPGAP1 functions as a GPI inositol-deacylase required for efficient transport of GPI-anchored proteins. Plant Physiology, 2021, 187, 2156-2173.	2.3	16
2269	Multistep Signaling in Nature: A Close-Up of Geobacter Chemotaxis Sensing. International Journal of Molecular Sciences, 2021, 22, 9034.	1.8	3
2270	Comparison of differential expression genes in ovaries and testes of Pearlscale angelfish Centropyge vrolikii based on RNA-Seq analysis. Fish Physiology and Biochemistry, 2021, 47, 1565-1583.	0.9	8
2271	Full-length transcriptome analysis of <i>Spodoptera frugiperda</i> larval brain reveals detoxification genes. PeerJ, 2021, 9, e12069.	0.9	6
2272	The genomic basis of army ant chemosensory adaptations. Molecular Ecology, 2021, 30, 6627-6641.	2.0	9
2274	Trends in the Application of â€œOmicsâ€• to Ecotoxicology and Stress Ecology. Genes, 2021, 12, 1481.	1.0	22
2275	Hidden service publishing flow homology comparison using profileâ€hidden markov model. International Journal of Intelligent Systems, 0, , .	3.3	1
2276	Systematic genome-wide analysis of the ethylene-responsive ACS gene family: Contributions to sex form differentiation and development in melon and watermelon. Gene, 2021, 805, 145910.	1.0	10
2277	Biochemical characterization of LysVpKK5 endolysin from a marine vibriophage. Protein Expression and Purification, 2021, 188, 105971.	0.6	2
2278	Comparative in silico analysis of phosphate transporter gene family, PHT, in Camelina sativa gemome. Gene Reports, 2021, 25, 101351.	0.4	2

#	ARTICLE	IF	CITATIONS
2279	ELIHKSIR Web Server: Evolutionary Links Inferred for Histidine Kinase Sensors Interacting with Response Regulators. Entropy, 2021, 23, 170.	1.1	4
2280	The Dfam community resource of transposable element families, sequence models, and genome annotations. Mobile DNA, 2021, 12, 2.	1.3	279
2281	antiSMASH. , 2012, , 1-6.		1
2282	Bioinformatics and Biochemical Methods to Study the Structural and Functional Elements of DEAD-Box RNA Helicases. Methods in Molecular Biology, 2015, 1259, 165-181.	0.4	5
2283	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. Methods in Molecular Biology, 2017, 1558, 127-138.	0.4	12
2284	Coevolutionary Analysis of Protein Sequences for Molecular Modeling. Methods in Molecular Biology, 2019, 2022, 379-397.	0.4	7
2285	Multiple Sequence Alignment with DIALIGN. Methods in Molecular Biology, 2014, 1079, 191-202.	0.4	7
2286	DisMeta: A Meta Server for Construct Design and Optimization. Methods in Molecular Biology, 2014, 1091, 3-16.	0.4	64
2287	Annotating Functional RNAs in Genomes Using Infernal. Methods in Molecular Biology, 2014, 1097, 163-197.	0.4	49
2288	Integrative Data-Mining Tools to Link Gene and Function. Methods in Molecular Biology, 2014, 1101, 43-66.	0.4	4
2289	Cell-Free Translation of Biofuel Enzymes. Methods in Molecular Biology, 2014, 1118, 71-95.	0.4	24
2290	Annotated Stochastic Context Free Grammars for Analysis and Synthesis of Proteins. Lecture Notes in Computer Science, 2011, , 77-88.	1.0	4
2291	Structure and Function of RNase H Enzymes. Nucleic Acids and Molecular Biology, 2011, , 299-317.	0.2	5
2292	Integrating Protein Family Sequence Similarities with Gene Expression to Find Signature Gene Networks in Breast Cancer Metastasis. Lecture Notes in Computer Science, 2011, , 247-259.	1.0	4
2293	Pyrenophora tritici-repentis: A Plant Pathogenic Fungus with Global Impact. , 2014, , 1-39.		20
2295	Transcription Factor Effector Domains. Sub-Cellular Biochemistry, 2011, 52, 261-277.	1.0	45
2296	Function and Evolution of C2H2 Zinc Finger Arrays. Sub-Cellular Biochemistry, 2011, 52, 75-94.	1.0	37
2297	Bioinformatics Tools for Predicting GPCR Gene Functions. Advances in Experimental Medicine and Biology, 2014, 796, 205-224.	0.8	5

#	ARTICLE	IF	CITATIONS
2298	Metagenomic Data Mining in Oil Spill Studies. , 2019, , 211-223.		2
2299	Chloroplast development at low temperature requires the pseudouridine synthase gene TCD3 in rice. Scientific Reports, 2020, 10, 8518.	1.6	14
2300	Approaches to Fungal Genome Annotation. Mycology, 2011, 2, 118-141.	2.0	109
2301	O-antigen biosynthesis gene clusters of Escherichia albertii: their diversity and similarity to Escherichia coli gene clusters and the development of an O-genotyping method. Microbial Genomics, 2019, 5, .	1.0	27
2302	Peptide-utilizing carbon starvation gene yjiY is required for flagella-mediated infection caused by Salmonella. Microbiology (United Kingdom), 2016, 162, 100-116.	0.7	17
2303	Lipoproteins of Enterococcus faecalis: bioinformatic identification, expression analysis and relation to virulence. Microbiology (United Kingdom), 2011, 157, 3001-3013.	0.7	34
2315	Transcription Factors, Gene Regulatory Networks and Agronomic Traits. Advances in Agroecology, 2011, , 65-94.	0.3	1
2316	Efficient Experimental Design and Analysis Strategies for the Detection of Differential Expression Using RNA-Sequencing. , 2014, , 279-310.		2
2317	A domain sequence approach to pangenomics: applications to Escherichia coli. F1000Research, 2012, 1, 19.	0.8	8
2318	A domain sequence approach to pangenomics: applications to Escherichia coli. F1000Research, 2012, 1, 19.	0.8	12
2319	Computational genome-wide identification of heat shock protein genes in the bovine genome. F1000Research, 2018, 7, 1504.	0.8	10
2320	Cocos: Constructing multi-domain protein phylogenies. PLOS Currents, 2011, 3, RRN1240.	1.4	1
2321	A Dynamic View of Domain-Motif Interactions. PLoS Computational Biology, 2012, 8, e1002341.	1.5	48
2322	Improvement in Protein Domain Identification Is Reached by Breaking Consensus, with the Agreement of Many Profiles and Domain Co-occurrence. PLoS Computational Biology, 2016, 12, e1005038.	1.5	38
2323	Oncodomains: A protein domain-centric framework for analyzing rare variants in tumor samples. PLoS Computational Biology, 2017, 13, e1005428.	1.5	25
2324	Contact- and Protein Transfer-Dependent Stimulation of Assembly of the Gliding Motility Machinery in Myxococcus xanthus. PLoS Genetics, 2015, 11, e1005341.	1.5	49
2325	Improved Microarray-Based Decision Support with Graph Encoded Interactome Data. PLoS ONE, 2010, 5, e10225.	1.1	6
2326	The Distribution of GYR- and YLP-Like Motifs in Drosophila Suggests a General Role in Cuticle Assembly and Other Protein-Protein Interactions. PLoS ONE, 2010, 5, e12536.	1.1	17

#	ARTICLE	IF	CITATIONS
2327	Machine Learning Methods for Prediction of CDK-Inhibitors. PLoS ONE, 2010, 5, e13357.	1.1	9
2328	Identification, Activity and Disulfide Connectivity of C-di-GMP Regulating Proteins in Mycobacterium tuberculosis. PLoS ONE, 2010, 5, e15072.	1.1	47
2329	Specificity of the E. coli LysR-Type Transcriptional Regulators. PLoS ONE, 2010, 5, e15189.	1.1	25
2330	A Mighty Small Heart: The Cardiac Proteome of Adult Drosophila melanogaster. PLoS ONE, 2011, 6, e18497.	1.1	81
2331	The Complete Genome Sequence of Fibrobacter succinogenes S85 Reveals a Cellulolytic and Metabolic Specialist. PLoS ONE, 2011, 6, e18814.	1.1	199
2332	Differential Control of Yersinia pestis Biofilm Formation In Vitro and in the Flea Vector by Two c-di-GMP Diguanylate Cyclases. PLoS ONE, 2011, 6, e19267.	1.1	82
2333	Involvement of a Toxoplasma gondii Chromatin Remodeling Complex Ortholog in Developmental Regulation. PLoS ONE, 2011, 6, e19570.	1.1	12
2334	Evaluating the Fidelity of De Novo Short Read Metagenomic Assembly Using Simulated Data. PLoS ONE, 2011, 6, e19984.	1.1	65
2335	Extending the Aerolysin Family: From Bacteria to Vertebrates. PLoS ONE, 2011, 6, e20349.	1.1	107
2336	Transcriptome Sequencing of the Blind Subterranean Mole Rat, Spalax galili: Utility and Potential for the Discovery of Novel Evolutionary Patterns. PLoS ONE, 2011, 6, e21227.	1.1	32
2337	Characterisation of a Desmosterol Reductase Involved in Phytosterol Dealkylation in the Silkworm, Bombyx mori. PLoS ONE, 2011, 6, e21316.	1.1	23
2338	New Structural and Functional Contexts of the Dx[DN]xDG Linear Motif: Insights into Evolution of Calcium-Binding Proteins. PLoS ONE, 2011, 6, e21507.	1.1	53
2339	Comparative Genomics of the Mating-Type Loci of the Mushroom Flammulina velutipes Reveals Widespread Synteny and Recent Inversions. PLoS ONE, 2011, 6, e22249.	1.1	54
2340	The Genome Sequence of the North-European Cucumber (Cucumis sativus L.) Unravels Evolutionary Adaptation Mechanisms in Plants. PLoS ONE, 2011, 6, e22728.	1.1	112
2341	Comprehensive Structural and Substrate Specificity Classification of the Saccharomyces cerevisiae Methyltransferome. PLoS ONE, 2011, 6, e23168.	1.1	50
2342	N-Termini of Fungal CSL Transcription Factors Are Disordered, Enriched in Regulatory Motifs and Inhibit DNA Binding in Fission Yeast. PLoS ONE, 2011, 6, e23650.	1.1	8
2343	Hydrophilic Aromatic Residue and in silico Structure for Carbohydrate Binding Module. PLoS ONE, 2011, 6, e24814.	1.1	6
2344	Identification of Plasmodium vivax Proteins with Potential Role in Invasion Using Sequence Redundancy Reduction and Profile Hidden Markov Models. PLoS ONE, 2011, 6, e25189.	1.1	10

#	ARTICLE	IF	CITATIONS
2345	Putting into Practice Domain-Linear Motif Interaction Predictions for Exploration of Protein Networks. PLoS ONE, 2011, 6, e25376.	1.1	37
2346	Bioinformatic Analysis of Pathogenic Missense Mutations of Activin Receptor Like Kinase 1 Ectodomain. PLoS ONE, 2011, 6, e26431.	1.1	14
2347	Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624.	1.1	75
2348	Whole-Genome Comparison of Two Campylobacter jejuni Isolates of the Same Sequence Type Reveals Multiple Loci of Different Ancestral Lineage. PLoS ONE, 2011, 6, e27121.	1.1	25
2349	Uncovering the Prevalence and Diversity of Integrating Conjugative Elements in Actinobacteria. PLoS ONE, 2011, 6, e27846.	1.1	56
2350	Comparative Genomic and Transcriptomic Characterization of the Toxigenic Marine Dinoflagellate Alexandrium ostenfeldii. PLoS ONE, 2011, 6, e28012.	1.1	92
2351	Active Site Detection by Spatial Conformity and Electrostatic Analysisâ€"Unravelling a Proteolytic Function in Shrimp Alkaline Phosphatase. PLoS ONE, 2011, 6, e28470.	1.1	41
2352	Protein 3D Structure Computed from Evolutionary Sequence Variation. PLoS ONE, 2011, 6, e28766.	1.1	975
2353	The Origin of GPCRs: Identification of Mammalian like Rhodopsin, Adhesion, Glutamate and Frizzled GPCRs in Fungi. PLoS ONE, 2012, 7, e29817.	1.1	152
2354	Bisulfite Sequencing Reveals That Aspergillus flavus Holds a Hollow in DNA Methylation. PLoS ONE, 2012, 7, e30349.	1.1	74
2355	Contribution of a Genomic Accessory Region Encoding a Putative Cellobiose Phosphotransferase System to Virulence of Streptococcus pneumoniae. PLoS ONE, 2012, 7, e32385.	1.1	27
2356	Membrane Topology and Predicted RNA-Binding Function of the â€˜Early Responsive to Dehydration (ERD4)â€™ Plant Protein. PLoS ONE, 2012, 7, e32658.	1.1	35
2357	The Natural Product Domain Seeker NaPDoS: A Phylogeny Based Bioinformatic Tool to Classify Secondary Metabolite Gene Diversity. PLoS ONE, 2012, 7, e34064.	1.1	422
2358	SH3 Domain Tyrosine Phosphorylation â€" Sites, Role and Evolution. PLoS ONE, 2012, 7, e36310.	1.1	30
2359	Characterization of Modular Bacteriophage Endolysins from Myoviridae Phages OBP, 201Ï†2-1 and PVP-SE1. PLoS ONE, 2012, 7, e36991.	1.1	109
2360	NMR Structure of Lipoprotein YxeF from Bacillus subtilis Reveals a Calycin Fold and Distant Homology with the Lipocalin Blc from Escherichia coli. PLoS ONE, 2012, 7, e37404.	1.1	6
2361	Predicting Inter-Species Cross-Talk in Two-Component Signalling Systems. PLoS ONE, 2012, 7, e37737.	1.1	2
2362	Collagen-Like Proteins in Pathogenic E. coli Strains. PLoS ONE, 2012, 7, e37872.	1.1	32

#	ARTICLE	IF	CITATIONS
2363	Flexibility in MuA Transposase Family Protein Structures: Functional Mapping with Scanning Mutagenesis and Sequence Alignment of Protein Homologues. PLoS ONE, 2012, 7, e37922.	1.1	5
2364	HEMD: An Integrated Tool of Human Epigenetic Enzymes and Chemical Modulators for Therapeutics. PLoS ONE, 2012, 7, e39917.	1.1	25
2365	Genes for the Major Structural Components of Thermotogales Speciesâ€™ Togas Revealed by Proteomic and Evolutionary Analyses of OmpA and OmpB Homologs. PLoS ONE, 2012, 7, e40236.	1.1	22
2366	GmcA Is a Putative Glucose-Methanol-Choline Oxidoreductase Required for the Induction of Asexual Development in Aspergillus nidulans. PLoS ONE, 2012, 7, e40292.	1.1	29
2367	Metagenomic Insights into the Fibrolytic Microbiome in Yak Rumen. PLoS ONE, 2012, 7, e40430.	1.1	98
2368	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	1.1	42
2369	Novel Insights into the Transcriptome of Dirofilaria immitis. PLoS ONE, 2012, 7, e41639.	1.1	15
2370	Increasing Coverage of Transcription Factor Position Weight Matrices through Domain-level Homology. PLoS ONE, 2012, 7, e42779.	1.1	8
2371	Susceptibility towards Enterotoxigenic Escherichia coli F4ac Diarrhea Is Governed by the MUC13 Gene in Pigs. PLoS ONE, 2012, 7, e44573.	1.1	70
2372	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.	1.1	43
2373	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	1.1	55
2374	Identification of Nucleotide-Binding Sites in Protein Structures: A Novel Approach Based on Nucleotide Modularity. PLoS ONE, 2012, 7, e50240.	1.1	6
2375	Genome-Wide Survey of Pseudogenes in 80 Fully Re-sequenced Arabidopsis thaliana Accessions. PLoS ONE, 2012, 7, e51769.	1.1	14
2376	Mining of Novel Thermo-Stable Cellulolytic Genes from a Thermophilic Cellulose-Degrading Consortium by Metagenomics. PLoS ONE, 2013, 8, e53779.	1.1	44
2377	Evolutionary, Structural and Functional Interplay of the IÎºB Family Members. PLoS ONE, 2013, 8, e54178.	1.1	30
2378	Signal Balancing by the CetABC and CetZ Chemoreceptors Controls Energy Taxis in Campylobacter jejuni. PLoS ONE, 2013, 8, e54390.	1.1	38
2379	Planarians as a Model to Assess In Vivo the Role of Matrix Metalloproteinase Genes during Homeostasis and Regeneration. PLoS ONE, 2013, 8, e55649.	1.1	38
2380	Reciprocal Influence of Protein Domains in the Cold-Adapted Acyl Aminoacyl Peptidase from Sporosarcina psychrophila. PLoS ONE, 2013, 8, e56254.	1.1	12

#	ARTICLE	IF	CITATIONS
2381	Predicting the Binding Patterns of Hub Proteins: A Study Using Yeast Protein Interaction Networks. PLoS ONE, 2013, 8, e56833.	1.1	13
2382	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. PLoS ONE, 2013, 8, e57848.	1.1	6
2383	Sequencing and Comparative Analysis of the Straw Mushroom (Volvariella volvacea) Genome. PLoS ONE, 2013, 8, e58294.	1.1	143
2384	CLCAs - A Family of Metalloproteases of Intriguing Phylogenetic Distribution and with Cases of Substituted Catalytic Sites. PLoS ONE, 2013, 8, e62272.	1.1	19
2385	Database Citation in Full Text Biomedical Articles. PLoS ONE, 2013, 8, e63184.	1.1	33
2386	Evolution of and Horizontal Gene Transfer in the Endornavirus Genus. PLoS ONE, 2013, 8, e64270.	1.1	24
2387	Drug Promiscuity in PDB: Protein Binding Site Similarity Is Key. PLoS ONE, 2013, 8, e65894.	1.1	129
2388	Systematic Mutational Analysis of the Putative Hydrolase PqsE: Toward a Deeper Molecular Understanding of Virulence Acquisition in Pseudomonas aeruginosa. PLoS ONE, 2013, 8, e73727.	1.1	13
2389	Elementary Flux Modes Analysis of Functional Domain Networks Allows a Better Metabolic Pathway Interpretation. PLoS ONE, 2013, 8, e76143.	1.1	5
2390	Protein Kinase C-Dependent Signaling Controls the Midgut Epithelial Barrier to Malaria Parasite Infection in Anopheline Mosquitoes. PLoS ONE, 2013, 8, e76535.	1.1	21
2391	Classification of Î±-Helical Membrane Proteins Using Predicted Helix Architectures. PLoS ONE, 2013, 8, e77491.	1.1	4
2392	Generalized Baum-Welch Algorithm Based on the Similarity between Sequences. PLoS ONE, 2013, 8, e80565.	1.1	3
2393	Snf2 Family Gene Distribution in Higher Plant Genomes Reveals DRD1 Expansion and Diversification in the Tomato Genome. PLoS ONE, 2013, 8, e81147.	1.1	9
2394	New Insights into Histidine Triad Proteins: Solution Structure of a Streptococcus pneumoniae PhtD Domain and Zinc Transfer to AdcAII. PLoS ONE, 2013, 8, e81168.	1.1	48
2395	Large Scale Identification and Categorization of Protein Sequences Using Structured Logistic Regression. PLoS ONE, 2014, 9, e85139.	1.1	12
2396	Strong Genome-Wide Selection Early in the Evolution of Prochlorococcus Resulted in a Reduced Genome through the Loss of a Large Number of Small Effect Genes. PLoS ONE, 2014, 9, e88837.	1.1	58
2397	Characterization of Human Papillomavirus Type 154 and Tissue Tropism of Gammapapillomaviruses. PLoS ONE, 2014, 9, e89342.	1.1	15
2398	Insights into the Origin of Nematode Chemosensory GPCRs: Putative Orthologs of the Srw Family Are Found across Several Phyla of Protostomes. PLoS ONE, 2014, 9, e93048.	1.1	26

#	ARTICLE	IF	CITATIONS
2399	Biochemical Properties and Atomic Resolution Structure of a Proteolytically Processed Î²-Mannanase from Cellulolytic Streptomyces sp. SirexAA-E. PLoS ONE, 2014, 9, e94166.	1.1	18
2400	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PilO2Bp S-SAD Crystal Structure. PLoS ONE, 2014, 9, e94981.	1.1	4
2401	De Novo Transcriptomes of a Mixotrophic and a Heterotrophic Ciliate from Marine Plankton. PLoS ONE, 2014, 9, e101418.	1.1	29
2402	Genome-Wide Identification and Expression Analysis of NBS-Encoding Genes in Malus x domestica and Expansion of NBS Genes Family in Rosaceae. PLoS ONE, 2014, 9, e107987.	1.1	80
2403	Evolutionary Strategies of Viruses, Bacteria and Archaea in Hydrothermal Vent Ecosystems Revealed through Metagenomics. PLoS ONE, 2014, 9, e109696.	1.1	72
2404	Early Chordate Origin of the Vertebrate Integrin Î±I Domains. PLoS ONE, 2014, 9, e112064.	1.1	7
2405	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from Mycobacterium tuberculosis. PLoS ONE, 2014, 9, e116249.	1.1	6
2406	In Silico Screening for Novel Inhibitors of DNA Polymerase III Alpha Subunit of Mycobacterium tuberculosis (MtbDnaE2, H37Rv). PLoS ONE, 2015, 10, e0119760.	1.1	15
2407	De novo Transcriptome Assembly and the Putative Biosynthetic Pathway of Steroidal Sapogenins of Dioscorea composita. PLoS ONE, 2015, 10, e0124560.	1.1	19
2408	Evolution of the SH3 Domain Specificity Landscape in Yeasts. PLoS ONE, 2015, 10, e0129229.	1.1	8
2409	Structure and Assembly of TP901-1 Virion Unveiled by Mutagenesis. PLoS ONE, 2015, 10, e0131676.	1.1	19
2410	Identification of VPS13C as a Galectin-12-Binding Protein That Regulates Galectin-12 Protein Stability and Adipogenesis. PLoS ONE, 2016, 11, e0153534.	1.1	35
2411	A Large and Phylogenetically Diverse Class of Type 1 Opsins Lacking a Canonical Retinal Binding Site. PLoS ONE, 2016, 11, e0156543.	1.1	11
2412	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. PLoS ONE, 2016, 11, e0159627.	1.1	5
2413	Comparative Genomics of Acetobacterpasteurianus Ab3, an Acetic Acid Producing Strain Isolated from Chinese Traditional Rice Vinegar Meiguichu. PLoS ONE, 2016, 11, e0162172.	1.1	12
2414	Differential Communications between Fungi and Host Plants Revealed by Secretome Analysis of Phylogenetically Related Endophytic and Pathogenic Fungi. PLoS ONE, 2016, 11, e0163368.	1.1	20
2415	DNA Barcodes for the Northern European Tachinid Flies (Diptera: Tachinidae). PLoS ONE, 2016, 11, e0164933.	1.1	20
2416	Identification and expression analyses of WRKY genes reveal their involvement in growth and abiotic stress response in watermelon (Citrullus lanatus). PLoS ONE, 2018, 13, e0191308.	1.1	61

#	Article	IF	Citations
2417	Multispecies reconstructions uncover widespread conservation, and lineage-specific elaborations in eukaryotic mRNA metabolism. PLoS ONE, 2018, 13, e0192633.	1.1	20
2418	Transcriptome analysis of wheat grain using RNA-Seq. Frontiers of Agricultural Science and Engineering, 2014, 1, 214.	0.9	8
2419	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.	0.6	5
2420	Metals from cell to environment: Connecting Metallomics with other omics. Open Journal of Plant Science, 0, , 001-014.	0.2	3
2421	Comprehensive transcriptional landscape of porcine cardiac and skeletal muscles reveals differences of aging. Oncotarget, 2018, 9, 1524-1541.	0.8	41
2422	Cloning of an <I>ABC1</I>-like Gene <I>ZmABC1-10</I> and Its Responses to Cadmium and Other Abiotic Stresses in Maize (<I>Zea mays</I> L.). Acta Agronomica Sinica(China), 2011, 36, 2073-2083.	0.1	1
2423	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. Standards in Genomic Sciences, 2013, 7, 382-398.	1.5	12
2424	Structure and Function of the Small MutS-Related Domain. Molecular Biology International, 2011, 2011, 1-9.	1.7	34
2425	iRhoms; Its Functions and Essential Roles. Biomolecules and Therapeutics, 2016, 24, 109-114.	1.1	13
2426	Collagen-Induced Arthritis Analysis in <i>Rhbdf2</i> Knockout Mouse. Biomolecules and Therapeutics, 2018, 26, 298-305.	1.1	9
2427	Genome sequencing and next-generation sequence data analysis: A comprehensive compilation of bioinformatics tools and databases. American Journal of Molecular Biology, 2013, 03, 115-130.	0.1	8
2428	Bioinformatic Game Theory and Its Application to Biological Affinity Networks. Applied Mathematics, 2013, 04, 92-108.	0.1	1
2429	Identification of a xylem sap germin-like protein and its expression under short-day and non-freezing low-temperature conditions in poplar root. Plant Biotechnology, 2016, 33, 123-127.	0.5	5
2430	Bioinformatic Identification of Rare Codon Clusters (RCCs) in HBV Genome and Evaluation of RCCs in Proteins Structure of Hepatitis B Virus. Hepatitis Monthly, 2016, 16, e39909.	0.1	12
2431	Homology modeling, comparative genomics and functional annotation of Mycoplasma genitalium hypothetical protein MG_237. Bioinformation, 2011, 7, 299-303.	0.2	14
2432	Prediction and analysis of paralogous proteins in Trichomonas vaginalis genome. Bioinformation, 2011, 6, 31-34.	0.2	9
2433	An alignment-free domain architecture similarity search (ADASS) algorithm for inferring homology between multi-domain proteins. Bioinformation, 2013, 9, 491-499.	0.2	11
2434	Structure and functional annotation of hypothetical proteins having putative Rubisco activase function from Vitis vinifera. Bioinformation, 2015, 11, 11-16.	0.2	5

#	Article	IF	Citations
2435	Characterizing protein domain associations by Small-molecule ligand binding. Journal of Proteome Science and Computational Biology, 2012, 1, 6.	1.0	5
2436	Annotation of glycoside hydrolases in Sorghum bicolor using proteins interaction approach. Journal of Proteome Science and Computational Biology, 2013, 2, 2.	1.0	6
2437	A deletion polymorphism in the Caenorhabditis elegans RIG-I homolog disables viral RNA dicing and antiviral immunity. ELife, 2013, 2, e00994.	2.8	156
2438	Mapping and analysis of Caenorhabditis elegans transcription factor sequence specificities. ELife, 2015, 4, .	2.8	85
2439	Dynamics of venom composition across a complex life cycle. ELife, 2018, 7, .	2.8	83
2440	<i>Burkholderia pseudomallei</i>type III secreted protein BipC: role in actin modulation and translocation activities required for the bacterial intracellular lifecycle. PeerJ, 2016, 4, e2532.	0.9	6
2441	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. PeerJ, 2016, 4, e2620.	0.9	37
2442	Genome-wide identification of CBL family and expression analysis of <i>CBLs</i> in response to potassium deficiency in cotton. PeerJ, 2017, 5, e3653.	0.9	36
2443	Genome-wide identification of the<i>MADS-box</i>transcription factor family in pear (<i>Pyrus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4	0.9	38
2444	Genome-wide identification and characterization of GRAS transcription factors in tomato (<i>Solanum lycopersicum</i>). PeerJ, 2017, 5, e3955.	0.9	50
2445	Comprehensive transcriptional profiling of aging porcine liver. PeerJ, 2019, 7, e6949.	0.9	6
2446	Cyclic nucleotide binding and structural changes in the isolated GAF domain of<i>Anabaena</i>adenylyl cyclase, CyaB2. PeerJ, 2015, 3, e882.	0.9	26
2447	Genome-wide identification and characterization of TCP family genes in <i>Brassica juncea</i> var. tumida. PeerJ, 2020, 8, e9130.	0.9	11
2448	Bioinformatics Resources of the Korean Bioinformation Center (KOBIC). Genomics and Informatics, 2010, 8, 165-169.	0.4	0
2449	In Silico Identification of Novel G Protein-Coupled Receptors. Neuromethods, 2011, , 3-18.	0.2	0
2450	TransDomain: A Transitive Domain-Based Method in Proteinâ€“Protein Interaction Prediction. Lecture Notes in Computer Science, 2011, , 240-252.	1.0	0
2451	Omega Loops of Proteins in Homo Sapiens: Role in Diseases. Communications in Computer and Information Science, 2011, , 362-367.	0.4	0
2454	Function Prediction of Genes: From Molecular Function to Cellular Function. , 2011, , 197-214.		0

#	ARTICLE	IF	CITATIONS
2455	Expressed Sequence Tag Analysis of the Erythrocytic Stage ofPlasmodium berghei. Korean Journal of Parasitology, 2011, 49, 221.	0.5	0
2456	Solution Structure of Water-soluble Mutant of Crambin and Implication for Protein Solubility. Bulletin of the Korean Chemical Society, 2011, 32, 1640-1644.	1.0	1
2457	Basics of the Cytoskeleton: Myosins. , 2012, , 73-100.		0
2458	Aligning Discovered Patterns from Protein Family Sequences. Lecture Notes in Computer Science, 2012, , 243-254.	1.0	0
2459	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
2461	Functional Annotation. Chapman & Hall/CRC Mathematical and Computational Biology Series, 2012, , .	0.1	0
2463	Taxonomic Classification of Metagenomic Shotgun Sequences with CARMA3. , 2013, , 1-8.		0
2464	Variable Selection to Improve Classification of Metagenomes. , 2013, , 1-9.		0
2465	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.	0.8	0
2466	A fragmented alignment method detects a putative phosphorylation site and a putative BRC repeat in the Drosophila melanogaster BRCA2 protein. F1000Research, 2013, 2, 143.	0.8	2
2467	Sequence analysis, structure and binding site prediction of Sigma 1 receptor protein by in silico method. Bioinformation, 2013, 9, 944-951.	0.2	0
2468	PCR Amplification, Sequencing, and In Silico Characterization of Pectin Lyase Genes from Aspergillus flavus NIICC8142. , 2014, , 413-421.		2
2469	Transparent Incremental Updates for Genomics Data Analysis Pipelines. Lecture Notes in Computer Science, 2014, , 311-320.	1.0	5
2470	The Courseâ€™s SIB Libraries. Communications in Computer and Information Science, 2014, , 30-44.	0.4	0
2471	Persistence and Antigenic Variation. , 0, , 366-390.		0
2472	Predicting Protein Functions Based on Dynamic Protein Interaction Networks. Lecture Notes in Computer Science, 2015, , 390-401.	1.0	1
2473	Structural Annotation of the Mycobacterium tuberculosis Proteome. , 0, , 261-280.		0
2475	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. , 2016, , 137-165.		0

#	Article	IF	Citations
2480	Storage Size Estimation for Schemaless Big Data Applications: A JSON-Based Overview. Lecture Notes in Networks and Systems, 2018, , 315-323.	0.5	0
2482	Genome-Wide Identification, Classification and Evolutionary Expansion of KNOX Gene Family in Rice (&lt;i&gt;Oryza sativa&lt;/i&gt;) and &lt;i&gt;Populus&lt;/i&gt; (&lt;i&gt;Populustrichocarpa&lt;/i&gt;). American Journal of Plant Sciences, 2018, 09, 1071-1092.	0.3	7
2483	Reef-Building Corals as a Tool for Climate Change Research in the Genomics Era. Results and Problems in Cell Differentiation, 2018, 65, 529-546.	0.2	3
2491	Categorizing Molecular Features of NOTCH4 Involved in Breast Cancer. International Journal of Scientific Research in Science and Technology, 2019, , 408-413.	0.1	0
2503	Genome-Wide Identification, Characterization and Expression Profiling of Aluminum-Activated Malate Transporters in Eriobotrya japonica Lindl.. Horticulturae, 2021, 7, 441.	1.2	13
2505	An In Silico Approach for Function Prediction of Hypothetical Proteins of Listeria monocytogenes. SSRN Electronic Journal, 0, , .	0.4	2
2507	Bioinformatic-Based Approaches for Disease-Resistance Gene Discovery in Plants. Agronomy, 2021, 11, 2259.	1.3	3
2508	How to resist soil desiccation: Transcriptional changes in a Mediterranean earthworm during aestivation. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2022, 264, 111112.	0.8	5
2509	Evolutionary history of dimethylsulfoniopropionate (DMSP) demethylation enzyme DmdA in marine bacteria. PeerJ, 2020, 8, e9861.	0.9	4
2510	The hypothetical periplasmic protein PA1624 from<i>Pseudomonas aeruginosa</i>folds into a unique two-domain structure. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 609-615.	0.4	1
2511	Intrinsic disorder within and flanking the DNA-binding domains of human transcription factors. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 104-15.	0.7	17
2512	Fungal genome resources at NCBI. Mycology, 2011, 2, 142-160.	2.0	5
2514	Assessment of vocation of rifabutin and rifapentine in replace of rifampcin in drug resistance leprosy patients: a molecular simulation study. Molecular Biology Research Communications, 2017, 6, 113-122.	0.2	1
2515	Current trends in algal biotechnology for the generation of sustainable biobased products. , 2022, , 213-239.		1
2516	Centromere-Specific Retrotransposons and Very-Long-Chain Fatty Acid Biosynthesis in the Genome of Yellowhorn (Xanthoceras sorbifolium, Sapindaceae), an Oil-Producing Tree With Significant Drought Resistance. Frontiers in Plant Science, 2021, 12, 766389.	1.7	6
2517	Integrative genome, transcriptome, microRNA, and degradome analysis of water dropwort (Oenanthe) Tj ETQq1 1 0.784314 rgBT /Overl	2.9	31
2518	Recurrent expansions of B30.2-associated immune receptor families in fish. Immunogenetics, 2022, 74, 129-147.	1.2	6
2519	Proteomic characterization of pilot scale hot-water extracts from the industrial carrageenan red seaweed Eucheuma denticulatum. Algal Research, 2022, 62, 102619.	2.4	11

#	Article	IF	Citations
2520	Physiological, Biochemical and Transcriptomic Analysis of the Aerial Parts (Leaf-Blade and Petiole) of Asarum sieboldii Responding to Drought Stress. International Journal of Molecular Sciences, 2021, 22, 13402.	1.8	1
2521	Transcription Factor RrANT1 of Rosa rugosa Positively Regulates Flower Organ Size in Petunia hybrida. International Journal of Molecular Sciences, 2022, 23, 1236.	1.8	0
2522	Characterizing the oral and distal gut microbiota of the threatened southern sea otter (<i>Enhydra) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	7
2524	Transcriptome Analysis and Functional Validation Identify a Putative bZIP Transcription Factor, Fpkapc, that Regulates Development, Stress Responses, and Virulence in <i>Fusarium pseudograminearum</i>. Phytopathology, 2022, 112, 1299-1309.	1.1	6
2525	A quinoprotein dehydrogenase from Pelagibacterium halotolerans ANSP101 oxidizes deoxynivalenol to 3-keto-deoxynivalenol. Food Control, 2022, 136, 108834.	2.8	15
2526	Isolation, Characterization and Draft Genome Analysis of Bacteriophages Infecting Acidovorax citrulli. Frontiers in Microbiology, 2021, 12, 803789.	1.5	3
2528	Genome-Wide In Silico Analysis and Expression Profiling of Phosphoenolpyruvate Carboxylase Genes in Loquat, Apple, Peach, Strawberry and Pear. Agronomy, 2022, 12, 25.	1.3	7
2530	Genome-Wide Analysis of Late Embryogenesis Abundant Protein Gene Family in Vigna Species and Expression of VrLEA Encoding Genes in Vigna glabrescens Reveal Its Role in Heat Tolerance. Frontiers in Plant Science, 2022, 13, 843107.	1.7	9
2531	Partially Resistant Avocado Rootstock DusaÂ® Shows Prolonged Upregulation of Nucleotide Binding-Leucine Rich Repeat Genes in Response to Phytophthora cinnamomi Infection. Frontiers in Plant Science, 2022, 13, 793644.	1.7	6
2532	Genome-wide identification, characterization of expansin gene family of banana and their expression pattern under various stresses. 3 Biotech, 2022, 12, 101.	1.1	1
2533	Effects of neonatal methoxychlor exposure on the ovarian transcriptome in piglets. Animal Reproduction Science, 2022, 238, 106956.	0.5	2
2534	Identification of TIFY gene family in walnut and analysis of its expression under abiotic stresses. BMC Genomics, 2022, 23, 190.	1.2	6
2535	Snake Venomics: Fundamentals, Recent Updates, and a Look to the Next Decade. Toxins, 2022, 14, 247.	1.5	19
2536	AU-Rich Element RNA Binding Proteins: At the Crossroads of Post-Transcriptional Regulation and Genome Integrity. International Journal of Molecular Sciences, 2022, 23, 96.	1.8	19
2537	Unique roles of vaginal Megasphaera phylotypes in reproductive health. Microbial Genomics, 2021, 7, .	1.0	6
2538	High Molecular Weight Kininogen: A Review of the Structural Literature. International Journal of Molecular Sciences, 2021, 22, 13370.	1.8	15
2539	Phylogenetic Analysis with Prediction of Cofactor or Ligand Binding for Pseudomonas aeruginosa PAS and Cache Domains. Microbiology Spectrum, 2021, 9, e0102621.	1.2	4
2540	Mutations in PpAGO3 Lead to Enhanced Virulence of Phytophthora parasitica by Activation of 25â€“26â€‰nt sRNA-Associated Effector Genes. Frontiers in Microbiology, 2022, 13, 856106.	1.5	0

#	ARTICLE	IF	CITATIONS
2541	Cisplatin resistance-related multi-omics differences and the establishment of machine learning models. Journal of Translational Medicine, 2022, 20, 171.	1.8	18
2542	Genome-wide analysis and functional characterization of CHYR gene family associated with abiotic stress tolerance in bread wheat (Triticum aestivum L.). BMC Plant Biology, 2022, 22, 204.	1.6	8
2618	Analysis of the Î²-Glucosidase Family Reveals Genes Involved in the Lignification of Stone Cells in Chinese White Pear (Pyrus bretschneideri Rehd.). Frontiers in Plant Science, 2022, 13, .	1.7	2
2619	Recent advances in immobilized Ï‰-transaminase for chiral amine synthesis. Materials Today Chemistry, 2022, 24, 100922.	1.7	5
2620	HDACs Gene Family Analysis of Eight Rosaceae Genomes Reveals the Genomic Marker of Cold Stress in Prunus mume. International Journal of Molecular Sciences, 2022, 23, 5957.	1.8	7
2621	Performance assessment of genomic island prediction tools with an improved version of Design-Island. Computational Biology and Chemistry, 2022, 98, 107698.	1.1	1
2622	Genome-Wide Identification and Expression Pattern Analysis of KNOX Gene Family in Orchidaceae. Frontiers in Plant Science, 2022, 13, .	1.7	12
2623	Comparative Transcriptomics and Metabolites Analysis of Two Closely Related Euphorbia Species Reveal Environmental Adaptation Mechanism and Active Ingredients Difference. Frontiers in Plant Science, 2022, 13, .	1.7	5
2624	Exploring the SiCCT Gene Family and Its Role in Heading Date in Foxtail Millet. Frontiers in Plant Science, 0, 13, .	1.7	0
2625	Genome-wide identification, expression and evolution analysis of OVATE family proteins in cotton (Gossypium spp.). Gene, 2022, 834, 146653.	1.0	1
2626	Genome assembly provided new insights into the Cinnamomum burmannii evolution and D-borneol biosynthesis differences between chemotypes. Industrial Crops and Products, 2022, 186, 115181.	2.5	6
2627	Chromosome-level assembly and analysis of the Thymus genome provide insights into glandular secretory trichome formation and monoterpenoid biosynthesis in thyme. Plant Communications, 2022, 3, 100413.	3.6	20
2628	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. Genes, 2022, 13, 1464.	1.0	1
2629	<i>In silico</i> subtractive genomics approach characterizes a hypothetical protein (MG_476) from <i>microplasma genitalium</i> G37. Journal of Clinical and Experimental Investigations, 2022, 13, em00805.	0.1	0
2632	Genome-Wide Identification, In Silico Analysis and Expression Profiling of SWEET Gene Family in Loquat (Eriobotrya japonica Lindl.). Agriculture (Switzerland), 2022, 12, 1312.	1.4	6
2633	Transcriptomic Analysis of Radish (Raphanus sativus L.) Roots with CLE41 Overexpression. Plants, 2022, 11, 2163.	1.6	4
2634	A Plasmid Carrying blaIMP-56 in Pseudomonas aeruginosa Belonging to a Novel Resistance Plasmid Family. Microorganisms, 2022, 10, 1863.	1.6	3
2635	Development of de-novo transcriptome assembly and SSRs in allohexaploid Brassica with functional annotations and identification of heat-shock proteins for thermotolerance. Frontiers in Genetics, 0, 13, .	1.1	2

#	Article	IF	Citations
2636	Investigating NAC Transcription Factor Role in Redox Homeostasis in Solanum lycopersicum L.: Bioinformatics, Physiological and Expression Analysis under Drought Stress. Plants, 2022, 11, 2930.	1.6	1
2637	Expansion and Neofunctionalization of Actinoporin-like Genes in Mediterranean Mussel (<i>Mytilus) Tj ETQq1 1 0.784314 rgBT /Overl	1.1	1
2639	ROS generated from biotic stress: Effects on plants and alleviation by endophytic microbes. Frontiers in Plant Science, 0, 13, .	1.7	44
2640	SNP-based high-density linkage map construction and QTL mapping of black spot disease resistance in Chinese sand pear. Journal of Applied Genetics, 0, , .	1.0	0
2641	Transcriptome and Regional Association Analyses Reveal the Effects of Oleosin Genes on the Accumulation of Oil Content in Brassica napus. Plants, 2022, 11, 3140.	1.6	5
2642	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. Communications Biology, 2022, 5, .	2.0	3
2643	Functional regulation of Responsive to abscisic acid (Rab) genes from representative plant species and their stress response. Plant Physiology Reports, 2022, 27, 653-664.	0.7	3
2644	Rice TCD8 Encoding a Multi-Domain GTPase Is Crucial for Chloroplast Development of Early Leaf Stage at Low Temperatures. Biology, 2022, 11, 1738.	1.3	0
2645	Population diversity analyses provide insights into key horticultural traits of Chinese native thymes. Horticulture Research, 2023, 10, .	2.9	2
2646	Integrative omics analyses of the ligninolytic Rhodosporidium fluviale LM-2 disclose catabolic pathways for biobased chemical production. , 2023, 16, .		2
2647	Identification of drug and protein-protein interaction network among stress and depression: A bioinformatics approach. Informatics in Medicine Unlocked, 2023, 37, 101174.	1.9	7
2648	Genome-wide identification and analysis of TCP transcription factor genes in <i>Rosa chinensis</i> in response to abiotic stress and fungal diseases. Ornamental Plant Research, 2023, 3, 1-11.	0.2	0
2649	Genome-Wide Prediction of Disease Resistance Gene Analogs in Flax. Compendium of Plant Genomes, 2023, , 217-233.	0.3	0
2650	The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in Arabidopsis thaliana. International Journal of Molecular Sciences, 2023, 24, 3580.	1.8	1
2651	An evolutionarily conserved bimodular domain anchors ZC3HC1 and its yeast homologue Pml39p to the nuclear basket. Molecular Biology of the Cell, 2023, 34, .	0.9	1
2652	Multifaceted functions of RNA-binding protein vigilin in gene silencing, genome stability, and autism-related disorders. Journal of Biological Chemistry, 2023, 299, 102988.	1.6	2
2653	The Bcl-2-associated athanogene gene family in tobacco (Nicotiana tabacum) and the function of NtBAG5 in leaf senescence. Frontiers in Plant Science, 0, 14, .	1.7	0
2654	HuCoPIA: An Atlas of Human vs. SARS-CoV-2 Interactome and the Comparative Analysis with Other Coronaviridae Family Viruses. Viruses, 2023, 15, 492.	1.5	1

#	ARTICLE	IF	CITATIONS
2655	Genome-Wide Identification, Classification, and Expression Analyses of the CsDGAT Gene Family in Cannabis sativa L. and Their Response to Cold Treatment. International Journal of Molecular Sciences, 2023, 24, 4078.	1.8	1
2656	Genome-wide identification and expression analysis of the <i>CHYR</i> gene family in <i>Phaseolus vulgaris</i> under abiotic stress at the seeding stage. Journal of Plant Interactions, 2023, 18, .	1.0	0
2657	Data-driven design of orthogonal protein-protein interactions. Science Signaling, 2023, 16, .	1.6	0
2658	Genomic Analysis, Evolution and Characterization of E3 Ubiquitin Protein Ligase (TRIM) Gene Family in Common Carp (Cyprinus carpio). Genes, 2023, 14, 667.	1.0	0
2659	The first chromosome-level <i>Fallopia multiflora</i> genome assembly provides insights into stilbene biosynthesis. Horticulture Research, 2023, 10, .	2.9	1
2660	Antibiotic resistance in Neisseria gonorrhoeae: broad-spectrum drug target identification using subtractive genomics. Genomics and Informatics, 2023, 21, e5.	0.4	1
2661	Omics-assisted characterization of two-component system genes from Gossypium Raimondii in response to salinity and molecular interaction with abscisic acid. Frontiers in Plant Science, 0, 14, .	1.7	1
2686	Bioinformatics Databases. Interdisciplinary Applied Mathematics, 2023, , 13-25.	0.2	0
2693	Mining bioparts for the biosynthesis of plant-derived bioactive compounds via omics and bioinformatics technologies. , 2024, , 1-32.		0