

The Pfam protein families database

Nucleic Acids Research

40, D290-D301

DOI: [10.1093/nar/gkr1065](https://doi.org/10.1093/nar/gkr1065)

Citation Report

#	ARTICLE	IF	CITATIONS
2	Adding unaligned sequences into an existing alignment using MAFFT and LAST. <i>Bioinformatics</i> , 2012, 28, 3144-3146.	1.8	217
3	Genome Reduction and Co-evolution between the Primary and Secondary Bacterial Symbionts of Psyllids. <i>Molecular Biology and Evolution</i> , 2012, 29, 3781-3792.	3.5	175
4	The Arabidopsis HEI10 Is a New ZMM Protein Related to Zip3. <i>PLoS Genetics</i> , 2012, 8, e1002799.	1.5	208
5	Proteins of Unknown Function in the Protein Data Bank (PDB): An Inventory of True Uncharacterized Proteins and Computational Tools for Their Analysis. <i>International Journal of Molecular Sciences</i> , 2012, 13, 12761-12772.	1.8	41
6	CombFunc: predicting protein function using heterogeneous data sources. <i>Nucleic Acids Research</i> , 2012, 40, W466-W470.	6.5	63
7	Loss of the DnaK-DnaJ-GrpE Chaperone System among the Aquificales. <i>Molecular Biology and Evolution</i> , 2012, 29, 3485-3495.	3.5	31
8	Side-chain rotamer changes upon ligand binding: common, crucial, correlate with entropy and rearrange hydrogen bonding. <i>Bioinformatics</i> , 2012, 28, i423-i430.	1.8	61
9	Draft Genome Sequence of <i>Brevibacterium massiliense</i> Strain 541308T. <i>Journal of Bacteriology</i> , 2012, 194, 5151-5152.	1.0	7
10	OrySPSSP: a comparative Platform for Small Secreted Proteins from rice and other plants. <i>Nucleic Acids Research</i> , 2012, 41, D1192-D1198.	6.5	18
11	A Global Comparison of the Human and <i>T. brucei</i> Degradomes Gives Insights about Possible Parasite Drug Targets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1942.	1.3	3
12	Draft Genome Sequence of <i>Actinomyces massiliensis</i> Strain 4401292T. <i>Journal of Bacteriology</i> , 2012, 194, 5121-5121.	1.0	4
13	Genome-Wide Identification and in Silico Analysis of Poplar Peptide Deformylases. <i>International Journal of Molecular Sciences</i> , 2012, 13, 5112-5124.	1.8	4
14	ProteinHistorian: Tools for the Comparative Analysis of Eukaryote Protein Origin. <i>PLoS Computational Biology</i> , 2012, 8, e1002567.	1.5	89
15	State of the Art in Silico Tools for the Study of Signaling Pathways in Cancer. <i>International Journal of Molecular Sciences</i> , 2012, 13, 6561-6581.	1.8	4
16	Eleven diverse nuclear-encoded phylogenetic markers for the subfamily Panicoideae (Poaceae). <i>American Journal of Botany</i> , 2012, 99, e443-6.	0.8	7
17	The Csr/Rsm system of <i>Yersinia</i> and related pathogens. <i>RNA Biology</i> , 2012, 9, 379-391.	1.5	87
18	A Response Regulator Interfaces between the Frz Chemosensory System and the MglA/MglB GTPase/GAP Module to Regulate Polarity in <i>Myxococcus xanthus</i> . <i>PLoS Genetics</i> , 2012, 8, e1002951.	1.5	60
19	Structure of the <i>Plasmodium</i> 6-cysteine s48/45 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6692-6697.	3.3	69

#	ARTICLE	IF	CITATIONS
20	Genome Sequence of <i>Rickettsia conorii</i> subsp. <i>caspia</i> , the Agent of Astrakhan Fever. <i>Journal of Bacteriology</i> , 2012, 194, 4763-4764.	1.0	6
21	Heptahelical protein PQLC2 is a lysosomal cationic amino acid exporter underlying the action of cysteamine in cystinosis therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3434-43.	3.3	138
22	Genome Sequence of <i>Reyranella massiliensis</i> , a Bacterium Associated with Amoebae. <i>Journal of Bacteriology</i> , 2012, 194, 5698-5698.	1.0	6
23	Genomic Comparison of <i>Rickettsia helvetica</i> and Other <i>Rickettsia</i> Species. <i>Journal of Bacteriology</i> , 2012, 194, 2751-2751.	1.0	9
24	NPIDB: nucleic acid-protein interaction database. <i>Nucleic Acids Research</i> , 2012, 41, D517-D523.	6.5	55
25	AntiFam: a tool to help identify spurious ORFs in protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas003-bas003.	1.4	38
26	GenColors-based comparative genome databases for small eukaryotic genomes. <i>Nucleic Acids Research</i> , 2012, 41, D692-D699.	6.5	7
27	Structural study of MCP1P1 N-terminal conserved domain reveals a PIN-like RNase. <i>Nucleic Acids Research</i> , 2012, 40, 6957-6965.	6.5	73
28	TIGRFAMs and Genome Properties in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D387-D395.	6.5	484
29	Multidomain Carbohydrate-binding Proteins Involved in <i>Bacteroides thetaiotaomicron</i> Starch Metabolism. <i>Journal of Biological Chemistry</i> , 2012, 287, 34614-34625.	1.6	93
30	Genome Sequence of <i>Legionella tunisiensis</i> Strain LegM ^T , a New <i>Legionella</i> Species Isolated from Hypersaline Lake Water. <i>Journal of Bacteriology</i> , 2012, 194, 5978-5978.	1.0	4
31	Genomic Comparison of <i>Kingella kingae</i> Strains. <i>Journal of Bacteriology</i> , 2012, 194, 5972-5972.	1.0	12
32	N-Acetylgalactosamine Utilization Pathway and Regulon in Proteobacteria. <i>Journal of Biological Chemistry</i> , 2012, 287, 28047-28056.	1.6	30
33	RNApathwaysDB—a database of RNA maturation and decay pathways. <i>Nucleic Acids Research</i> , 2012, 41, D268-D272.	6.5	9
34	ESTHER, the database of the Î±/Î²-hydrolase fold superfamily of proteins: tools to explore diversity of functions. <i>Nucleic Acids Research</i> , 2012, 41, D423-D429.	6.5	244
35	MoNetFamily: a web server to infer homologous modules and module-module interaction networks in vertebrates. <i>Nucleic Acids Research</i> , 2012, 40, W263-W270.	6.5	15
36	Role of ATG8 and Autophagy in Programmed Nuclear Degradation in <i>Tetrahymena thermophila</i> . <i>Eukaryotic Cell</i> , 2012, 11, 494-506.	3.4	50
37	SANS: high-throughput retrieval of protein sequences allowing 50% mismatches. <i>Bioinformatics</i> , 2012, 28, i438-i443.	1.8	22

#	ARTICLE	IF	CITATIONS
38	ChromoHub: a data hub for navigators of chromatin-mediated signalling. <i>Bioinformatics</i> , 2012, 28, 2205-2206.	1.8	82
39	Genome Sequence of <i>Rickettsia conorii</i> subsp. <i>israelensis</i> , the Agent of Israeli Spotted Fever. <i>Journal of Bacteriology</i> , 2012, 194, 5130-5131.	1.0	9
40	Identification of Cj1051c as a Major Determinant for the Restriction Barrier of <i>Campylobacter jejuni</i> Strain NCTC11168. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7841-7848.	1.4	29
41	Genome Sequence of <i>Rickettsia conorii</i> subsp. <i>indica</i> , the Agent of Indian Tick Typhus. <i>Journal of Bacteriology</i> , 2012, 194, 3288-3289.	1.0	15
42	Draft Genome Sequence of <i>Staphylococcus massiliensis</i> Strain 5402776 ^T . <i>Journal of Bacteriology</i> , 2012, 194, 6984-6985.	1.0	1
43	SIFTS: Structure Integration with Function, Taxonomy and Sequences resource. <i>Nucleic Acids Research</i> , 2012, 41, D483-D489.	6.5	238
44	Sequence, structure and functional diversity of PD-(D/E)XK phosphodiesterase superfamily. <i>Nucleic Acids Research</i> , 2012, 40, 7016-7045.	6.5	122
45	Complete Genome Sequence of the Giant <i>Pseudomonas</i> Phage Lu11. <i>Journal of Virology</i> , 2012, 86, 6369-6370.	1.5	25
46	Assignment of protein sequences to existing domain and family classification systems: Pfam and the PDB. <i>Bioinformatics</i> , 2012, 28, 2763-2772.	1.8	56
47	Extensive evolutionary and functional diversity among mammalian AIM2-like receptors. <i>Journal of Experimental Medicine</i> , 2012, 209, 1969-1983.	4.2	200
48	Functional prediction and physiological characterization of a novel short trans-membrane protein 1 as a subunit of mitochondrial respiratory complexes. <i>Physiological Genomics</i> , 2012, 44, 1133-1140.	1.0	16
49	Minireview: Progress and Challenges in Proteomics Data Management, Sharing, and Integration. <i>Molecular Endocrinology</i> , 2012, 26, 1660-1674.	3.7	10
50	PseudoDomain. , 2012, , .		0
51	The RCSB Protein Data Bank: new resources for research and education. <i>Nucleic Acids Research</i> , 2012, 41, D475-D482.	6.5	418
52	Activity of the Osmotically Regulated <i>yqiH</i> Promoter from <i>Bacillus subtilis</i> Is Controlled at a Distance. <i>Journal of Bacteriology</i> , 2012, 194, 5197-5208.	1.0	13
53	Crystal structure of LpxK, the 4 ϵ -kinase of lipid A biosynthesis and atypical P-loop kinase functioning at the membrane interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12956-12961.	3.3	17
54	The <i>Saccharomyces cerevisiae</i> Actin Patch Protein App1p Is a Phosphatidate Phosphatase Enzyme. <i>Journal of Biological Chemistry</i> , 2012, 287, 40186-40196.	1.6	48
55	Sequence and Annotation of <i>Rickettsia sibirica</i> Genome. <i>Journal of Bacteriology</i> , 2012, 194, 2377-2377.	1.0	7

#	ARTICLE	IF	CITATIONS
56	Complete Genome Sequence of Marinomonas Bacteriophage P12026. Journal of Virology, 2012, 86, 8909-8910.	1.5	11
57	Genome Sequence of Afipia birgiae, a Rare Bacterium Associated with Amoebae. Journal of Bacteriology, 2012, 194, 7018-7018.	1.0	3
58	Genome Sequence of Diplorickettsia massiliensis, an Emerging Ixodes ricinus-Associated Human Pathogen. Journal of Bacteriology, 2012, 194, 3287-3287.	1.0	9
59	An adaptation of Pfam profiles to predict protein sub-cellular localization in Gram positive bacteria. , 2012, 2012, 5554-7.		4
60	Diversity in the Protein N-Glycosylation Pathways Within the Campylobacter Genus. Molecular and Cellular Proteomics, 2012, 11, 1203-1219.	2.5	84
61	Activation of the Carbon Concentrating Mechanism by CO ₂ Deprivation Coincides with Massive Transcriptional Restructuring in <i>Chlamydomonas reinhardtii</i> . Plant Cell, 2012, 24, 1860-1875.	3.1	121
62	Evolution of the FGF Gene Family. International Journal of Evolutionary Biology, 2012, 2012, 1-12.	1.0	42
63	Genomic Analysis of Rickettsia japonica Strain YH ^T . Journal of Bacteriology, 2012, 194, 6992-6992.	1.0	5
64	PDBTM: Protein Data Bank of transmembrane proteins after 8 years. Nucleic Acids Research, 2012, 41, D524-D529.	6.5	245
65	Structure and Location of the Regulatory \hat{I}^2 Subunits in the $(\hat{I}^2\hat{I}^3\hat{I}^1)$ 4 Phosphorylase Kinase Complex. Journal of Biological Chemistry, 2012, 287, 36651-36661.	1.6	16
66	DECIPHER: web-based, community resource for clinical interpretation of rare variants in developmental disorders. Human Molecular Genetics, 2012, 21, R37-R44.	1.4	74
67	Genome Sequence of <i>Rickettsia sibirica</i> subsp. <i>mongolitimonae</i> . Journal of Bacteriology, 2012, 194, 2389-2390.	1.0	7
68	Complete Genome Sequence of Geobacillus thermoglucosidans TNO-09.020, a Thermophilic Sporeformer Associated with a Dairy-Processing Environment. Journal of Bacteriology, 2012, 194, 4118-4118.	1.0	31
69	Complete Genome Sequence of Serratia plymuthica Bacteriophage \hat{I} -MAM1. Journal of Virology, 2012, 86, 13872-13873.	1.5	8
70	MetalPDB: a database of metal sites in biological macromolecular structures. Nucleic Acids Research, 2012, 41, D312-D319.	6.5	157
71	LUCApedia: a database for the study of ancient life. Nucleic Acids Research, 2012, 41, D1079-D1082.	6.5	42
72	Genome Sequence of a New Streptomyces coelicolor Generalized Transducing Bacteriophage, \hat{I} -CAM. Journal of Virology, 2012, 86, 13860-13860.	1.5	5
73	Complete Genome Sequence of Croceibacter Bacteriophage P2559S. Journal of Virology, 2012, 86, 8912-8913.	1.5	22

#	ARTICLE	IF	CITATIONS
74	Characterization of Novel Phages Isolated in Coagulase-Negative Staphylococci Reveals Evolutionary Relationships with Staphylococcus aureus Phages. <i>Journal of Bacteriology</i> , 2012, 194, 5829-5839.	1.0	50
75	Autoinhibition of the formin Cappuccino in the absence of canonical autoinhibitory domains. <i>Molecular Biology of the Cell</i> , 2012, 23, 3801-3813.	0.9	32
76	Making your database available through Wikipedia: the pros and cons. <i>Nucleic Acids Research</i> , 2012, 40, D9-D12.	6.5	31
77	Characterization of a Viral Synergism in the Monocot <i>Brachypodium distachyon</i> Reveals Distinctly Altered Host Molecular Processes Associated with Disease. <i>Plant Physiology</i> , 2012, 160, 1432-1452.	2.3	60
78	The classification of esterases: an important gene family involved in insecticide resistance - A review. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2012, 107, 437-449.	0.8	190
79	Cardiac mitochondrial matrix and respiratory complex protein phosphorylation. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2012, 303, H940-H966.	1.5	86
80	Evolutionary Diversity of the Mitochondrial Calcium Uniporter. <i>Science</i> , 2012, 336, 886-886.	6.0	146
81	Regulation of archaeella expression by the FHA and von Willebrand domain-containing proteins ArnA and ArnB in <i>Sulfolobus acidocaldarius</i> . <i>Molecular Microbiology</i> , 2012, 86, 24-36.	1.2	72
82	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i> : towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , 2012, 14, 2870-2890.	1.8	235
83	Tagaturonate-fructuronate epimerase (UxaE), a novel enzyme in the hexuronate catabolic network in <i>Thermotoga maritima</i> . <i>Environmental Microbiology</i> , 2012, 14, 2920-2934.	1.8	41
84	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
85	Urocanate reductase: identification of a novel anaerobic respiratory pathway in <i>Shewanella oneidensis</i> . <i>Molecular Microbiology</i> , 2012, 86, 1452-1463.	1.2	39
86	Diverse circular ssDNA viruses discovered in dragonflies (Odonata: Epiprocta). <i>Journal of General Virology</i> , 2012, 93, 2668-2681.	1.3	163
87	Fragment and Conquer: From Structure to Complexes to Function. <i>Structure</i> , 2012, 20, 1617-1619.	1.6	2
88	Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174.	1.1	59
89	Characterization of the Salmonella bacteriophage vB_SenS-Ent1. <i>Journal of General Virology</i> , 2012, 93, 2046-2056.	1.3	30
90	Bacterial Biosynthetic Gene Clusters Encoding the Anti-cancer Haterumalide Class of Molecules. <i>Journal of Biological Chemistry</i> , 2012, 287, 39125-39138.	1.6	80
91	Data mining for microbiologists. <i>Methods in Microbiology</i> , 2012, 39, 27-79.	0.4	8

#	ARTICLE	IF	CITATIONS
92	Cysteine peptidases and their inhibitors in <i>Tetranychus urticae</i> : a comparative genomic approach. <i>BMC Genomics</i> , 2012, 13, 307.	1.2	38
93	Fife, a <i>Drosophila</i> Piccolo-RIM Homolog, Promotes Active Zone Organization and Neurotransmitter Release. <i>Journal of Neuroscience</i> , 2012, 32, 17048-17058.	1.7	42
94	Conserved rules govern genetic interaction degree across species. <i>Genome Biology</i> , 2012, 13, R57.	13.9	48
95	Endosomal crosstalk: meeting points for signaling pathways. <i>Trends in Cell Biology</i> , 2012, 22, 447-456.	3.6	104
96	Proteome variation among <i>Filifactor aloicis</i> strains. <i>Proteomics</i> , 2012, 12, 3343-3364.	1.3	32
97	A novel synthetic peptide from a tomato defensin exhibits antibacterial activities against <i>Helicobacter pylori</i> . <i>Journal of Peptide Science</i> , 2012, 18, 755-762.	0.8	24
98	Recent duplications drive rapid diversification of trypsin genes in 12 <i>Drosophila</i> . <i>Genetica</i> , 2012, 140, 297-305.	0.5	5
99	Enhancer Binding Proteins Act as Hetero-oligomers and Link Secondary Metabolite Production to Myxococcal Development, Motility, and Predation. <i>Chemistry and Biology</i> , 2012, 19, 1447-1459.	6.2	35
100	â€œ ⁶ â€ Type anionâ€ in biomolecular recognition. <i>FEBS Letters</i> , 2012, 586, 4180-4185.	1.3	49
101	In silico prediction of a disease-associated STIL mutant and its affect on the recruitment of centromere protein J (CENPJ). <i>FEBS Open Bio</i> , 2012, 2, 285-293.	1.0	53
102	A systematic, functional genomics, and reverse vaccinology approach to the identification of vaccine candidates in the cattle tick, <i>Rhipicephalus microplus</i> . <i>Ticks and Tick-borne Diseases</i> , 2012, 3, 179-187.	1.1	49
103	CancerProView: A graphical image database of cancer-related genes and proteins. <i>Genomics</i> , 2012, 100, 81-92.	1.3	2
104	Functional studies of soybean (<i>Glycine max</i> L.) seed LEA proteins GmPM6, GmPM11, and GmPM30 by CD and FTIR spectroscopy. <i>Plant Science</i> , 2012, 196, 152-159.	1.7	54
105	metaMicrobesOnline: phylogenomic analysis of microbial communities. <i>Nucleic Acids Research</i> , 2012, 41, D648-D654.	6.5	17
106	Identification of the Replication Region of a 111-kb Circular Plasmid from <i>Rhodococcus opacus</i> B-4 by Red Recombination-Based Deletion Analysis. <i>Bioscience, Biotechnology and Biochemistry</i> , 2012, 76, 1758-1764.	0.6	3
107	Current opportunities and challenges in microbial metagenome analysis—a bioinformatic perspective. <i>Briefings in Bioinformatics</i> , 2012, 13, 728-742.	3.2	193
108	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2012, 41, D70-D82.	6.5	243
109	Three Arabidopsis DUF579 Domain-Containing GXM Proteins are Methyltransferases Catalyzing 4-O-Methylation of Glucuronic Acid on Xylan. <i>Plant and Cell Physiology</i> , 2012, 53, 1934-1949.	1.5	84

#	ARTICLE	IF	CITATIONS
110	The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. <i>Nucleic Acids Research</i> , 2012, 40, D1-D8.	6.5	104
111	Predicting protein-RNA residue-base contacts using two-dimensional conditional random field. , 2012, , .		1
112	A Multidimensional Matrix for Systems Biology Research and Its Application to Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 5204-5220.	1.8	5
113	Hydrophobic Contributions to the Membrane Docking of Synaptotagmin 7 C2A Domain: Mechanistic Contrast between Isoforms 1 and 7. <i>Biochemistry</i> , 2012, 51, 7654-7664.	1.2	32
114	The Structure of the BfrBâ€“Bfd Complex Reveals Proteinâ€“Protein Interactions Enabling Iron Release from Bacterioferritin. <i>Journal of the American Chemical Society</i> , 2012, 134, 13470-13481.	6.6	71
115	Distant plant homologues: donâ€™t throw out the baby. <i>Trends in Plant Science</i> , 2012, 17, 126-128.	4.3	3
116	Caldicellulosiruptor Core and Pangenomes Reveal Determinants for Noncellulosomal Thermophilic Deconstruction of Plant Biomass. <i>Journal of Bacteriology</i> , 2012, 194, 4015-4028.	1.0	96
117	EFICAz2.5: application of a high-precision enzyme function predictor to 396 proteomes. <i>Bioinformatics</i> , 2012, 28, 2687-2688.	1.8	63
118	The Structure and Catalytic Cycle of a Sodium-Pumping Pyrophosphatase. <i>Science</i> , 2012, 337, 473-476.	6.0	123
119	Structure of the Sensor Domain of Mycobacterium tuberculosis PknH Receptor Kinase Reveals a Conserved Binding Cleft. <i>Journal of Molecular Biology</i> , 2012, 422, 488-494.	2.0	18
120	The role of MAP4K3 in lifespan regulation of Caenorhabditis elegans. <i>Biochemical and Biophysical Research Communications</i> , 2012, 425, 413-418.	1.0	6
121	The emerging contribution of sequence context to the specificity of protein interactions mediated by PDZ domains. <i>FEBS Letters</i> , 2012, 586, 2648-2661.	1.3	108
122	Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. <i>FEBS Letters</i> , 2012, 586, 2631-2637.	1.3	43
123	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	1.8	140
124	Three-Dimensional Structures of Membrane Proteins from Genomic Sequencing. <i>Cell</i> , 2012, 149, 1607-1621.	13.5	478
125	A guideline to proteomeâ€“wide Î±â€“helical membrane protein topology predictions. <i>Proteomics</i> , 2012, 12, 2282-2294.	1.3	29
126	Solution structure and siRNAâ€“mediated knockdown analysis of the mitochondrial diseaseâ€“related protein C12orf65. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2629-2642.	1.5	27
127	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. <i>BMC Bioinformatics</i> , 2012, 13, 264.	1.2	20

#	ARTICLE	IF	CITATIONS
128	Identifying structural domains of proteins using clustering. <i>BMC Bioinformatics</i> , 2012, 13, 286.	1.2	11
129	Exploring metazoan evolution through dynamic and holistic changes in protein families and domains. <i>BMC Evolutionary Biology</i> , 2012, 12, 138.	3.2	9
130	The immune gene repertoire of an important viral reservoir, the Australian black flying fox. <i>BMC Genomics</i> , 2012, 13, 261.	1.2	104
131	Optimizing de novo common wheat transcriptome assembly using short-read RNA-Seq data. <i>BMC Genomics</i> , 2012, 13, 392.	1.2	104
132	Transcriptome-scale homoeolog-specific transcript assemblies of bread wheat. <i>BMC Genomics</i> , 2012, 13, 492.	1.2	51
133	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	1.2	52
134	Identification of essential genes of the periodontal pathogen <i>Porphyromonas gingivalis</i> . <i>BMC Genomics</i> , 2012, 13, 578.	1.2	123
135	Dynamics of domain coverage of the protein sequence universe. <i>BMC Genomics</i> , 2012, 13, 634.	1.2	10
136	A Toolkit for bulk PCR-based marker design from next-generation sequence data: application for development of a framework linkage map in bulb onion (<i>Allium cepa</i> L.). <i>BMC Genomics</i> , 2012, 13, 637.	1.2	38
137	Genome-Wide Characterization of the Phosphate Starvation Response in <i>Schizosaccharomyces pombe</i> . <i>BMC Genomics</i> , 2012, 13, 697.	1.2	62
138	Evaluation method for the potential functionome harbored in the genome and metagenome. <i>BMC Genomics</i> , 2012, 13, 699.	1.2	65
139	Cloning, expression and characterization of an aryl-alcohol dehydrogenase from the white-rot fungus <i>Phanerochaete chrysosporium</i> strain BKM-F-1767. <i>BMC Microbiology</i> , 2012, 12, 126.	1.3	16
140	ST proteins, a new family of plant tandem repeat proteins with a DUF2775 domain mainly found in Fabaceae and Asteraceae. <i>BMC Plant Biology</i> , 2012, 12, 207.	1.6	11
141	The tomato RLK superfamily: phylogeny and functional predictions about the role of the LRRIL-RLK subfamily in antiviral defense. <i>BMC Plant Biology</i> , 2012, 12, 229.	1.6	119
142	Structure Motivator: A tool for exploring small three-dimensional elements in proteins. <i>BMC Structural Biology</i> , 2012, 12, 26.	2.3	9
143	Re-annotation of the CAZy genes of <i>Trichoderma reesei</i> and transcription in the presence of lignocellulosic substrates. <i>Microbial Cell Factories</i> , 2012, 11, 134.	1.9	173
144	MESSA: MEta-Server for protein Sequence Analysis. <i>BMC Biology</i> , 2012, 10, 82.	1.7	43
145	The UCSC Genome Browser. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit1.4.	25.8	86

#	ARTICLE	IF	CITATIONS
146	CDD: conserved domains and protein three-dimensional structure. <i>Nucleic Acids Research</i> , 2012, 41, D348-D352.	6.5	766
147	General secretion signal for the mycobacterial type VII secretion pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11342-11347.	3.3	177
148	Single-domain Î²2â€œthymosins: the family history. <i>Annals of the New York Academy of Sciences</i> , 2012, 1269, 7-15.	1.8	2
149	Template-based protein structure modeling using the RaptorX web server. <i>Nature Protocols</i> , 2012, 7, 1511-1522.	5.5	1,474
150	The PWAPA cassette: Intimate association of a PHD-like finger and a winged-helix domain in proteins included in histone-modifying complexes. <i>Biochimie</i> , 2012, 94, 2006-2012.	1.3	5
151	An improved understanding of TNFL/TNFR interactions using structure-based classifications. <i>Trends in Biochemical Sciences</i> , 2012, 37, 353-363.	3.7	31
152	Crystal Structures of Penicillin-Binding Protein 3 (PBP3) from Methicillin-Resistant <i>Staphylococcus aureus</i> in the Apo and Cefotaximeâ€œBound Forms. <i>Journal of Molecular Biology</i> , 2012, 423, 351-364.	2.0	48
153	The Structural Domains of <i>Pseudomonas aeruginosa</i> Phosphorylcholine Phosphatase Cooperate in Substrate Hydrolysis: 3D Structure and Enzymatic Mechanism. <i>Journal of Molecular Biology</i> , 2012, 423, 503-514.	2.0	6
154	Using Bioinformatics to Develop and Test Hypotheses: <i>E. coli</i> -Specific Virulence Determinants. <i>Journal of Microbiology and Biology Education</i> , 2012, 13, 161-169.	0.5	5
155	Engineering ecosystems and synthetic ecologies. <i>Molecular BioSystems</i> , 2012, 8, 2470.	2.9	112
156	Chemical composition is maintained in poorly conserved intrinsically disordered regions and suggests a means for their classification. <i>Molecular BioSystems</i> , 2012, 8, 3262.	2.9	48
157	Genomic Approaches for Interrogating the Biochemistry of Medicinal Plant Species. <i>Methods in Enzymology</i> , 2012, 517, 139-159.	0.4	46
158	Molecular Evolution of Translin Superfamily Proteins Within the Genomes of Eubacteria, Archaea and Eukaryotes. <i>Journal of Molecular Evolution</i> , 2012, 75, 155-167.	0.8	14
159	FastAnnotator- an efficient transcript annotation web tool. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	51
160	Stage-specific expression of protease genes in the apicomplexan parasite, <i>Eimeria tenella</i> . <i>BMC Genomics</i> , 2012, 13, 685.	1.2	30
161	Genomic resources for a model in adaptation and speciation research: characterization of the <i>Poecilia mexicana</i> transcriptome. <i>BMC Genomics</i> , 2012, 13, 652.	1.2	25
162	Genome sequence of the necrotrophic fungus <i>Penicillium digitatum</i> , the main postharvest pathogen of citrus. <i>BMC Genomics</i> , 2012, 13, 646.	1.2	205
163	SS18 Together with Animal-Specific Factors Defines Human BAF-Type SWI/SNF Complexes. <i>PLoS ONE</i> , 2012, 7, e33834.	1.1	102

#	ARTICLE	IF	CITATIONS
164	Predictive Sequence Analysis of the Candidatus Liberibacter asiaticus Proteome. PLoS ONE, 2012, 7, e41071.	1.1	22
165	A BCAM0223 Mutant of Burkholderia cenocepacia Is Deficient in Hemagglutination, Serum Resistance, Adhesion to Epithelial Cells and Virulence. PLoS ONE, 2012, 7, e41747.	1.1	33
166	Phylogenetic and Functional Metagenomic Profiling for Assessing Microbial Biodiversity in Environmental Monitoring. PLoS ONE, 2012, 7, e43630.	1.1	47
167	Dynamic Hubs Show Competitive and Static Hubs Non-Competitive Regulation of Their Interaction Partners. PLoS ONE, 2012, 7, e48209.	1.1	7
168	Human More Complex than Mouse at Cellular Level. PLoS ONE, 2012, 7, e41753.	1.1	10
169	Metagenomic Profiling of Microbial Composition and Antibiotic Resistance Determinants in Puget Sound. PLoS ONE, 2012, 7, e48000.	1.1	50
170	The Rice B-Box Zinc Finger Gene Family: Genomic Identification, Characterization, Expression Profiling and Diurnal Analysis. PLoS ONE, 2012, 7, e48242.	1.1	120
171	Insights into the Evolutionary Features of Human Neurodegenerative Diseases. PLoS ONE, 2012, 7, e48336.	1.1	10
172	TgpA, a Protein with a Eukaryotic-Like Transglutaminase Domain, Plays a Critical Role in the Viability of Pseudomonas aeruginosa. PLoS ONE, 2012, 7, e50323.	1.1	12
173	Multiple Inter-Kingdom Horizontal Gene Transfers in the Evolution of the Phosphoenolpyruvate Carboxylase Gene Family. PLoS ONE, 2012, 7, e51159.	1.1	7
174	Non-Traditional Antibacterial Screening Approaches for the Identification of Novel Inhibitors of the Glyoxylate Shunt in Gram-Negative Pathogens. PLoS ONE, 2012, 7, e51732.	1.1	45
175	Development of Transcriptomic Resources for Interrogating the Biosynthesis of Monoterpene Indole Alkaloids in Medicinal Plant Species. PLoS ONE, 2012, 7, e52506.	1.1	150
176	Comparative genomic and transcriptional analyses of CRISPR systems across the genus Pyrobaculum. Frontiers in Microbiology, 2012, 3, 251.	1.5	28
177	The Investigation of Gene Regulation and Variation in Human Cancers and Other Diseases. , 2012, , .		0
178	Crystal structure of DeSlâ€1, a novel deSUMOylase belonging to a putative isopeptidase superfamily. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2099-2104.	1.5	29
179	Automated identification of binding sites for phosphorylated ligands in protein structures. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2347-2358.	1.5	3
180	Sequence and structure relationships within von Willebrand factor. Blood, 2012, 120, 449-458.	0.6	251
181	Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 2012, 13, 711-727.	3.2	150

#	ARTICLE	IF	CITATIONS
182	Two-component signal transduction in <i>Corynebacterium glutamicum</i> and other corynebacteria: on the way towards stimuli and targets. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1131-1150.	1.7	35
183	Sequence fingerprints of enzyme specificities from the glycoside hydrolase family GH57. <i>Extremophiles</i> , 2012, 16, 497-506.	0.9	54
184	The use of evolutionary patterns in protein annotation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 316-325.	2.6	28
185	Structural genomics plucks high-hanging membrane proteins. <i>Current Opinion in Structural Biology</i> , 2012, 22, 326-332.	2.6	38
186	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. <i>Molecular Plant Pathology</i> , 2012, 13, 1120-1134.	2.0	14
187	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 744-750.	0.7	11
188	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. <i>Molecular Microbiology</i> , 2012, 85, 1072-1089.	1.2	68
189	Interplay of RsbM and RsbK controls the σ^B activity of <i>Bacillus cereus</i> . <i>Environmental Microbiology</i> , 2012, 14, 2788-2799.	1.8	9
190	Pneumococcal surface proteins: when the whole is greater than the sum of its parts. <i>Molecular Oral Microbiology</i> , 2012, 27, 221-245.	1.3	92
191	Structural mimicry between SLA/LP and Rickettsia surface antigens as a driver of autoimmune hepatitis: insights from an in silico study. <i>Theoretical Biology and Medical Modelling</i> , 2013, 10, 25.	2.1	12
192	Identification of diverse full-length endogenous betaretroviruses in megabats and microbats. <i>Retrovirology</i> , 2013, 10, 35.	0.9	45
193	Interactome map uncovers phosphatidylserine transport by oxysterol-binding proteins. <i>Nature</i> , 2013, 501, 257-261.	13.7	279
194	A de novo assembly of the newt transcriptome combined with proteomic validation identifies new protein families expressed during tissue regeneration. <i>Genome Biology</i> , 2013, 14, R16.	13.9	104
195	Detailed analysis of metagenome datasets obtained from biogas-producing microbial communities residing in biogas reactors does not indicate the presence of putative pathogenic microorganisms. <i>Biotechnology for Biofuels</i> , 2013, 6, 49.	6.2	31
196	De novo prediction of the genomic components and capabilities for microbial plant biomass degradation from (meta-)genomes. <i>Biotechnology for Biofuels</i> , 2013, 6, 24.	6.2	18
197	Identification of novel arthropod vector G protein-coupled receptors. <i>Parasites and Vectors</i> , 2013, 6, 150.	1.0	9
198	Genome sequence of a novel deep-sea vent epsilonproteobacterial phage provides new insight into the co-evolution of Epsilonproteobacteria and their phages. <i>Extremophiles</i> , 2013, 17, 405-419.	0.9	22
199	Comparative docking and ADMET study of some curcumin derivatives and herbal congeners targeting β^2 -amyloid. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 13-27.	1.2	30

#	ARTICLE	IF	CITATIONS
200	Endonuclease V: an unusual enzyme for repair of DNA deamination. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 3145-3156.	2.4	47
201	Genome-Wide Analysis of Mitogen-Activated Protein Kinase Gene Family in Maize. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1446-1460.	1.0	74
202	A tandem K-unit protease inhibitor (KPI106) serine carboxypeptidase (SCP1) controls mycorrhiza establishment and arbuscule development in <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2013, 75, 711-725.	2.8	30
203	Environmental responses and the control of iron homeostasis in fungal systems. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 939-955.	1.7	25
204	In silico investigation of PHD3 specific HIF1α proline 567 hydroxylation: A new player in the VHL/HIF1α interaction pathway?. <i>FEBS Letters</i> , 2013, 587, 2996-3001.	1.3	11
205	A conserved START domain coenzyme Q-binding polypeptide is required for efficient Q biosynthesis, respiratory electron transport, and antioxidant function in <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013, 1831, 776-791.	1.2	34
206	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2937-2943.	1.4	26
207	Effects of MACPF/CDC proteins on lipid membranes. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 2083-2098.	2.4	71
208	MS-desi, a desiccation-related protein in the floral nectar of the evergreen velvet bean (<i>Mucuna</i>). <i>Journal of Proteomics</i> , 2013, 10, 33-42.	1.6	33
209	IS-Dom: a dataset of independent structural domains automatically delineated from protein structures. <i>Journal of Computer-Aided Molecular Design</i> , 2013, 27, 419-426.	1.3	2
210	Analysis and consensus of currently available intrinsic protein disorder annotation sources in the MobiDB database. <i>BMC Bioinformatics</i> , 2013, 14, S3.	1.2	30
211	Inferring homologous protein-protein interactions through pair position specific scoring matrix. <i>BMC Bioinformatics</i> , 2013, 14, S11.	1.2	4
212	Jenner-predict server: prediction of protein vaccine candidates (PVCs) in bacteria based on host-pathogen interactions. <i>BMC Bioinformatics</i> , 2013, 14, 211.	1.2	62
213	A protein domain-centric approach for the comparative analysis of human and yeast phenotypically relevant mutations. <i>BMC Genomics</i> , 2013, 14, S5.	1.2	26
214	Assessment of computational methods for predicting the effects of missense mutations in human cancers. <i>BMC Genomics</i> , 2013, 14, S7.	1.2	153
215	Identification of G protein-coupled receptor signaling pathway proteins in marine diatoms using comparative genomics. <i>BMC Genomics</i> , 2013, 14, 503.	1.2	20
216	Reannotation and extended community resources for the genome of the non-seed plant <i>Physcomitrella patens</i> provide insights into the evolution of plant gene structures and functions. <i>BMC Genomics</i> , 2013, 14, 498.	1.2	170
217	KONAGAbase: a genomic and transcriptomic database for the diamondback moth, <i>Plutella xylostella</i> . <i>BMC Genomics</i> , 2013, 14, 464.	1.2	47

#	ARTICLE	IF	CITATIONS
218	Cytosine methylation is a conserved epigenetic feature found throughout the phylum Platyhelminthes. <i>BMC Genomics</i> , 2013, 14, 462.	1.2	35
219	Evolutionary origins, molecular cloning and expression of carotenoid hydroxylases in eukaryotic photosynthetic algae. <i>BMC Genomics</i> , 2013, 14, 457.	1.2	31
220	Frequent loss of lineages and deficient duplications accounted for low copy number of disease resistance genes in Cucurbitaceae. <i>BMC Genomics</i> , 2013, 14, 335.	1.2	74
221	Differential transcript isoform usage pre- and post-zygotic genome activation in zebrafish. <i>BMC Genomics</i> , 2013, 14, 331.	1.2	33
222	MGcV: the microbial genomic context viewer for comparative genome analysis. <i>BMC Genomics</i> , 2013, 14, 209.	1.2	53
223	Deep sequencing for de novo construction of a marine fish (<i>Sparus aurata</i>) transcriptome database with a large coverage of protein-coding transcripts. <i>BMC Genomics</i> , 2013, 14, 178.	1.2	90
224	Transcriptome analyses reveal protein and domain families that delineate stage-related development in the economically important parasitic nematodes, <i>Ostertagia ostertagi</i> and <i>Cooperia oncophora</i> . <i>BMC Genomics</i> , 2013, 14, 118.	1.2	31
225	phiBIOTICS: catalogue of therapeutic enzybiotics, relevant research studies and practical applications. <i>BMC Microbiology</i> , 2013, 13, 53.	1.3	20
226	A 1,681-locus consensus genetic map of cultivated cucumber including 67 NB-LRR resistance gene homolog and ten gene loci. <i>BMC Plant Biology</i> , 2013, 13, 53.	1.6	58
227	A novel function prediction approach using protein overlap networks. <i>BMC Systems Biology</i> , 2013, 7, 61.	3.0	13
228	BioBin: a bioinformatics tool for automating the binning of rare variants using publicly available biological knowledge. <i>BMC Medical Genomics</i> , 2013, 6, S6.	0.7	55
229	Identification and physiological characterization of phosphatidic acid phosphatase enzymes involved in triacylglycerol biosynthesis in <i>Streptomyces coelicolor</i> . <i>Microbial Cell Factories</i> , 2013, 12, 9.	1.9	40
230	Identification of triacylglycerol and steryl ester synthases of the methylotrophic yeast <i>Pichia pastoris</i> . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013, 1831, 1158-1166.	1.2	12
231	Pharmacophore Binding Motifs for Nicotinamide Adenine Dinucleotide Analogues Across Multiple Protein Families: A Detailed Contact-Based Analysis of the Interaction between Proteins and NAD(P) Cofactors. <i>Journal of Medicinal Chemistry</i> , 2013, 56, 6175-6189.	2.9	11
232	Genome-Wide Analysis of Nucleotide-Binding Site (NBS) Disease Resistance (R) Genes in Sacred Lotus (<i>Nelumbo nucifera</i> Gaertn.) Reveals Their Transition Role During Early Evolution of Land Plants. <i>Tropical Plant Biology</i> , 2013, 6, 98-116.	1.0	10
233	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. <i>Human Genetics</i> , 2013, 132, 899-911.	1.8	13
234	Long Noncoding RNA: a New Player of Heart Failure?. <i>Journal of Cardiovascular Translational Research</i> , 2013, 6, 876-883.	1.1	101
235	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. <i>Biotechnology Advances</i> , 2013, 31, 1109-1119.	6.0	23

#	ARTICLE	IF	CITATIONS
236	Structure of the PilZâ€“FimXEALâ€“c-di-GMP Complex Responsible for the Regulation of Bacterial Type IV Pilus Biogenesis. <i>Journal of Molecular Biology</i> , 2013, 425, 2174-2197.	2.0	49
237	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	3.6	61
238	Genome sequence analysis of the <i>Vibrio parahaemolyticus</i> lytic bacteriophage VPMS1. <i>Archives of Virology</i> , 2013, 158, 2409-2413.	0.9	8
239	Improving lignocellulolytic enzyme production with <i>Penicillium</i> : from strain screening to systems biology. <i>Biofuels</i> , 2013, 4, 523-534.	1.4	37
240	Evolutionary and Functional Analysis of the Key Pluripotency Factor Oct4 and Its Family Proteins. <i>Journal of Genetics and Genomics</i> , 2013, 40, 399-412.	1.7	7
241	Metagenomic insights into microbial metabolism affecting arsenic dispersion in Mediterranean marine sediments. <i>Molecular Ecology</i> , 2013, 22, 4870-4883.	2.0	36
242	Insights into the structureâ€“function relationship of disease resistance protein HCTR in maize (<i>Zea mays</i>). <i>Plant Physiology</i> , 2013, 159, 50-64.	1.3	9
243	Sigma factors in a thousand <i>Escherichia coli</i> genomes. <i>Environmental Microbiology</i> , 2013, 15, 3121-3129.	1.8	32
244	Characterization and genome sequencing of a novel bacteriophage infecting <i>Streptococcus agalactiae</i> with high similarity to a phage from <i>Streptococcus pyogenes</i> . <i>Archives of Virology</i> , 2013, 158, 1733-1741.	0.9	35
245	Detection of African swine fever virus-like sequences in ponds in the Mississippi Delta through metagenomic sequencing. <i>Virus Genes</i> , 2013, 46, 441-446.	0.7	21
246	Predominant archaea in marine sediments degrade detrital proteins. <i>Nature</i> , 2013, 496, 215-218.	13.7	526
247	Branched Signal Wiring of an Essential Bacterial Cell-Cycle Phosphotransfer Protein. <i>Structure</i> , 2013, 21, 1590-1601.	1.6	23
248	Structural Insight into the Giant Ca ²⁺ -Binding Adhesin SiiE: Implications for the Adhesion of <i>Salmonella enterica</i> to Polarized Epithelial Cells. <i>Structure</i> , 2013, 21, 741-752.	1.6	46
249	Interplay of flagellar motility and mucin degradation stimulates the association of <i>Pseudomonas aeruginosa</i> with human epithelial colorectal adenocarcinoma (Caco-2) cells. <i>Journal of Infection and Chemotherapy</i> , 2013, 19, 305-315.	0.8	15
250	Lecithin cholesterol acyltransferase (LCAT) activity in the presence of Apo-AI-derived peptides exposed to disorderâ€“order conformational transitions. <i>Biochemical and Biophysical Research Communications</i> , 2013, 441, 469-475.	1.0	6
251	PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. <i>Pain</i> , 2013, 154, 2586e1-2586e12.	2.0	50
252	Transcriptomic analysis of the dimorphic transition of <i>Ustilago maydis</i> induced in vitro by a change in pH. <i>Fungal Genetics and Biology</i> , 2013, 58-59, 116-125.	0.9	21
253	PPM-Dom: A novel method for domain position prediction. <i>Computational Biology and Chemistry</i> , 2013, 47, 8-15.	1.1	3

#	ARTICLE	IF	CITATIONS
254	Guardians of the actin monomer. <i>European Journal of Cell Biology</i> , 2013, 92, 316-332.	1.6	62
255	antiSMASH 2.0 – a versatile platform for genome mining of secondary metabolite producers. <i>Nucleic Acids Research</i> , 2013, 41, W204-W212.	6.5	753
256	Missense substitutions reflecting regulatory control of transmitter phosphatase activity in two-component signalling. <i>Molecular Microbiology</i> , 2013, 88, 459-472.	1.2	19
257	The mycobacterial antibiotic resistance determinant <i>WhiB7</i> acts as a transcriptional activator by binding the primary sigma factor <i>SigA</i> (<i>RpoV</i>). <i>Nucleic Acids Research</i> , 2013, 41, 10062-10076.	6.5	83
258	Lacto-N-biosidase Encoded by a Novel Gene of <i>Bifidobacterium longum</i> Subspecies <i>longum</i> Shows Unique Substrate Specificity and Requires a Designated Chaperone for Its Active Expression. <i>Journal of Biological Chemistry</i> , 2013, 288, 25194-25206.	1.6	83
259	Phenotypic variation caused by variation in the relative copy number of pDU1-based plasmids expressing the GAF domain of <i>Pkn41</i> or <i>Pkn42</i> in <i>Anabaena</i> sp. PCC 7120. <i>Research in Microbiology</i> , 2013, 164, 127-135.	1.0	20
260	Proteins and Domains Vary in Their Tolerance of Non-Synonymous Single Nucleotide Polymorphisms (nsSNPs). <i>Journal of Molecular Biology</i> , 2013, 425, 1274-1286.	2.0	32
261	Identification of novel phospholipase A2 group IX members in metazoans. <i>Biochimie</i> , 2013, 95, 1534-1543.	1.3	8
262	The c-di-GMP recognition mechanism of the PilZ domain of bacterial cellulose synthase subunit A. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 802-807.	1.0	42
263	IntApop: A web service for predicting apoptotic protein interactions in humans. <i>BioSystems</i> , 2013, 114, 238-244.	0.9	4
264	DGIdb: mining the druggable genome. <i>Nature Methods</i> , 2013, 10, 1209-1210.	9.0	443
265	Akirins in sea lice: First steps towards a deeper understanding. <i>Experimental Parasitology</i> , 2013, 135, 188-199.	0.5	15
266	High-resolution network biology: connecting sequence with function. <i>Nature Reviews Genetics</i> , 2013, 14, 865-879.	7.7	92
267	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.4	479
268	Optimizing multiple sequence alignments using a genetic algorithm based on three objectives: structural information, non-gaps percentage and totally conserved columns. <i>Bioinformatics</i> , 2013, 29, 2112-2121.	1.8	48
269	From the <i>Flavobacterium</i> genus to the phylum <i>Bacteroidetes</i> : genomic analysis of <i>dnd</i> gene clusters. <i>FEMS Microbiology Letters</i> , 2013, 348, 26-35.	0.7	6
270	The Evolutionary Origin of Epithelial Cell-Cell Adhesion Mechanisms. <i>Current Topics in Membranes</i> , 2013, 72, 267-311.	0.5	53
271	The <i>WbaK</i> acetyltransferase of <i>Salmonella enterica</i> group E gives insights into O antigen evolution. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2316-2322.	0.7	12

#	ARTICLE	IF	CITATIONS
272	A network of epigenetic regulators guides developmental haematopoiesis in vivo. <i>Nature Cell Biology</i> , 2013, 15, 1516-1525.	4.6	81
273	Remarkable similarities between the hemichordate (<i>Saccoglossus kowalevskii</i>) and vertebrate GPCR repertoire. <i>Gene</i> , 2013, 526, 122-133.	1.0	50
274	Novel Cold-Adapted Esterase MHLip from an Antarctic Soil Metagenome. <i>Biology</i> , 2013, 2, 177-188.	1.3	19
275	The RclR Protein Is a Reactive Chlorine-specific Transcription Factor in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 32574-32584.	1.6	71
276	Atomistic Modelling of Phosphopeptide Recognition for Modular Domains. <i>Annual Reports in Computational Chemistry</i> , 2013, 9, 61-84.	0.9	1
277	Transcription factor evolution in eukaryotes and the assembly of the regulatory toolkit in multicellular lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4858-66.	3.3	183
278	Integration of Protein Abundance and Structure Data Reveals Competition in the ErbB Signaling Network. <i>Science Signaling</i> , 2013, 6, ra109.	1.6	48
279	A phenylalanine rotameric switch for signal-state control in bacterial chemoreceptors. <i>Nature Communications</i> , 2013, 4, 2881.	5.8	37
280	Functional implications of splicing polymorphisms in the human genome. <i>Human Molecular Genetics</i> , 2013, 22, 3449-3459.	1.4	19
281	Protease Families, Evolution and Mechanism of Action. , 2013, , 1-36.		8
282	Experimental and computational analysis of the secretome of the hyperthermophilic archaeon <i>Pyrococcus furiosus</i> . <i>Extremophiles</i> , 2013, 17, 921-930.	0.9	8
283	Investigation of anti-cancer mechanisms by comparative analysis of naked mole rat and rat. <i>BMC Systems Biology</i> , 2013, 7, S5.	3.0	10
284	Bioinformatics opportunities for identification and study of medicinal plants. <i>Briefings in Bioinformatics</i> , 2013, 14, 238-250.	3.2	80
285	Pandoraviruses: Amoeba Viruses with Genomes Up to 2.5 Mb Reaching That of Parasitic Eukaryotes. <i>Science</i> , 2013, 341, 281-286.	6.0	509
286	Effect of Alternative Splicing on the Degree Centrality of Nodes in Protein-Protein Interaction Networks of <i>Homo sapiens</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1980-1988.	1.8	12
287	Making automated multiple alignments of very large numbers of protein sequences. <i>Bioinformatics</i> , 2013, 29, 989-995.	1.8	49
288	Untangling structure-function relationships in the rhomboid family of intramembrane proteases. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2862-2872.	1.4	29
289	Identification of genome-wide single nucleotide polymorphisms in allopolyploid crop <i>Brassica napus</i> . <i>BMC Genomics</i> , 2013, 14, 717.	1.2	70

#	ARTICLE	IF	CITATIONS
290	Integrating microRNA and mRNA expression profiling in <i>Symbiodinium microadriaticum</i> , a dinoflagellate symbiont of reef-building corals. <i>BMC Genomics</i> , 2013, 14, 704.	1.2	109
291	Web Apollo: a web-based genomic annotation editing platform. <i>Genome Biology</i> , 2013, 14, R93.	13.9	329
292	Crystal structure of c5321: a protective antigen present in uropathogenic <i>Escherichia coli</i> strains displaying an SLR fold. <i>BMC Structural Biology</i> , 2013, 13, 19.	2.3	17
293	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2013, 14, 664.	1.2	99
294	The genome and transcriptome of the enteric parasite <i>Entamoeba invadens</i> , a model for encystation. <i>Genome Biology</i> , 2013, 14, R77.	13.9	111
295	The bilaterian roots of cordon-bleu. <i>BMC Research Notes</i> , 2013, 6, 393.	0.6	3
296	Genome and transcriptome sequencing of the halophilic fungus <i>Wallemia ichthyophaga</i> : haloadaptations present and absent. <i>BMC Genomics</i> , 2013, 14, 617.	1.2	107
297	Two Pfam protein families characterized by a crystal structure of protein Ipg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013, 14, 265.	1.2	3
298	Identification, expression, and comparative genomic analysis of the IPT and CKX gene families in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>BMC Genomics</i> , 2013, 14, 594.	1.2	65
299	Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT/Overfoc 1.2 172	1.2	172
300	Functional requirements driving the gene duplication in 12 <i>Drosophila</i> species. <i>BMC Genomics</i> , 2013, 14, 555.	1.2	11
301	Probabilistic grammatical model for helix-helix contact site classification. <i>Algorithms for Molecular Biology</i> , 2013, 8, 31.	0.3	6
302	In silico prediction of structure and functions for some proteins of male-specific region of the human Y chromosome. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 258-269.	2.2	3
303	Two-component systems in <i>Streptomyces</i> : key regulators of antibiotic complex pathways. <i>Microbial Cell Factories</i> , 2013, 12, 127.	1.9	93
304	A new computational strategy for predicting essential genes. <i>BMC Genomics</i> , 2013, 14, 910.	1.2	34
305	Graph representation of high-dimensional alpha-helical membrane protein data. <i>BioData Mining</i> , 2013, 6, 21.	2.2	2
306	Prediction of protein-RNA residue-base contacts using two-dimensional conditional random field with the lasso. <i>BMC Systems Biology</i> , 2013, 7, S15.	3.0	10
307	PhaP phasins play a principal role in poly- β -hydroxybutyrate accumulation in free-living <i>Bradyrhizobium japonicum</i> . <i>BMC Microbiology</i> , 2013, 13, 290.	1.3	17

#	ARTICLE	IF	CITATIONS
308	Transcriptome analysis of the filamentous fungus <i>Aspergillus nidulans</i> directed to the global identification of promoters. <i>BMC Genomics</i> , 2013, 14, 847.	1.2	56
309	The planarian regeneration transcriptome reveals a shared but temporally shifted regulatory program between opposing head and tail scenarios. <i>BMC Genomics</i> , 2013, 14, 797.	1.2	50
310	Transferring functional annotations of membrane transporters on the basis of sequence similarity and sequence motifs. <i>BMC Bioinformatics</i> , 2013, 14, 343.	1.2	20
311	Evolution and dynamics of megaplasmids with genome sizes larger than 100 kb in the <i>Bacillus cereus</i> group. <i>BMC Evolutionary Biology</i> , 2013, 13, 262.	3.2	36
312	Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). <i>BMC Bioinformatics</i> , 2013, 14, 335.	1.2	86
313	A whole transcriptomal linkage analysis of gene co-regulation in insecticide resistant house flies, <i>Musca domestica</i> . <i>BMC Genomics</i> , 2013, 14, 803.	1.2	37
314	SHARP: genome-scale identification of gene-protein-reaction associations in cyanobacteria. <i>Photosynthesis Research</i> , 2013, 118, 181-190.	1.6	6
315	Training Based on Ligand Efficiency Improves Prediction of Bioactivities of Ligands and Drug Target Proteins in a Machine Learning Approach. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2525-2537.	2.5	16
316	Assessing the Human Gut Microbiota in Metabolic Diseases. <i>Diabetes</i> , 2013, 62, 3341-3349.	0.3	384
317	Molecular cloning and characterization of major vault protein of <i>Echinococcus multilocularis</i> . <i>Experimental Parasitology</i> , 2013, 134, 102-108.	0.5	2
318	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1243-1249.	3.6	153
319	Global versus Local Hubs in Human Protein-Protein Interaction Network. <i>Journal of Proteome Research</i> , 2013, 12, 5436-5446.	1.8	24
320	<i>foxl2</i> and <i>foxl3</i> are two ancient paralogs that remain fully functional in teleosts. <i>General and Comparative Endocrinology</i> , 2013, 194, 81-93.	0.8	42
321	<i>Acinetobacter baylyi</i> long-term stationary-phase protein StiP is a protease required for normal cell morphology and resistance to tellurite. <i>Canadian Journal of Microbiology</i> , 2013, 59, 726-736.	0.8	4
322	Genetic determinants of swimming motility in the squid light organ symbiont <i>Vibrio fischeri</i> . <i>MicrobiologyOpen</i> , 2013, 2, 576-594.	1.2	58
323	COMBat: Visualizing co-occurrence of annotation terms. , 2013, , .		2
324	Episodes of horizontal gene-transfer and gene-fusion led to co-existence of different metal-ion specific glyoxalase I. <i>Scientific Reports</i> , 2013, 3, 3076.	1.6	48
325	Modeling the calcium and phosphate mineralization of American lobster cuticle. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2013, 70, 1601-1611.	0.7	13

#	ARTICLE	IF	CITATIONS
326	Mercury Methylation by the Methanogen <i>Methanospirillum hungatei</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 6325-6330.	1.4	119
327	Histidine-rich proteins in prokaryotes: metal homeostasis and environmental habitat-related occurrence. <i>Metalomics</i> , 2013, 5, 1423.	1.0	26
328	Evaluating Optimization Strategies for HMMer Acceleration on GPU. , 2013, , .		1
329	Drift and conservation of differential exon usage across tissues in primate species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15377-15382.	3.3	103
330	An endo-1,4- β -glucanase PdCel5C from cellulytic fungus <i>Penicillium decumbens</i> with distinctive domain composition and hydrolysis product profile. <i>Enzyme and Microbial Technology</i> , 2013, 52, 190-195.	1.6	30
331	On the functional and structural characterization of hubs in protein-protein interaction networks. <i>Biotechnology Advances</i> , 2013, 31, 274-286.	6.0	54
332	Solution Structure of <i>Escherichia coli</i> FeoA and Its Potential Role in Bacterial Ferrous Iron Transport. <i>Journal of Bacteriology</i> , 2013, 195, 46-55.	1.0	50
333	Interactome3D: adding structural details to protein networks. <i>Nature Methods</i> , 2013, 10, 47-53.	9.0	449
334	Molecular and microscopic evidence of viruses in marine copepods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1375-1380.	3.3	67
335	Structural Determinants of Skeletal Muscle Ryanodine Receptor Gating*. <i>Journal of Biological Chemistry</i> , 2013, 288, 6154-6165.	1.6	48
336	BtaE, an Adhesin That Belongs to the Trimeric Autotransporter Family, Is Required for Full Virulence and Defines a Specific Adhesive Pole of <i>Brucella suis</i> . <i>Infection and Immunity</i> , 2013, 81, 996-1007.	1.0	40
337	Identification and Characterization of a High-Affinity Choline Uptake System of <i>Brucella abortus</i> . <i>Journal of Bacteriology</i> , 2013, 195, 493-501.	1.0	11
338	Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature. <i>Natural Product Reports</i> , 2013, 30, 108-160.	5.2	1,692
339	RNA sequencing reveals a diverse and dynamic repertoire of the <i>Xenopus tropicalis</i> transcriptome over development. <i>Genome Research</i> , 2013, 23, 201-216.	2.4	128
340	Predicting enzymatic function from global binding site descriptors. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 479-489.	1.5	13
341	Counterbalance of ligand- and self-coupled motions characterizes multispecificity of ubiquitin. <i>Protein Science</i> , 2013, 22, 168-178.	3.1	8
342	Behavioural and genetic analyses of <i>Nasonia</i> shed light on the evolution of sex pheromones. <i>Nature</i> , 2013, 494, 345-348.	13.7	110
343	Abstracting knowledge from the protein data bank. <i>Biopolymers</i> , 2013, 99, 183-188.	1.2	6

#	ARTICLE	IF	CITATIONS
344	Predicting the Functional, Molecular, and Phenotypic Consequences of Amino Acid Substitutions using Hidden Markov Models. <i>Human Mutation</i> , 2013, 34, 57-65.	1.1	1,057
345	Prediction of protein domain boundaries from inverse covariances. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 253-260.	1.5	13
346	The Glove-like Structure of the Conserved Membrane Protein TatC Provides Insight into Signal Sequence Recognition in Twin-Arginine Translocation. <i>Structure</i> , 2013, 21, 777-788.	1.6	67
347	Mdm10 is an ancient eukaryotic porin co-occurring with the ERMES complex. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 3314-3325.	1.9	68
348	Density peaks of paralog pairs in human and mouse genomes. <i>Gene</i> , 2013, 527, 55-61.	1.0	3
349	Identification of Immunity-related Genes in Arabidopsis and Cassava Using Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 345-353.	3.0	8
350	A continuous fluorescence assay for the characterization of Nudix hydrolases. <i>Analytical Biochemistry</i> , 2013, 437, 178-184.	1.1	4
351	Classification and nomenclature of the superfamily of short-chain dehydrogenases/reductases (SDRs). <i>Chemico-Biological Interactions</i> , 2013, 202, 111-115.	1.7	123
352	The evolution and putative function of phosducin-like proteins in the malaria parasite Plasmodium. <i>Infection, Genetics and Evolution</i> , 2013, 13, 49-55.	1.0	2
353	Position-specific scoring matrix and hidden Markov model complement each other for the prediction of conopeptide superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 717-724.	1.1	12
354	The photoconvertible water-soluble chlorophyll-binding protein of <i>Chenopodium album</i> is a member of DUF538, a superfamily that distributes in Embryophyta. <i>Journal of Plant Physiology</i> , 2013, 170, 1549-1552.	1.6	21
355	Analysis of sequence repeats of proteins in the PDB. <i>Computational Biology and Chemistry</i> , 2013, 47, 156-166.	1.1	18
356	The superfamily of mitochondrial Complex1_LYR motif-containing (LYRM) proteins. <i>Biochemical Society Transactions</i> , 2013, 41, 1335-1341.	1.6	49
357	The architectural design of networks of protein domain architectures. <i>Biology Letters</i> , 2013, 9, 20130268.	1.0	6
358	The 216-bp <i>marB</i> gene of the <i>marRAB</i> operon in <i>Escherichia coli</i> encodes a periplasmic protein which reduces the transcription rate of <i>marA</i> . <i>FEMS Microbiology Letters</i> , 2013, 345, 49-55.	0.7	29
359	Bacterial second messengers, cGMP and c-di-GMP, in a quest for regulatory dominance. <i>EMBO Journal</i> , 2013, 32, 2421-2423.	3.5	24
360	SNVDis: A Proteome-wide Analysis Service for Evaluating nsSNVs in Protein Functional Sites and Pathways. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 122-126.	3.0	15
361	A Zinc Lock on GGDEF Domain Dimerization Inhibits <i>E. coli</i> Biofilms. <i>Structure</i> , 2013, 21, 1067-1068.	1.6	1

#	ARTICLE	IF	CITATIONS
362	Helix Bundle Loops Determine Whether Histidine Kinases Autophosphorylate in cis or in trans. <i>Journal of Molecular Biology</i> , 2013, 425, 1198-1209.	2.0	61
363	Rapid modulation of gene expression profiles in the telencephalon of male goldfish following exposure to waterborne sex pheromones. <i>General and Comparative Endocrinology</i> , 2013, 192, 204-213.	0.8	16
364	Lipopolysaccharide-induced TNF- α factor in grass carp (<i>Ctenopharyngodon idella</i>): Evidence for its involvement in antiviral innate immunity. <i>Fish and Shellfish Immunology</i> , 2013, 34, 538-545.	1.6	31
365	Regulation of ethylene biosynthesis at the level of 1-aminocyclopropane-1-carboxylate oxidase (ACO) gene. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 295-307.	1.0	94
366	The structure of a novel glucuronoyl esterase from <i>Myceliophthora thermophila</i> gives new insights into its role as a potential biocatalyst. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 63-73.	2.5	38
367	The AEROPATH project targeting <i>Pseudomonas aeruginosa</i> : crystallographic studies for assessment of potential targets in early-stage drug discovery. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 25-34.	0.7	30
369	Subpocket Analysis Method for Fragment-Based Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 131-141.	2.5	23
370	Expression of sulfatases in <i>Rhodopirellula baltica</i> and the diversity of sulfatases in the genus <i>Rhodopirellula</i> . <i>Marine Genomics</i> , 2013, 9, 51-61.	0.4	145
371	Bioinformatic prediction of the exportome of <i>Babesia bovis</i> and identification of novel proteins in parasite-infected red blood cells. <i>International Journal for Parasitology</i> , 2013, 43, 409-416.	1.3	18
372	<i>GsmR</i> , a response regulator with an HD-related output domain in <i>Xanthomonas campestris</i> , is positively controlled by <i>C_{lp}</i> and is involved in the expression of genes responsible for flagellum synthesis. <i>FEBS Journal</i> , 2013, 280, 199-213.	2.2	16
373	Reassessment of the <i>Listeria monocytogenes</i> pan-genome reveals dynamic integration hotspots and mobile genetic elements as major components of the accessory genome. <i>BMC Genomics</i> , 2013, 14, 47.	1.2	212
374	Genomes of marine cyanopodoviruses reveal multiple origins of diversity. <i>Environmental Microbiology</i> , 2013, 15, 1356-1376.	1.8	99
375	Sequencing and annotation of the <i>Ophiostoma ulmigenome</i> . <i>BMC Genomics</i> , 2013, 14, 162.	1.2	40
376	A Time to Scatter Genes and a Time to Gather Them. <i>Advances in Botanical Research</i> , 2013, 66, 1-35.	0.5	8
377	Transcriptional Regulation of Seven ERFs in Rice Under Oxygen Depletion and Iron Overload Stress. <i>Tropical Plant Biology</i> , 2013, 6, 16-25.	1.0	12
378	Quantification and functional analysis of modular protein evolution in a dense phylogenetic tree. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 898-907.	1.1	29
379	Cyclic di-GMP: the First 25 Years of a Universal Bacterial Second Messenger. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 1-52.	2.9	1,479
380	Untangling the transcriptome from fungus-infected plant tissues. <i>Gene</i> , 2013, 519, 238-244.	1.0	6

#	ARTICLE	IF	CITATIONS
381	Structure of <i>Ostertagia ostertagi</i> ASP-1: insights into disulfide-mediated cyclization and dimerization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 493-503.	2.5	29
382	Using Analyses of Amino Acid Coevolution to Understand Protein Structure and Function. <i>Methods in Enzymology</i> , 2013, 523, 191-212.	0.4	13
383	The Genetic Basis for Bacterial Mercury Methylation. <i>Science</i> , 2013, 339, 1332-1335.	6.0	778
384	Bioinformatics tools for secretome analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2442-2453.	1.1	93
385	Intersection of selenoproteins and kinase signalling. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1279-1284.	1.1	8
386	Bioinformatic survey for new physiological substrates of Cyclin-dependent kinase 5. <i>Genomics</i> , 2013, 101, 221-228.	1.3	13
387	Proteins with an alpha/beta hydrolase fold: Relationships between subfamilies in an ever-growing superfamily. <i>Chemico-Biological Interactions</i> , 2013, 203, 266-268.	1.7	39
388	Archaeal and eukaryotic homologs of Hfq. <i>RNA Biology</i> , 2013, 10, 636-651.	1.5	75
389	Identification of Expressed Resistance Gene Analogs from Peanut (<i>Arachis hypogaea</i> L.) Expressed Sequence Tags. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 453-461.	4.1	15
390	Glycerol assimilation and production of 1,3-propanediol by <i>Citrobacter amalonaticus</i> Y19. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5001-5011.	1.7	38
391	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
392	The role of structural bioinformatics resources in the era of integrative structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 710-721.	2.5	17
393	Cloning, purification and metal binding of the HNH motif from colicin E7. <i>Protein Expression and Purification</i> , 2013, 89, 210-218.	0.6	6
394	One Stop Shop for Everything Dictyostelium: dictyBase and the Dicty Stock Center in 2012. <i>Methods in Molecular Biology</i> , 2013, 983, 59-92.	0.4	151
395	In Search of Actionable Targets for Agrigenomics and Microalgal Biofuel Production: Sequence-Structural Diversity Studies on Algal and Higher Plants with a Focus on GPAT Protein. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 173-186.	1.0	20
396	Elements of Coevolution in Biological Sequences. <i>Physical Review Letters</i> , 2013, 110, 178102.	2.9	29
397	Evidence for the widespread distribution of CRISPR-Cas system in the Phylum <i>Cyanobacteria</i> . <i>RNA Biology</i> , 2013, 10, 687-693.	1.5	86
398	Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and development. <i>Toxicology and Applied Pharmacology</i> , 2013, 270, 149-157.	1.3	61

#	ARTICLE	IF	CITATIONS
399	PPlevo : Proteinâ€“protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013, 102, 237-242.	1.3	131
400	Adaptive Smith-Waterman residue match seeding for protein structural alignment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1823-1839.	1.5	2
401	Analysis of DNA Repair and Protection in the Tardigrade <i>Ramazzottius varieornatus</i> and <i>Hypsibius dujardini</i> after Exposure to UVC Radiation. <i>PLoS ONE</i> , 2013, 8, e64793.	1.1	75
402	Genome-wide identification, phylogeny and expression analysis of SUN, OFP and YABBY gene family in tomato. <i>Molecular Genetics and Genomics</i> , 2013, 288, 111-129.	1.0	178
403	Novel inositol catabolic pathway in <i>Thermotoga maritima</i> . <i>Environmental Microbiology</i> , 2013, 15, 2254-2266.	1.8	23
404	Identification of Human Protein Interaction Domains using an ORFeome-based Yeast Two-hybrid Fragment Library. <i>Journal of Proteome Research</i> , 2013, 12, 3181-3192.	1.8	14
405	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	3.2	253
406	Comparative analysis of cation/proton antiporter superfamily in plants. <i>Gene</i> , 2013, 521, 245-251.	1.0	34
407	Molecular Methods of Virus Detection in Lymphoma. <i>Methods in Molecular Biology</i> , 2013, 971, 277-293.	0.4	6
408	Screening and Expression of Genes from Metagenomes. <i>Advances in Applied Microbiology</i> , 2013, 83, 1-68.	1.3	43
409	DNA marker applications to molecular genetics and genomics in tomato. <i>Breeding Science</i> , 2013, 63, 21-30.	0.9	35
410	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
411	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	9.4	1,176
412	Transcriptome of the <i>Lymantria dispar</i> (Gypsy Moth) Larval Midgut in Response to Infection by <i>Bacillus thuringiensis</i> . <i>PLoS ONE</i> , 2013, 8, e61190.	1.1	46
413	Genetic diversity in cultured and wild marine cyanomyoviruses reveals phosphorus stress as a strong selective agent. <i>ISME Journal</i> , 2013, 7, 1827-1841.	4.4	67
414	Proteinâ€“Ligand Interactions: Fundamentals. <i>Methods in Molecular Biology</i> , 2013, 1008, 3-34.	0.4	22
415	Protein Engineering and Stabilization from Sequence Statistics. <i>Methods in Enzymology</i> , 2013, 523, 237-256.	0.4	25
416	Cyclic di-AMP: another second messenger enters the fray. <i>Nature Reviews Microbiology</i> , 2013, 11, 513-524.	13.6	338

#	ARTICLE	IF	CITATIONS
417	An Extracellular Interactome of Immunoglobulin and LRR Proteins Reveals Receptor-Ligand Networks. <i>Cell</i> , 2013, 154, 228-239.	13.5	207
418	Computational analysis of xanthine dehydrogenase enzyme from different source organisms. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2013, 2, 185-189.	1.2	6
419	Plant Cell Wall Deconstruction by Ascomycete Fungi. <i>Annual Review of Microbiology</i> , 2013, 67, 477-498.	2.9	328
420	Comparative analyses of stress-responsive genes in <i>Arabidopsis thaliana</i> : insight from genomic data mining, functional enrichment, pathway analysis and phenomics. <i>Molecular BioSystems</i> , 2013, 9, 1888.	2.9	26
421	The molecular basis of targeting protein kinases in cancer therapeutics. <i>Seminars in Cancer Biology</i> , 2013, 23, 235-242.	4.3	74
422	Structure-guided discovery of the metabolite carboxy-SAM that modulates tRNA function. <i>Nature</i> , 2013, 498, 123-126.	13.7	84
423	Paleoproteomic study of the Iceman's brain tissue. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 3709-3722.	2.4	44
424	Exploring the diversity of SPRY/B30.2-mediated interactions. <i>Trends in Biochemical Sciences</i> , 2013, 38, 38-46.	3.7	67
425	Enlarging Cells Initiating Apomixis in <i>Hieracium praealtum</i> Transition to an Embryo Sac Program prior to Entering Mitosis. <i>Plant Physiology</i> , 2013, 163, 216-231.	2.3	78
426	wks13, a New Biocontrol Agent for <i>Salmonella enterica</i> Serovars Enteritidis and Typhimurium in Foods: Characterization, Application, Sequence Analysis, and Oral Acute Toxicity Study. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1956-1968.	1.4	75
427	RECENT ADVANCES IN FUNCTIONAL REGION PREDICTION BY USING STRUCTURAL AND EVOLUTIONARY INFORMATION – REMAINING PROBLEMS AND FUTURE EXTENSIONS. <i>Computational and Structural Biotechnology Journal</i> , 2013, 8, e201308007.	1.9	8
428	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013, 14, 327.	1.2	74
429	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
430	Emergence of novel domains in proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 47.	3.2	36
431	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. <i>Proteome Science</i> , 2013, 11, S3.	0.7	34
432	HMPAS: Human Membrane Protein Analysis System. <i>Proteome Science</i> , 2013, 11, S7.	0.7	10
433	Evolutionary Acquisition and Loss of Saxitoxin Biosynthesis in Dinoflagellates: the Second "Core" Gene, <i>sxtG</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 2128-2136.	1.4	70
436	Identification and expression profiling analysis of goose melanoma differentiation associated gene 5 (MDA5) gene. <i>Poultry Science</i> , 2013, 92, 2618-2624.	1.5	12

#	ARTICLE	IF	CITATIONS
437	Deubiquitylases From Genes to Organism. <i>Physiological Reviews</i> , 2013, 93, 1289-1315.	13.1	350
438	The structure of Rv3717 reveals a novel amidase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2543-2554.	2.5	25
439	Regulation of H2O2 Stress-responsive Genes through a Novel Transcription Factor in the Protozoan Pathogen <i>Entamoeba histolytica</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 4462-4474.	1.6	48
440	Toxicological evaluation of proteins introduced into food crops. <i>Critical Reviews in Toxicology</i> , 2013, 43, 25-42.	1.9	88
441	Elucidation of Gephyronic Acid Biosynthetic Pathway Revealed Unexpected SAM-Dependent Methylations. <i>Journal of Natural Products</i> , 2013, 76, 2269-2276.	1.5	29
442	Next-Generation Sequencing-Based Transcriptional Profiling of Sacred Lotus "China Antique". <i>Tropical Plant Biology</i> , 2013, 6, 161-179.	1.0	13
443	Calciomics: integrative studies of Ca ²⁺ -binding proteins and their interactomes in biological systems. <i>Metallomics</i> , 2013, 5, 29-42.	1.0	77
444	Functional Identification of Valerena-1,10-diene Synthase, a Terpene Synthase Catalyzing a Unique Chemical Cascade in the Biosynthesis of Biologically Active Sesquiterpenes in <i>Valeriana officinalis</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 3163-3173.	1.6	39
445	Evolutionary analysis of CBL-interacting protein kinase gene family in plants. <i>Plant Growth Regulation</i> , 2013, 71, 49-56.	1.8	21
446	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. <i>ISME Journal</i> , 2013, 7, 2287-2300.	4.4	113
447	Viral Metagenome Annotation Pipeline. , 2013, , 1-12.		1
448	Mechanistic Characterization of the Tetraacyldisaccharide-1-phosphate 4 ⁺ -Kinase LpxK Involved in Lipid A Biosynthesis. <i>Biochemistry</i> , 2013, 52, 2280-2290.	1.2	6
449	Type I pyridoxal 5 ⁺ -phosphate dependent enzymatic domains embedded within multimodular nonribosomal peptide synthetase and polyketide synthase assembly lines. <i>BMC Structural Biology</i> , 2013, 13, 26.	2.3	22
450	Complete Genome Sequence of <i>Anoxybacillus flavithermus</i> TNO-09.006, a Thermophilic Sporeformer Associated with a Dairy-Processing Environment. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
451	Complete Genome Sequence of the <i>Arcobacter butzleri</i> Cattle Isolate 7h1h. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
452	Complete Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>testudinum</i> Strain 03-427 ^T. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
453	A Chemical Proteomics Approach to Profiling the ATP-binding Proteome of <i>Mycobacterium tuberculosis</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1644-1660.	2.5	41
454	Novel <i>Burkholderia mallei</i> Virulence Factors Linked to Specific Host-Pathogen Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3036-3051.	2.5	38

#	ARTICLE	IF	CITATIONS
455	A Significant Fraction of 21-Nucleotide Small RNA Originates from Phased Degradation of Resistance Genes in Several Perennial Species. <i>Plant Physiology</i> , 2013, 162, 741-754.	2.3	74
456	Formin™ cellular structures. <i>Communicative and Integrative Biology</i> , 2013, 6, e27634.	0.6	36
457	Metagenomic <i>De Novo</i> Assembly of an Aquatic Representative of the Verrucomicrobial Class <i>Spartobacteria</i> . <i>MBio</i> , 2013, 4, e00569-12.	1.8	107
458	Between-strand disulfides: forbidden disulfides linking adjacent β^2 -strands. <i>RSC Advances</i> , 2013, 3, 24680.	1.7	8
459	An Overview on Semantic Analysis of Proteomics Data. , 2013, , .		0
460	DNA-binding specificity changes in the evolution of forkhead transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12349-12354.	3.3	150
461	Improving the Prediction of Kinase Binding Affinity Using Homology Models. , 2013, , .		2
462	Ecological Patterns of <i>nifH</i> Genes in Four Terrestrial Climatic Zones Explored with Targeted Metagenomics Using FrameBot, a New Informatics Tool. <i>MBio</i> , 2013, 4, e00592-13.	1.8	279
463	The folding capacity of the mature domain of the dual-targeted plant tRNA nucleotidyltransferase influences organelle selection. <i>Biochemical Journal</i> , 2013, 453, 401-412.	1.7	12
464	Mining the bacterial unknown proteome: identification and characterization of a novel family of highly conserved protective antigens in <i>Staphylococcus aureus</i> . <i>Biochemical Journal</i> , 2013, 455, 273-284.	1.7	26
465	DBATE: database of alternative transcripts expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat050.	1.4	11
466	Evolution of Animal and Plant Dicers: Early Parallel Duplications and Recurrent Adaptation of Antiviral RNA Binding in Plants. <i>Molecular Biology and Evolution</i> , 2013, 30, 627-641.	3.5	138
467	CodonPhyML: Fast Maximum Likelihood Phylogeny Estimation under Codon Substitution Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 1270-1280.	3.5	99
468	Kinannotate, a computer program to identify and classify members of the eukaryotic protein kinase superfamily. <i>Bioinformatics</i> , 2013, 29, 2387-2394.	1.8	43
469	The Complex NOD-Like Receptor Repertoire of the Coral <i>Acropora digitifera</i> Includes Novel Domain Combinations. <i>Molecular Biology and Evolution</i> , 2013, 30, 167-176.	3.5	109
470	MYRF Is a Membrane-Associated Transcription Factor That Autoproteolytically Cleaves to Directly Activate Myelin Genes. <i>PLoS Biology</i> , 2013, 11, e1001625.	2.6	198
471	Investigating the beneficial traits of <i>Trichoderma hamatum</i> GD12 for sustainable agriculture—insights from genomics. <i>Frontiers in Plant Science</i> , 2013, 4, 258.	1.7	119
472	A contribution to the study of plant development evolution based on gene co-expression networks. <i>Frontiers in Plant Science</i> , 2013, 4, 291.	1.7	22

#	ARTICLE	IF	CITATIONS
473	The Methyltransferase NSD3 Has Chromatin-binding Motifs, PHD5-C5HCH, That Are Distinct from Other NSD (Nuclear Receptor SET Domain) Family Members in Their Histone H3 Recognition. <i>Journal of Biological Chemistry</i> , 2013, 288, 4692-4703.	1.6	56
474	APPRIS: annotation of principal and alternative splice isoforms. <i>Nucleic Acids Research</i> , 2013, 41, D110-D117.	6.5	205
475	webPDBinder: a server for the identification of ligand binding sites on protein structures. <i>Nucleic Acids Research</i> , 2013, 41, W308-W313.	6.5	5
476	Functional Analysis of Pneumococcal Drug Efflux Pumps Associates the MATE DinF Transporter with Quinolone Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 248-253.	1.4	37
477	Schistosoma mansoni Sirtuins: Characterization and Potential as Chemotherapeutic Targets. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2428.	1.3	77
478	GEMINI: Integrative Exploration of Genetic Variation and Genome Annotations. <i>PLoS Computational Biology</i> , 2013, 9, e1003153.	1.5	377
479	Assembly of the Type II Secretion System such as Found in <i>Vibrio cholerae</i> Depends on the Novel Pilotin AspS. <i>PLoS Pathogens</i> , 2013, 9, e1003117.	2.1	59
480	Computational Protein Design Quantifies Structural Constraints on Amino Acid Covariation. <i>PLoS Computational Biology</i> , 2013, 9, e1003313.	1.5	35
481	A Network of HMG-box Transcription Factors Regulates Sexual Cycle in the Fungus <i>Podospora anserina</i> . <i>PLoS Genetics</i> , 2013, 9, e1003642.	1.5	58
482	Transposon Domestication versus Mutualism in Ciliate Genome Rearrangements. <i>PLoS Genetics</i> , 2013, 9, e1003659.	1.5	42
483	From Principal Component to Direct Coupling Analysis of Coevolution in Proteins: Low-Eigenvalue Modes are Needed for Structure Prediction. <i>PLoS Computational Biology</i> , 2013, 9, e1003176.	1.5	113
484	Discovery of diversity in xylan biosynthetic genes by transcriptional profiling of a heteroxylan containing mucilaginous tissue. <i>Frontiers in Plant Science</i> , 2013, 4, 183.	1.7	31
485	The Repertoires of Ubiquitinating and Deubiquitinating Enzymes in Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 1172-1187.	3.5	70
486	The <i>Tarenaya hassleriana</i> Genome Provides Insight into Reproductive Trait and Genome Evolution of Crucifers. <i>Plant Cell</i> , 2013, 25, 2813-2830.	3.1	95
487	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. <i>Bioinformatics</i> , 2013, 29, 1577-1579.	1.8	129
488	KIDFamMap: a database of kinase-inhibitor-disease family maps for kinase inhibitor selectivity and binding mechanisms. <i>Nucleic Acids Research</i> , 2013, 41, D430-D440.	6.5	23
489	The pneumococcal MgaSpn virulence transcriptional regulator generates multimeric complexes on linear double-stranded DNA. <i>Nucleic Acids Research</i> , 2013, 41, 6975-6991.	6.5	30
490	Adjusting scoring matrices to correct overextended alignments. <i>Bioinformatics</i> , 2013, 29, 3007-3013.	1.8	12

#	ARTICLE	IF	CITATIONS
491	Gymnosperm B-sister genes may be involved in ovule/seed development and, in some species, in the growth of fleshy fruit-like structures. <i>Annals of Botany</i> , 2013, 112, 535-544.	1.4	19
492	ToPS: A Framework to Manipulate Probabilistic Models of Sequence Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003234.	1.5	6
493	PUMA: A Unified Framework for Penalized Multiple Regression Analysis of GWAS Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003101.	1.5	38
494	Low Frequency Variants, Collapsed Based on Biological Knowledge, Uncover Complexity of Population Stratification in 1000 Genomes Project Data. <i>PLoS Genetics</i> , 2013, 9, e1003959.	1.5	35
495	DNA Topoisomerase II Is Involved in Regulation of Cyst Wall Protein Genes and Differentiation in <i>Giardia lamblia</i> . <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2218.	1.3	11
496	Signatures of Pleiotropy, Economy and Convergent Evolution in a Domain-Resolved Map of Human-Virus Protein-Protein Interaction Networks. <i>PLoS Pathogens</i> , 2013, 9, e1003778.	2.1	47
497	A Compendium of <i>Caenorhabditis elegans</i> RNA Binding Proteins Predicts Extensive Regulation at Multiple Levels. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 297-304.	0.8	31
498	Structural Disorder Provides Increased Adaptability for Vesicle Trafficking Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1003144.	1.5	46
499	The Genome of <i>Spraguea lophii</i> and the Basis of Host-Microsporidian Interactions. <i>PLoS Genetics</i> , 2013, 9, e1003676.	1.5	66
500	TRIAD1 and HHARI bind to and are activated by distinct neddylated Cullin-RING ligase complexes. <i>EMBO Journal</i> , 2013, 32, 2848-2860.	3.5	84
501	Brittle Culm1, a COBRA-Like Protein, Functions in Cellulose Assembly through Binding Cellulose Microfibrils. <i>PLoS Genetics</i> , 2013, 9, e1003704.	1.5	129
502	Tiki, at the head of a new superfamily of enzymes. <i>Bioinformatics</i> , 2013, 29, 2371-2374.	1.8	11
503	Structure-Based Function Prediction of Uncharacterized Protein Using Binding Sites Comparison. <i>PLoS Computational Biology</i> , 2013, 9, e1003341.	1.5	38
504	Functional and Evolutionary Analysis of the Genome of an Obligate Fungal Symbiont. <i>Genome Biology and Evolution</i> , 2013, 5, 891-904.	1.1	54
505	Recombineering in <i>Corynebacterium glutamicum</i> combined with optical nanosensors: a general strategy for fast producer strain generation. <i>Nucleic Acids Research</i> , 2013, 41, 6360-6369.	6.5	141
506	Structures of RNA polymerase II complexes with Bye1, a chromatin-binding PHF3/DIDO homologue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15277-15282.	3.3	38
507	The First Structure of a Mycobacteriophage, the <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> Phage Araucaria. <i>Journal of Virology</i> , 2013, 87, 8099-8109.	1.5	35
508	Genome-Wide Characterization of Endogenous Retroviruses in the Bat <i>Myotis lucifugus</i> Reveals Recent and Diverse Infections. <i>Journal of Virology</i> , 2013, 87, 8493-8501.	1.5	46

#	ARTICLE	IF	CITATIONS
509	Control of RNA Stability by NrrF, an Iron-Regulated Small RNA in <i>Neisseria gonorrhoeae</i> . <i>Journal of Bacteriology</i> , 2013, 195, 5166-5173.	1.0	22
510	Genetic Control and Comparative Genomic Analysis of Flowering Time in <i>Setaria</i> (Poaceae). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 283-295.	0.8	97
511	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. <i>Nucleic Acids Research</i> , 2013, 41, 790-803.	6.5	44
512	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. <i>Briefings in Functional Genomics</i> , 2013, 12, 366-380.	1.3	57
513	Proteogenomic Analysis of <i>Bradyrhizobium japonicum</i> USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3388-3397.	2.5	39
514	Evolution of Tre-2/Bub2/Cdc16 (TBC) Rab GTPase-activating proteins. <i>Molecular Biology of the Cell</i> , 2013, 24, 1574-1583.	0.9	57
515	Improving the Lethal Effect of Cpl-7, a Pneumococcal Phage Lysozyme with Broad Bactericidal Activity, by Inverting the Net Charge of Its Cell Wall-Binding Module. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 5355-5365.	1.4	89
516	MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. <i>Molecular Biology and Evolution</i> , 2013, 30, 772-780.	3.5	32,012
517	Phylogenetic Distribution of Potential Cellulases in Bacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1545-1554.	1.4	267
518	The Evolution of MicroRNA Pathway Protein Components in Cnidaria. <i>Molecular Biology and Evolution</i> , 2013, 30, 2541-2552.	3.5	57
519	Putting the Pieces Together: High-performance LC-MS/MS Provides Network-, Pathway-, and Protein-level Perspectives in <i>Populus</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 106-119.	2.5	26
520	Mapping of Genotype-Phenotype Diversity among Clinical Isolates of <i>Mycobacterium tuberculosis</i> by Sequence-Based Transcriptional Profiling. <i>Genome Biology and Evolution</i> , 2013, 5, 1849-1862.	1.1	69
521	CEP89 is required for mitochondrial metabolism and neuronal function in man and fly. <i>Human Molecular Genetics</i> , 2013, 22, 3138-3151.	1.4	38
522	Protein Similarity Networks Reveal Relationships among Sequence, Structure, and Function within the Cupin Superfamily. <i>PLoS ONE</i> , 2013, 8, e74477.	1.1	53
523	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	6.5	745
524	The Genetic Architecture of Degenerin/Epithelial Sodium Channels in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 441-450.	0.8	85
525	Global analysis of <i>Drosophila</i> Cys2-His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. <i>Genome Research</i> , 2013, 23, 928-940.	2.4	70
526	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. <i>Genomics and Informatics</i> , 2013, 11, 102.	0.4	117

#	ARTICLE	IF	CITATIONS
527	FunGene: the functional gene pipeline and repository. <i>Frontiers in Microbiology</i> , 2013, 4, 291.	1.5	518
528	HAMAP in 2013, new developments in the protein family classification and annotation system. <i>Nucleic Acids Research</i> , 2013, 41, D584-D589.	6.5	57
529	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013, 41, D445-D451.	6.5	99
530	A Genomic Survey of HECT Ubiquitin Ligases in Eukaryotes Reveals Independent Expansions of the HECT System in Several Lineages. <i>Genome Biology and Evolution</i> , 2013, 5, 833-847.	1.1	35
531	Draft Genome Sequences of Human Pathogenic Fungus <i>Geomyces pannorum</i> Sensu Lato and Bat White Nose Syndrome Pathogen <i>Geomyces</i> (<i>Pseudogymnoascus</i>) <i>destructans</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	27
532	eProSâ€”a database and toolbox for investigating protein sequenceâ€”structureâ€”function relationships through energy profiles. <i>Nucleic Acids Research</i> , 2013, 41, D320-D326.	6.5	8
533	MISTIC: mutual information server to infer coevolution. <i>Nucleic Acids Research</i> , 2013, 41, W8-W14.	6.5	157
534	Identification of SPOR Domain Amino Acids Important for Septal Localization, Peptidoglycan Binding, and a Disulfide Bond in the Cell Division Protein FtsN. <i>Journal of Bacteriology</i> , 2013, 195, 5308-5315.	1.0	20
535	Inherited mutations in the helicase RTEL1 cause telomere dysfunction and Hoyeraalâ€”Hreidarsson syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3408-16.	3.3	127
536	Fragment recruitment on metabolic pathways: comparative metabolic profiling of metagenomes and metatranscriptomes. <i>Bioinformatics</i> , 2013, 29, 790-791.	1.8	8
537	Association of candidate genes with drought tolerance traits in diverse perennial ryegrass accessions. <i>Journal of Experimental Botany</i> , 2013, 64, 1537-1551.	2.4	83
538	Structures of apo- and ssDNA-bound YdbC from <i>Lactococcus lactis</i> uncover the function of protein domain family DUF2128 and expand the single-stranded DNA-binding domain proteome. <i>Nucleic Acids Research</i> , 2013, 41, 2756-2768.	6.5	10
539	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013, 41, D246-D251.	6.5	488
540	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , 2013, 41, 4549-4564.	6.5	108
541	An Unbiased Approach to Identifying Tau Kinases That Phosphorylate Tau at Sites Associated with Alzheimer Disease. <i>Journal of Biological Chemistry</i> , 2013, 288, 23331-23347.	1.6	99
542	Mediation of Clathrin-Dependent Trafficking during Cytokinesis and Cell Expansion by <i>Arabidopsis</i> STOMATAL CYTOKINESIS DEFECTIVE Proteins. <i>Plant Cell</i> , 2013, 25, 3910-3925.	3.1	44
543	Structural studies of <i>Pseudomonas</i> and <i>Chromobacterium</i> %aminotransferases provide insights into their differing substrate specificity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 564-576.	2.5	51
544	Structure of <i>Neisseria meningitidis</i> lipoprotein GNA1162. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 362-368.	0.7	6

#	ARTICLE	IF	CITATIONS
545	Cloning, overexpression, purification and preliminary X-ray analysis of the catalytic domain of the ethylene receptor ETR1 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1307-1309.	0.7	3
546	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. <i>Journal of Bacteriology</i> , 2013, 195, 4466-4475.	1.0	16
547	<i>Pseudomonas syringae</i> pv. tomato DC3000 CmaL (PSPTO4723), a DUF1330 Family Member, Is Needed To Produce <i>l</i> -isoleucine, a Precursor for the Phytotoxin Coronatine. <i>Journal of Bacteriology</i> , 2013, 195, 287-296.	1.0	28
548	Transcription Regulation of Plastid Genes Involved in Sulfate Transport in Viridiplantae. <i>BioMed Research International</i> , 2013, 2013, 1-6.	0.9	12
549	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat023.	1.4	22
550	Overexpressed TPX2 causes ectopic formation of microtubular arrays in the nuclei of acentrosomal plant cells. <i>Journal of Experimental Botany</i> , 2013, 64, 4575-4587.	2.4	31
551	Different functions for the domains of the <i>Arabidopsis thaliana</i> RMI1 protein in DNA cross-link repair, somatic and meiotic recombination. <i>Nucleic Acids Research</i> , 2013, 41, 9349-9360.	6.5	25
552	An estimated 5% of new protein structures solved today represent a new Pfam family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2186-2193.	2.5	12
553	Utilization of Heme as an Iron Source by Marine Alphaproteobacteria in the Roseobacter Clade. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5753-5762.	1.4	31
554	Two RNA-binding motifs in eIF3 direct HCV IRES-dependent translation. <i>Nucleic Acids Research</i> , 2013, 41, 7512-7521.	6.5	64
555	Genes involved in host-parasite interactions can be revealed by their correlated expression. <i>Nucleic Acids Research</i> , 2013, 41, 1508-1518.	6.5	38
556	Nucleotide-independent cytoskeletal scaffolds in bacteria. <i>Cytoskeleton</i> , 2013, 70, 409-423.	1.0	50
557	Improved contact prediction in proteins: Using pseudolikelihoods to infer Potts models. <i>Physical Review E</i> , 2013, 87, 012707.	0.8	545
558	Analysis of periplasmic sensor domains from <i>Anaeromyxobacter dehalogenans</i> CP: Structure of one sensor domain from a histidine kinase and another from a chemotaxis protein. <i>MicrobiologyOpen</i> , 2013, 2, 766-777.	1.2	7
559	Crystal Structure and Site-directed Mutagenesis of 3-Ketosteroid 1-Dehydrogenase from <i>Rhodococcus erythropolis</i> SQ1 Explain Its Catalytic Mechanism. <i>Journal of Biological Chemistry</i> , 2013, 288, 35559-35568.	1.6	48
560	Identification of mycobacterial lectins from genomic data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 644-657.	1.5	15
561	Characterization of an M28 metalloprotease family member residing in the yeast vacuole. <i>FEMS Yeast Research</i> , 2013, 13, 471-484.	1.1	9
562	The network of stabilizing contacts in proteins studied by coevolutionary data. <i>Journal of Chemical Physics</i> , 2013, 139, 155103.	1.2	33

#	ARTICLE	IF	CITATIONS
563	The catalytic domain CysPc of the <sc>DEK</sc>1 calpain is functionally conserved in land plants. <i>Plant Journal</i> , 2013, 75, 742-754.	2.8	27
564	Complete mitochondrial genome of the aluminum-tolerant fungus <i><sc>R</sc>hodotorula taiwanensis</i> <sc>RS</sc>1 and comparative analysis of <i><sc>B</sc>asidiomycota</i> mitochondrial genomes. <i>MicrobiologyOpen</i> , 2013, 2, 308-317.	1.2	14
565	A comparison of multi-label techniques based on problem transformation for protein functional prediction. , 2013, 2013, 2688-91.		2
566	Insights into the oligomerization of <sc>CRMP</sc>s: crystal structure of human collapsin response mediator protein 5. <i>Journal of Neurochemistry</i> , 2013, 125, 855-868.	2.1	25
568	The expanding superfamily of gelsolin homology domain proteins. <i>Cytoskeleton</i> , 2013, 70, 775-795.	1.0	39
569	Searching algorithm for type IV secretion system effectors 1.0: a tool for predicting type IV effectors and exploring their genomic context. <i>Nucleic Acids Research</i> , 2013, 41, 9218-9229.	6.5	50
570	<i>COLLAPSED ABNORMAL POLLEN1</i> Gene Encoding the Arabinokinase-Like Protein Is Involved in Pollen Development in Rice. <i>Plant Physiology</i> , 2013, 162, 858-871.	2.3	45
571	Rice DB : an Oryza Information Portal linking annotation, subcellular location, function, expression, regulation, and evolutionary information for rice and Arabidopsis. <i>Plant Journal</i> , 2013, 76, 1057-1073.	2.8	29
572	Role of <sc>C</sc>a²⁺ in folding the tandem Î²-sandwich extender domains of a bacterial ice-binding adhesin. <i>FEBS Journal</i> , 2013, 280, 5919-5932.	2.2	20
573	Crystal structure of the Î³-aminotransferase from <i>Paracoccus denitrificans</i> and its phylogenetic relationship with other class III amino-transferases that have biotechnological potential. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 774-787.	1.5	39
574	Solution structure of the recombinant target recognition domain of zoocin A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 722-727.	1.5	7
575	A Thermophilic Alkalophilic Î±-Amylase from <i>Bacillus</i> sp. AAH-31 Shows a Novel Domain Organization among Glycoside Hydrolase Family 13 Enzymes. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 1867-1873.	0.6	7
576	In Silico Ionomics Segregates Parasitic from Free-Living Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 1902-1909.	1.1	4
577	The CD225 Domain of IFITM3 Is Required for both IFITM Protein Association and Inhibition of Influenza A Virus and Dengue Virus Replication. <i>Journal of Virology</i> , 2013, 87, 7837-7852.	1.5	154
578	Two potentially novel amylolytic enzyme specificities in the prokaryotic glycoside hydrolase Î±-amylase family GH57. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2584-2593.	0.7	18
579	Coupling mutagenesis and parallel deep sequencing to probe essential residues in a genome or gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E848-57.	3.3	36
580	Identification of a Mammalian-type Phosphatidylglycerophosphate Phosphatase in the Eubacterium <i>Rhodopirellula baltica</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 5176-5185.	1.6	6
581	Eukaryotic resistance to fluoride toxicity mediated by a widespread family of fluoride export proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19018-19023.	3.3	108

#	ARTICLE	IF	CITATIONS
582	Computational identification of novel biochemical systems involved in oxidation, glycosylation and other complex modifications of bases in DNA. <i>Nucleic Acids Research</i> , 2013, 41, 7635-7655.	6.5	115
583	Isoform-selective Oligomer Formation of <i>Saccharomyces cerevisiae</i> p24 Family Proteins. <i>Journal of Biological Chemistry</i> , 2013, 288, 37057-37070.	1.6	18
584	Characterization of the Yeast Actin Patch Protein App1p Phosphatidate Phosphatase. <i>Journal of Biological Chemistry</i> , 2013, 288, 6427-6437.	1.6	20
585	A Conserved Hydrolase Responsible for the Cleavage of Aminoacylphosphatidylglycerol in the Membrane of <i>Enterococcus faecium</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 22768-22776.	1.6	19
586	Genome-Wide SNP Genotyping to Infer the Effects on Gene Functions in Tomato. <i>DNA Research</i> , 2013, 20, 221-233.	1.5	58
587	All or Nothing: Protein Complexes Flip Essentiality between Distantly Related Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 1049-1059.	1.1	38
588	Mechanisms and Dynamics of Orphan Gene Emergence in Insect Genomes. <i>Genome Biology and Evolution</i> , 2013, 5, 439-455.	1.1	128
589	The Genome of the Anaerobic Fungus <i>Orpinomyces</i> sp. Strain C1A Reveals the Unique Evolutionary History of a Remarkable Plant Biomass Degrader. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4620-4634.	1.4	224
590	Cooperative Degradation of Chitin by Extracellular and Cell Surface-Expressed Chitinases from <i>Paenibacillus</i> sp. Strain FPU-7. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7482-7490.	1.4	66
591	The mutational landscape of phosphorylation signaling in cancer. <i>Scientific Reports</i> , 2013, 3, 2651.	1.6	149
592	CRITERIA FOR AN UPDATED CLASSIFICATION OF HUMAN TRANSCRIPTION FACTOR DNA-BINDING DOMAINS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340007.	0.3	9
593	A link between host plant adaptation and pesticide resistance in the polyphagous spider mite <i>Tetranychus urticae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E113-22.	3.3	347
594	On the Origin of Large Flexibility of P-glycoprotein in the Inward-facing State. <i>Journal of Biological Chemistry</i> , 2013, 288, 19211-19220.	1.6	120
595	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013, 41, e121-e121.	6.5	1,214
596	dcGO: database of domain-centric ontologies on functions, phenotypes, diseases and more. <i>Nucleic Acids Research</i> , 2013, 41, D536-D544.	6.5	98
597	Evolution of the JAK-STAT pathway. <i>Jak-stat</i> , 2013, 2, e22756.	2.2	59
598	Horizontal Transfer and Evolution of Prokaryote Transposable Elements in Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 822-832.	1.1	38
599	PIECE: a database for plant gene structure comparison and evolution. <i>Nucleic Acids Research</i> , 2013, 41, D1159-D1166.	6.5	50

#	ARTICLE	IF	CITATIONS
600	Exon-phase symmetry and intrinsic structural disorder promote modular evolution in the human genome. <i>Nucleic Acids Research</i> , 2013, 41, 4409-4422.	6.5	15
601	Propeptides of eukaryotic proteases encode histidines to exploit organelle pH for regulation. <i>FASEB Journal</i> , 2013, 27, 2939-2945.	0.2	2
602	Transcriptomic and biochemical analyses identify a family of chlorhexidine efflux proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20254-20259.	3.3	138
603	Protein-protein interaction networks studies and importance of 3D structure knowledge. <i>Expert Review of Proteomics</i> , 2013, 10, 511-520.	1.3	17
604	To Tree or Not to Tree? Genome-Wide Quantification of Recombination and Reticulate Evolution during the Diversification of Strict Intracellular Bacteria. <i>Genome Biology and Evolution</i> , 2013, 5, 2305-2317.	1.1	21
605	Transcriptomic analysis of <i>Ustilago maydis</i> infecting <i>Arabidopsis</i> reveals important aspects of the fungus pathogenic mechanisms. <i>Plant Signaling and Behavior</i> , 2013, 8, e25059.	1.2	25
606	PPR proteins of green algae. <i>RNA Biology</i> , 2013, 10, 1526-1542.	1.5	34
607	Genomic Reconstruction of the Transcriptional Regulatory Network in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2463-2473.	1.0	54
608	<i>Coxiella burnetii</i> effector protein subverts clathrin-mediated vesicular trafficking for pathogen vacuole biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4770-9.	3.3	85
610	Identification, characterization and preliminary X-ray diffraction analysis of the rolling-circle replication initiator protein from plasmid pSTK1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1123-1126.	0.7	1
611	PlantTFcat: an online plant transcription factor and transcriptional regulator categorization and analysis tool. <i>BMC Bioinformatics</i> , 2013, 14, 321.	1.2	119
612	Characterization and transcript profiling of the pectin methylesterase (PME) and pectin methylesterase inhibitor (PMEI) gene families in flax (<i>Linum usitatissimum</i>). <i>BMC Genomics</i> , 2013, 14, 742.	1.2	56
613	RegPrecise 3.0 - A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	1.2	408
614	Genomic and expression analysis of the flax (<i>Linum usitatissimum</i>) family of glycosyl hydrolase 35 genes. <i>BMC Genomics</i> , 2013, 14, 344.	1.2	24
615	The Complete Genome Sequence of <i>Methanobrevibacter</i> sp. AbM4. <i>Standards in Genomic Sciences</i> , 2013, 8, 215-227.	1.5	42
616	Non-contiguous finished genome sequence and description of <i>Anaerococcus pacaensis</i> sp. nov., a new species of anaerobic bacterium. <i>Standards in Genomic Sciences</i> , 2013, 8, 548-560.	1.5	9
617	Non-contiguous genome sequence of <i>Mycobacterium simiae</i> strain DSM 44165T. <i>Standards in Genomic Sciences</i> , 2013, 8, 306-317.	1.5	5
618	Large-scale multiple sequence alignment visualization through gradient vector flow analysis. , 2013, , .		4

#	ARTICLE	IF	CITATIONS
619	A potential source for cellulolytic enzyme discovery and environmental aspects revealed through metagenomics of Brazilian mangroves. <i>AMB Express</i> , 2013, 3, 65.	1.4	40
620	The switches.ELM Resource: A Compendium of Conditional Regulatory Interaction Interfaces. <i>Science Signaling</i> , 2013, 6, rs7.	1.6	101
621	Inference of Hopfield-Potts patterns from covariation in protein families: calculation and statistical error bars. <i>Journal of Physics: Conference Series</i> , 2013, 473, 012010.	0.3	1
622	MisPred: a resource for identification of erroneous protein sequences in public databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat053.	1.4	17
623	Complete Genome Sequence of the Thermophilic and Facultatively Chemolithoautotrophic Sulfate Reducer <i>Archaeoglobus sulfaticallidus</i> Strain PM70-1 ^T. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
624	Feature-Based Classification of Amino Acid Substitutions outside Conserved Functional Protein Domains. <i>Scientific World Journal, The</i> , 2013, 2013, 1-10.	0.8	5
625	Ecogenomic Perspectives on Domains of Unknown Function: Correlation-Based Exploration of Marine Metagenomes. <i>PLoS ONE</i> , 2013, 8, e50869.	1.1	11
626	Integron Gene Cassettes: A Repository of Novel Protein Folds with Distinct Interaction Sites. <i>PLoS ONE</i> , 2013, 8, e52934.	1.1	11
627	De Novo Transcriptome Sequencing and Analysis for <i>Venturia inaequalis</i> , the Devastating Apple Scab Pathogen. <i>PLoS ONE</i> , 2013, 8, e53937.	1.1	32
628	Prediction of Contact Residue Pairs Based on Co-Substitution between Sites in Protein Structures. <i>PLoS ONE</i> , 2013, 8, e54252.	1.1	14
629	Increasing Sequence Search Sensitivity with Transitive Alignments. <i>PLoS ONE</i> , 2013, 8, e54422.	1.1	3
630	Improving Microbial Genome Annotations in an Integrated Database Context. <i>PLoS ONE</i> , 2013, 8, e54859.	1.1	54
631	Staring at the Cold Sun: Blue Light Regulation Is Distributed within the Genus <i>Acinetobacter</i> . <i>PLoS ONE</i> , 2013, 8, e55059.	1.1	49
632	Evolution of the Ferric Reductase Domain (FRD) Superfamily: Modularity, Functional Diversification, and Signature Motifs. <i>PLoS ONE</i> , 2013, 8, e58126.	1.1	68
633	Horizontal Transfer of a Subtilisin Gene from Plants into an Ancestor of the Plant Pathogenic Fungal Genus <i>Colletotrichum</i> . <i>PLoS ONE</i> , 2013, 8, e59078.	1.1	28
634	Reduce Manual Curation by Combining Gene Predictions from Multiple Annotation Engines, a Case Study of Start Codon Prediction. <i>PLoS ONE</i> , 2013, 8, e63523.	1.1	12
635	Transcriptomic Analysis of a Tertiary Relict Plant, Extreme Xerophyte <i>Reaumuria soongorica</i> to Identify Genes Related to Drought Adaptation. <i>PLoS ONE</i> , 2013, 8, e63993.	1.1	55
636	Tracing Evolutionary Footprints to Identify Novel Gene Functional Linkages. <i>PLoS ONE</i> , 2013, 8, e66817.	1.1	3

#	ARTICLE	IF	CITATIONS
637	Systematic Analysis and Comparison of Nucleotide-Binding Site Disease Resistance Genes in a Diploid Cotton <i>Gossypium raimondii</i> . PLoS ONE, 2013, 8, e68435.	1.1	55
638	Structural Basis of the Novel <i>S. pneumoniae</i> Virulence Factor, GHIP, a Glycosyl Hydrolase 25 Participating in Host-Cell Invasion. PLoS ONE, 2013, 8, e68647.	1.1	13
639	Plant F-Box Protein Evolution Is Determined by Lineage-Specific Timing of Major Gene Family Expansion Waves. PLoS ONE, 2013, 8, e68672.	1.1	25
640	TCW: Transcriptome Computational Workbench. PLoS ONE, 2013, 8, e69401.	1.1	17
641	Increments and Duplication Events of Enzymes and Transcription Factors Influence Metabolic and Regulatory Diversity in Prokaryotes. PLoS ONE, 2013, 8, e69707.	1.1	18
642	Metagenomic Guilt by Association: An Operonic Perspective. PLoS ONE, 2013, 8, e71484.	1.1	11
643	Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. PLoS ONE, 2013, 8, e74056.	1.1	12
644	High-Throughput RNA Sequencing of <i>Pseudomonas</i> -Infected <i>Arabidopsis</i> Reveals Hidden Transcriptome Complexity and Novel Splice Variants. PLoS ONE, 2013, 8, e74183.	1.1	82
645	A Proteomic Investigation of Soluble Olfactory Proteins in <i>Anopheles gambiae</i> . PLoS ONE, 2013, 8, e75162.	1.1	37
646	Automatic Identification of Highly Conserved Family Regions and Relationships in Genome Wide Datasets Including Remote Protein Sequences. PLoS ONE, 2013, 8, e75458.	1.1	7
647	Turnerbactin, a Novel Triscatecholate Siderophore from the Shipworm Endosymbiont <i>Teredinibacter turnerae</i> T7901. PLoS ONE, 2013, 8, e76151.	1.1	55
648	DIRS and Ngaro Retrotransposons in Fungi. PLoS ONE, 2013, 8, e76319.	1.1	16
649	Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. PLoS ONE, 2013, 8, e77181.	1.1	88
650	Identification of Novel Vaccine Candidates against Multidrug-Resistant <i>Acinetobacter baumannii</i> . PLoS ONE, 2013, 8, e77631.	1.1	80
651	SIFT Indel: Predictions for the Functional Effects of Amino Acid Insertions/Deletions in Proteins. PLoS ONE, 2013, 8, e77940.	1.1	108
652	Integrative Pathway-Based Approach for Genome-Wide Association Studies: Identification of New Pathways for Rheumatoid Arthritis and Type 1 Diabetes. PLoS ONE, 2013, 8, e78577.	1.1	9
653	The BtaF Trimeric Autotransporter of <i>Brucella suis</i> Is Involved in Attachment to Various Surfaces, Resistance to Serum and Virulence. PLoS ONE, 2013, 8, e79770.	1.1	26
654	Putative Sugar Transporters of the Mustard Leaf Beetle <i>Phaedon cochleariae</i> : Their Phylogeny and Role for Nutrient Supply in Larval Defensive Glands. PLoS ONE, 2013, 8, e84461.	1.1	16

#	ARTICLE	IF	CITATIONS
655	Homologs of the yeast Tvp38 vesicle-associated protein are conserved in chloroplasts and cyanobacteria. <i>Frontiers in Plant Science</i> , 2013, 4, 467.	1.7	24
656	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. <i>Frontiers in Genetics</i> , 2013, 4, 62.	1.1	7
657	Meta4: a web application for sharing and annotating metagenomic gene predictions using web services. <i>Frontiers in Genetics</i> , 2013, 4, 168.	1.1	8
658	Interaction between the genomes of <i>Lactococcus lactis</i> and phages of the P335 species. <i>Frontiers in Microbiology</i> , 2013, 4, 257.	1.5	36
659	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.	1.5	44
660	Exploiting a Reference Genome in Terms of Duplications: The Network of Paralogs and Single Copy Genes in <i>Arabidopsis thaliana</i> . <i>Biology</i> , 2013, 2, 1465-1487.	1.3	6
661	The Clip-Segment of the von Willebrand Domain 1 of the BMP Modulator Protein Crossveinless 2 Is Preformed. <i>Molecules</i> , 2013, 18, 11658-11682.	1.7	9
662	NRF2-ome: An Integrated Web Resource to Discover Protein Interaction and Regulatory Networks of NRF2. <i>Oxidative Medicine and Cellular Longevity</i> , 2013, 2013, 1-9.	1.9	38
663	Structure Topology Prediction of Discriminative Sequence Motifs in Membrane Proteins with Domains of Unknown Functions. <i>Structural Biology</i> , 2013, 2013, 1-10.	0.0	2
664	Activation of an Endogenous Retrotransposon Associated with Epigenetic Changes in <i>Lotus japonicus</i> : A Tool for Functional Genomics in Legumes. <i>Plant Genome</i> , 2013, 6, plantgenome2013.04.0009.	1.6	6
665	Flexibility of the Linker between the Domains of DNA Methyltransferase SsoII Revealed by Small-Angle X-Ray Scattering: Implications for Transcription Regulation in SsoII Restriction-Modification System. <i>PLoS ONE</i> , 2014, 9, e93453.	1.1	7
666	Intrinsic Disorder in the BK Channel and Its Interactome. <i>PLoS ONE</i> , 2014, 9, e94331.	1.1	16
667	Evolution of Mitochondria Reconstructed from the Energy Metabolism of Living Bacteria. <i>PLoS ONE</i> , 2014, 9, e96566.	1.1	52
668	Transcriptome Analysis of the Oil-Rich Tea Plant, <i>Camellia oleifera</i> , Reveals Candidate Genes Related to Lipid Metabolism. <i>PLoS ONE</i> , 2014, 9, e104150.	1.1	73
669	An Improved Method for Including Upper Size Range Plasmids in Metamobilomes. <i>PLoS ONE</i> , 2014, 9, e104405.	1.1	35
670	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. <i>PLoS ONE</i> , 2014, 9, e87645.	1.1	34
671	Novel Genes Participating in the Formation of Prismatic and Nacreous Layers in the Pearl Oyster as Revealed by Their Tissue Distribution and RNA Interference Knockdown. <i>PLoS ONE</i> , 2014, 9, e84706.	1.1	44
672	Sequencing, De Novo Assembly and Annotation of the Colorado Potato Beetle, <i>Leptinotarsa decemlineata</i> , Transcriptome. <i>PLoS ONE</i> , 2014, 9, e86012.	1.1	60

#	ARTICLE	IF	CITATIONS
673	Genome and Transcriptome Analysis of the Basidiomycetous Yeast <i>Pseudozyma antarctica</i> Producing Extracellular Glycolipids, Mannosylerythritol Lipids. PLoS ONE, 2014, 9, e86490.	1.1	45
674	RNA Viral Metagenome of Whiteflies Leads to the Discovery and Characterization of a Whitefly-Transmitted Carlavirus in North America. PLoS ONE, 2014, 9, e86748.	1.1	46
675	Training Set Selection for the Prediction of Essential Genes. PLoS ONE, 2014, 9, e86805.	1.1	38
676	Citrus sinensis Annotation Project (CAP): A Comprehensive Database for Sweet Orange Genome. PLoS ONE, 2014, 9, e87723.	1.1	47
677	Transcriptomics and Identification of the Chemoreceptor Superfamily of the Pupal Parasitoid of the Oriental Fruit Fly, <i>Spalangia endius</i> Walker (Hymenoptera: Pteromalidae). PLoS ONE, 2014, 9, e87800.	1.1	14
678	Hundreds of Circular Novel Plasmids and DNA Elements Identified in a Rat Cecum Metamobilome. PLoS ONE, 2014, 9, e87924.	1.1	107
679	Functionally Enigmatic Genes: A Case Study of the Brain Ignorome. PLoS ONE, 2014, 9, e88889.	1.1	77
680	Inferring Domain-Domain Interactions from Protein-Protein Interactions with Formal Concept Analysis. PLoS ONE, 2014, 9, e88943.	1.1	6
681	Improved Lanthipeptide Detection and Prediction for antiSMASH. PLoS ONE, 2014, 9, e89420.	1.1	45
682	Hsp90-Dependent Assembly of the DBC2/RhoBTB2-Cullin3 E3-Ligase Complex. PLoS ONE, 2014, 9, e90054.	1.1	16
683	High Precision Prediction of Functional Sites in Protein Structures. PLoS ONE, 2014, 9, e91240.	1.1	15
684	De Novo Structure Prediction of Globular Proteins Aided by Sequence Variation-Derived Contacts. PLoS ONE, 2014, 9, e92197.	1.1	98
685	MP3: A Software Tool for the Prediction of Pathogenic Proteins in Genomic and Metagenomic Data. PLoS ONE, 2014, 9, e93907.	1.1	112
686	Unraveling Patterns of Site-to-Site Synonymous Rates Variation and Associated Gene Properties of Protein Domains and Families. PLoS ONE, 2014, 9, e95034.	1.1	17
687	Characterization of an Archaeal Two-Component System That Regulates Methanogenesis in <i>Methanosaeta harundinacea</i> . PLoS ONE, 2014, 9, e95502.	1.1	17
688	Chitinase-Like (CTL) and Cellulose Synthase (CESA) Gene Expression in Gelatinous-Type Cellulosic Walls of Flax (<i>Linum usitatissimum</i> L.) Bast Fibers. PLoS ONE, 2014, 9, e97949.	1.1	59
689	Transcriptome Profiling to Discover Putative Genes Associated with Paraquat Resistance in Goosegrass (<i>Eleusine indica</i> L.). PLoS ONE, 2014, 9, e99940.	1.1	58
690	Genome Duplication and Gene Loss Affect the Evolution of Heat Shock Transcription Factor Genes in Legumes. PLoS ONE, 2014, 9, e102825.	1.1	79

#	ARTICLE	IF	CITATIONS
691	De Novo Assembly of the Perennial Ryegrass Transcriptome Using an RNA-Seq Strategy. PLoS ONE, 2014, 9, e103567.	1.1	44
692	Phosphorylation Site Dynamics of Early T-cell Receptor Signaling. PLoS ONE, 2014, 9, e104240.	1.1	54
693	Molecular and Evolutionary Analysis of NEAr-Iron Transporter (NEAT) Domains. PLoS ONE, 2014, 9, e104794.	1.1	43
694	Transcriptomic Analysis of Tail Regeneration in the Lizard <i>Anolis carolinensis</i> Reveals Activation of Conserved Vertebrate Developmental and Repair Mechanisms. PLoS ONE, 2014, 9, e105004.	1.1	112
695	Structural Insights into the Recognition of Phosphopeptide by the FHA Domain of Kanadaptin. PLoS ONE, 2014, 9, e107309.	1.1	6
696	Full-Length Enriched cDNA Libraries and ORFeome Analysis of Sugarcane Hybrid and Ancestor Genotypes. PLoS ONE, 2014, 9, e107351.	1.1	26
697	Combining Structural Modeling with Ensemble Machine Learning to Accurately Predict Protein Fold Stability and Binding Affinity Effects upon Mutation. PLoS ONE, 2014, 9, e107353.	1.1	71
698	Sequence and Annotation of the Apicoplast Genome of the Human Pathogen <i>Babesia microti</i> . PLoS ONE, 2014, 9, e107939.	1.1	26
699	Hybrid and Rogue Kinases Encoded in the Genomes of Model Eukaryotes. PLoS ONE, 2014, 9, e107956.	1.1	3
700	Two Structural Motifs within Canonical EF-Hand Calcium-Binding Domains Identify Five Different Classes of Calcium Buffers and Sensors. PLoS ONE, 2014, 9, e109287.	1.1	61
701	Genome-Wide Identification and Tissue-Specific Expression Analysis of UDP-Glycosyltransferases Genes Confirm Their Abundance in <i>Cicer arietinum</i> (Chickpea) Genome. PLoS ONE, 2014, 9, e109715.	1.1	44
702	Dissemination of the Transmissible Quinolone-Resistance Gene <i>qnrS1</i> by IncX Plasmids in Nigeria. PLoS ONE, 2014, 9, e110279.	1.1	17
703	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. PLoS ONE, 2014, 9, e111122.	1.1	14
704	Community Structure Detection for Overlapping Modules through Mathematical Programming in Protein Interaction Networks. PLoS ONE, 2014, 9, e112821.	1.1	18
705	Toward Computational Cumulative Biology by Combining Models of Biological Datasets. PLoS ONE, 2014, 9, e113053.	1.1	8
706	Structure of Putrescine Aminotransferase from <i>Escherichia coli</i> Provides Insights into the Substrate Specificity among Class III Aminotransferases. PLoS ONE, 2014, 9, e113212.	1.1	16
707	Computational and Experimental Analysis of the Secretome of <i>Methylococcus capsulatus</i> (Bath). PLoS ONE, 2014, 9, e114476.	1.1	7
708	An in Silico Approach for Characterization of an Aminoglycoside Antibiotic-Resistant Methyltransferase Protein from <i>Pyrococcus furiosus</i> (DSM 3638). Bioinformatics and Biology Insights, 2014, 8, BBI.S14620.	1.0	6

#	ARTICLE	IF	CITATIONS
709	Efficient mapping of genomic sequences to optimize multiple pairwise alignment in hybrid cluster platforms. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 60-71.	1.0	0
710	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. <i>Genes</i> , 2014, 5, 957-981.	1.0	76
711	Alternative splicing during Arabidopsis flower development results in constitutive and stage-regulated isoforms. <i>Frontiers in Genetics</i> , 2014, 5, 25.	1.1	45
712	Analysis pipeline for the epistasis search – statistical versus biological filtering. <i>Frontiers in Genetics</i> , 2014, 5, 106.	1.1	57
713	A Hypothetical Protein of <i>Alteromonas macleodii</i> AltDE1 (amad1_06475) Predicted to be a Cold-Shock Protein with RNA Chaperone Activity. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S20802.	2.3	2
714	Multi-PAS domain-mediated protein oligomerization of PpsR from <i>Rhodobacter sphaeroides</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 863-876.	2.5	11
715	Bioinformatics: A Molecular Microbiologist's Perspective. <i>Current Bioinformatics</i> , 2014, 9, 8-17.	0.7	2
716	Comprehensive analysis of patched domain-containing genes reveals a unique evolutionary pattern. <i>Genetics and Molecular Research</i> , 2014, 13, 7318-7331.	0.3	16
717	Expansion of specialized metabolism-related superfamily genes via whole genome duplications during angiosperm evolution. <i>Plant Biotechnology</i> , 2014, 31, 579-584.	0.5	9
718	Identification of novel and conserved microRNAs in <i>Coffea canephora</i> and <i>Coffea arabica</i> . <i>Genetics and Molecular Biology</i> , 2014, 37, 671-682.	0.6	15
719	In-silico Structural and Functional Analysis of Hypothetical Proteins of <i>Leptospira Interrogans</i> . <i>Biochemistry & Pharmacology: Open Access</i> , 2014, 03, .	0.2	8
720	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. <i>International Journal of Knowledge Discovery in Bioinformatics</i> , 2014, 4, 24-41.	0.8	2
721	Evolution and Expression Analysis of the CCCH Zinc Finger Gene Family in <i>Vitis vinifera</i> . <i>Plant Genome</i> , 2014, 7, plantgenome2014.05.0019.	1.6	15
723	Structural Systems Biology: Modeling Interactions and Networks for Systems Studies. , 2014, , 9-19.		0
724	Evolution and Classification of Myosins, a Eukaryotic Whole-Genome Approach. <i>Genome Biology and Evolution</i> , 2014, 6, 290-305.	1.1	121
725	CAMP: Collection of sequences and structures of antimicrobial peptides. <i>Nucleic Acids Research</i> , 2014, 42, D1154-D1158.	6.5	219
726	Meiosis Gene Inventory of Four Ciliates Reveals the Prevalence of a Synaptonemal Complex-Independent Crossover Pathway. <i>Molecular Biology and Evolution</i> , 2014, 31, 660-672.	3.5	32
727	Amyloplast-Localized SUBSTANDARD STARCH GRAIN4 Protein Influences the Size of Starch Grains in Rice Endosperm. <i>Plant Physiology</i> , 2014, 164, 623-636.	2.3	98

#	ARTICLE	IF	CITATIONS
728	Simulated hatchery system to assess bacteriophage efficacy against <i>Vibrio harveyi</i> . <i>Diseases of Aquatic Organisms</i> , 2014, 112, 113-119.	0.5	21
729	REPERTOIRE OF PROTEIN KINASES ENCODED IN THE GENOME OF ZEBRAFISH SHOWS REMARKABLY LARGE POPULATION OF PIM KINASES. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1350014.	0.3	3
730	Cyanobacteriochrome SesA Is a Diguanylate Cyclase That Induces Cell Aggregation in <i>Thermosynechococcus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 24801-24809.	1.6	103
731	A Comparative Study of Lectin Affinity Based Plant N-Glycoproteome Profiling Using Tomato Fruit as a Model. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 566-579.	2.5	55
732	A Soybean Acyl Carrier Protein, GmACP, Is Important for Root Nodule Symbiosis. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 415-423.	1.4	16
733	A DEK Domain-Containing Protein Modulates Chromatin Structure and Function in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 4328-4344.	3.1	57
734	A Genomic Analysis Pipeline and Its Application to Pediatric Cancers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 826-839.	1.9	2
735	Knowledge-driven genomic interactions: an application in ovarian cancer. <i>BioData Mining</i> , 2014, 7, 20.	2.2	21
736	New gene models and alternative splicing in the maize pathogen <i>Colletotrichum graminicola</i> revealed by RNA-Seq analysis. <i>BMC Genomics</i> , 2014, 15, 842.	1.2	59
737	Small non-coding RNA profiling and the role of piRNA pathway genes in the protection of chicken primordial germ cells. <i>BMC Genomics</i> , 2014, 15, 757.	1.2	29
738	Carnitine metabolism to trimethylamine by an unusual Rieske-type oxygenase from human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4268-4273.	3.3	264
739	Evolved Osmotolerant <i>Escherichia coli</i> Mutants Frequently Exhibit Defective N-Acetylglucosamine Catabolism and Point Mutations in Cell Shape-Regulating Protein MreB. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3729-3740.	1.4	53
740	An Expanded Genomic Representation of the Phylum Cyanobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 1031-1045.	1.1	326
741	iLIR. <i>Autophagy</i> , 2014, 10, 913-925.	4.3	187
742	Microsporidian Genomes Harbor a Diverse Array of Transposable Elements that Demonstrate an Ancestry of Horizontal Exchange with Metazoans. <i>Genome Biology and Evolution</i> , 2014, 6, 2289-2300.	1.1	34
743	GmFLD, a soybean homolog of the autonomous pathway gene FLOWERING LOCUS D, promotes flowering in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2014, 14, 263.	1.6	22
744	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014, 14, 329.	1.6	42
745	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. <i>Genome Biology</i> , 2014, 15, 512.	3.8	475

#	ARTICLE	IF	CITATIONS
746	Functional phylogenomics analysis of bacteria and archaea using consistent genome annotation with UniFam. <i>BMC Evolutionary Biology</i> , 2014, 14, 207.	3.2	22
747	Genetic analysis of vegetative branching in sorghum. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2387-2403.	1.8	35
748	Tomato nuclear proteome reveals the involvement of specific E2 ubiquitin-conjugating enzymes in fruit ripening. <i>Genome Biology</i> , 2014, 15, 548.	3.8	91
749	Molecular cloning and in-silico characterization of high temperature stress responsive pAPX gene isolated from heat tolerant Indian wheat cv. Raj 3765. <i>BMC Research Notes</i> , 2014, 7, 713.	0.6	18
750	Identification of conserved, centrosome-targeting ASH domains in TRAPP11 complex subunits and TRAPPC8. <i>Cilia</i> , 2014, 3, 6.	1.8	40
751	Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1132-1148.	3.5	62
752	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. <i>BMC Genomics</i> , 2014, 15, 901.	1.2	11
753	Rapid Evolution of piRNA Pathway in the Teleost Fish: Implication for an Adaptation to Transposon Diversity. <i>Genome Biology and Evolution</i> , 2014, 6, 1393-1407.	1.1	46
754	Bioinformatic characterisation of genes encoding cell wall degrading enzymes in the <i>Phytophthora parasitica</i> genome. <i>BMC Genomics</i> , 2014, 15, 785.	1.2	89
755	The GPCR repertoire in the demosponge <i>Amphimedon queenslandica</i> : insights into the GPCR system at the early divergence of animals. <i>BMC Evolutionary Biology</i> , 2014, 14, 270.	3.2	42
756	Systematic exploration of guide-tree topology effects for small protein alignments. <i>BMC Bioinformatics</i> , 2014, 15, 338.	1.2	27
757	PIGD: a database for intronless genes in the Poaceae. <i>BMC Genomics</i> , 2014, 15, 832.	1.2	22
758	CRISPR adaptive immune systems of Archaea. <i>RNA Biology</i> , 2014, 11, 156-167.	1.5	129
759	A highly conserved family of domains related to the DNA-glycosylase fold helps predict multiple novel pathways for RNA modifications. <i>RNA Biology</i> , 2014, 11, 360-372.	1.5	35
760	New Tricks for "Old" Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. <i>Genome Biology and Evolution</i> , 2014, 6, 2897-2917.	1.1	14
761	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	6.5	270
762	The Evolution of the GPCR Signaling System in Eukaryotes: Modularity, Conservation, and the Transition to Metazoan Multicellularity. <i>Genome Biology and Evolution</i> , 2014, 6, 606-619.	1.1	145
763	Deorphanizing the human transmembrane genome: A landscape of uncharacterized membrane proteins. <i>Acta Pharmacologica Sinica</i> , 2014, 35, 11-23.	2.8	34

#	ARTICLE	IF	CITATIONS
764	An antimicrobial protein of the gut symbiont <i>Bacteroides fragilis</i> with a MACPF domain of host immune proteins. <i>Molecular Microbiology</i> , 2014, 94, 1361-1374.	1.2	70
765	Dissemination of 6S RNA among Bacteria. <i>RNA Biology</i> , 2014, 11, 1467-1478.	1.5	40
766	Single cell genomic study of <i>Dehalococcoides</i> species from deep-sea sediments of the Peruvian Margin. <i>ISME Journal</i> , 2014, 8, 1831-1842.	4.4	117
767	New Insights into Chloramphenicol Biosynthesis in <i>Streptomyces venezuelae</i> ATCC 10712. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7441-7450.	1.4	74
768	SCOP2 prototype: a new approach to protein structure mining. <i>Nucleic Acids Research</i> , 2014, 42, D310-D314.	6.5	260
769	Transcriptome analysis of the salivary glands of <i>Nephotettix cincticeps</i> (Uhler). <i>Journal of Insect Physiology</i> , 2014, 71, 170-176.	0.9	44
770	Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. <i>Environmental Microbiology</i> , 2014, 16, 3548-3561.	1.8	76
771	Metagenomic Frameworks for Monitoring Antibiotic Resistance in Aquatic Environments. <i>Environmental Health Perspectives</i> , 2014, 122, 222-228.	2.8	89
772	Proteomics of a fuzzy organelle: interphase chromatin. <i>EMBO Journal</i> , 2014, 33, 648-664.	3.5	58
773	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. <i>PLoS Biology</i> , 2014, 12, e1001843.	2.6	79
774	Functional Organization of a Multimodular Bacterial Chemosensory Apparatus. <i>PLoS Genetics</i> , 2014, 10, e1004164.	1.5	32
775	Effect of Wnt3a on Keratinocytes Utilizing in Vitro and Bioinformatics Analysis. <i>International Journal of Molecular Sciences</i> , 2014, 15, 5472-5495.	1.8	1
776	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau022.	1.4	62
777	Structure of a Membrane-Embedded Prenyltransferase Homologous to UBIAD1. <i>PLoS Biology</i> , 2014, 12, e1001911.	2.6	89
778	Improving Contact Prediction along Three Dimensions. <i>PLoS Computational Biology</i> , 2014, 10, e1003847.	1.5	71
779	ECOD: An Evolutionary Classification of Protein Domains. <i>PLoS Computational Biology</i> , 2014, 10, e1003926.	1.5	321
780	Local Effect of Enhancer of Zeste-Like Reveals Cooperation of Epigenetic and cis-Acting Determinants for Zygotic Genome Rearrangements. <i>PLoS Genetics</i> , 2014, 10, e1004665.	1.5	66
781	Functional Characterisation of Germinant Receptors in <i>Clostridium botulinum</i> and <i>Clostridium sporogenes</i> Presents Novel Insights into Spore Germination Systems. <i>PLoS Pathogens</i> , 2014, 10, e1004382.	2.1	40

#	ARTICLE	IF	CITATIONS
782	Genomic insights into the fungal lignocellulolytic system of <i>Myceliophthora thermophila</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 281.	1.5	87
783	Assembly of viral genomes from metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 714.	1.5	44
784	A Taxonomy of Bacterial Microcompartment Loci Constructed by a Novel Scoring Method. <i>PLoS Computational Biology</i> , 2014, 10, e1003898.	1.5	227
785	Cysteine-2 and Cys30 are essential for chlorophyll-binding activity of the water-soluble chlorophyll-binding protein (WSCP) of <i>Chenopodium album</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 1825-1832.	0.6	4
786	Comparative Analysis of <i>Salmonella</i> Genomes Identifies a Metabolic Network for Escalating Growth in the Inflamed Gut. <i>MBio</i> , 2014, 5, e00929-14.	1.8	165
787	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	3
788	AvrBsT Acetylates Arabidopsis ACIP1, a Protein that Associates with Microtubules and Is Required for Immunity. <i>PLoS Pathogens</i> , 2014, 10, e1003952.	2.1	81
789	A comprehensive analysis of the Omp85/TpsB protein superfamily structural diversity, taxonomic occurrence, and evolution. <i>Frontiers in Microbiology</i> , 2014, 5, 370.	1.5	78
790	Characterization of the surfaceome of the metal-reducing bacterium <i>Desulfotomaculum reducens</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 432.	1.5	22
791	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003788.	1.5	72
792	dcGOR: An R Package for Analysing Ontologies and Protein Domain Annotations. <i>PLoS Computational Biology</i> , 2014, 10, e1003929.	1.5	18
793	Cyclic di-GMP-dependent Signaling Pathways in the Pathogenic Firmicute <i>Listeria monocytogenes</i> . <i>PLoS Pathogens</i> , 2014, 10, e1004301.	2.1	80
794	TM6SF2 and MAC30, new enzyme homologs in sterol metabolism and common metabolic disease. <i>Frontiers in Genetics</i> , 2014, 5, 439.	1.1	50
795	Genome-Wide Prediction and Validation of Peptides That Bind Human Prosurvival Bcl-2 Proteins. <i>PLoS Computational Biology</i> , 2014, 10, e1003693.	1.5	35
796	A mortise-tenon joint in the transmembrane domain modulates autotransporter assembly into bacterial outer membranes. <i>Nature Communications</i> , 2014, 5, 4239.	5.8	46
797	Presence-Absence Variation in <i>A. thaliana</i> Is Primarily Associated with Genomic Signatures Consistent with Relaxed Selective Constraints. <i>Molecular Biology and Evolution</i> , 2014, 31, 59-69.	3.5	36
798	Unconventionally secreted effectors of two filamentous pathogens target plant salicylate biosynthesis. <i>Nature Communications</i> , 2014, 5, 4686.	5.8	283
799	Manually curated database of rice proteins. <i>Nucleic Acids Research</i> , 2014, 42, D1214-D1221.	6.5	19

#	ARTICLE	IF	CITATIONS
800	Transcription-Independent Functions of an RNA Polymerase II Subunit, Rpb2, During Genome Rearrangement in the Ciliate, <i>Oxytricha trifallax</i> . <i>Genetics</i> , 2014, 197, 839-849.	1.2	23
801	Global Patterns of Protein Domain Gain and Loss in Superkingdoms. <i>PLoS Computational Biology</i> , 2014, 10, e1003452.	1.5	65
802	Genomic Insights into Processes Driving the Infection of <i>Alexandrium tamarense</i> by the Parasitoid <i>Amoebophrya</i> sp. <i>Eukaryotic Cell</i> , 2014, 13, 1439-1449.	3.4	42
803	Symbiotic Adaptation Drives Genome Streamlining of the Cyanobacterial Sponge Symbiont <i>Candidatus</i> <i>Synechococcus spongiarum</i> . <i>MBio</i> , 2014, 5, e00079-14.	1.8	83
804	Evolution of a Cellular Immune Response in <i>Drosophila</i> : A Phenotypic and Genomic Comparative Analysis. <i>Genome Biology and Evolution</i> , 2014, 6, 273-289.	1.1	51
805	Large-Scale Genomic Analysis Suggests a Neutral Punctuated Dynamics of Transposable Elements in Bacterial Genomes. <i>PLoS Computational Biology</i> , 2014, 10, e1003680.	1.5	32
806	Genes That Bias Mendelian Segregation. <i>PLoS Genetics</i> , 2014, 10, e1004387.	1.5	80
807	Discovery and Confirmation of Ligand Binding Specificities of the <i>Schistosoma japonicum</i> Polarity Protein Scribble. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2837.	1.3	5
808	Characterizing Protein Interactions Employing a Genome-Wide siRNA Cellular Phenotyping Screen. <i>PLoS Computational Biology</i> , 2014, 10, e1003814.	1.5	10
809	FSim: A Novel Functional Similarity Search Algorithm and Tool for Discovering Functionally Related Gene Products. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	2
810	Gene Expansion Shapes Genome Architecture in the Human Pathogen <i>Lichtheimia corymbifera</i> : An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). <i>PLoS Genetics</i> , 2014, 10, e1004496.	1.5	80
811	A Scalable and Accurate Targeted Gene Assembly Tool (SAT-Assembler) for Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003737.	1.5	31
812	Synonymous Constraint Elements Show a Tendency to Encode Intrinsically Disordered Protein Segments. <i>PLoS Computational Biology</i> , 2014, 10, e1003607.	1.5	21
813	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907.	1.5	49
814	Zinc Finger Transcription Factors Displaced SREBP Proteins as the Major Sterol Regulators during <i>Saccharomycotina</i> Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004076.	1.5	63
815	Evidence of a Bacterial Receptor for Lysozyme: Binding of Lysozyme to the Anti- β Factor RsiV Controls Activation of the ECF β Factor β V. <i>PLoS Genetics</i> , 2014, 10, e1004643.	1.5	40
816	Phylogeny and phylogeography of functional genes shared among seven terrestrial subsurface metagenomes reveal N-cycling and microbial evolutionary relationships. <i>Frontiers in Microbiology</i> , 2014, 5, 531.	1.5	87
817	Metagenomic evidence for metabolism of trace atmospheric gases by high-elevation desert Actinobacteria. <i>Frontiers in Microbiology</i> , 2014, 5, 698.	1.5	62

#	ARTICLE	IF	CITATIONS
818	Structure of RDE-4 dsRBDs and mutational studies provide insights into dsRNA recognition in the <i>Caenorhabditis elegans</i> RNAi pathway. <i>Biochemical Journal</i> , 2014, 458, 119-130.	1.7	7
819	Ca ²⁺ -stabilized adhesin helps an Antarctic bacterium reach out and bind ice. <i>Bioscience Reports</i> , 2014, 34, .	1.1	32
821	Genome-wide comparative analysis of NBS-encoding genes between Brassica species and <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2014, 15, 3.	1.2	147
822	Identification of <i>Giardia lamblia</i> DHHC Proteins and the Role of Protein S-palmitoylation in the Encystation Process. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2997.	1.3	23
823	Genome-Wide Analysis of the Cyclin Gene Family in Tomato. <i>International Journal of Molecular Sciences</i> , 2014, 15, 120-140.	1.8	28
824	Genome of brown tide virus (AaV), the little giant of the Megaviridae, elucidates NCLDV genome expansion and host-virus coevolution. <i>Virology</i> , 2014, 466-467, 60-70.	1.1	86
825	Computational methods for analysis and inference of kinase/inhibitor relationships. <i>Frontiers in Genetics</i> , 2014, 5, 196.	1.1	16
826	Analysis of two domains with novel RNA-processing activities throws light on the complex evolution of ribosomal RNA biogenesis. <i>Frontiers in Genetics</i> , 2014, 5, 424.	1.1	21
827	SeqDepot: streamlined database of biological sequences and precomputed features. <i>Bioinformatics</i> , 2014, 30, 295-297.	1.8	10
828	Network Assessor: An automated method for quantitative assessment of a network's potential for gene function prediction. <i>Frontiers in Genetics</i> , 2014, 5, 123.	1.1	10
829	Structural Comparison, Substrate Specificity, and Inhibitor Binding of AGPase Small Subunit from Monocot and Dicot: Present Insight and Future Potential. <i>BioMed Research International</i> , 2014, 2014, 1-20.	0.9	9
830	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2198-2212.	2.5	5
831	Mutations Enabling Displacement of Tryptophan by 4-Fluorotryptophan as a Canonical Amino Acid of the Genetic Code. <i>Genome Biology and Evolution</i> , 2014, 6, 629-641.	1.1	31
832	MycCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	6.5	1,187
833	Draft Genome Sequence of <i>Mycobacterium cosmeticum</i> DSM 44829. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
834	Draft Genome Sequence of <i>Mycobacterium vulneris</i> DSM 45247 ^T. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
835	Draft Genome Sequence of <i>Rickettsia aeschlimannii</i> , Associated with <i>Hyalomma marginatum</i> Ticks. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
836	Genome Sequence of <i>Rickettsia tamurae</i> , a Recently Detected Human Pathogen in Japan. <i>Genome Announcements</i> , 2014, 2, .	0.8	7

#	ARTICLE	IF	CITATIONS
837	Genome Sequence of <i>Rickettsia hoogstraalii</i> , a Geographically Widely Distributed Tick-Associated Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
838	Genome Sequence of <i>Bacillus simplex</i> Strain P558, Isolated from a Human Fecal Sample. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
839	First Closed Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>intermedius</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	9
840	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . <i>MBio</i> , 2014, 5, e01980.	1.8	39
841	Genome Sequence of the $\hat{\mu}$ -Poly- <i>l</i> -Lysine-Producing Strain <i>Streptomyces albulus</i> NK660, Isolated from Soil in Gutian, Fujian Province, China. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
842	Genome-Scale Metabolic Network Validation of <i>Shewanella oneidensis</i> Using Transposon Insertion Frequency Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003848.	1.5	25
843	AlgaePath: comprehensive analysis of metabolic pathways using transcript abundance data from next-generation sequencing in green algae. <i>BMC Genomics</i> , 2014, 15, 196.	1.2	36
844	The mitochondrial and chloroplast genomes of the haptophyte <i>Chrysochromulina tobin</i> contain unique repeat structures and gene profiles. <i>BMC Genomics</i> , 2014, 15, 604.	1.2	30
845	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
846	Characterization and regulation of the Resistance-Nodulation-Cell Division-type multidrug efflux pumps MdtABC and MdtUVW from the fire blight pathogen <i>Erwinia amylovora</i> . <i>BMC Microbiology</i> , 2014, 14, 185.	1.3	40
847	Adaptive evolution and divergent expression of heat stress transcription factors in grasses. <i>BMC Evolutionary Biology</i> , 2014, 14, 147.	3.2	29
848	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	5.8	173
849	Comparison of gene expression of <i>Paramecium bursaria</i> with and without <i>Chlorella variabilis</i> symbionts. <i>BMC Genomics</i> , 2014, 15, 183.	1.2	57
850	A pipeline for the de novo assembly of the <i>Themira biloba</i> (Sepsidae: Diptera) transcriptome using a multiple k-mer length approach. <i>BMC Genomics</i> , 2014, 15, 188.	1.2	14
851	Complete Genome Sequence and Annotation of a <i>Campylobacter jejuni</i> Strain, MTVDSJCj20, Isolated from a Naturally Colonized Farm-Raised Chicken. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
852	Experimental evidence validating the computational inference of functional associations from gene fusion events: a critical survey. <i>Briefings in Bioinformatics</i> , 2014, 15, 443-454.	3.2	19
853	Genome Sequence of <i>Legionella massiliensis</i> , Isolated from a Cooling Tower Water Sample. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
854	IRBIS: a systematic search for conserved complementarity. <i>Rna</i> , 2014, 20, 1519-1531.	1.6	16

#	ARTICLE	IF	CITATIONS
855	Draft Genome Sequence of <i>Mycobacterium austroafricanum</i> DSM 44191. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
856	Draft Genome Sequence of <i>Mycobacterium asiaticum</i> Strain DSM 44297. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
857	Draft Genome Sequence of <i>Mycobacterium mageritense</i> DSM 44476 ^T. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
858	Draft Genome Sequence of <i>Mycobacterium triplex</i> DSM 44626. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
859	Draft Genome Sequence of <i>Mycobacterium farcinogenes</i> NCTC 10955. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
860	Evidence of Extensive DNA Transfer between <i>Bacteroidales</i> Species within the Human Gut. <i>MBio</i> , 2014, 5, e01305-14.	1.8	126
861	TIR-domain-containing protein repertoire of nine anthozoan species reveals coral-specific expansions and uncharacterized proteins. <i>Developmental and Comparative Immunology</i> , 2014, 46, 480-488.	1.0	80
862	Powerful Sequence Similarity Search Methods and In-Depth Manual Analyses Can Identify Remote Homologs in Many Apparently "Orphan" Viral Proteins. <i>Journal of Virology</i> , 2014, 88, 10-20.	1.5	116
863	Association mapping of brassinosteroid candidate genes and plant architecture in a diverse panel of <i>Sorghum bicolor</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 2645-2662.	1.8	31
864	Identification and characterization of genes involved in the jasmonate biosynthetic and signaling pathways in mulberry (<i>Morus notabilis</i>). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 663-672.	4.1	6
865	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47
866	Comparative single-cell genomics reveals potential ecological niches for the freshwater actinobacteria lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	4.4	137
867	Rapid similarity search of proteins using alignments of domain arrangements. <i>Bioinformatics</i> , 2014, 30, 274-281.	1.8	37
868	Preventive <scp>DNA</scp> repair by sanitizing the cellular (deoxy)nucleoside triphosphate pool. <i>FEBS Journal</i> , 2014, 281, 4207-4223.	2.2	38
869	DoMosaics: software for domain arrangement visualization and domain-centric analysis of proteins. <i>Bioinformatics</i> , 2014, 30, 282-283.	1.8	52
870	Structure of Pneumococcal Peptidoglycan Hydrolase LytB Reveals Insights into the Bacterial Cell Wall Remodeling and Pathogenesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 23403-23416.	1.6	62
871	Functional elucidation of antibacterial phage ORFans targeting <i>Pseudomonas aeruginosa</i>. <i>Cellular Microbiology</i> , 2014, 16, 1822-1835.	1.1	47
872	Draft genomic DNA sequence of the facultatively methylotrophic bacterium <i>Acidomonas methanolicatypa</i> strain MB58. <i>FEMS Microbiology Letters</i> , 2014, 351, 9-13.	0.7	7

#	ARTICLE	IF	CITATIONS
873	Deletion of membrane-associated <i>Asp</i> 23 leads to upregulation of cell wall stress genes in <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2014, 93, 1259-1268.	1.2	58
874	Potentially novel copper resistance genes in copper-enriched activated sludge revealed by metagenomic analysis. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 10255-10266.	1.7	30
875	Symbiotic adaptations in the fungal cultivar of leaf-cutting ants. <i>Nature Communications</i> , 2014, 5, 5675.	5.8	84
876	Molecular evolution of the bacterial pseudouridine 5-phosphate glycosidase protein family. <i>FEBS Journal</i> , 2014, 281, 4439-4449.	2.2	18
877	Genome-wide identification and expression analyses of cytochrome <i>P450</i> genes in mulberry (<i>Morus notabilis</i>). <i>Journal of Integrative Plant Biology</i> , 2014, 56, 887-901.	4.1	53
878	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. <i>Nucleic Acids Research</i> , 2014, 42, D364-D373.	6.5	156
879	Prevalence, Evolution, and <i>cis</i> -Regulation of Diel Transcription in <i>Chlamydomonas reinhardtii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2461-2471.	0.8	29
880	Proteomic analysis of <i>Lawsonia intracellularis</i> reveals expression of outer membrane proteins during infection. <i>Veterinary Microbiology</i> , 2014, 174, 448-455.	0.8	17
881	PredictProtein ³ an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	6.5	589
882	Cooperative binding of LysM domains determines the carbohydrate affinity of a bacterial endopeptidase protein. <i>FEBS Journal</i> , 2014, 281, 1196-1208.	2.2	45
883	Identification of a broad family of lipid <i>A</i> late acyltransferases with non-canonical substrate specificity. <i>Molecular Microbiology</i> , 2014, 91, 887-899.	1.2	17
884	Heteromeric transposase elements: generators of genomic islands across diverse bacteria. <i>Molecular Microbiology</i> , 2014, 93, 1084-1092.	1.2	48
885	Network-based identification of key proteins involved in apoptosis and cell cycle regulation. <i>Cell Proliferation</i> , 2014, 47, 356-368.	2.4	2
886	A comparative systems analysis of polysaccharide-elicited responses in <i>Neurospora crassa</i> reveals carbon source-specific cellular adaptations. <i>Molecular Microbiology</i> , 2014, 91, 275-299.	1.2	95
887	Origin and Evolution of European Community-Acquired Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2014, 5, e01044-14.	1.8	112
888	The Structure-Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	6.5	210
889	Protein universe containing a <i>PUA</i> RNA-binding domain. <i>FEBS Journal</i> , 2014, 281, 74-87.	2.2	18
890	A Comprehensive Phylogenetic and Structural Analysis of the Carcinoembryonic Antigen (CEA) Gene Family. <i>Genome Biology and Evolution</i> , 2014, 6, 1314-1326.	1.1	26

#	ARTICLE	IF	CITATIONS
891	Identification and characterization of trimethylamine <i>N</i> -oxide (TMAO) demethylase and TMAO permease in <i>Methylophilus methylotrophus</i> . Environmental Microbiology, 2014, 16, 3318-3330.	1.8	18
892	Structural basis for adaptation of lactobacilli to gastrointestinal mucus. Environmental Microbiology, 2014, 16, 888-903.	1.8	102
893	Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. Structure, 2014, 22, 1799-1809.	1.6	10
894	Structural basis and dynamics of multidrug recognition in a minimal bacterial multidrug resistance system. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5498-507.	3.3	18
895	A bioinformatic and computational study of myosin phosphatase subunit diversity. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2014, 307, R256-R270.	0.9	21
896	CasCleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. Bioinformatics, 2014, 30, 71-80.	1.8	63
897	Accurate prediction of interfacial residues in two-domain proteins using evolutionary information: Implications for three-dimensional modeling. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1219-1234.	1.5	7
898	Spotlite: Web Application and Augmented Algorithms for Predicting Co-Complexed Proteins from Affinity Purification - Mass Spectrometry Data. Journal of Proteome Research, 2014, 13, 5944-5955.	1.8	18
899	Identification of Low-Molecular-Weight Compounds Inhibiting Growth of Corynebacteria: Potential Lead Compounds for Antibiotics. ChemMedChem, 2014, 9, 282-285.	1.6	3
900	Clustal Omega. Current Protocols in Bioinformatics, 2014, 48, 3.13.1-16.	25.8	461
901	New perspectives on the diversification of the RNA interference system: insights from comparative genomics and small RNA sequencing. Wiley Interdisciplinary Reviews RNA, 2014, 5, 141-181.	3.2	62
902	Structural characterization of MepB from <i>Staphylococcus aureus</i> reveals homology to endonucleases. Protein Science, 2014, 23, 594-602.	3.1	6
903	Genomic Characterization of Variable Surface Antigens Reveals a Telomere Position Effect as a Prerequisite for RNA Interference-Mediated Silencing in <i>Paramecium tetraurelia</i> . MBio, 2014, 5, e01328.	1.8	13
904	Draft Genome Sequence of the Pathogenic Fungus <i>Scedosporium apiospermum</i> . Genome Announcements, 2014, 2, .	0.8	42
905	Analysis of the Skin Transcriptome in Two Oujiang Color Varieties of Common Carp. PLoS ONE, 2014, 9, e90074.	1.1	38
906	Towards a comprehensive Plasmodium falciparum merozoite cell surface and secreted recombinant protein library. Malaria Journal, 2014, 13, 93.	0.8	35
907	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
908	Obligate Insect Endosymbionts Exhibit Increased Ortholog Length Variation and Loss of Large Accessory Proteins Concurrent with Genome Shrinkage. Genome Biology and Evolution, 2014, 6, 763-775.	1.1	10

#	ARTICLE	IF	CITATIONS
909	Kin-Driver: a database of driver mutations in protein kinases. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau104-bau104.	1.4	23
910	P3DB 3.0: From plant phosphorylation sites to protein networks. Nucleic Acids Research, 2014, 42, D1206-D1213.	6.5	75
911	Genome-wide identification, splicing, and expression analysis of the myosin gene family in maize (<i>Zea mays</i>). <i>PLoS ONE</i> , 2014, 9, e101010.	2.4	14
912	The palmitoyl acyltransferase HIP14 shares a high proportion of interactors with huntingtin: implications for a role in the pathogenesis of Huntington's disease. <i>Human Molecular Genetics</i> , 2014, 23, 4142-4160.	1.4	58
913	Evolutionary and Structural Analyses of Mammalian Haloacid Dehalogenase-type Phosphatases AUM and Chronophin Provide Insight into the Basis of Their Different Substrate Specificities. <i>Journal of Biological Chemistry</i> , 2014, 289, 3416-3431.	1.6	24
914	Structural genomics analysis of uncharacterized protein families overrepresented in human gut bacteria identifies a novel glycoside hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 112.	1.2	13
915	Novel and unique domains in aminoacyl-tRNA synthetases from human fungal pathogens <i>Aspergillus niger</i> , <i>Candida albicans</i> and <i>Cryptococcus neoformans</i> . <i>BMC Genomics</i> , 2014, 15, 1069.	1.2	14
916	Alkane hydroxylase genes in psychrophile genomes and the potential for cold active catalysis. <i>BMC Genomics</i> , 2014, 15, 1120.	1.2	25
917	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. <i>BMC Genomics</i> , 2014, 15, 1159.	1.2	10
918	Interspecific and host-related gene expression patterns in nematode-trapping fungi. <i>BMC Genomics</i> , 2014, 15, 968.	1.2	30
919	The <i>Vibrio cholerae</i> diguanylate cyclase VCA0965 has an AGDEF active site and synthesizes cyclic di-GMP. <i>BMC Microbiology</i> , 2014, 14, 22.	1.3	40
920	Comparative genomics for mycobacterial peptidoglycan remodelling enzymes reveals extensive genetic multiplicity. <i>BMC Microbiology</i> , 2014, 14, 75.	1.3	42
921	RNA sequencing and de novo assembly of the digestive gland transcriptome in <i>Mytilus galloprovincialis</i> fed with toxinogenic and non-toxic strains of <i>Alexandrium minutum</i> . <i>BMC Research Notes</i> , 2014, 7, 722.	0.6	47
922	The loose evolutionary relationships between transcription factors and other gene products across prokaryotes. <i>BMC Research Notes</i> , 2014, 7, 928.	0.6	2
923	Unique features of apicoplast DNA gyrases from <i>Toxoplasma gondii</i> and <i>Plasmodium falciparum</i> . <i>BMC Bioinformatics</i> , 2014, 15, 416.	1.2	14
924	Phylogenomic analysis of glycogen branching and debranching enzymatic duo. <i>BMC Evolutionary Biology</i> , 2014, 14, 183.	3.2	27
925	Loss and retention of resistance genes in five species of the Brassicaceae family. <i>BMC Plant Biology</i> , 2014, 14, 298.	1.6	27
926	A curated <i>C. difficile</i> strain 630 metabolic network: prediction of essential targets and inhibitors. <i>BMC Systems Biology</i> , 2014, 8, 117.	3.0	39

#	ARTICLE	IF	CITATIONS
927	The other face of restriction: modification-dependent enzymes. <i>Nucleic Acids Research</i> , 2014, 42, 56-69.	6.5	149
928	Regulatory networks, genes and glycerophospholipid biosynthesis pathway in schistosomiasis: A systems biology view for pharmacological intervention. <i>Gene</i> , 2014, 550, 214-222.	1.0	3
929	The Transporter Classification Database. <i>Nucleic Acids Research</i> , 2014, 42, D251-D258.	6.5	437
930	Biophysics of protein evolution and evolutionary protein biophysics. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140419.	1.5	202
931	Comparative Analyses of Nonpathogenic, Opportunistic, and Totally Pathogenic Mycobacteria Reveal Genomic and Biochemical Variabilities and Highlight the Survival Attributes of Mycobacterium tuberculosis. <i>MBio</i> , 2014, 5, e02020.	1.8	64
932	canSAR: updated cancer research and drug discovery knowledgebase. <i>Nucleic Acids Research</i> , 2014, 42, D1040-D1047.	6.5	69
933	Draft Genome Sequence of Mycobacterium neoaurum Strain DSM 44074 ^T. <i>Genome Announcements</i> , 2014, 2, .	0.8	2
934	Toward rationally redesigning bacterial two-component signaling systems using coevolutionary information. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E563-71.	3.3	117
935	UniHI 7: an enhanced database for retrieval and interactive analysis of human molecular interaction networks. <i>Nucleic Acids Research</i> , 2014, 42, D408-D414.	6.5	91
936	The Draft Assembly of the Radically Organized Stylonychia lemnae Macronuclear Genome. <i>Genome Biology and Evolution</i> , 2014, 6, 1707-1723.	1.1	58
937	Single-cell genomics reveals metabolic strategies for microbial growth and survival in an oligotrophic aquifer. <i>Microbiology (United Kingdom)</i> , 2014, 160, 362-372.	0.7	10
938	The endocytic activity of the flagellar pocket in <i>Trypanosoma brucei</i> is regulated by an adjacent phosphatidylinositol phosphate kinase. <i>Journal of Cell Science</i> , 2014, 127, 2351-64.	1.2	35
939	Function and Localization Dynamics of Bifunctional Penicillin-Binding Proteins in <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1627-1639.	1.0	24
940	<i>Arabidopsis</i> ANGULATA10 is required for thylakoid biogenesis and mesophyll development. <i>Journal of Experimental Botany</i> , 2014, 65, 2391-2404.	2.4	13
941	Ancestral repeats have shaped epigenome and genome composition for millions of years in <i>Arabidopsis thaliana</i> . <i>Nature Communications</i> , 2014, 5, 4104.	5.8	74
942	3did: a catalog of domain-based interactions of known three-dimensional structure. <i>Nucleic Acids Research</i> , 2014, 42, D374-D379.	6.5	249
943	Diversity of O-Antigen Repeat Unit Structures Can Account for the Substantial Sequence Variation of Wzx Translocases. <i>Journal of Bacteriology</i> , 2014, 196, 1713-1722.	1.0	57
944	Comparative Genomics of the <i>Campylobacter lari</i> Group. <i>Genome Biology and Evolution</i> , 2014, 6, 3252-3266.	1.1	69

#	ARTICLE	IF	CITATIONS
945	In <i>Candida albicans</i> , phosphorylation of Exo84 by Cdk1-Hgc1 is necessary for efficient hyphal extension. <i>Molecular Biology of the Cell</i> , 2014, 25, 1097-1110.	0.9	29
946	KBDOCK 2013: a spatial classification of 3D protein domain family interactions. <i>Nucleic Acids Research</i> , 2014, 42, D389-D395.	6.5	31
947	MetaProx: the database of metagenomic proximons. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	7
948	Exonic splicing signals impose constraints upon the evolution of enzymatic activity. <i>Nucleic Acids Research</i> , 2014, 42, 5790-5798.	6.5	8
949	The evolution of the ribosome biogenesis pathway from a yeast perspective. <i>Nucleic Acids Research</i> , 2014, 42, 1509-1523.	6.5	87
950	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e172-e172.	6.5	33
951	A Novel Mutation in the <i>ROGDI</i> Gene in a Patient with Kohlschütter-Täufel Syndrome. <i>Molecular Syndromology</i> , 2014, 5, 293-298.	0.3	18
952	topPTM: a new module of dbPTM for identifying functional post-translational modifications in transmembrane proteins. <i>Nucleic Acids Research</i> , 2014, 42, D537-D545.	6.5	34
953	Transcript Profiling Reveals Auxin and Cytokinin Signaling Pathways and Transcription Regulation during In Vitro Organogenesis of Ramie (<i>Boehmeria nivea</i> L. Gaud). <i>PLoS ONE</i> , 2014, 9, e113768.	1.1	29
954	The eukaryotic linear motif resource ELM: 10 years and counting. <i>Nucleic Acids Research</i> , 2014, 42, D259-D266.	6.5	260
955	Fifteen Million Years of Evolution in the <i>Oryza</i> Genus Shows Extensive Gene Family Expansion. <i>Molecular Plant</i> , 2014, 7, 642-656.	3.9	54
956	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2014, 42, D285-D291.	6.5	133
957	Chromosomal Replication Dynamics and Interaction with the \hat{I}^2 Sliding Clamp Determine Orientation of Bacterial Transposable Elements. <i>Genome Biology and Evolution</i> , 2014, 6, 727-740.	1.1	18
958	A novel missense mutation in <i>CCDC88C</i> activates the JNK pathway and causes a dominant form of spinocerebellar ataxia. <i>Journal of Medical Genetics</i> , 2014, 51, 590-595.	1.5	64
959	Computational and Experimental Prediction of Human C-Type Lectin Receptor Druggability. <i>Frontiers in Immunology</i> , 2014, 5, 323.	2.2	45
960	Structure and Function of the LmbE-like Superfamily. <i>Biomolecules</i> , 2014, 4, 527-545.	1.8	11
961	TreeFam v9: a new website, more species and orthology-on-the-fly. <i>Nucleic Acids Research</i> , 2014, 42, D922-D925.	6.5	125
962	Bioprospecting in the Genomic Age. <i>Advances in Applied Microbiology</i> , 2014, 87, 111-146.	1.3	10

#	ARTICLE	IF	CITATIONS
963	Analysis of Expressed Genes of the Bacterium <i>Candidatus Phytoplasma Mali</i> ™ Highlights Key Features of Virulence and Metabolism. PLoS ONE, 2014, 9, e94391.	1.1	29
964	CRISPRstrand: predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci. Bioinformatics, 2014, 30, i489-i496.	1.8	57
965	Integrated omics study delineates the dynamics of lipid droplets in <i>Rhodococcus opacus</i> PD630. Nucleic Acids Research, 2014, 42, 1052-1064.	6.5	79
967	CLYBL is a polymorphic human enzyme with malate synthase and Î ² -methylmalate synthase activity. Human Molecular Genetics, 2014, 23, 2313-2323.	1.4	29
968	Genome-Wide Search for Eliminating Domains Reveals Novel Function for BLES03-Like Proteins. Genome Biology and Evolution, 2014, 6, 2017-2033.	1.1	2
969	Identifying transcription factor complexes and their roles. Bioinformatics, 2014, 30, i415-i421.	1.8	25
970	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau006-bau006.	1.4	64
971	Trends in structural coverage of the protein universe and the impact of the Protein Structure Initiative. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3733-3738.	3.3	79
972	Analysis of the Opsin Repertoire in the Tardigrade <i>Hypsibius dujardini</i> Provides Insights into the Evolution of Opsin Genes in Panarthropoda. Genome Biology and Evolution, 2014, 6, 2380-2391.	1.1	54
973	Entropy-driven partitioning of the hierarchical protein space. Bioinformatics, 2014, 30, i624-i630.	1.8	2
974	Expanding the catalog of <i>cas</i> genes with metagenomes. Nucleic Acids Research, 2014, 42, 2448-2459.	6.5	25
975	PDBsum additions. Nucleic Acids Research, 2014, 42, D292-D296.	6.5	279
976	Correlating Information Contents of Gene Ontology Terms to Infer Semantic Similarity of Gene Products. Computational and Mathematical Methods in Medicine, 2014, 2014, 1-9.	0.7	10
977	Helminth Allergens, Parasite-Specific IgE, and Its Protective Role in Human Immunity. Frontiers in Immunology, 2014, 5, 61.	2.2	136
978	Sex-Determination System in the Diploid Yeast <i>Zygosaccharomyces sapae</i> . G3: Genes, Genomes, Genetics, 2014, 4, 1011-1025.	0.8	12
979	Soybean knowledge base (SoyKB): a web resource for integration of soybean translational genomics and molecular breeding. Nucleic Acids Research, 2014, 42, D1245-D1252.	6.5	102
980	Protein Domains of Unknown Function Are Essential in Bacteria. MBo, 2014, 5, e00744-13.	1.8	112
981	Predicting virus mutations through statistical relational learning. BMC Bioinformatics, 2014, 15, 309.	1.2	6

#	ARTICLE	IF	CITATIONS
982	HMM-ModE: implementation, benchmarking and validation with HMMER3. BMC Research Notes, 2014, 7, 483.	0.6	10
983	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	13.9	424
984	Structural Basis of Lipid Binding for the Membrane-embedded Tetraacyldisaccharide-1-phosphate 4â€²-Kinase LpxK. Journal of Biological Chemistry, 2014, 289, 24059-24068.	1.6	8
985	PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors. Nucleic Acids Research, 2014, 42, D1182-D1187.	6.5	800
986	CentrosomeDB: a new generation of the centrosomal proteins database for <i>Human</i> and <i>Drosophila melanogaster</i> . Nucleic Acids Research, 2014, 42, D430-D436.	6.5	47
987	PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome. Nucleic Acids Research, 2014, 42, D897-D902.	6.5	264
988	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	6.5	5,425
989	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
990	IMG 4 version of the integrated microbial genomes comparative analysis system. Nucleic Acids Research, 2014, 42, D560-D567.	6.5	555
991	Comparative Genomics of Taphrina Fungi Causing Varying Degrees of Tumorous Deformity in Plants. Genome Biology and Evolution, 2014, 6, 861-872.	1.1	33
992	Comparative Genomics Suggests That the Human Pathogenic Fungus <i>Pneumocystis jirovecii</i> Acquired Obligate Biotrophy through Gene Loss. Genome Biology and Evolution, 2014, 6, 1938-1948.	1.1	49
993	Discovery of a Novel Bottleneck Dolphin Coronavirus Reveals a Distinct Species of Marine Mammal Coronavirus in Gammacoronavirus. Journal of Virology, 2014, 88, 1318-1331.	1.5	126
994	Crystal structure of human CRMP-4: correction of intensities for lattice-translocation disorder. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1680-1694.	2.5	20
995	Preliminary crystallographic analysis of a double mutant of the acetyl xylo-oligosaccharide esterase Axe2 in its dimeric form. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 476-481.	0.4	8
996	Long non-coding RNAs: modulators of nuclear structure and function. Current Opinion in Cell Biology, 2014, 26, 10-18.	2.6	219
997	SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features. Journal of Molecular Biology, 2014, 426, 2692-2701.	2.0	189
998	Functional characterization of WalRK: A twoâ€²-component signal transduction system from <i>Bacillus anthracis</i> . FEBS Open Bio, 2014, 4, 65-76.	1.0	29
999	Discovery of Unconventional Kinetochores in Kinetoplastids. Cell, 2014, 156, 1247-1258.	13.5	217

#	ARTICLE	IF	CITATIONS
1000	Chemistry of the Retinoid (Visual) Cycle. <i>Chemical Reviews</i> , 2014, 114, 194-232.	23.0	285
1001	A common structural scaffold in CTD phosphatases that supports distinct catalytic mechanisms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 103-118.	1.5	3
1002	Complete genome of a new <i>Firmicutes</i> species belonging to the dominant human colonic microbiota (<i>Ruminococcus bicirculans</i>) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890.	1.8	62
1003	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. <i>Molecular Neurobiology</i> , 2014, 49, 88-102.	1.9	231
1004	The pH dependence of flavivirus envelope protein structure: insights from molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1563-1574.	2.0	17
1005	Functional Protein Prediction Using HMM Based Feature Representation and Relevance Analysis. <i>Advances in Intelligent Systems and Computing</i> , 2014, , 71-76.	0.5	0
1006	Enrichment and characterization of an anaerobic cellulolytic microbial consortium SQD-1.1 from mangrove soil. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 465-474.	1.7	28
1007	Evidence of positive selection at codon sites localized in the C-terminal peptide of ORC6. <i>Biotechnology Letters</i> , 2014, 36, 251-256.	1.1	0
1008	Skyalign: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models. <i>BMC Bioinformatics</i> , 2014, 15, 7.	1.2	298
1009	Evolutionary origins of sensation in metazoans: functional evidence for a new sensory organ in sponges. <i>BMC Evolutionary Biology</i> , 2014, 14, 3.	3.2	92
1010	New mini-zincin structures provide a minimal scaffold for members of this metallopeptidase superfamily. <i>BMC Bioinformatics</i> , 2014, 15, 1.	1.2	541
1011	Tracking the Origin and Divergence of Cholinesterases and Neuroligins: The Evolution of Synaptic Proteins. <i>Journal of Molecular Neuroscience</i> , 2014, 53, 362-369.	1.1	11
1012	A special member of the rice SRO family, OsSRO1c, mediates responses to multiple abiotic stresses through interaction with various transcription factors. <i>Plant Molecular Biology</i> , 2014, 84, 693-705.	2.0	48
1013	A Novel Missense Mutation in AFG3L2 Associated with Late Onset and Slow Progression of Spinocerebellar Ataxia Type 28. <i>Journal of Molecular Neuroscience</i> , 2014, 52, 493-496.	1.1	22
1014	β -Glucuronidase from <i>Lactobacillus brevis</i> useful for baicalin hydrolysis belongs to glycoside hydrolase family 30. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4021-4032.	1.7	42
1015	Cell Wall-Related Proteins of Unknown Function: Missing Links in Plant Cell Wall Development. <i>Plant and Cell Physiology</i> , 2014, 55, 1031-1043.	1.5	25
1016	NeuroPID: a predictor for identifying neuropeptide precursors from metazoan proteomes. <i>Bioinformatics</i> , 2014, 30, 931-940.	1.8	29
1017	Prokka: rapid prokaryotic genome annotation. <i>Bioinformatics</i> , 2014, 30, 2068-2069.	1.8	12,881

#	ARTICLE	IF	CITATIONS
1018	Biogenesis and functions of bacterial S-layers. <i>Nature Reviews Microbiology</i> , 2014, 12, 211-222.	13.6	287
1019	Recombinant expression and purification of an ATP-dependent DNA ligase from <i>Aliivibrio salmonicida</i> . <i>Protein Expression and Purification</i> , 2014, 97, 29-36.	0.6	16
1020	Evolutionary comparisons of miRNA regulation system in six model organisms. <i>Genetica</i> , 2014, 142, 109-118.	0.5	7
1021	The Mi-2 Homolog Mit1 Actively Positions Nucleosomes within Heterochromatin To Suppress Transcription. <i>Molecular and Cellular Biology</i> , 2014, 34, 2046-2061.	1.1	29
1022	Dependency of codon usage on protein sequence patterns: a statistical study. <i>Theoretical Biology and Medical Modelling</i> , 2014, 11, 2.	2.1	2
1023	Dormancy within <i>Staphylococcus epidermidis</i> biofilms: a transcriptomic analysis by RNA-seq. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 2585-2596.	1.7	25
1024	TPX2: of spindle assembly, DNA damage response, and cancer. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 3027-3047.	2.4	155
1025	ComPlex: conservation and divergence of co-expression networks in <i>A. thaliana</i> , <i>Populus</i> and <i>O. sativa</i> . <i>BMC Genomics</i> , 2014, 15, 106.	1.2	69
1026	Land Use Type Significantly Affects Microbial Gene Transcription in Soil. <i>Microbial Ecology</i> , 2014, 67, 919-930.	1.4	48
1027	Summer Squash Identification by High-Resolution-Melting (HRM) Analysis Using Gene-Based ESTâ€™SSR Molecular Markers. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 395-405.	1.0	17
1028	Functional Divergence and Evolutionary Dynamics of the Putative AAAP Gene Family in <i>Brassica rapa</i> . <i>Plant Molecular Biology Reporter</i> , 2014, 32, 517-530.	1.0	7
1029	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	1.2	375
1030	Comparative genomics of <i>Cylindrospermopsis raciborskii</i> strains with differential toxicities. <i>BMC Genomics</i> , 2014, 15, 83.	1.2	64
1031	Endogenous viral elements in algal genomes. <i>Acta Oceanologica Sinica</i> , 2014, 33, 102-107.	0.4	11
1032	Comparative Genomic Analysis of Two-Component Signal Transduction Systems in Probiotic <i>Lactobacillus casei</i> . <i>Indian Journal of Microbiology</i> , 2014, 54, 293-301.	1.5	7
1033	Rapid identification of novel antigens of <i>Salmonella Enteritidis</i> by microarray-based immunoscreening. <i>Mikrochimica Acta</i> , 2014, 181, 1707-1714.	2.5	7
1034	Analysis of the bovine rumen microbiome reveals a diversity of Sus-like polysaccharide utilization loci from the bacterial phylum <i>Bacteroidetes</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 601-606.	1.4	41
1035	Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data. <i>BMC Bioinformatics</i> , 2014, 15, 28.	1.2	12

#	ARTICLE	IF	CITATIONS
1036	On the Origin and Evolution of Plant Brassinosteroid Receptor Kinases. <i>Journal of Molecular Evolution</i> , 2014, 78, 118-129.	0.8	28
1037	Genome-wide analysis of the bHLH transcription factor family in Chinese cabbage (<i>Brassica rapa</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overlo 1.0 104	1.0	104
1038	Overexpression of a new stress-repressive gene OsDSR2 encoding a protein with a DUF966 domain increases salt and simulated drought stress sensitivities and reduces ABA sensitivity in rice. <i>Plant Cell Reports</i> , 2014, 33, 323-336.	2.8	49
1039	Genomic comparison of sporeforming bacilli isolated from milk. <i>BMC Genomics</i> , 2014, 15, 26.	1.2	27
1040	Disordered binding regions of Ewing's sarcoma fusion proteins. <i>Russian Journal of Bioorganic Chemistry</i> , 2014, 40, 16-25.	0.3	1
1041	Comparative phylogenetic analysis of genome-wide Mlo gene family members from <i>Glycine max</i> and <i>Arabidopsis thaliana</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 345-359.	1.0	38
1042	Crystal structures of the human Dysferlin inner DysF domain. <i>BMC Structural Biology</i> , 2014, 14, 3.	2.3	26
1043	Bioinformatic analysis of the four transcription factors used to induce pluripotent stem cells. <i>Cytotechnology</i> , 2014, 66, 967-978.	0.7	4
1044	Catalytic mechanism and origin of high activity of cellulase TmCel12A at high temperature: a quantum mechanical/molecular mechanical study. <i>Cellulose</i> , 2014, 21, 937-949.	2.4	9
1045	Molecular Characterization and Evolution of a Gene Family Encoding Both Female- and Male-Specific Reproductive Proteins in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 1554-1567.	3.5	39
1046	Characterization of <i>Euglenaformis</i> gen. nov. and the chloroplast genome of <i>Euglenaformis</i> [<i>Euglena</i>] <i>proxima</i> (Euglenophyta). <i>Phycologia</i> , 2014, 53, 66-73.	0.6	36
1047	A putative role of the Sup35p C-terminal domain in the cytoskeleton organization during yeast mitosis. <i>Molecular BioSystems</i> , 2014, 10, 925-940.	2.9	5
1048	Structure-guided approach for detecting large domain inserts in protein sequences as illustrated using the haloacid dehalogenase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1896-1906.	1.5	3
1049	Metrics for the Human Proteome Project 2013-2014 and Strategies for Finding Missing Proteins. <i>Journal of Proteome Research</i> , 2014, 13, 15-20.	1.8	124
1050	The substrate specificity, enantioselectivity and structure of the α -selective amine:pyruvate transaminase from <i>Nectria haematococca</i> . <i>FEBS Journal</i> , 2014, 281, 2240-2253.	2.2	60
1051	Studies on the regulation of the human E1 subunit of the 2-oxoglutarate dehydrogenase complex, including the identification of a novel calcium-binding site. <i>Biochemical Journal</i> , 2014, 459, 369-381.	1.7	34
1052	Identification and Characterization of a Gene Cluster Required for Proper Rod Shape, Cell Division, and Pathogenesis in <i>Clostridium difficile</i> . <i>Journal of Bacteriology</i> , 2014, 196, 2290-2300.	1.0	44
1053	Transcriptome-wide identification of bread wheat WRKY transcription factors in response to drought stress. <i>Molecular Genetics and Genomics</i> , 2014, 289, 765-781.	1.0	116

#	ARTICLE	IF	CITATIONS
1054	Activating Mutations Cluster in the <i>α</i> -Molecular Brake Regions of Protein Kinases and Do Not Associate with Conserved or Catalytic Residues. <i>Human Mutation</i> , 2014, 35, 318-328.	1.1	20
1055	Molecular and ultrastructural analysis of forisome subunits reveals the principles of forisome assembly. <i>Annals of Botany</i> , 2014, 113, 1121-1137.	1.4	16
1056	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. <i>Nucleic Acids Research</i> , 2014, 42, D496-D502.	6.5	52
1057	Biofilm formation and antibiotic production in <i>U. oregonensis</i> are influenced by intracellular concentrations of cyclic dimeric guanosinmonophosphate. <i>Environmental Microbiology</i> , 2014, 16, 1252-1266.	1.8	44
1058	The major cockroach allergen Bla g 4 binds tyramine and octopamine. <i>Molecular Immunology</i> , 2014, 60, 86-94.	1.0	22
1059	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. <i>Genome Research</i> , 2014, 24, 1308-1315.	2.4	235
1060	MHF 1 plays Fanconi anaemia complementation group M protein (FANCM)-dependent and FANCM-independent roles in DNA repair and homologous recombination in plants. <i>Plant Journal</i> , 2014, 78, 822-833.	2.8	19
1061	Connectivity between Catalytic Landscapes of the Metallo-β-Lactamase Superfamily. <i>Journal of Molecular Biology</i> , 2014, 426, 2442-2456.	2.0	94
1062	Characterization of the pyrophosphate-dependent 6-phosphofructokinase from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Archives of Biochemistry and Biophysics</i> , 2014, 546, 53-63.	1.4	14
1063	Identification and genetic characterization of a novel picornavirus from chickens. <i>Journal of General Virology</i> , 2014, 95, 1094-1103.	1.3	28
1064	Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. <i>Bioinformatics</i> , 2014, 30, 2093-2097.	1.8	11
1065	Genome-wide identification of members in the YTH domain-containing RNA-binding protein family in apple and expression analysis of their responsiveness to senescence and abiotic stresses. <i>Gene</i> , 2014, 538, 292-305.	1.0	38
1066	A <i>de novo</i> transcriptome of European pollen beetle populations and its analysis, with special reference to insecticide action and resistance. <i>Insect Molecular Biology</i> , 2014, 23, 511-526.	1.0	29
1067	Genetically distinct pathways guide effector export through the type VI secretion system. <i>Molecular Microbiology</i> , 2014, 92, 529-542.	1.2	192
1068	Structural and functional analysis of hypothetical and conserved proteins of <i>Clostridium tetani</i> . <i>Journal of Infection and Public Health</i> , 2014, 7, 296-307.	1.9	44
1069	Computational analysis of riboswitch-based regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 900-907.	0.9	9
1070	Recurrent mutation of <i>JAK3</i> in T-cell polyclonal leukemia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 309-316.	1.5	79
1071	ATP Modulates Acute Inflammation In Vivo through Dual Oxidase-Derived H ₂ O ₂ Production and NF-κB Activation. <i>Journal of Immunology</i> , 2014, 192, 5710-5719.	0.4	66

#	ARTICLE	IF	CITATIONS
1072	Gene expression of lactobacilli in murine forestomach biofilms. <i>Microbial Biotechnology</i> , 2014, 7, 347-359.	2.0	31
1073	Metagenomic analysis of the microbial community in fermented grape marc reveals that <i>Lactobacillus fabifermentans</i> is one of the dominant species: insights into its genome structure. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6015-6037.	1.7	35
1074	Cystomanamides: Structure and Biosynthetic Pathway of a Family of Glycosylated Lipopeptides from Myxobacteria. <i>Organic Letters</i> , 2014, 16, 2414-2417.	2.4	24
1075	The genetic potential for key biogeochemical processes in Arctic frost flowers and young sea ice revealed by metagenomic analysis. <i>FEMS Microbiology Ecology</i> , 2014, 89, 376-387.	1.3	25
1076	Evolution of the Cation Chloride Cotransporter Family: Ancient Origins, Gene Losses, and Subfunctionalization through Duplication. <i>Molecular Biology and Evolution</i> , 2014, 31, 434-447.	3.5	54
1077	Structural and molecular insights into novel surface-exposed mucus adhesins from <i>Lactobacillus reuteri</i> human strains. <i>Molecular Microbiology</i> , 2014, 92, 543-556.	1.2	29
1078	Overview of Recent Progress in Protein-Expression Technologies for Small-Molecule Screening. <i>Journal of Biomolecular Screening</i> , 2014, 19, 1000-1013.	2.6	11
1079	Virus induced gene silencing of three putative prolyl 4-hydroxylases enhances plant growth in tomato (<i>Solanum lycopersicum</i>). <i>Plant Molecular Biology</i> , 2014, 85, 459-471.	2.0	35
1080	Antibacterial enzymes from the functional screening of metagenomic libraries hosted in <i>Ralstonia metallidurans</i> . <i>FEMS Microbiology Letters</i> , 2014, 354, 19-26.	0.7	33
1081	Complete sequence analysis of two cryptic plasmids from <i>Bifidobacterium kashiwanohense</i> ... JCM 15439 (type strain) isolated from healthy infant feces. <i>Animal Science Journal</i> , 2014, 85, 158-163.	0.6	5
1082	Bioenergetics and anaerobic respiratory chains of acetoclastic methanogens. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1130-1147.	0.5	212
1083	Systematic analysis of a wasp parasitism arsenal. <i>Molecular Ecology</i> , 2014, 23, 890-901.	2.0	108
1084	High-throughput sequencing exclusively identified a novel Torque teno virus genotype in serum of a patient with fatal fever. <i>Virologica Sinica</i> , 2014, 29, 112-118.	1.2	16
1085	Core structure of the U6 small nuclear ribonucleoprotein at 1.7-Å... resolution. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 544-551.	3.6	65
1086	footprintDB: a database of transcription factors with annotated cis elements and binding interfaces. <i>Bioinformatics</i> , 2014, 30, 258-265.	1.8	72
1087	Localization-controlled specificity of FAD:threonine flavin transferases in <i>Klebsiella pneumoniae</i> and its implications for the mechanism of Na ⁺ -translocating NADH:quinone oxidoreductase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1122-1129.	0.5	22
1088	The Genome of the Foraminiferan <i>Reticulomyxa filosa</i> . <i>Current Biology</i> , 2014, 24, 11-18.	1.8	73
1089	An update on sugar transport and signalling in grapevine. <i>Journal of Experimental Botany</i> , 2014, 65, 821-832.	2.4	147

#	ARTICLE	IF	CITATIONS
1090	DNA assembly techniques for next-generation combinatorial biosynthesis of natural products. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 469-477.	1.4	51
1091	The evolution of lncRNA repertoires and expression patterns in tetrapods. <i>Nature</i> , 2014, 505, 635-640.	13.7	898
1092	Take five – Type VII secretion systems of Mycobacteria. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1707-1716.	1.9	180
1093	Interplay between phosphoinositide lipids and calcium signals at the leading edge of chemotaxing amoeboid cells. <i>Chemistry and Physics of Lipids</i> , 2014, 182, 73-79.	1.5	21
1094	Overlapping and Distinct Roles of <i>Aspergillus fumigatus</i> UDP-glucose 4-Epimerases in Galactose Metabolism and the Synthesis of Galactose-containing Cell Wall Polysaccharides. <i>Journal of Biological Chemistry</i> , 2014, 289, 1243-1256.	1.6	102
1095	Novel roles of plant RETINOBLASTOMA-RELATED (RBR) protein in cell proliferation and asymmetric cell division. <i>Journal of Experimental Botany</i> , 2014, 65, 2657-2666.	2.4	49
1096	Functional Diversification of Dicer-like Proteins and Small RNAs Required for Genome Sculpting. <i>Developmental Cell</i> , 2014, 28, 174-188.	3.1	87
1097	A novel splicing outcome reveals more than 2000 new mammalian protein isoforms. <i>Bioinformatics</i> , 2014, 30, 151-156.	1.8	11
1098	Health effects of wheat lectins: A review. <i>Journal of Cereal Science</i> , 2014, 59, 112-117.	1.8	47
1099	Creating functional engineered variants of the single-module non-ribosomal peptide synthetase IndC by T domain exchange. <i>Molecular BioSystems</i> , 2014, 10, 1709-1718.	2.9	35
1100	Microbial genomics, transcriptomics and proteomics: new discoveries in decomposition research using complementary methods. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1531-1537.	1.7	49
1101	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. <i>Bioinformatics</i> , 2014, 30, 1112-1119.	1.8	57
1102	Habitat-specific type I polyketide synthases in soils and street sediments. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 75-85.	1.4	21
1103	Marine Tubeworm Metamorphosis Induced by Arrays of Bacterial Phage Tail-Like Structures. <i>Science</i> , 2014, 343, 529-533.	6.0	223
1104	Rice NARROW LEAF1 Regulates Leaf and Adventitious Root Development. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 270-281.	1.0	38
1105	Use of in silico tools for classification of novel missense mutations identified in dystrophin gene in developing countries. <i>Gene</i> , 2014, 535, 250-254.	1.0	6
1106	Minke whale genome and aquatic adaptation in cetaceans. <i>Nature Genetics</i> , 2014, 46, 88-92.	9.4	227
1107	Integrating In Silico Resources to Map a Signaling Network. <i>Methods in Molecular Biology</i> , 2014, 1101, 197-245.	0.4	18

#	ARTICLE	IF	CITATIONS
1108	Identification and developmental expression of the enzymes responsible for dopamine, histamine, octopamine and serotonin biosynthesis in the copepod crustacean <i>Calanus finmarchicus</i> . <i>General and Comparative Endocrinology</i> , 2014, 195, 28-39.	0.8	32
1109	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , 2014, 346, 763-767.	6.0	2,096
1110	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	7.2	82
1111	Gene3D: Multi-domain annotations for protein sequence and comparative genome analysis. <i>Nucleic Acids Research</i> , 2014, 42, D240-D245.	6.5	50
1112	EBI metagenomics—a new resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2014, 42, D600-D606.	6.5	127
1113	Selecting Protein Families for Environmental Features Based on Manifold Regularization. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 104-108.	2.2	1
1114	InterProScan 5: genome-scale protein function classification. <i>Bioinformatics</i> , 2014, 30, 1236-1240.	1.8	6,553
1115	Metabolic regulation of phytoplasma malic enzyme and phosphotransacetylase supports the use of malate as an energy source in these plant pathogens. <i>Microbiology (United Kingdom)</i> , 2014, 160, 2794-2806.	0.7	8
1116	Different transcription regulation routes are exerted by L- and D-amino acid enantiomers of peptide hormones. <i>Journal of Experimental Biology</i> , 2014, 217, 4337-46.	0.8	7
1117	Essential Letters in the Fungal Alphabet. <i>Advances in Genetics</i> , 2014, 85, 201-253.	0.8	84
1118	Estimation of relative effectiveness of phylogenetic programs by machine learning. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1441004.	0.3	0
1119	Broad-range Glycosidase Activity Profiling. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2787-2800.	2.5	55
1120	Rigid-body motions of interacting proteins dominate multispecific binding of ubiquitin in a shape-dependent manner. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 77-89.	1.5	7
1121	Sustainable harvest: managing plasticity for resilient crops. <i>Plant Biotechnology Journal</i> , 2014, 12, 517-533.	4.1	34
1122	Phenylethanol promotes adhesion and biofilm formation of the antagonistic yeast <i>Kloeckera apiculata</i> for the control of blue mold on citrus. <i>FEMS Yeast Research</i> , 2014, 14, 536-546.	1.1	63
1123	Age-dependent deterioration of locomotion in <i>Drosophila melanogaster</i> deficient in the homologue of amyotrophic lateral sclerosis 2. <i>Genes To Cells</i> , 2014, 19, 464-477.	0.5	7
1124	RNA-Seq transcriptome analysis to identify genes involved in metabolism-based diclofop resistance in <i>Lolium rigidum</i> . <i>Plant Journal</i> , 2014, 78, 865-876.	2.8	185
1125	Comprehensive analysis of DNA polymerase III β subunits and their homologs in bacterial genomes. <i>Nucleic Acids Research</i> , 2014, 42, 1393-1413.	6.5	59

#	ARTICLE	IF	CITATIONS
1126	Transcriptomic analysis of the role of Rim101/PacC in the adaptation of <i>Ustilago maydis</i> to an alkaline environment. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1985-1998.	0.7	28
1127	Comparative analysis of deep-sea bacterioplankton OMICS revealed the occurrence of habitat-specific genomic attributes. <i>Marine Genomics</i> , 2014, 17, 1-8.	0.4	11
1128	Heme in the marine environment: from cells to the iron cycle. <i>Metallomics</i> , 2014, 6, 1107-1120.	1.0	63
1129	New Insights about Enzyme Evolution from Large Scale Studies of Sequence and Structure Relationships. <i>Journal of Biological Chemistry</i> , 2014, 289, 30221-30228.	1.6	57
1130	The relationship between classification of multi-domain proteins using an alignment-free approach and their functions: a case study with immunoglobulins. <i>Molecular BioSystems</i> , 2014, 10, 1082.	2.9	8
1131	Lineage and species-specific long noncoding RNAs during erythro-megakaryocytic development. <i>Blood</i> , 2014, 123, 1927-1937.	0.6	169
1132	Identification of HilD-Regulated Genes in <i>Salmonella enterica</i> Serovar Typhimurium. <i>Journal of Bacteriology</i> , 2014, 196, 1094-1101.	1.0	45
1133	Nucleophilic 1,4-Additions for Natural Product Discovery. <i>ACS Chemical Biology</i> , 2014, 9, 2014-2022.	1.6	58
1134	Systematic Identification of Hypothetical Bacteriophage Proteins Targeting Key Protein Complexes of <i>Pseudomonas aeruginosa</i> . <i>Journal of Proteome Research</i> , 2014, 13, 4446-4456.	1.8	54
1135	A novel Fibroblast Growth Factor Receptor family member promotes neuronal outgrowth and synaptic plasticity in <i>Aplysia</i> . <i>Amino Acids</i> , 2014, 46, 2477-2488.	1.2	10
1136	Data, Databases, Data Format, Database Search, Data Retrieval Systems, and Genome Browsers. , 2014, , 77-131.		0
1137	Variability of the transporter gene complement in ammonia-oxidizing archaea. <i>Trends in Microbiology</i> , 2014, 22, 665-675.	3.5	81
1138	The protein Compromised Hydrolysis of Triacylglycerols 7 (CHT7) acts as a repressor of cellular quiescence in <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15833-15838.	3.3	105
1139	Using THz time-scale infrared spectroscopy to examine the role of collective, thermal fluctuations in the formation of myoglobin allosteric communication pathways and ligand specificity. <i>Soft Matter</i> , 2014, 10, 4387.	1.2	13
1140	A Root-Expressed <i>Phenylalanine:4-Hydroxyphenylpyruvate Aminotransferase</i> Is Required for Tropane Alkaloid Biosynthesis in <i>Atropa belladonna</i> . <i>Plant Cell</i> , 2014, 26, 3745-3762.	3.1	69
1141	The landscape of kinase fusions in cancer. <i>Nature Communications</i> , 2014, 5, 4846.	5.8	769
1142	Structural insights into the unique single-stranded DNA-binding mode of <i>Helicobacter pylori</i> DprA. <i>Nucleic Acids Research</i> , 2014, 42, 3478-3491.	6.5	23
1143	Chitin-induced activation of immune signaling by the rice receptor CEBiP relies on a unique sandwich-type dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E404-13.	3.3	271

#	ARTICLE	IF	CITATIONS
1144	Proteome-wide analysis of human disease mutations in short linear motifs: neglected players in cancer?. <i>Molecular BioSystems</i> , 2014, 10, 2626-2642.	2.9	80
1145	HNH proteins are a widespread component of phage DNA packaging machines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6022-6027.	3.3	110
1146	Pneumocandin Biosynthesis: Involvement of a <i>trans</i> -selective Proline Hydroxylase. <i>ChemBioChem</i> , 2014, 15, 2365-2369.	1.3	47
1147	RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014, 42, D352-D357.	6.5	53
1148	The Structure and Specificity of the Type III Secretion System Effector NleC Suggest a DNA Mimicry Mechanism of Substrate Recognition. <i>Biochemistry</i> , 2014, 53, 5131-5139.	1.2	28
1149	<i>scp</i> GIL, a new c-di-GMP-binding protein domain involved in regulation of cellulose synthesis in enterobacteria. <i>Molecular Microbiology</i> , 2014, 93, 439-452.	1.2	118
1150	Homogalacturonan-modifying enzymes: structure, expression, and roles in plants. <i>Journal of Experimental Botany</i> , 2014, 65, 5125-5160.	2.4	242
1151	Asymmetric mRNA localization contributes to fidelity and sensitivity of spatially localized systems. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 833-839.	3.6	57
1152	Identification, Expression, and Regulation of Anti-M β 1/Allerian Hormone Type-II Receptor in the Embryonic Chicken Gonad1. <i>Biology of Reproduction</i> , 2014, 90, 106.	1.2	28
1153	EnsembleGASVR: a novel ensemble method for classifying missense single nucleotide polymorphisms. <i>Bioinformatics</i> , 2014, 30, 2324-2333.	1.8	17
1154	Non-coding RNA: a new frontier in regulatory biology. <i>National Science Review</i> , 2014, 1, 190-204.	4.6	175
1155	Genome-Wide Identification, Phylogeny, Duplication, and Expression Analyses of Two-Component System Genes in Chinese Cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>DNA Research</i> , 2014, 21, 379-396.	1.5	53
1156	Crystal structures of three representatives of a new <i>P</i> -fam family PF14869 (DUF4488) suggest they function in sugar binding/uptake. <i>Protein Science</i> , 2014, 23, 1380-1391.	3.1	3
1157	“Come into the fold”: A comparative analysis of bacterial redox enzyme maturation protein members of the NarJ subfamily. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 2971-2984.	1.4	18
1158	Molecular characterization and expression analysis of the complement factor I (CpFI) in the whitespotted bamboo shark (<i>Chiloscyllium plagiosum</i>). <i>Fish and Shellfish Immunology</i> , 2014, 40, 414-423.	1.6	6
1159	T cell transcripts and T cell activities in the gills of the teleost fish sea bass (<i>Dicentrarchus labrax</i>). <i>Developmental and Comparative Immunology</i> , 2014, 47, 309-318.	1.0	58
1160	Characterization and Phylogenetic Analysis of Allergenic Tryp_alpha_amyl Protein Family in Plants. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 270-278.	2.4	4
1161	A Novel Mercuric Reductase from the Unique Deep Brine Environment of Atlantis II in the Red Sea. <i>Journal of Biological Chemistry</i> , 2014, 289, 1675-1687.	1.6	36

#	ARTICLE	IF	CITATIONS
1162	Expression of cytoskeletal and molt-related genes is temporally scheduled in the hypodermis of the crayfish <i>Procambarus clarkii</i> during premolt. <i>Journal of Experimental Biology</i> , 2014, 217, 4193-202.	0.8	27
1163	Unraveling novel broad-spectrum antibacterial targets in food and waterborne pathogens using comparative genomics and protein interaction network analysis. <i>Infection, Genetics and Evolution</i> , 2014, 27, 300-308.	1.0	36
1164	Evolutionarily Distinct Versions of the Multidomain Enzyme β -Isopropylmalate Synthase Share Discrete Mechanisms of V-Type Allosteric Regulation. <i>Biochemistry</i> , 2014, 53, 4847-4856.	1.2	10
1165	X-ray structure of a CDP-alcohol phosphatidyltransferase membrane enzyme and insights into its catalytic mechanism. <i>Nature Communications</i> , 2014, 5, 4169.	5.8	39
1166	Comparative Phosphoproteome Analysis of the Developing Grains in Bread Wheat (<i>Triticum aestivum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 4281-4297.	1.8	54
1167	Nucleotide polymorphism and copy number variant detection using exome capture and next-generation sequencing in the polyploid grass <i>Panicum virgatum</i> . <i>Plant Journal</i> , 2014, 79, 993-1008.	2.8	39
1168	Nanoliter qPCR Platform for Highly Parallel, Quantitative Assessment of Reductive Dehalogenase Genes and Populations of Dehalogenating Microorganisms in Complex Environments. <i>Environmental Science & Technology</i> , 2014, 48, 9659-9667.	4.6	22
1169	Molecular dynamics simulations of lectin domain of FimH and immunoinformatics for the design of potential vaccine candidates. <i>Computational Biology and Chemistry</i> , 2014, 52, 18-24.	1.1	11
1170	De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. <i>Nature Biotechnology</i> , 2014, 32, 1045-1052.	9.4	535
1171	Catechol 2,3-dioxygenase and other <i>meta</i> -cleavage catabolic pathway genes in the "anaerobic" termite gut spirochete <i>Reponema primitia</i> . <i>Molecular Ecology</i> , 2014, 23, 1531-1543.	2.0	34
1172	Comparative analysis of zygospore transcripts during early germination in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Plant Physiology</i> , 2014, 171, 1685-1692.	1.6	8
1173	Visualization of protein sequence features using JavaScript and SVG with pViz.js. <i>Bioinformatics</i> , 2014, 30, 3408-3409.	1.8	19
1174	Realizing the promise of parasite genomics. <i>Trends in Parasitology</i> , 2014, 30, 321-323.	1.5	10
1175	CutProtFam-Pred: Detection and classification of putative structural cuticular proteins from sequence alone, based on profile Hidden Markov Models. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 52, 51-59.	1.2	98
1176	Swine interferon-induced transmembrane protein, sIFITM3, inhibits foot-and-mouth disease virus infection in vitro and in vivo. <i>Antiviral Research</i> , 2014, 109, 22-29.	1.9	25
1177	The robustness and innovability of protein folds. <i>Current Opinion in Structural Biology</i> , 2014, 26, 131-138.	2.6	108
1178	Whole exome sequencing identifies three novel mutations in <i>ANTXR1</i> in families with GAPO syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2014, 164, 2328-2334.	0.7	20
1179	Leveraging structure for enzyme function prediction: methods, opportunities, and challenges. <i>Trends in Biochemical Sciences</i> , 2014, 39, 363-371.	3.7	31

#	ARTICLE	IF	CITATIONS
1180	An integrative computational model for large-scale identification of metalloproteins in microbial genomes: a focus on iron-sulfur cluster proteins. <i>Metallomics</i> , 2014, 6, 1913-1930.	1.0	20
1181	Insights into Secondary Metabolism from a Global Analysis of Prokaryotic Biosynthetic Gene Clusters. <i>Cell</i> , 2014, 158, 412-421.	13.5	801
1182	Biosynthesis of Crocacin Involves an Unusual Hydrolytic Release Domain Showing Similarity to Condensation Domains. <i>Chemistry and Biology</i> , 2014, 21, 855-865.	6.2	42
1183	Transcription of Two Adjacent Carbohydrate Utilization Gene Clusters in <i>Bifidobacterium breve</i> UCC2003 Is Controlled by LacI- and Repressor Open Reading Frame Kinase (ROK)-Type Regulators. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3604-3614.	1.4	29
1184	Fast pseudolikelihood maximization for direct-coupling analysis of protein structure from many homologous amino-acid sequences. <i>Journal of Computational Physics</i> , 2014, 276, 341-356.	1.9	155
1185	Paenilarvins: Iturin Family Lipopeptides from the Honey Bee Pathogen <i>Paenibacillus larvae</i> . <i>ChemBioChem</i> , 2014, 15, 1947-1955.	1.3	51
1186	A New Formulation of Protein Evolutionary Models that Account for Structural Constraints. <i>Molecular Biology and Evolution</i> , 2014, 31, 736-749.	3.5	25
1187	Family 34 glycosyltransferase (GT34) genes and proteins in <i>Pinus radiata</i> (radiata) Tj ETQq1 1 0,784314 rgBT /Overd	2.8	1
1188	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014, 42, D490-D495.	6.5	5,443
1189	A sugar phosphatase regulates the methylerythritol phosphate (MEP) pathway in malaria parasites. <i>Nature Communications</i> , 2014, 5, 4467.	5.8	69
1191	New phylogenomic and comparative analyses provide corroborating evidence that Myxozoa is Cnidaria. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 10-18.	1.2	34
1192	Bioinformatics Analysis of Pancreas Cancer Genome in High-Throughput Genomic Technologies. , 2014, , 93-131.		1
1193	Cold Response in <i>Phalaenopsis aphrodite</i> and Characterization of PaCBF1 and PaICE1. <i>Plant and Cell Physiology</i> , 2014, 55, 1623-1635.	1.5	29
1194	Identification of novel leads applying <i>in silico</i> studies for <i>Mycobacterium</i> multidrug resistant (MMR) protein. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1889-1906.	2.0	18
1195	Bioinformatic approaches to augment study of epithelial-to-mesenchymal transition in lung cancer. <i>Physiological Genomics</i> , 2014, 46, 699-724.	1.0	26
1196	Structure- and context-based analysis of the GxGYxYP family reveals a new putative class of Glycoside Hydrolase. <i>BMC Bioinformatics</i> , 2014, 15, 196.	1.2	8
1197	Homology-based prediction of interactions between proteins using Averaged One-Dependence Estimators. <i>BMC Bioinformatics</i> , 2014, 15, 213.	1.2	77
1198	Identification and phylogenetic analyses of VAS _t , an uncharacterized protein domain associated with lipid-binding domains in Eukaryotes. <i>BMC Bioinformatics</i> , 2014, 15, 222.	1.2	38

#	ARTICLE	IF	CITATIONS
1199	Large-scale phosphoproteome analysis in seedling leaves of <i>Brachypodium distachyon</i> L.. BMC Genomics, 2014, 15, 375.	1.2	37
1200	Differential gene expression between functionally specialized polyps of the colonial hydrozoan <i>Hydractinia symbiolongicarpus</i> (Phylum Cnidaria). BMC Genomics, 2014, 15, 406.	1.2	45
1201	Genome-wide analysis of regulatory proteases sequences identified through bioinformatics data mining in <i>Taenia solium</i> . BMC Genomics, 2014, 15, 428.	1.2	6
1202	Quantitative phosphoproteomic profiling of fiber differentiation and initiation in a fiberless mutant of cotton. BMC Genomics, 2014, 15, 466.	1.2	33
1203	The genome and occlusion bodies of marine <i>Penaeus monodon</i> nudivirus (PmNV, also known as MBV) Tj ETQq0 0 0 rgBT /Overlock 10 T terrestrial nudiviruses. BMC Genomics, 2014, 15, 628.	1.2	38
1204	Inspecting the potential physiological and biomedical value of 44 conserved uncharacterised proteins of <i>Streptococcus pneumoniae</i> . BMC Genomics, 2014, 15, 652.	1.2	10
1205	Gene co-expression network analysis in <i>Rhodobacter capsulatus</i> and application to comparative expression analysis of <i>Rhodobacter sphaeroides</i> . BMC Genomics, 2014, 15, 730.	1.2	19
1206	Proteomic analysis of the <i>Plasmodium</i> male gamete reveals the key role for glycolysis in flagellar motility. Malaria Journal, 2014, 13, 315.	0.8	50
1207	Crystal structure of the lytic CHAPK domain of the endolysin LysK from <i>Staphylococcus aureus</i> bacteriophage K. Virology Journal, 2014, 11, 133.	1.4	47
1208	Profiling the orphan enzymes. Biology Direct, 2014, 9, 10.	1.9	43
1209	Understanding the sequence requirements of protein families: insights from the BioVis 2013 contests. BMC Proceedings, 2014, 8, S1.	1.8	4
1210	De novo assembly and characterization of the transcriptome in the desiccation-tolerant moss <i>Syntrichia caninervis</i> . BMC Research Notes, 2014, 7, 490.	0.6	69
1211	Identification of G protein-coupled receptors in <i>Schistosoma haematobium</i> and <i>S. mansoni</i> by comparative genomics. Parasites and Vectors, 2014, 7, 242.	1.0	37
1212	Genome-wide survey and expression analysis of the bHLH-PAS genes in the amphioxus <i>Branchiostoma floridae</i> reveal both conserved and diverged expression patterns between cephalochordates and vertebrates. EvoDevo, 2014, 5, 20.	1.3	12
1213	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. Genome Medicine, 2014, 6, 57.	3.6	101
1214	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. Genome Medicine, 2014, 6, 59.	3.6	20
1215	Biology of ferritin in mammals: an update on iron storage, oxidative damage and neurodegeneration. Archives of Toxicology, 2014, 88, 1787-1802.	1.9	135
1216	The Architecture of a Scrambled Genome Reveals Massive Levels of Genomic Rearrangement during Development. Cell, 2014, 158, 1187-1198.	13.5	152

#	ARTICLE	IF	CITATIONS
1217	An improved method for specificity annotation shows a distinct evolutionary divergence among the microbial enzymes of the cholyglycine hydrolase family. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1162-1174.	0.7	22
1218	Integrative Network Analysis of the Signaling Cascades in Seedling Leaves of Bread Wheat by Large-Scale Phosphoproteomic Profiling. <i>Journal of Proteome Research</i> , 2014, 13, 2381-2395.	1.8	42
1219	Xylan utilization in human gut commensal bacteria is orchestrated by unique modular organization of polysaccharide-degrading enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3708-17.	3.3	137
1220	Aggregation Factor as an Inhibitor of Bacterial Binding to Gut Mucosa. <i>Microbial Ecology</i> , 2014, 68, 633-644.	1.4	22
1221	Genomic analysis of cyclic-di-GMP-related genes in rhizobial type strains and functional analysis in <i>Rhizobium etli</i> . <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4589-4602.	1.7	23
1222	The first mouse mutants of D14Abb1e (Fam208a) show that it is critical for early development. <i>Mammalian Genome</i> , 2014, 25, 293-303.	1.0	30
1223	Assembly and nuclear export of pre-ribosomal particles in budding yeast. <i>Chromosoma</i> , 2014, 123, 327-344.	1.0	44
1224	Genome-wide identification, classification and expression analysis of the heat shock transcription factor family in Chinese cabbage. <i>Molecular Genetics and Genomics</i> , 2014, 289, 541-551.	1.0	59
1225	Genome-wide analysis and identification of stress-responsive genes of the CCCH zinc finger family in <i>Solanum lycopersicum</i> . <i>Molecular Genetics and Genomics</i> , 2014, 289, 965-979.	1.0	49
1226	MetalS3, a database-mining tool for the identification of structurally similar metal sites. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 937-945.	1.1	28
1227	Diversity of the metal-transporting P1B-type ATPases. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 947-960.	1.1	98
1228	Protein-protein interaction network of the marine microalga <i>Tetraselmis subcordiformis</i> : prediction and application for starch metabolism analysis. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 1287-1296.	1.4	18
1229	GhPSY, a phytoene synthase gene, is related to the red plant phenotype in upland cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	19
1230	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
1231	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> . <i>New Phytologist</i> , 2014, 202, 554-564.	3.5	52
1232	Classification of Intrinsically Disordered Regions and Proteins. <i>Chemical Reviews</i> , 2014, 114, 6589-6631.	23.0	1,618
1233	Large-Scale Genetic Perturbations Reveal Regulatory Networks and an Abundance of Gene-Specific Repressors. <i>Cell</i> , 2014, 157, 740-752.	13.5	248
1234	PTP-central: A comprehensive resource of protein tyrosine phosphatases in eukaryotic genomes. <i>Methods</i> , 2014, 65, 156-164.	1.9	16

#	ARTICLE	IF	CITATIONS
1235	Benchmarking of Methods for Genomic Taxonomy. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1529-1539.	1.8	241
1236	Signaling through C2 domains: More than one lipid target. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1536-1547.	1.4	189
1237	Evolution and diversity of the 2-oxoglutarate-dependent dioxygenase superfamily in plants. <i>Plant Journal</i> , 2014, 78, 328-343.	2.8	313
1238	Small auxin upregulated RNA (<i>SAUR</i>) gene family in maize: Identification, evolution, and its phylogenetic comparison with <i>Arabidopsis</i>, rice, and sorghum. <i>Journal of Integrative Plant Biology</i> , 2014, 56, 133-150.	4.1	93
1239	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
1240	Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. <i>Human Molecular Genetics</i> , 2014, 23, 5866-5878.	1.4	463
1241	Alginate-Dependent Gene Expression Mechanism in <i>Sphingomonas</i> sp. Strain A1. <i>Journal of Bacteriology</i> , 2014, 196, 2691-2700.	1.0	14
1242	Complete <i>Bordetella avium</i>, <i>Bordetella hinzii</i> and <i>Bordetella trematum</i> lipid A structures and genomic sequence analyses of the loci involved in their modifications. <i>Innate Immunity</i> , 2014, 20, 659-672.	1.1	10
1243	The ABC-F protein EttA gates ribosome entry into the translation elongation cycle. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 143-151.	3.6	109
1244	Elastic network models capture the motions apparent within ensembles of RNA structures. <i>Rna</i> , 2014, 20, 792-804.	1.6	33
1245	Bacterial methionine biosynthesis. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1571-1584.	0.7	178
1246	In silico study of wall-associated kinase family reveals large-scale genomic expansion potentially connected with functional diversification in <i>Populus</i> . <i>Tree Genetics and Genomes</i> , 2014, 10, 1135-1147.	0.6	17
1247	Genomewide analysis of LATERAL ORGAN BOUNDARIES Domain gene family in <i>Zea mays</i> . <i>Journal of Genetics</i> , 2014, 93, 79-91.	0.4	48
1248	Homology Modeling and Comparative Profiling of Superoxide Dismutase Among Extremophiles: <i>Exiguobacterium</i> as a Model Organism. <i>Indian Journal of Microbiology</i> , 2014, 54, 450-458.	1.5	5
1249	A comprehensive study of small non-frameshift insertions/deletions in proteins and prediction of their phenotypic effects by a machine learning method (KD4i). <i>BMC Bioinformatics</i> , 2014, 15, 111.	1.2	21
1250	Metavir 2: new tools for viral metagenome comparison and assembled virome analysis. <i>BMC Bioinformatics</i> , 2014, 15, 76.	1.2	217
1251	spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 81.	1.2	100
1252	Target network differences between western drugs and Chinese herbal ingredients in treating cardiovascular disease. <i>BMC Bioinformatics</i> , 2014, 15, S3.	1.2	7

#	ARTICLE	IF	CITATIONS
1253	A multilocus timescale for oomycete evolution estimated under three distinct molecular clock models. <i>BMC Evolutionary Biology</i> , 2014, 14, 101.	3.2	53
1254	Functional genomics reveals that <i>Clostridium difficile</i> Spo0A coordinates sporulation, virulence and metabolism. <i>BMC Genomics</i> , 2014, 15, 160.	1.2	145
1255	Secretome analysis reveals effector candidates associated with broad host range necrotrophy in the fungal plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>BMC Genomics</i> , 2014, 15, 336.	1.2	241
1256	Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. <i>BMC Genomics</i> , 2014, 15, 356.	1.2	13
1257	High-throughput screening and whole genome sequencing identifies an antimicrobially active inhibitor of <i>Vibrio cholerae</i> . <i>BMC Microbiology</i> , 2014, 14, 49.	1.3	10
1258	Genes associated with agronomic traits in non-heading Chinese cabbage identified by expression profiling. <i>BMC Plant Biology</i> , 2014, 14, 71.	1.6	21
1259	Genome-scale metabolic reconstructions of <i>Bifidobacterium adolescentis</i> L2-32 and <i>Faecalibacterium prausnitzii</i> A2-165 and their interaction. <i>BMC Systems Biology</i> , 2014, 8, 41.	3.0	88
1260	Bioinformatic analysis of proteomics data. <i>BMC Systems Biology</i> , 2014, 8, S3.	3.0	131
1261	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. <i>Marine Genomics</i> , 2014, 18, 97-99.	0.4	14
1262	The Interplay of Light and Oxygen in the Reactive Oxygen Stress Response of <i>Chlamydomonas reinhardtii</i> Dissected by Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 969-989.	2.5	29
1263	Orphans and new gene origination, a structural and evolutionary perspective. <i>Current Opinion in Structural Biology</i> , 2014, 26, 73-83.	2.6	27
1264	Maintaining a microbial genome & metagenome data analysis system in an academic setting. , 2014, , .		5
1265	Engineering adenylate cyclases regulated by near-infrared window light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10167-10172.	3.3	104
1266	Abundant and Diverse Clustered Regularly Interspaced Short Palindromic Repeat Spacers in <i>Clostridium difficile</i> Strains and Prophages Target Multiple Phage Types within This Pathogen. <i>MBio</i> , 2014, 5, e01045-13.	1.8	67
1267	Repurposing TRASH: Emergence of the enzyme organomercurial lyase from a non-catalytic zinc finger scaffold. <i>Journal of Structural Biology</i> , 2014, 188, 16-21.	1.3	11
1268	e-Driver: a novel method to identify protein regions driving cancer. <i>Bioinformatics</i> , 2014, 30, 3109-3114.	1.8	116
1269	Prediction of protein post-translational modifications: main trends and methods. <i>Russian Chemical Reviews</i> , 2014, 83, 143-154.	2.5	6
1270	Conserved expression of lincRNA during human and macaque prefrontal cortex development and maturation. <i>Rna</i> , 2014, 20, 1103-1111.	1.6	59

#	ARTICLE	IF	CITATIONS
1271	Mechanistic and Bioinformatic Investigation of a Conserved Active Site Helix in β -Isopropylmalate Synthase from <i>Mycobacterium tuberculosis</i> , a Member of the DRE-TIM Metallolyase Superfamily. <i>Biochemistry</i> , 2014, 53, 2915-2925.	1.2	14
1272	LRRsearch: An asynchronous server-based application for the prediction of leucine-rich repeat motifs and an integrative database of NOD-like receptors. <i>Computers in Biology and Medicine</i> , 2014, 53, 164-170.	3.9	34
1273	Influence of Impaired Lipoprotein Biogenesis on Surface and Exoproteome of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteome Research</i> , 2014, 13, 650-667.	1.8	45
1274	Broad-Enrich: functional interpretation of large sets of broad genomic regions. <i>Bioinformatics</i> , 2014, 30, i393-i400.	1.8	21
1275	Identification of potential drug targets by subtractive genome analysis of <i>Bacillus anthracis</i> A0248: An in silico approach. <i>Computational Biology and Chemistry</i> , 2014, 52, 66-72.	1.1	29
1276	Structural basis for a pH-sensitive calcium leak across membranes. <i>Science</i> , 2014, 344, 1131-1135.	6.0	86
1277	Purification, characterization, molecular cloning, and extracellular production of a novel bacterial glycerophosphocholine cholinephosphodiesterase from <i>Streptomyces sanglieri</i> . <i>Journal of Bioscience and Bioengineering</i> , 2014, 117, 422-430.	1.1	6
1278	Phosphoglucan phosphatase function sheds light on starch degradation. <i>Trends in Plant Science</i> , 2014, 19, 471-478.	4.3	73
1279	Genome-wide analysis of terpene synthases in soybean: functional characterization of GmTPS3. <i>Gene</i> , 2014, 544, 83-92.	1.0	29
1280	Sequencing and analysis of the transcriptome of the acorn worm <i>Ptychodera flava</i> , an indirect developing hemichordate. <i>Marine Genomics</i> , 2014, 15, 35-43.	0.4	16
1281	Assembly of Robust Bacterial Microcompartment Shells Using Building Blocks from an Organelle of Unknown Function. <i>Journal of Molecular Biology</i> , 2014, 426, 2217-2228.	2.0	102
1282	MoTlg2, a t-SNARE component is important for formation of the Spitzenkörper and polar deposition of chitin in <i>Magnaporthe oryzae</i> . <i>Physiological and Molecular Plant Pathology</i> , 2014, 87, 9-18.	1.3	4
1283	C19orf12 mutation leads to a pallido-pyramidal syndrome. <i>Gene</i> , 2014, 537, 352-356.	1.0	28
1284	Genome-wide analysis of the GRAS gene family in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Genomics</i> , 2014, 103, 135-146.	1.3	114
1285	TRDistiller: A rapid filter for enrichment of sequence datasets with proteins containing tandem repeats. <i>Journal of Structural Biology</i> , 2014, 186, 386-391.	1.3	11
1286	Proteome compression via protein domain compositions. <i>Methods</i> , 2014, 67, 380-385.	1.9	9
1287	Incomplete sterols and hopanoids pathways in ciliates: Gene loss and acquisition during evolution as a source of biosynthetic genes. <i>Molecular Phylogenetics and Evolution</i> , 2014, 74, 122-134.	1.2	21
1288	Structure of allergens and structure based epitope predictions. <i>Methods</i> , 2014, 66, 3-21.	1.9	82

#	ARTICLE	IF	CITATIONS
1289	Gene encoding a novel invertase from a xerophilic <i>Aspergillus niger</i> strain and production of the enzyme in <i>Pichia pastoris</i> . <i>Enzyme and Microbial Technology</i> , 2014, 63, 28-33.	1.6	16
1290	Systematic Detection of Internal Symmetry in Proteins Using CE-Symm. <i>Journal of Molecular Biology</i> , 2014, 426, 2255-2268.	2.0	44
1291	Genomic analysis and expression investigation of caleosin gene family in <i>Arabidopsis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2014, 448, 365-371.	1.0	37
1292	Metaproteomics: Extracting and Mining Proteome Information to Characterize Metabolic Activities in Microbial Communities. <i>Current Protocols in Bioinformatics</i> , 2014, 46, 13.26.1-14.	25.8	18
1293	ChEpiMod: a knowledgebase for chemical modulators of epigenome reader domains. <i>Bioinformatics</i> , 2014, 30, 1481-1483.	1.8	11
1294	Unique Features of the Loblolly Pine (<i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
1295	The European Bioinformatics Institute's data resources 2014. <i>Nucleic Acids Research</i> , 2014, 42, D18-D25.	6.5	71
1296	Intrinsically Disordered Proteins and Intrinsically Disordered Protein Regions. <i>Annual Review of Biochemistry</i> , 2014, 83, 553-584.	5.0	850
1297	Improving transcriptome construction in non-model organisms: integrating manual and automated gene definition in <i>Emiliana huxleyi</i> . <i>BMC Genomics</i> , 2014, 15, 148.	1.2	31
1298	Crystal structure of a member of a novel family of dioxygenases (PF10014) reveals a conserved cupin fold and active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 164-170.	1.5	15
1299	Crosstalk and the evolution of specificity in two-component signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5550-5555.	3.3	95
1300	Transporter taxonomy – a comparison of different transport protein classification schemes. <i>Drug Discovery Today: Technologies</i> , 2014, 12, e37-e46.	4.0	7
1301	A Code for RanGDP Binding in Ankyrin Repeats Defines a Nuclear Import Pathway. <i>Cell</i> , 2014, 157, 1130-1145.	13.5	67
1302	Characterization of the biosynthetic gene cluster for the ribosomally synthesized cyclic peptide ustiloxin B in <i>Aspergillus flavus</i> . <i>Fungal Genetics and Biology</i> , 2014, 68, 23-30.	0.9	130
1303	Crystal structure of <i>Arabidopsis</i> glutamyl-tRNA reductase in complex with its stimulator protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6630-6635.	3.3	58
1304	The identification of four histidine kinases that influence sporulation in <i>Clostridium thermocellum</i> . <i>Anaerobe</i> , 2014, 28, 109-119.	1.0	33
1305	The bacterial septal ring protein <i>RlpA</i> is a lytic transglycosylase that contributes to rod shape and daughter cell separation in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2014, 93, 113-128.	1.2	95
1306	Overview of Plant Chitinases Identified as Food Allergens. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 5734-5742.	2.4	14

#	ARTICLE	IF	CITATIONS
1307	Omics and the Future of Sustainable Biomaterials. ACS Symposium Series, 2014, , 59-79.	0.5	3
1308	Metatranscriptome profiling of a harmful algal bloom. Harmful Algae, 2014, 37, 75-83.	2.2	45
1309	Large $\hat{\pm}$ -aminonitrilase activity screening of nitrilase superfamily members: Access to conversion and enantiospecificity by LC $\hat{\pm}$ MS. Journal of Molecular Catalysis B: Enzymatic, 2014, 107, 79-88.	1.8	6
1310	Diffusible gas transmitter signaling in the copepod crustacean <i>Calanus finmarchicus</i> : Identification of the biosynthetic enzymes of nitric oxide (NO), carbon monoxide (CO) and hydrogen sulfide (H ₂ S) using a de novo assembled transcriptome. General and Comparative Endocrinology, 2014, 202, 76-86.	0.8	18
1311	Effective identification of kinase-specific phosphorylation sites based on domain $\hat{\pm}$ domain interactions. Chemometrics and Intelligent Laboratory Systems, 2014, 136, 97-103.	1.8	4
1312	Ligand heterogeneity of the cysteine protease binding protein family in the parasitic protist <i>Entamoeba histolytica</i> . International Journal for Parasitology, 2014, 44, 625-635.	1.3	32
1313	A novel sea anemone peptide that inhibits acid-sensing ion channels. Peptides, 2014, 53, 3-12.	1.2	54
1314	Biological network extraction from scientific literature: state of the art and challenges. Briefings in Bioinformatics, 2014, 15, 856-877.	3.2	55
1315	Molecular Cloning and Yeast Expression of Cinnamate 4-Hydroxylase from <i>Ornithogalum saundersiae</i> Baker. Molecules, 2014, 19, 1608-1621.	1.7	18
1316	ENTROPY MEASURES BASED METHOD FOR THE CLASSIFICATION OF PROTEIN DOMAINS INTO FAMILIES AND CLANS. , 2014, , .		0
1319	Tn7. Microbiology Spectrum, 2014, 2, .	1.2	67
1320	Inference of domain-domain interactions by matrix factorisation and domain-level features. International Journal of Functional Informatics and Personalised Medicine, 2014, 4, 259.	0.4	0
1321	Molecular Docking and Panicytic Effect of 8-Prenylnaringenin in the Elevated T-Maze. Chemical and Pharmaceutical Bulletin, 2014, 62, 1231-1237.	0.6	4
1322	The complete genome sequence of the rumen methanogen <i>Methanobacterium formicicum</i> BRM9. Standards in Genomic Sciences, 2014, 9, 15.	1.5	27
1323	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. Evolutionary Bioinformatics, 2014, 10, EBO.S13759.	0.6	23
1324	Complete Genome Sequence of <i>Campylobacter iguaniorum</i> Strain 1485E T , Isolated from a Bearded Dragon (<i>Pogona vitticeps</i>). Genome Announcements, 2014, 2, .	0.8	10
1325	Genome Sequence of <i>Afpia felis</i> Strain 76713, Isolated in Hospital Water Using an Amoeba Co-Culture Procedure. Genome Announcements, 2014, 2, .	0.8	1
1326	Non-contiguous finished genome sequence and description of <i>Anaerococcus provenciensis</i> sp. nov.. Standards in Genomic Sciences, 2014, 9, 1198-1210.	1.5	15

#	ARTICLE	IF	CITATIONS
1327	The Genome Sequence of a Type ST239 Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate from a Malaysian Hospital. <i>Standards in Genomic Sciences</i> , 2014, 9, 933-939.	1.5	2
1328	Non-contiguous finished genome sequence and description of <i>Sulfurimonas hongkongensis</i> sp. nov., a strictly anaerobic denitrifying, hydrogen- and sulfur-oxidizing chemolithoautotroph isolated from marine sediment. <i>Standards in Genomic Sciences</i> , 2014, 9, 1302-1310.	1.5	30
1329	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <i>Standards in Genomic Sciences</i> , 2014, 9, 1259-1274.	1.5	31
1330	Non-contiguous finished genome sequence and description of <i>Bacteroides neonati</i> sp. nov., a new species of anaerobic bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 794-806.	1.5	8
1331	High quality draft genome sequence of <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i> strain hu-01. <i>Standards in Genomic Sciences</i> , 2014, 9, 755-762.	1.5	8
1332	Genome Sequence of <i>Legionella anisa</i> , Isolated from a Respiratory Sample, Using an Amoebal Coculture Procedure. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
1333	Draft Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> HP T , the First Defined-Strain Dairy Starter Culture Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
1334	SysPTM 2.0: an updated systematic resource for post-translational modification. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau025-bau025.	1.4	58
1335	Noncontiguous finished genome sequence and description of <i>Virgibacillus massiliensis</i> sp. nov., a moderately halophilic bacterium isolated from human gut. <i>New Microbes and New Infections</i> , 2015, 8, 78-88.	0.8	10
1336	Most partial domains in proteins are alignment and annotation artifacts. <i>Genome Biology</i> , 2015, 16, 99.	3.8	27
1337	Identification, molecular characterization and expression analysis of <i>RPL24</i> genes in three Cucurbitaceae family members: cucumber, melon and watermelon. <i>Biotechnology and Biotechnological Equipment</i> , 2015, 29, 1024-1034.	0.5	12
1338	<i>Cryptococcus gattii</i> urease as a virulence factor and the relevance of enzymatic activity in cryptococcosis pathogenesis. <i>FEBS Journal</i> , 2015, 282, 1406-1418.	2.2	47
1339	Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. <i>Genetic Epidemiology</i> , 2015, 39, 376-384.	0.6	20
1340	Pyrosequencing and de novo assembly of A antarctic krill (<i>Euphausia superba</i>) transcriptome to study the adaptability of krill to climate-induced environmental changes. <i>Molecular Ecology Resources</i> , 2015, 15, 1460-1471.	2.2	30
1341	An unusually simple HP1 gene set in Hymenopteran insects. <i>Biochemistry and Cell Biology</i> , 2015, 93, 596-603.	0.9	5
1342	Emergence of <i>de novo</i> proteins from "dark genomic matter"™ by "grow slow and moult"™. <i>Biochemical Society Transactions</i> , 2015, 43, 867-873.	1.6	38
1343	Large scale transcriptome analysis reveals interplay between development of forest trees and a beneficial mycorrhiza helper bacterium. <i>BMC Genomics</i> , 2015, 16, 658.	1.2	28
1344	Comparative genome-based identification of a cell wall-anchored protein from <i>Lactobacillus plantarum</i> increases adhesion of <i>Lactococcus lactis</i> to human epithelial cells. <i>Scientific Reports</i> , 2015, 5, 14109.	1.6	29

#	ARTICLE	IF	CITATIONS
1345	Characterization of the Granule-Bound Starch Synthase I Gene in <i>Chenopodium</i> . <i>Plant Genome</i> , 2015, 8, eplantgenome2014.09.0051.	1.6	11
1346	Functional and structural properties of a novel cellulosome-like multienzyme complex: efficient glycoside hydrolysis of water-insoluble 7-xylosyl-10-deacetylpaclitaxel. <i>Scientific Reports</i> , 2015, 5, 13768.	1.6	23
1347	Generation and Analysis of Microbial Metatranscriptomes. , 2015, , 2.4.5-1-2.4.5-19.		1
1348	Cross-strand disulfides in the non-hydrogen bonding site of antiparallel β -sheet (aCSDNs): poised for biological switching. <i>RSC Advances</i> , 2015, 5, 86303-86321.	1.7	4
1349	De novo transcriptome profiling of highly purified human lymphocytes primary cells. <i>Scientific Data</i> , 2015, 2, 150051.	2.4	33
1350	Structural insight into the <scp>TRIAP</scp> 1/ <scp>PRELI</scp> -like domain family of mitochondrial phospholipid transfer complexes. <i>EMBO Reports</i> , 2015, 16, 824-835.	2.0	68
1351	Regulatory RNA at the root of animals: dynamic expression of developmental lincRNAs in the calcisponge <i>Sycon ciliatum</i>. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151746.	1.2	16
1352	Homology-Based Prediction of Potential Protein-Protein Interactions between Human Erythrocytes and <i>Plasmodium falciparum</i> . <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S31880.	1.0	21
1353	Identification of an Ideal-like Fingerprint for a Protein Fold using Overlapped Conserved Residues based Approach. <i>Scientific Reports</i> , 2015, 4, 5643.	1.6	6
1354	Systematic analyses reveal uniqueness and origin of the CFEM domain in fungi. <i>Scientific Reports</i> , 2015, 5, 13032.	1.6	46
1355	Genome wide discovery of long intergenic non-coding RNAs in Diamondback moth (<i>Plutella</i>) Tj ETQq0 0 0 rgBT /Overlock 10 If 50 342 T	1.6	18
1356	The Phylogenetic Signature Underlying ATP Synthase c-Ring Compliance. <i>Biophysical Journal</i> , 2015, 109, 975-987.	0.2	11
1357	Genome-wide identification and expression profiling of annexins in <i>Brassica rapa</i> and their phylogenetic sequence comparison with <i>B. juncea</i> and <i>A. thaliana</i> annexins. <i>Plant Gene</i> , 2015, 4, 109-124.	1.4	19
1358	Pangenome analysis of <i>Bifidobacterium longum</i> and site-directed mutagenesis through by-pass of restriction-modification systems. <i>BMC Genomics</i> , 2015, 16, 832.	1.2	89
1359	Characterization and annotation of <i>Babesia orientalis</i> apicoplast genome. <i>Parasites and Vectors</i> , 2015, 8, 543.	1.0	25
1360	The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). <i>Standards in Genomic Sciences</i> , 2015, 10, 86.	1.5	287
1361	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015, 31, 926-932.	1.8	1,223
1362	The pan-genome of <i>Lactobacillus reuteri</i> strains originating from the pig gastrointestinal tract. <i>BMC Genomics</i> , 2015, 16, 1023.	1.2	64

#	ARTICLE	IF	CITATIONS
1363	A novel RING finger in the C-terminal domain of the coatomer protein $\hat{\pm}$ -COP. <i>Biology Direct</i> , 2015, 10, 70.	1.9	7
1364	Conformational thermodynamics of biomolecular complexes: The histogram-based method. <i>Journal of Physics: Conference Series</i> , 2015, 638, 012013.	0.3	3
1365	MnTEdb, a collective resource for mulberry transposable elements. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	25
1366	Using PepExplorer to Filter and Organize <i><i>De Novo</i></i> Peptide Sequencing Results. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 13.27.1-13.27.9.	25.8	4
1367	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MT43, a Representative of the Manu2 Genotype. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
1368	Draft Genome Sequence of <i>Mycobacterium mucogenicum</i> Strain CSUR P2099. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
1369	Better prediction of functional effects for sequence variants. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	478
1370	High quality genome sequence and description of <i>Enterobacter mori</i> strain 5â€“4, isolated from a mixture of formation water and crude-oil. <i>Standards in Genomic Sciences</i> , 2015, 10, 9.	1.5	6
1371	Phylogenomics and sequence-structure-function relationships in the GmrSD family of Type IV restriction enzymes. <i>BMC Bioinformatics</i> , 2015, 16, 336.	1.2	24
1372	Parameterizing sequence alignment with an explicit evolutionary model. <i>BMC Bioinformatics</i> , 2015, 16, 406.	1.2	26
1373	Comparative genomics between human and animal associated subspecies of the <i>Mycobacterium avium</i> complex: a basis for pathogenicity. <i>BMC Genomics</i> , 2015, 16, 695.	1.2	22
1374	The rumen microbial metagenome associated with high methane production in cattle. <i>BMC Genomics</i> , 2015, 16, 839.	1.2	306
1375	Multifunctional polyketide synthase genes identified by genomic survey of the symbiotic dinoflagellate, <i>Symbiodinium minutum</i> . <i>BMC Genomics</i> , 2015, 16, 941.	1.2	28
1376	Metagenome from a <i>Spirulina</i> digesting biogas reactor: analysis via binning of contigs and classification of short reads. <i>BMC Microbiology</i> , 2015, 15, 277.	1.3	32
1377	Implications of ethylene biosynthesis and signaling in soybean drought stress tolerance. <i>BMC Plant Biology</i> , 2015, 15, 213.	1.6	110
1378	Three-dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. <i>BMC Structural Biology</i> , 2015, 15, 20.	2.3	4
1379	BioDB extractor: customized data extraction system for commonly used bioinformatics databases. <i>BioData Mining</i> , 2015, 8, 31.	2.2	2
1380	The UBR-box and its relationship to binuclear RING-like treble clef zinc fingers. <i>Biology Direct</i> , 2015, 10, 36.	1.9	7

#	ARTICLE	IF	CITATIONS
1381	Pan-genomic analysis to redefine species and subspecies based on quantum discontinuous variation: the <i>Klebsiella</i> paradigm. <i>Biology Direct</i> , 2015, 10, 55.	1.9	33
1382	Draft genome of <i>Brugia pahangi</i> : high similarity between <i>B. pahangi</i> and <i>B. malayi</i> . <i>Parasites and Vectors</i> , 2015, 8, 451.	1.0	19
1383	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	0.6	38
1384	Genome sequence of <i>Oceanobacillus picturae</i> strain S1, an halophilic bacterium first isolated in human gut. <i>Standards in Genomic Sciences</i> , 2015, 10, 91.	1.5	16
1385	Characterization of the dextran-binding domain in the glucan-binding protein C of <i>Streptococcus mutans</i> . <i>Journal of Applied Microbiology</i> , 2015, 119, 1148-1157.	1.4	12
1386	A quantitative hybridization approach using 17 DNA markers for identification and clustering analysis of <i>Ralstonia solanacearum</i> . <i>Plant Pathology</i> , 2015, 64, 1270-1283.	1.2	2
1387	Draft Genome Sequence of <i>Mycobacterium neworleansense</i> Strain ATCC 49404 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
1388	SInCR structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav060.	1.4	10
1389	Draft Genome Sequence of <i>Streptomyces ahygroscopicus</i> subsp. <i>wuyiensis</i> CK-15, Isolated from Soil in Fujian Province, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
1390	<i>Streptococcus pneumoniae</i> Genome-wide Identification and Characterization of BOX Element-binding Domains. <i>Molecular Informatics</i> , 2015, 34, 742-752.	1.4	0
1391	Selection of recombinant anti-SH3 domain antibodies by high-throughput phage display. <i>Protein Science</i> , 2015, 24, 1890-1900.	3.1	15
1392	Rock, Paper, Scissors: Harnessing Complementarity in Ortholog Detection Methods Improves Comparative Genomic Inference. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 629-638.	0.8	10
1393	PspF-binding domain PspA ¹⁴⁴ and the PspA-F complex: New insights into the coiled-coil-dependent regulation of AAA ⁺ proteins. <i>Molecular Microbiology</i> , 2015, 98, 743-759.	1.2	33
1394	Draft Genome Sequence of <i>Mycobacterium peregrinum</i> Strain CSUR P2098. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
1395	Complete Genome Sequences of <i>Campylobacter jejuni</i> Strains RM3196 (233.94) and RM3197 (308.95) Isolated from Patients with Guillain-Barré Syndrome. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
1396	A new signal characterization and signal-based Chou's PseAAC representation of protein sequences. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550024.	0.3	30
1397	Dissecting helices: sequence, structure and function. <i>FEBS Journal</i> , 2015, 282, 4415-4432.	2.2	32
1398	Novel host-specific iron acquisition system in the zoonotic pathogen <i>Vibrio vulnificus</i> . <i>Environmental Microbiology</i> , 2015, 17, 2076-2089.	1.8	35

#	ARTICLE	IF	CITATIONS
1399	Patterns of Wnt signaling in the life cycle of <i>Podocoryna carnea</i> and its implications for medusae evolution in Hydrozoa (Cnidaria). <i>Evolution & Development</i> , 2015, 17, 325-336.	1.1	24
1400	EvoDB: a database of evolutionary rate profiles, associated protein domains and phylogenetic trees for PFAM-A. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav065.	1.4	1
1401	Draft Genome Sequence of <i>Mycobacterium lentiflavum</i> CSUR P1491. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
1402	Identification, modeling, and characterization studies of <i>Tetrahymena thermophila</i> myosin <sc>FERM</sc> domains suggests a conserved core fold but functional differences. <i>Cytoskeleton</i> , 2015, 72, 585-596.	1.0	1
1403	Quantitative assessment of protein function prediction programs. <i>Genetics and Molecular Research</i> , 2015, 14, 17555-17566.	0.3	2
1404	Positive selection sites in tertiary structure of Leguminosae Chalcone isomerase 1. <i>Genetics and Molecular Research</i> , 2015, 14, 1957-1967.	0.3	2
1405	Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses. <i>Viruses</i> , 2015, 7, 5388-5409.	1.5	16
1406	Statistical Approaches to Detecting and Analyzing Tandem Repeats in Genomic Sequences. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 31.	2.0	19
1407	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 95.	2.0	26
1408	Comprehensive Protein Interactome Analysis of a Key RNA Helicase: Detection of Novel Stress Granule Proteins. <i>Biomolecules</i> , 2015, 5, 1441-1466.	1.8	26
1409	Identification of novel esterase-active enzymes from hot environments by use of the host bacterium <i>Thermus thermophilus</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 275.	1.5	65
1410	Antibacterial phage ORFans of <i>Pseudomonas aeruginosa</i> phage LUZ24 reveal a novel MvaT inhibiting protein. <i>Frontiers in Microbiology</i> , 2015, 6, 1242.	1.5	31
1411	Anatomy of protein disorder, flexibility and disease-related mutations. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 47.	1.6	16
1412	The Semantics of the Modular Architecture of Protein Structures. <i>Current Protein and Peptide Science</i> , 2015, 17, 62-71.	0.7	8
1413	A Hormone-Responsive C1-Domain-Containing Protein At5g17960 Mediates Stress Response in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2015, 10, e0115418.	1.1	13
1414	The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. <i>PLoS ONE</i> , 2015, 10, e0118606.	1.1	10
1415	Molecular Evolution and Phylogenetic Analysis of Eight COL Superfamily Genes in Group I Related to Photoperiodic Regulation of Flowering Time in Wild and Domesticated Cotton (<i>Gossypium</i>) Species. <i>PLoS ONE</i> , 2015, 10, e0118669.	1.1	18
1416	Insight into Neutral and Disease-Associated Human Genetic Variants through Interpretable Predictors. <i>PLoS ONE</i> , 2015, 10, e0120729.	1.1	2

#	ARTICLE	IF	CITATIONS
1417	Genome-Wide Comparative Analysis Reveals Similar Types of NBS Genes in Hybrid Citrus sinensis Genome and Original Citrus clementine Genome and Provides New Insights into Non-TIR NBS Genes. PLoS ONE, 2015, 10, e0121893.	1.1	9
1418	Building a Better Fragment Library for De Novo Protein Structure Prediction. PLoS ONE, 2015, 10, e0123998.	1.1	25
1419	Transcriptome-Wide Identification of Salt-Responsive Members of the WRKY Gene Family in Gossypium aridum. PLoS ONE, 2015, 10, e0126148.	1.1	83
1420	Est10: A Novel Alkaline Esterase Isolated from Bovine Rumen Belonging to the New Family XV of Lipolytic Enzymes. PLoS ONE, 2015, 10, e0126651.	1.1	10
1421	Phylogenomic Analysis Reveals Deep Divergence and Recombination in an Economically Important Grapevine Virus. PLoS ONE, 2015, 10, e0126819.	1.1	30
1422	Computational Analysis and Low-Scale Constitutive Expression of Laccases Synthetic Genes GILCC1 from Ganoderma lucidum and POXA 1B from Pleurotus ostreatus in Pichia pastoris. PLoS ONE, 2015, 10, e0116524.	1.1	36
1423	Characterization of the Xylella fastidiosa PD1671 Gene Encoding Degenerate c-di-GMP GGDEF/EAL Domains, and Its Role in the Development of Pierce's Disease. PLoS ONE, 2015, 10, e0121851.	1.1	13
1424	Molecular Determinants Underlying Binding Specificities of the ABL Kinase Inhibitors: Combining Alanine Scanning of Binding Hot Spots with Network Analysis of Residue Interactions and Coevolution. PLoS ONE, 2015, 10, e0130203.	1.1	36
1425	Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. PLoS Computational Biology, 2015, 11, e1004325.	1.5	80
1426	How Co-translational Folding of Multi-domain Protein Is Affected by Elongation Schedule: Molecular Simulations. PLoS Computational Biology, 2015, 11, e1004356.	1.5	22
1427	Identification of Ohnolog Genes Originating from Whole Genome Duplication in Early Vertebrates, Based on Synteny Comparison across Multiple Genomes. PLoS Computational Biology, 2015, 11, e1004394.	1.5	113
1428	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. PLoS Computational Biology, 2015, 11, e1004465.	1.5	17
1429	Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Computational Biology, 2015, 11, e1004467.	1.5	36
1430	Functional Basis of Microorganism Classification. PLoS Computational Biology, 2015, 11, e1004472.	1.5	37
1431	Beyond the E-Value: Stratified Statistics for Protein Domain Prediction. PLoS Computational Biology, 2015, 11, e1004509.	1.5	19
1432	Reproductive Mode and the Evolution of Genome Size and Structure in Caenorhabditis Nematodes. PLoS Genetics, 2015, 11, e1005323.	1.5	102
1433	Genome-Wide Collation of the Plasmodium falciparum WDR Protein Superfamily Reveals Malarial Parasite-Specific Features. PLoS ONE, 2015, 10, e0128507.	1.1	9
1434	Proteins Related to the Type I Secretion System Are Associated with Secondary SecA_DEAD Domain Proteins in Some Species of Planctomycetes, Verrucomicrobia, Proteobacteria, Nitrospirae and Chlorobi. PLoS ONE, 2015, 10, e0129066.	1.1	1

#	ARTICLE	IF	CITATIONS
1435	A de novo Assembly of the Common Frog (<i>Rana temporaria</i>) Transcriptome and Comparison of Transcription Following Exposure to Ranavirus and <i>Batrachochytrium dendrobatidis</i> . PLoS ONE, 2015, 10, e0130500.	1.1	32
1436	A Unique Set of the Burkholderia Collagen-Like Proteins Provides Insight into Pathogenesis, Genome Evolution and Niche Adaptation, and Infection Detection. PLoS ONE, 2015, 10, e0137578.	1.1	27
1437	Genome-Wide Characterization and Expression Analysis of Major Intrinsic Proteins during Abiotic and Biotic Stresses in Sweet Orange (<i>Citrus sinensis</i> L. Osb.). PLoS ONE, 2015, 10, e0138786.	1.1	65
1438	Functional Advantages of Conserved Intrinsic Disorder in RNA-Binding Proteins. PLoS ONE, 2015, 10, e0139731.	1.1	100
1439	Extending Protein Domain Boundary Predictors to Detect Discontinuous Domains. PLoS ONE, 2015, 10, e0141541.	1.1	5
1440	Coevolved Mutations Reveal Distinct Architectures for Two Core Proteins in the Bacterial Flagellar Motor. PLoS ONE, 2015, 10, e0142407.	1.1	8
1441	Relationships between predicted moonlighting proteins, human diseases, and comorbidities from a network perspective. Frontiers in Physiology, 2015, 6, 171.	1.3	14
1442	Genome-wide identification of CAMTA gene family members in <i>Medicago truncatula</i> and their expression during root nodule symbiosis and hormone treatments. Frontiers in Plant Science, 2015, 6, 459.	1.7	41
1443	Comparative analysis of the phycocyanin gene family in 10 plant species: a focus on <i>Zea mays</i> . Frontiers in Plant Science, 2015, 6, 515.	1.7	36
1444	The heat shock factor gene family in <i>Salix suchowensis</i> : a genome-wide survey and expression profiling during development and abiotic stresses. Frontiers in Plant Science, 2015, 6, 748.	1.7	40
1445	Divergence of the bZIP Gene Family in Strawberry, Peach, and Apple Suggests Multiple Modes of Gene Evolution after Duplication. International Journal of Genomics, 2015, 2015, 1-11.	0.8	21
1446	Comparative Analysis of Apicoplast-Targeted Protein Extension Lengths in Apicomplexan Parasites. BioMed Research International, 2015, 2015, 1-6.	0.9	7
1447	A Database of Plastid Protein Families from Red Algae and Apicomplexa and Expression Regulation of the <i>moeB</i> Gene. BioMed Research International, 2015, 2015, 1-5.	0.9	7
1448	A Large-Scale Structural Classification of Antimicrobial Peptides. BioMed Research International, 2015, 2015, 1-6.	0.9	123
1449	Evolutionary Influenced Interaction Pattern as Indicator for the Investigation of Natural Variants Causing Nephrogenic Diabetes Insipidus. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-6.	0.7	0
1450	SIFTER-T: A scalable and optimized framework for the SIFTER phylogenomic method of probabilistic protein domain annotation. BioTechniques, 2015, 58, 140-142.	0.8	1
1451	Molecular cloning of RBCS genes in <i>Selaginella</i> and the evolution of the <i>rbcS</i> gene family. Archives of Biological Sciences, 2015, 67, 373-383.	0.2	1
1452	Tn7. , 0, , 647-667.		13

#	ARTICLE	IF	CITATIONS
1453	NrichD database: sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. <i>Nucleic Acids Research</i> , 2015, 43, D300-D305.	6.5	12
1454	Recognition rules for binding of Zn-Cys2His2 transcription factors to operator DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 253-266.	2.0	10
1455	Learning HMMs for nucleotide sequences from amino acid alignments. <i>Bioinformatics</i> , 2015, 31, 1836-1838.	1.8	1
1456	Metagenome sequence of <i>E. coli</i> from sporocarp tissue reveals Ascomycota ectomycorrhizal fingerprints of genome expansion and a Proteobacteria-rich microbiome. <i>Environmental Microbiology</i> , 2015, 17, 2952-2968.	1.8	34
1457	Histone chaperones in Arabidopsis and rice: genome-wide identification, phylogeny, architecture and transcriptional regulation. <i>BMC Plant Biology</i> , 2015, 15, 42.	1.6	44
1458	The Classification and Evolution of Enzyme Function. <i>Biophysical Journal</i> , 2015, 109, 1082-1086.	0.2	95
1459	Protein structure prediction guided by crosslinking restraints – A systematic evaluation of the impact of the crosslinking spacer length. <i>Methods</i> , 2015, 89, 79-90.	1.9	39
1460	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. <i>Molecular Biology and Evolution</i> , 2015, 32, 2195-2207.	3.5	48
1461	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	1.8	17
1462	Conservation of inter-residue interactions and prediction of folding rates of domain repeats. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 534-551.	2.0	8
1463	Macyranones: Structure, Biosynthesis, and Binding Mode of an Unprecedented Epoxyketone that Targets the 20S Proteasome. <i>Journal of the American Chemical Society</i> , 2015, 137, 8121-8130.	6.6	34
1464	Multiple horizontally acquired genes from fungal and prokaryotic donors encode cellulolytic enzymes in the bdelloid rotifer <i>Adineta ricciae</i> . <i>Gene</i> , 2015, 566, 125-137.	1.0	22
1465	Biochemistry and regulatory functions of bacterial glucose kinases. <i>Archives of Biochemistry and Biophysics</i> , 2015, 577-578, 1-10.	1.4	12
1466	The central nervous system transcriptome of the weakly electric brown ghost knifefish (<i>Apteronotus</i>) Tj ETQq1 1 0.784314 rsgBT /Overl	1.2	19
1467	Pan-genome dynamics of <i>Pseudomonas</i> gene complements enriched across hexachlorocyclohexane dumpsite. <i>BMC Genomics</i> , 2015, 16, 313.	1.2	19
1468	Genome sequencing of the <i>Trichoderma reesei</i> QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. <i>BMC Genomics</i> , 2015, 16, 326.	1.2	31
1469	A novel essential domain perspective for exploring gene essentiality. <i>Bioinformatics</i> , 2015, 31, 2921-2929.	1.8	7
1470	Predicting Sub-cellular Location of Proteins Based on Hierarchical Clustering and Hidden Markov Models. <i>Lecture Notes in Computer Science</i> , 2015, , 256-263.	1.0	1

#	ARTICLE	IF	CITATIONS
1471	Environmental Sensing in Actinobacteria: a Comprehensive Survey on the Signaling Capacity of This Phylum. <i>Journal of Bacteriology</i> , 2015, 197, 2517-2535.	1.0	54
1472	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. <i>New Phytologist</i> , 2015, 208, 1227-1240.	3.5	165
1473	Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates. <i>Genome Biology and Evolution</i> , 2015, 7, evv172.	1.1	22
1474	Exploring the repeat protein universe through computational protein design. <i>Nature</i> , 2015, 528, 580-584.	13.7	227
1475	Comparative study of the effectiveness and limitations of current methods for detecting sequence coevolution. <i>Bioinformatics</i> , 2015, 31, 1929-1937.	1.8	22
1476	Improving compound-protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015, 31, i221-i229.	1.8	201
1477	Epigenetic regulation of serotype expression antagonizes transcriptome dynamics in <i>Paramecium tetraurelia</i> . <i>DNA Research</i> , 2015, 22, 293-305.	1.5	18
1478	The Rise and Fall of TRP-N, an Ancient Family of Mechanogated Ion Channels, in Metazoa. <i>Genome Biology and Evolution</i> , 2015, 7, 1713-1727.	1.1	36
1479	Interspecific Differential Expression Analysis of RNA-Seq Data Yields Insight into Life Cycle Variation in Hydractiniid Hydrozoans. <i>Genome Biology and Evolution</i> , 2015, 7, 2417-2431.	1.1	22
1480	A common tRNA modification at an unusual location: the discovery of wyosine biosynthesis in mitochondria. <i>Nucleic Acids Research</i> , 2015, 43, 4262-4273.	6.5	22
1481	By the company they keep: interaction networks define the binding ability of transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, e125-e125.	6.5	12
1482	Complete genome sequence of bacteriophage P8625, the first lytic phage that infects Verrucomicrobia. <i>Standards in Genomic Sciences</i> , 2015, 10, 96.	1.5	1
1483	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MT11, Which Represents a New Lineage. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
1484	Complete Genome Sequences of Four Novel <i>Escherichia coli</i> Bacteriophages Belonging to New Phage Groups. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
1485	Draft Genome Sequence of <i>Mycobacterium europaeum</i> Strain CSUR P1344. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
1486	Draft Genome Sequence of the <i>Lactobacillus agilis</i> Strain Marseille. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
1487	Draft Genome Sequence of <i>Mycobacterium bohemicum</i> Strain DSM 44277 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
1488	The Peptidoglycan-Binding Protein SjcF1 Influences Septal Junction Function and Channel Formation in the Filamentous Cyanobacterium <i>Anabaena</i> . <i>MBio</i> , 2015, 6, e00376.	1.8	33

#	ARTICLE	IF	CITATIONS
1489	Complete genome of the marine bacterium <i>Wenzhouxiangella marina</i> KCTC 42284T. <i>Marine Genomics</i> , 2015, 24, 277-280.	0.4	10
1490	Phylogeny, Morphology, and Metabolic and Invasive Capabilities of Epicellular Fish Coccidium <i>Goussia janae</i> . <i>Protist</i> , 2015, 166, 659-676.	0.6	16
1491	In-depth analysis of the critical genes and pathways in colorectal cancer. <i>International Journal of Molecular Medicine</i> , 2015, 36, 923-930.	1.8	20
1492	Genome-Wide Analysis and Expression Patterns of the YUCCA Genes in Maize. <i>Journal of Genetics and Genomics</i> , 2015, 42, 707-710.	1.7	22
1493	The YhhN protein of <i>Legionella pneumophila</i> is a Lysoplasmalogenase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 742-751.	1.4	22
1494	In silico analysis and prioritization of drug targets in <i>Fusarium solani</i> . <i>Medical Hypotheses</i> , 2015, 84, 81-84.	0.8	8
1495	Enriching the annotation of <i>Mycobacterium tuberculosis</i> H37Rv proteome using remote homology detection approaches: Insights into structure and function. <i>Tuberculosis</i> , 2015, 95, 14-25.	0.8	9
1496	The eyestalk transcriptome of red swamp crayfish <i>Procambarus clarkii</i> . <i>Gene</i> , 2015, 557, 28-34.	1.0	60
1497	Identification and expression analyses of calmodulin-binding transcription activator genes in soybean. <i>Plant and Soil</i> , 2015, 386, 205-221.	1.8	52
1498	Codon usage and protein sequence pattern dependency in different organisms: A Bioinformatics approach. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550002.	0.3	1
1499	A Basic Leucine Zipper Transcription Factor, AabZIP1, Connects Abscisic Acid Signaling with Artemisinin Biosynthesis in <i>Artemisia annua</i> . <i>Molecular Plant</i> , 2015, 8, 163-175.	3.9	198
1500	Structure and Evolution of N-domains in AAA Metalloproteases. <i>Journal of Molecular Biology</i> , 2015, 427, 910-923.	2.0	23
1501	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	3.6	109
1502	<i>Listeria monocytogenes</i> exopolysaccharide: origin, structure, biosynthetic machinery and cAMP-dependent regulation. <i>Molecular Microbiology</i> , 2015, 96, 728-743.	1.2	80
1503	Genomic Potential for Polysaccharide Deconstruction in Bacteria. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1513-1519.	1.4	155
1504	Glandular β -glucosidases in juvenile <i>Chrysomelina</i> leaf beetles support the evolution of a host-plant-dependent chemical defense. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 58, 28-38.	1.2	16
1505	Horizontal transfer of carbohydrate metabolism genes into ectomycorrhizal <i>Armanita</i> . <i>New Phytologist</i> , 2015, 205, 1552-1564.	3.5	17
1506	<i>ZIP3</i> is a cellular zinc transporter that mediates the tightly regulated import of zinc in <i>Leishmania infantum</i> parasites. <i>Molecular Microbiology</i> , 2015, 96, 581-595.	1.2	16

#	ARTICLE	IF	CITATIONS
1507	Arginine-rhamnosylation as new strategy to activate translation elongation factor P. <i>Nature Chemical Biology</i> , 2015, 11, 266-270.	3.9	116
1508	Molecular responses of <i>Frankia</i> sp. strain QA3 to naphthalene. <i>Canadian Journal of Microbiology</i> , 2015, 61, 281-292.	0.8	16
1509	Autophagy Regulatory Network "A systems-level bioinformatics resource for studying the mechanism and regulation of autophagy. <i>Autophagy</i> , 2015, 11, 155-165.	4.3	89
1510	Genome-Wide Analysis of Alternative Splicing Landscapes Modulated during Plant-Virus Interactions in <i>Brachypodium distachyon</i> . <i>Plant Cell</i> , 2015, 27, 71-85.	3.1	145
1511	A Similarity-Based Learning Algorithm Using Distance Transformation. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2015, 27, 1452-1464.	4.0	2
1512	Chaperone network composition in <i>Solanum lycopersicum</i> explored by transcriptome profiling and microarray meta-analysis. <i>Plant, Cell and Environment</i> , 2015, 38, 693-709.	2.8	71
1513	PHOTOSYSTEM II PROTEIN33, a Protein Conserved in the Plastid Lineage, Is Associated with the Chloroplast Thylakoid Membrane and Provides Stability to Photosystem II Supercomplexes in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2015, 167, 481-492.	2.3	46
1514	Characterization of glycerophosphoethanolamine ethanolaminephosphodiesterase from <i>Streptomyces sanglieri</i> . <i>Journal of Bioscience and Bioengineering</i> , 2015, 119, 123-130.	1.1	6
1515	Genetic and genomic analysis of RNases in model cyanobacteria. <i>Photosynthesis Research</i> , 2015, 126, 171-183.	1.6	23
1516	New Mode of Energy Metabolism in the Seventh Order of Methanogens as Revealed by Comparative Genome Analysis of <i>Candidatus Methanoplasma termitum</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1338-1352.	1.4	235
1518	Molecular Evolution of Nitrogen Assimilatory Enzymes in Marine Prasinophytes. <i>Journal of Molecular Evolution</i> , 2015, 80, 65-80.	0.8	8
1519	Relationship between amino acid usage and amino acid evolution in primates. <i>Gene</i> , 2015, 557, 182-187.	1.0	12
1520	GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. <i>Bioinformatics</i> , 2015, 31, 1411-1419.	1.8	167
1521	Cooperative Substrate Binding by a Diguanylate Cyclase. <i>Journal of Molecular Biology</i> , 2015, 427, 415-432.	2.0	22
1522	Bioinformatic analysis of a PLP-dependent enzyme superfamily suitable for biocatalytic applications. <i>Biotechnology Advances</i> , 2015, 33, 566-604.	6.0	193
1523	Hydrolysis of Wheat Arabinoxylan by Two Acetyl Xylan Esterases from <i>Chaetomium thermophilum</i> . <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 1139-1152.	1.4	8
1524	Current Functional Metagenomic Approaches Only Expand the Existing Protease Sequence Space, but does not Presently Add Any Novelty to it. <i>Current Microbiology</i> , 2015, 70, 19-26.	1.0	10
1525	The Same or Not the Same: Lineage-Specific Gene Expansions and Homology Relationships in Multigene Families in Nematodes. <i>Journal of Molecular Evolution</i> , 2015, 80, 18-36.	0.8	23

#	ARTICLE	IF	CITATIONS
1526	Engineering a high-performance, metagenomic-derived novel xylanase with improved soluble protein yield and thermostability. <i>Enzyme and Microbial Technology</i> , 2015, 70, 35-41.	1.6	33
1527	Tannase Sequence from a Xerophilic <i>Aspergillus niger</i> Strain and Production of the Enzyme in <i>Pichia pastoris</i> . <i>Molecular Biotechnology</i> , 2015, 57, 439-447.	1.3	12
1528	The Eukaryotic Ancestor Had a Complex Ubiquitin Signaling System of Archaeal Origin. <i>Molecular Biology and Evolution</i> , 2015, 32, 726-739.	3.5	58
1529	Discovery of Novel Genes Derived from Transposable Elements Using Integrative Genomic Analysis. <i>Molecular Biology and Evolution</i> , 2015, 32, 1487-1506.	3.5	49
1530	Dual analysis of host and pathogen transcriptomes in ostreid herpesvirus 1â€positive <i>Crassostrea gigas</i> . <i>Environmental Microbiology</i> , 2015, 17, 4200-4212.	1.8	75
1531	Regulation of the expression of the whole genome of <i>Ustilago maydis</i> by a MAPK pathway. <i>Archives of Microbiology</i> , 2015, 197, 575-588.	1.0	7
1532	Species-specific duplications driving the recent expansion of NBS-LRR genes in five Rosaceae species. <i>BMC Genomics</i> , 2015, 16, 77.	1.2	39
1533	Evolutionary and expression analysis of a MADS-box gene superfamily involved in ovule development of seeded and seedless grapevines. <i>Molecular Genetics and Genomics</i> , 2015, 290, 825-846.	1.0	46
1534	The genome and transcriptome of the zoonotic hookworm <i>Ancylostoma ceylanicum</i> identify infection-specific gene families. <i>Nature Genetics</i> , 2015, 47, 416-422.	9.4	91
1535	Genome-wide analysis of bHLH transcription factor and involvement in the infection by yellow leaf curl virus in tomato (<i>Solanum lycopersicum</i>). <i>BMC Genomics</i> , 2015, 16, 39.	1.2	102
1536	Terminal-Repeat Retrotransposons with GAG Domain in Plant Genomes: A New Testimony on the Complex World of Transposable Elements. <i>Genome Biology and Evolution</i> , 2015, 7, 493-504.	1.1	23
1537	Structure and Function of the Bacterial Root Microbiota in Wild and Domesticated Barley. <i>Cell Host and Microbe</i> , 2015, 17, 392-403.	5.1	1,102
1538	Prediction of Indel flanking regions in protein sequences using a variable-order Markov model. <i>Bioinformatics</i> , 2015, 31, 40-47.	1.8	5
1539	Genomic characterization of a temperate phage of the psychrotolerant deep-sea bacterium <i>Aurantimonas</i> sp.. <i>Extremophiles</i> , 2015, 19, 49-58.	0.9	15
1540	The Amaranthin-Like Lectin (LuALL) Genes of Flax: a Unique Gene Family with Members Inducible by Defence Hormones. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 731-741.	1.0	13
1541	Biosynthesis and genomic analysis of medium-chain hydrocarbon production by the endophytic fungal isolate <i>Nigrograna mackinnonii</i> E5202H. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3715-3728.	1.7	44
1542	Beyond Lysozyme: Antimicrobial Peptides Against Malaria. , 2015, , 91-101.		1
1544	RNA-seq for gene identification and transcript profiling in relation to root growth of bermudagrass (<i>Cynodon dactylon</i>) under salinity stress. <i>BMC Genomics</i> , 2015, 16, 575.	1.2	67

#	ARTICLE	IF	CITATIONS
1545	Draft Genome Sequence of the <i>Lactobacillus mucosae</i> Strain Marseille. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
1546	Genomic Analysis of the Evolution and Global Spread of Hyper-invasive Meningococcal Lineage 5. <i>EBioMedicine</i> , 2015, 2, 234-243.	2.7	20
1547	The insertion domain 1 of class IIA dimeric glycyl-tRNA synthetase is a rubredoxin-like zinc ribbon. <i>Journal of Structural Biology</i> , 2015, 190, 38-46.	1.3	5
1548	A rule-based expert system for inferring functional annotation. <i>Applied Soft Computing Journal</i> , 2015, 35, 373-385.	4.1	5
1549	Genome-wide identification, phylogeny, and expression analysis of the SWEET gene family in tomato. <i>Gene</i> , 2015, 573, 261-272.	1.0	141
1550	Genome-wide characterisation and analysis of bHLH transcription factors related to tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . <i>Scientific Reports</i> , 2015, 5, 11244.	1.6	97
1551	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015, 14, 2976-2987.	1.8	16
1552	Functional Networks of Highest-Connected Splice Isoforms: From The Chromosome 17 Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3484-3491.	1.8	28
1553	Molecular evolution and functional divergence of tubulin superfamily in the fungal tree of life. <i>Scientific Reports</i> , 2014, 4, 6746.	1.6	79
1554	Identification and genomic analysis of temperate <i>Pseudomonas</i> bacteriophage PstS-1 from the Japan trench at a depth of 7000Åm. <i>Research in Microbiology</i> , 2015, 166, 668-676.	1.0	12
1555	AguR, a Transmembrane Transcription Activator of the Putrescine Biosynthesis Operon in <i>Lactococcus lactis</i> , Acts in Response to the Agmatine Concentration. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6145-6157.	1.4	20
1556	Map-based cloning and characterization of <i>BPH29</i> , a B3 domain-containing recessive gene conferring brown planthopper resistance in rice. <i>Journal of Experimental Botany</i> , 2015, 66, 6035-6045.	2.4	148
1557	Genome-Wide Identification and Evolution of HECT Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2015, 16, 8517-8535.	1.8	15
1558	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	3.2	6
1559	The Secreted Proteins of <i>Achlya hypogyna</i> and <i>Thraustotheca clavata</i> Identify the Ancestral Oomycete Secretome and Reveal Gene Acquisitions by Horizontal Gene Transfer. <i>Genome Biology and Evolution</i> , 2015, 7, 120-135.	1.1	34
1560	Structural insight into operator dre-sites recognition and effector binding in the GntR/HutC transcription regulator NagR. <i>Nucleic Acids Research</i> , 2015, 43, 1283-1296.	6.5	36
1561	MetaRank: Ranking Microbial Taxonomic Units or Functional Groups for Comparative Analysis of Metagenomes. , 2015, , 442-447.		0
1562	In silico identification of AMPylating enzymes and study of their divergent evolution. <i>Scientific Reports</i> , 2015, 5, 10804.	1.6	32

#	ARTICLE	IF	CITATIONS
1563	Pervasive Variation of Transcription Factor Orthologs Contributes to Regulatory Network Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005011.	1.5	29
1564	Analysis of Arabidopsis floral transcriptome: detection of new florally expressed genes and expansion of Brassicaceae-specific gene families. <i>Frontiers in Plant Science</i> , 2015, 5, 802.	1.7	28
1565	Metagenomic analyses reveal no differences in genes involved in cellulose degradation under different tillage treatments. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv069.	1.3	38
1566	Molecular level biodegradation of phenol and its derivatives through dmp operon of <i>Pseudomonas putida</i> : A bio-molecular modeling and docking analysis. <i>Journal of Environmental Sciences</i> , 2015, 36, 144-151.	3.2	11
1567	Combined transcriptome and metabolite profiling reveals that <i>PLR1</i> plays an important role in lariciresinol accumulation in <i>Isatis indigotica</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 6259-6271.	2.4	38
1568	INGA: protein function prediction combining interaction networks, domain assignments and sequence similarity. <i>Nucleic Acids Research</i> , 2015, 43, W134-W140.	6.5	73
1569	Genome-wide identification of the auxin response factor (ARF) gene family and expression analysis of its role associated with pistil development in Japanese apricot (<i>Prunus mume</i> Sieb. et Zucc). <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	22
1570	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. <i>Journal of Experimental Botany</i> , 2015, 66, 4239-4250.	2.4	10
1571	Genome Sequence of <i>Clostridium acetobutylicum</i> GXAS18-1, a Novel Biobutanol Production Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
1572	The functional landscape bound to the transcription factors of <i>Escherichia coli</i> K-12. <i>Computational Biology and Chemistry</i> , 2015, 58, 93-103.	1.1	16
1573	Rumen Microbiology: From Evolution to Revolution. , 2015, , .		60
1574	Identification of SlpB, a Cytotoxic Protease from <i>Serratia marcescens</i> . <i>Infection and Immunity</i> , 2015, 83, 2907-2916.	1.0	35
1575	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <i>Frontiers in Microbiology</i> , 2015, 6, 199.	1.5	24
1576	Evolutionary hierarchy of vertebrate-like heterotrimeric G protein families. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 27-40.	1.2	35
1577	Origin and evolution of lysyl oxidases. <i>Scientific Reports</i> , 2015, 5, 10568.	1.6	86
1578	Solution structure of a soluble fragment derived from a membrane protein by shotgun proteolysis. <i>Protein Engineering, Design and Selection</i> , 2015, 28, 445-450.	1.0	4
1579	Evolutionary dynamics of rhomboid proteases in <i>Streptomyces</i> . <i>BMC Research Notes</i> , 2015, 8, 234.	0.6	0
1580	The origin of the ADAR gene family and animal RNA editing. <i>BMC Evolutionary Biology</i> , 2015, 15, 4.	3.2	65

#	ARTICLE	IF	CITATIONS
1581	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. <i>Frontiers in Plant Science</i> , 2014, 5, 759.	1.7	98
1582	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	13.6	544
1583	Elucidation of the serosal cuticle machinery in the beetle <i>Tribolium</i> by RNA sequencing and functional analysis of <i>Knickkopf1</i> , <i>Retroactive</i> and <i>Laccase2</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2015, 60, 7-12.	1.2	28
1584	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
1585	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	9.4	1,560
1586	PAV markers in <i>Sorghum bicolor</i> : genome pattern, affected genes and pathways, and genetic linkage map construction. <i>Theoretical and Applied Genetics</i> , 2015, 128, 623-637.	1.8	15
1587	Microbial Consortium Associated with the Antarctic Marine Ciliate <i>Euplotes focardii</i> : An Investigation from Genomic Sequences. <i>Microbial Ecology</i> , 2015, 70, 484-497.	1.4	42
1588	Structural organization of very small chromosomes: study on a single-celled evolutionary distant eukaryote <i>Giardia intestinalis</i> . <i>Chromosoma</i> , 2015, 124, 81-94.	1.0	23
1589	Genetic diversity of <i>Trichoderma atroviride</i> strains collected in Poland and identification of loci useful in detection of within-species diversity. <i>Folia Microbiologica</i> , 2015, 60, 297-307.	1.1	21
1590	Studies on Deimmunization of Antileukaemic L-Asparaginase to have Reduced Clinical Immunogenicity- An in silico Approach. <i>Pathology and Oncology Research</i> , 2015, 21, 909-920.	0.9	20
1591	Structure-based function analysis of putative conserved proteins with isomerase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 741-763.	1.1	14
1592	A heteromeric potassium channel involved in the modulation of the plasma membrane potential is essential for the survival of African trypanosomes. <i>FASEB Journal</i> , 2015, 29, 3228-3237.	0.2	21
1593	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	1.2	1,445
1594	MDAT- Aligning multiple domain arrangements. <i>BMC Bioinformatics</i> , 2015, 16, 19.	1.2	5
1595	MBBC: an efficient approach for metagenomic binning based on clustering. <i>BMC Bioinformatics</i> , 2015, 16, 36.	1.2	23
1596	DomSign: a top-down annotation pipeline to enlarge enzyme space in the protein universe. <i>BMC Bioinformatics</i> , 2015, 16, 96.	1.2	6
1597	Genome-wide analysis of the R2R3-MYB transcription factor genes in Chinese cabbage (<i>Brassica rapa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.2	71
1598	A novel <i>Schistosoma japonicum</i> endonuclease homologous to DNase II. <i>BMC Genomics</i> , 2015, 16, 126.	1.2	10

#	ARTICLE	IF	CITATIONS
1599	The observation of evolutionary interaction pattern pairs in membrane proteins. <i>BMC Structural Biology</i> , 2015, 15, 6.	2.3	1
1600	Mining the entire Protein DataBank for frequent spatially cohesive amino acid patterns. <i>BioData Mining</i> , 2015, 8, 4.	2.2	12
1601	The draft genome of <i>Primula veris</i> yields insights into the molecular basis of heterostyly. <i>Genome Biology</i> , 2015, 16, 12.	3.8	96
1602	Habitat Visualization and Genomic Analysis of <i>Candidatus Pantoea carbekii</i> , the Primary Symbiont of the Brown Marmorated Stink Bug. <i>Genome Biology and Evolution</i> , 2015, 7, 620-635.	1.1	50
1603	Molecular cloning and immune responsive expression of LGP2 gene, a pivotal member of the RLR gene family from Muscovy duck <i>Cairina moschata</i> . <i>Poultry Science</i> , 2015, 94, 1170-1176.	1.5	15
1604	X-Linked <i>TEX11</i> Mutations, Meiotic Arrest, and Azoospermia in Infertile Men. <i>New England Journal of Medicine</i> , 2015, 372, 2097-2107.	13.9	279
1605	Comparative transcriptome profiling approach to glean virulence and immunomodulation-related genes of <i>Fasciola hepatica</i> . <i>BMC Genomics</i> , 2015, 16, 366.	1.2	15
1606	Cancer3D: understanding cancer mutations through protein structures. <i>Nucleic Acids Research</i> , 2015, 43, D968-D973.	6.5	46
1607	A Computational Domain-Based Feature Grouping Approach for Prediction of Stability of SCF Ligases. <i>Lecture Notes in Computer Science</i> , 2015, , 630-640.	1.0	1
1608	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
1609	Genome Sequence, Comparative Analysis, and Evolutionary Insights into Chitinases of Entomopathogenic Fungus <i>Hirsutiella thompsonii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 916-930.	1.1	39
1610	The conjugative DNA-transfer apparatus of <i>Streptomyces</i> . <i>International Journal of Medical Microbiology</i> , 2015, 305, 224-229.	1.5	30
1611	Evolutionary Patterns in Coiled-Coils. <i>Genome Biology and Evolution</i> , 2015, 7, 545-556.	1.1	27
1612	Most Highly Expressed Protein-Coding Genes Have a Single Dominant Isoform. <i>Journal of Proteome Research</i> , 2015, 14, 1880-1887.	1.8	106
1613	Thermophilic microbial cellulose decomposition and methanogenesis pathways recharacterized by metatranscriptomic and metagenomic analysis. <i>Scientific Reports</i> , 2014, 4, 6708.	1.6	62
1614	Sensor response regulator interactions in a cross-regulated signal transduction network. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1504-1515.	0.7	10
1615	Novel Transcriptional Regulons for Autotrophic Cycle Genes in Crenarchaeota. <i>Journal of Bacteriology</i> , 2015, 197, 2383-2391.	1.0	11
1616	The role of RNA conformation in RNA-protein recognition. <i>RNA Biology</i> , 2015, 12, 720-727.	1.5	31

#	ARTICLE	IF	CITATIONS
1617	Mutations Associated with Reduced Surotomycin Susceptibility in <i>Clostridium difficile</i> and <i>Enterococcus</i> Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 4139-4147.	1.4	21
1618	Patterns of Evolutionary Conservation of Ascorbic Acid-Related Genes Following Whole-Genome Triplication in <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 299-313.	1.1	18
1619	Limited Portability of G-Patch Domains in Regulators of the Prp43 RNA Helicase Required for Pre-mRNA Splicing and Ribosomal RNA Maturation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2015, 200, 135-147.	1.2	14
1620	Characterization of a new ViI-like <i>Erwinia amylovora</i> bacteriophage phiEa2809. <i>FEMS Microbiology Letters</i> , 2015, 362, .	0.7	18
1621	Molecular modeling, simulation and virtual screening of MurD ligase protein from <i>Salmonella typhimurium</i> LT2. <i>Journal of Pharmacological and Toxicological Methods</i> , 2015, 73, 34-41.	0.3	12
1622	MadR1, a <i>Mycobacterium tuberculosis</i> cell cycle stress response protein that is a member of a widely conserved protein class of prokaryotic, eukaryotic and archeal origin. <i>Tuberculosis</i> , 2015, 95, 251-258.	0.8	5
1623	Loss of <i>Drosophila</i> pheromone reverses its role in sexual communication in <i>Drosophila suzukii</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20143018.	1.2	70
1624	Metagenomic analysis reveals adaptations to a cold-adapted lifestyle in a low-temperature acid mine drainage stream. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	75
1625	Hypothetical gene <i>C18orf42</i> encodes a novel protein kinase A-binding protein. <i>Genes To Cells</i> , 2015, 20, 267-280.	0.5	2
1626	Genome-wide identification of auxin response factor (ARF) genes and its tissue-specific prominent expression in <i>Gossypium raimondii</i> . <i>Functional and Integrative Genomics</i> , 2015, 15, 481-493.	1.4	41
1627	PPDMs—a resource for mapping small molecule bioactivities from ChEMBL to Pfam-A protein domains. <i>Bioinformatics</i> , 2015, 31, 776-778.	1.8	11
1628	Redox proteomic analysis of <i>mytilus edulis</i> gills: effects of the pharmaceutical diclofenac on a non-target organism. <i>Drug Testing and Analysis</i> , 2015, 7, 957-966.	1.6	11
1629	Personalized Biochemistry and Biophysics. <i>Biochemistry</i> , 2015, 54, 2551-2559.	1.2	31
1630	Carbohydrate-binding module tribes. <i>Biopolymers</i> , 2015, 103, 203-214.	1.2	24
1631	Functional diversification of the dehydrin gene family in apple and its contribution to cold acclimation during dormancy. <i>Physiologia Plantarum</i> , 2015, 155, 315-329.	2.6	18
1632	Genome-wide comparison of ferritin family from Archaea, Bacteria, Eukarya, and Viruses: its distribution, characteristic motif, and phylogenetic relationship. <i>Die Naturwissenschaften</i> , 2015, 102, 64.	0.6	21
1633	Functionally Structured Genomes in <i>Lactobacillus kunkeei</i> Colonizing the Honey Crop and Food Products of Honeybees and Stingless Bees. <i>Genome Biology and Evolution</i> , 2015, 7, 1455-1473.	1.1	50
1634	Whole transcriptomic analysis of the plant-beneficial rhizobacterium <i>Bacillus amyloliquefaciens</i> SQR9 during enhanced biofilm formation regulated by maize root exudates. <i>BMC Genomics</i> , 2015, 16, 685.	1.2	139

#	ARTICLE	IF	CITATIONS
1635	Associations of SNPs located at candidate genes to bovine growth traits, prioritized with an interaction networks construction approach. <i>BMC Genetics</i> , 2015, 16, 91.	2.7	16
1636	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. <i>BMC Genomics</i> , 2015, 16, 520.	1.2	173
1637	Plant Carbohydrate Active Enzyme (CAZyme) Repertoires: A Comparative Study. , 2015, , 115-134.		0
1638	Assessing sequence plasticity of a virus-like nanoparticle by evolution toward a versatile scaffold for vaccines and drug delivery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12360-12365.	3.3	117
1639	Baleen whales host a unique gut microbiome with similarities to both carnivores and herbivores. <i>Nature Communications</i> , 2015, 6, 8285.	5.8	184
1640	Comparative transcriptomic analysis revealed adaptation mechanism of <i>Phrynocephalus erythrurus</i> , the highest altitude Lizard living in the Qinghai-Tibet Plateau. <i>BMC Evolutionary Biology</i> , 2015, 15, 101.	3.2	50
1641	Unravelling the genome of Holy basil: an "incomparable" "elixir of life" of traditional Indian medicine. <i>BMC Genomics</i> , 2015, 16, 413.	1.2	60
1642	TMFoldRec: a statistical potential-based transmembrane protein fold recognition tool. <i>BMC Bioinformatics</i> , 2015, 16, 201.	1.2	11
1643	Ten Years of Maintaining and Expanding a Microbial Genome and Metagenome Analysis System. <i>Trends in Microbiology</i> , 2015, 23, 730-741.	3.5	20
1644	Prediction of host - pathogen protein interactions between <i>Mycobacterium tuberculosis</i> and <i>Homo sapiens</i> using sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 100.	1.2	51
1645	Domain similarity based orthology detection. <i>BMC Bioinformatics</i> , 2015, 16, 154.	1.2	11
1646	<i>Aspergillus niger</i> membrane-associated proteome analysis for the identification of glucose transporters. <i>Biotechnology for Biofuels</i> , 2015, 8, 150.	6.2	43
1647	Bioinformatic search for cellulose synthase genes in flax (<i>Linum usitatissimum</i>) and their phylogenetic analysis. <i>Cytology and Genetics</i> , 2015, 49, 279-287.	0.2	7
1648	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015, 1, 197-209.	2.9	94
1649	Tunicate pregnane X receptor (PXR) orthologs: Transcript characterization and natural variation. <i>Marine Genomics</i> , 2015, 23, 99-108.	0.4	4
1650	Functional and Structural Characterization of the Antiphagocytic Properties of a Novel Transglutaminase from <i>Streptococcus suis</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 19081-19092.	1.6	22
1651	Experimental Design and Bioinformatics Analysis for the Application of Metagenomics in Environmental Sciences and Biotechnology. <i>Environmental Science & Technology</i> , 2015, 49, 12628-12640.	4.6	72
1652	Structural and functional studies of a metallo- β -lactamase unveil a new type of structurally encoded nickel-containing heterodinuclear site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2054-2065.	2.5	3

#	ARTICLE	IF	CITATIONS
1653	Unearthing the genomes of plant-beneficial <i>Pseudomonas</i> model strains WCS358, WCS374 and WCS417. <i>BMC Genomics</i> , 2015, 16, 539.	1.2	184
1654	Whole transcriptome profiling of the vernalization process in <i>Lilium longiflorum</i> (cultivar White) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	45
1655	Depiction of carbohydrate-active enzyme diversity in <i>Caldicellulosiruptor</i> sp. F32 at the genome level reveals insights into distinct polysaccharide degradation features. <i>Molecular BioSystems</i> , 2015, 11, 3164-3173.	2.9	17
1656	REGULATOR: a database of metazoan transcription factors and maternal factors for developmental studies. <i>BMC Bioinformatics</i> , 2015, 16, 114.	1.2	13
1657	Genome-Wide Analysis of <i>PHOSPHOLIPID</i> : <i>DIACYLGLYCEROL ACYLTRANSFERASE</i> (<i>PDAT</i>) Genes in Plants Reveals the Eudicot-Wide <i>PDAT</i> Gene Expansion and Altered Selective Pressures Acting on the Core Eudicot <i>PDAT</i> Paralog. <i>Plant Physiology</i> , 2015, 167, 887-904.	2.3	39
1658	lncRNA-ID: Long non-coding RNA IDentification using balanced random forests. <i>Bioinformatics</i> , 2015, 31, 3897-3905.	1.8	85
1659	Evolution and Diversity of the Ras Superfamily of Small GTPases in Prokaryotes. <i>Genome Biology and Evolution</i> , 2015, 7, 57-70.	1.1	51
1660	Structural modeling and in silico analysis of non-synonymous single nucleotide polymorphisms of human 3 β -hydroxysteroid dehydrogenase type 2. <i>Meta Gene</i> , 2015, 5, 162-172.	0.3	37
1661	Computational approaches to natural product discovery. <i>Nature Chemical Biology</i> , 2015, 11, 639-648.	3.9	373
1662	Transcriptomic analysis of the <i>GCN5</i> gene reveals mechanisms of the epigenetic regulation of virulence and morphogenesis in <i>Ustilago maydis</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov055.	1.1	17
1663	KLF/SP Transcription Factor Family Evolution: Expansion, Diversification, and Innovation in Eukaryotes. <i>Genome Biology and Evolution</i> , 2015, 7, 2289-2309.	1.1	93
1664	Inntags: small self-structured epitopes for innocuous protein tagging. <i>Nature Methods</i> , 2015, 12, 955-958.	9.0	22
1665	CovRS-Regulated Transcriptome Analysis of a Hypervirulent M23 Strain of Group A <i>Streptococcus pyogenes</i> Provides New Insights into Virulence Determinants. <i>Journal of Bacteriology</i> , 2015, 197, 3191-3205.	1.0	17
1666	Histone Peptide Recognition by KDM5B-PHD1: A Case Study. <i>Biochemistry</i> , 2015, 54, 5766-5780.	1.2	13
1667	The <i>Brassica rapa</i> Genome. <i>Compendium of Plant Genomes</i> , 2015, , .	0.3	8
1668	<i>Clostridium butyricum</i> Strains and Dysbiosis Linked to Necrotizing Enterocolitis in Preterm Neonates. <i>Clinical Infectious Diseases</i> , 2015, 61, 1107-1115.	2.9	109
1669	Computational approaches to study the effects of small genomic variations. <i>Journal of Molecular Modeling</i> , 2015, 21, 251.	0.8	21
1670	Rumen Metagenomics. , 2015, , 223-245.		5

#	ARTICLE	IF	CITATIONS
1671	Methods of processing mass spectrometry data to identify peptides and proteins. Moscow University Chemistry Bulletin, 2015, 70, 211-222.	0.2	0
1673	The Little Known Universe of Short Proteins in Insects: A Machine Learning Approach. True Bugs (Heteroptera) of the Neotropics, 2015, , 177-202.	1.2	3
1674	Identifying three-dimensional structures of autophosphorylation complexes in crystals of protein kinases. Science Signaling, 2015, 8, rs13.	1.6	38
1676	The Kuâ€“Mar zinc finger: A segment-swapped zinc ribbon in MarR-like transcription regulators related to the Ku bridge. Journal of Structural Biology, 2015, 191, 281-289.	1.3	7
1677	EnzDP: Improved enzyme annotation for metabolic network reconstruction based on domain composition profiles. Journal of Bioinformatics and Computational Biology, 2015, 13, 1543003.	0.3	11
1678	Polyketide synthesis genes associated with toxin production in two species of Gambierdiscus (Dinophyceae). BMC Genomics, 2015, 16, 410.	1.2	56
1679	CDvist: a webserver for identification and visualization of conserved domains in protein sequences. Bioinformatics, 2015, 31, 1475-1477.	1.8	69
1680	The cell envelope proteome of <i>Aggregatibacter actinomycetemcomitans</i> . Molecular Oral Microbiology, 2015, 30, 97-110.	1.3	9
1681	Multiple histidines in the periplasmic domain of the <i>S</i> sensor kinase <i>SsrA</i> enhance signaling in response to extracellular acidification. Molecular Microbiology, 2015, 95, 678-691.	1.2	27
1682	The evolution and function of protein tandem repeats in plants. New Phytologist, 2015, 206, 397-410.	3.5	54
1683	Pooled assembly of marine metagenomic datasets: enriching annotation through chimerism. Bioinformatics, 2015, 31, 311-317.	1.8	26
1684	Metatranscriptomic Analyses of Plant Cell Wall Polysaccharide Degradation by Microorganisms in the Cow Rumen. Applied and Environmental Microbiology, 2015, 81, 1375-1386.	1.4	206
1685	A General Computational Approach for Repeat Protein Design. Journal of Molecular Biology, 2015, 427, 563-575.	2.0	72
1686	Identification and phylogenetic analysis of late embryogenesis abundant proteins family in tomato (<i>Solanum lycopersicum</i>). Planta, 2015, 241, 757-772.	1.6	93
1687	Accurate in silico identification of species-specific acetylation sites by integrating protein sequence-derived and functional features. Scientific Reports, 2014, 4, 5765.	1.6	71
1688	Iron â€“sulfur cluster biogenesis in mammalian cells: New insights into the molecular mechanisms of cluster delivery. Biochimica Et Biophysica Acta - Molecular Cell Research, 2015, 1853, 1493-1512.	1.9	170
1689	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus <i>Eucalyptus</i> . New Phytologist, 2015, 206, 1328-1336.	3.5	19
1690	The Crystal Structure of the Human Titin:Obscurin Complex Reveals a Conserved yet Specific Muscle M-Band Zipper Module. Journal of Molecular Biology, 2015, 427, 718-736.	2.0	20

#	ARTICLE	IF	CITATIONS
1691	Transport of L-Glutamine, L-Alanine, L-Arginine and L-Histidine by the Neuron-Specific Slc38a8 (SNAT8) in CNS. <i>Journal of Molecular Biology</i> , 2015, 427, 1495-1512.	2.0	53
1692	In-silico characterization of Formin Binding Protein 4 Family of proteins. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2015, 7, 43-64.	2.2	4
1693	Structural, evolutionary and functional analysis of the <sc>NAC</sc> domain protein family in <i>Eucalyptus</i>. <i>New Phytologist</i> , 2015, 206, 1337-1350.	3.5	69
1694	Arsenic hypertolerance in the protist <i>Euglena mutabilis</i> is mediated by specific transporters and functional integrity maintenance mechanisms. <i>Environmental Microbiology</i> , 2015, 17, 1941-1949.	1.8	12
1695	¹ H, ¹⁵ N and ¹³ C resonance assignments of the yeast Pih1 and Tah1 C-terminal domains complex. <i>Biomolecular NMR Assignments</i> , 2015, 9, 71-73.	0.4	3
1696	Genomes and gene expression across light and productivity gradients in eastern subtropical Pacific microbial communities. <i>ISME Journal</i> , 2015, 9, 1076-1092.	4.4	108
1697	Genome wide in silico characterization of Dof gene families of pigeonpea (<i>Cajanus cajan</i> (L) Millsp.). <i>Molecular Biology Reports</i> , 2015, 42, 535-552.	1.0	31
1698	Protein-protein interaction predictions using text mining methods. <i>Methods</i> , 2015, 74, 47-53.	1.9	73
1699	Bioinformatic Analysis of GJB2 Gene Missense Mutations. <i>Cell Biochemistry and Biophysics</i> , 2015, 71, 1623-1642.	0.9	16
1700	Genome-wide analysis of the MADS-box gene family in <i>Brassica rapa</i> (Chinese cabbage). <i>Molecular Genetics and Genomics</i> , 2015, 290, 239-255.	1.0	80
1701	Effects of Actin-Like Proteins Encoded by Two <i>Bacillus pumilus</i> Phages on Unstable Lysogeny, Revealed by Genomic Analysis. <i>Applied and Environmental Microbiology</i> , 2015, 81, 339-350.	1.4	21
1702	Molecular characterization of calponin in the catch muscle of the Yesso scallop <i>Mizuhopecten yessoensis</i> . <i>Fisheries Science</i> , 2015, 81, 155-162.	0.7	4
1703	Genome-wide identification and structure-function studies of proteases and protease inhibitors in <i>Cicer arietinum</i> (chickpea). <i>Computers in Biology and Medicine</i> , 2015, 56, 67-81.	3.9	7
1704	Myc and its interactors take shape. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 469-483.	0.9	102
1705	BurrH: a new modular DNA binding protein for genome engineering. <i>Scientific Reports</i> , 2014, 4, 3831.	1.6	45
1706	cddApp: a Cytoscape app for accessing the NCBI conserved domain database. <i>Bioinformatics</i> , 2015, 31, 134-136.	1.8	4
1707	Outer membrane vesicles are vehicles for the delivery of <sc>V</sc> <i>vibrio tasmaniensis</i> virulence factors to oyster immune cells. <i>Environmental Microbiology</i> , 2015, 17, 1152-1165.	1.8	75
1708	Structure-based functional annotation of putative conserved proteins having lyase activity from <i>Haemophilus influenzae</i> . <i>3 Biotech</i> , 2015, 5, 317-336.	1.1	15

#	ARTICLE	IF	CITATIONS
1709	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. ISME Journal, 2015, 9, 207-216.	4.4	540
1710	Mode of action of <i>Bacillus licheniformis</i> pectin methylesterase on highly methylesterified and acetylated pectins. Carbohydrate Polymers, 2015, 115, 540-550.	5.1	16
1711	Genomic comparison of chitinolytic enzyme systems from terrestrial and aquatic bacteria. Environmental Microbiology, 2016, 18, 38-49.	1.8	63
1712	Bacterial collagenases – A review. Critical Reviews in Microbiology, 2016, 42, 106-126.	2.7	136
1713	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Frontiers in Microbiology, 2016, 7, 238.	1.5	66
1714	Structure Prediction and Binding Site Analysis of Hepatotoxic Microcystin-LR Degrading MlrC-Like Protein from <i>Burkholderia</i> sp. using Computational Approaches. Current Research in Bioinformatics, 2016, 5, 1-9.	0.1	1
1715	Identification, characterization, and gene expression analysis of nucleotide binding site (NB)-type resistance gene homologues in switchgrass. BMC Genomics, 2016, 17, 892.	1.2	14
1716	QuaBingo: A Prediction System for Protein Quaternary Structure Attributes Using Block Composition. BioMed Research International, 2016, 2016, 1-10.	0.9	4
1717	In silico identification and characterization of the WRKY gene superfamily in pepper (<i>Capsicum annuum</i>) Tj ETQq0 0.0 rgBT /Overlock 10	0.3	22
1718	Steric Clash in the SET Domain of Histone Methyltransferase NSD1 as a Cause of Sotos Syndrome and Its Genetic Heterogeneity in a Brazilian Cohort. Genes, 2016, 7, 96.	1.0	9
1719	A transcriptional blueprint for a spiral-cleaving embryo. BMC Genomics, 2016, 17, 552.	1.2	20
1720	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. ELife, 2016, 5, e11888.	2.8	414
1721	Developmental Cycle and Genome Analysis of <i>Rubidus massiliensis</i> , a New <i>Vermamoeba vermiformis</i> Pathogen. Frontiers in Cellular and Infection Microbiology, 2016, 6, 31.	1.8	35
1722	PATyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	1.5	153
1723	Genomic Insights into a New <i>Citrobacter koseri</i> Strain Revealed Gene Exchanges with the Virulence-Associated <i>Yersinia pestis</i> pPCP1 Plasmid. Frontiers in Microbiology, 2016, 7, 340.	1.5	13
1724	Enantioselective Utilization of D-Amino Acids by Deep-Sea Microorganisms. Frontiers in Microbiology, 2016, 7, 511.	1.5	40
1725	The Role of Complement in Cnidarian-Dinoflagellate Symbiosis and Immune Challenge in the Sea Anemone <i>Aiptasia pallida</i> . Frontiers in Microbiology, 2016, 7, 519.	1.5	66
1726	Proteomic Analysis of a Novel <i>Bacillus Jumbo</i> Phage Revealing Glycoside Hydrolase As Structural Component. Frontiers in Microbiology, 2016, 7, 745.	1.5	33

#	ARTICLE	IF	CITATIONS
1727	Diversity of the Germination Apparatus in <i>Clostridium botulinum</i> Groups I, II, III, and IV. <i>Frontiers in Microbiology</i> , 2016, 7, 1702.	1.5	25
1728	Bioinformatic Analyses of Unique (Orphan) Core Genes of the Genus <i>Acidithiobacillus</i> : Functional Inferences and Use As Molecular Probes for Genomic and Metagenomic/Transcriptomic Interrogation. <i>Frontiers in Microbiology</i> , 2016, 7, 2035.	1.5	16
1729	Comparative Genomic Analysis of <i>Bacillus amyloliquefaciens</i> and <i>Bacillus subtilis</i> Reveals Evolutional Traits for Adaptation to Plant-Associated Habitats. <i>Frontiers in Microbiology</i> , 2016, 7, 2039.	1.5	54
1730	Long Noncoding RNA and mRNA Expression Profiles in the Thyroid Gland of Two Phenotypically Extreme Pig Breeds Using Ribo-Zero RNA Sequencing. <i>Genes</i> , 2016, 7, 34.	1.0	36
1731	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. <i>Genes</i> , 2016, 7, 89.	1.0	51
1732	Identification of Novel Pathways in Plant Lectin-Induced Cancer Cell Apoptosis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 228.	1.8	12
1733	Comparative Genomics of the Extreme Acidophile <i>Acidithiobacillus thiooxidans</i> Reveals Intraspecific Divergence and Niche Adaptation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1355.	1.8	39
1734	IGDD: a database of intronless genes in dicots. <i>BMC Bioinformatics</i> , 2016, 17, 289.	1.2	23
1735	Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. <i>Biology Direct</i> , 2016, 11, 27.	1.9	3
1736	Identification and functional characterization of novel xylose transporters from the cell factories <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 148.	6.2	71
1737	Dimerization and Transactivation Domains as Candidates for Functional Modulation and Diversity of Sox9. <i>PLoS ONE</i> , 2016, 11, e0156199.	1.1	8
1738	Identification of <i>Aedes aegypti</i> Long Intergenic Non-coding RNAs and Their Association with Wolbachia and Dengue Virus Infection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005069.	1.3	85
1739	A Factor Graph Approach to Automated GO Annotation. <i>PLoS ONE</i> , 2016, 11, e0146986.	1.1	5
1740	Biochemical Characterization of a Family 15 Carbohydrate Esterase from a Bacterial Marine Arctic Metagenome. <i>PLoS ONE</i> , 2016, 11, e0159345.	1.1	32
1741	Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624. <i>PLoS ONE</i> , 2016, 11, e0162983.	1.1	76
1742	Comparative genomic and transcriptomic analyses of the Fuzhuan brick tea-fermentation fungus <i>Aspergillus cristatus</i> . <i>BMC Genomics</i> , 2016, 17, 428.	1.2	55
1743	Glutathione S-Transferase Gene Family in <i>Gossypium raimondii</i> and <i>G. arboreum</i> : Comparative Genomic Study and their Expression under Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 139.	1.7	81
1744	Transcriptome Analysis Identifies Candidate Genes Related to Triacylglycerol and Pigment Biosynthesis and Photoperiodic Flowering in the Ornamental and Oil-Producing Plant, <i>Camellia reticulata</i> (Theaceae). <i>Frontiers in Plant Science</i> , 2016, 7, 163.	1.7	29

#	ARTICLE	IF	CITATIONS
1745	Analysis of the Prefoldin Gene Family in 14 Plant Species. <i>Frontiers in Plant Science</i> , 2016, 7, 317.	1.7	20
1746	Expansion and Functional Divergence of AP2 Group Genes in Spermatophytes Determined by Molecular Evolution and Arabidopsis Mutant Analysis. <i>Frontiers in Plant Science</i> , 2016, 7, 1383.	1.7	37
1747	A Developmental Transcriptome Map for Allotetraploid <i>Arachis hypogaea</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1446.	1.7	178
1748	Comparative Genomic Analysis of the GRF Genes in Chinese Pear (<i>Pyrus bretschneideri</i> Rehd), Poplar (<i>Populus</i>), Grape (<i>Vitis vinifera</i>), Arabidopsis and Rice (<i>Oryza sativa</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1750.	1.7	97
1749	Structural, Evolutionary, and Functional Analysis of the Class III Peroxidase Gene Family in Chinese Pear (<i>Pyrus bretschneideri</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 1874.	1.7	83
1750	Glutathione S-transferases and UDP-glycosyltransferases Are Involved in Response to Aluminum Stress in Flax. <i>Frontiers in Plant Science</i> , 2016, 7, 1920.	1.7	55
1751	OsSGL, a Novel DUF1645 Domain-Containing Protein, Confers Enhanced Drought Tolerance in Transgenic Rice and Arabidopsis. <i>Frontiers in Plant Science</i> , 2016, 7, 2001.	1.7	46
1752	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016, 32, 3566-3574.	1.8	25
1753	In Silico Analysis: Annotations about Structural and Functional Features of DUF 2726 Family Member Proteins. <i>Bangladesh Journal of Microbiology</i> , 2016, , 53-58.	0.2	0
1754	Identification of genetic and environmental factors stimulating excision from <i>ScpS</i> treptomyces scabiei chromosome of the toxicogenic region responsible for pathogenicity. <i>Molecular Plant Pathology</i> , 2016, 17, 501-509.	2.0	23
1755	Transcriptomic profiling of <i>Alexandrium fundyense</i> during physical interaction with or exposure to chemical signals from the parasite <i>Amoebophrya</i> . <i>Molecular Ecology</i> , 2016, 25, 1294-1307.	2.0	22
1756	Draft Genome Sequence of the Rumen Methanogen Methanobrevibacter olleyae YLM1. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
1757	Genome Sequence of a <i>Clostridium neonatale</i> Strain Isolated in a Canadian Neonatal Intensive Care Unit. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
1758	Identification of family determining residues in <i>Jumonji</i> lysine demethylases: A sequence-based, family wide classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 397-407.	1.5	4
1759	Disruption of <i>OssULTR3</i> reduces phytate and phosphorus concentrations and alters the metabolite profile in rice grains. <i>New Phytologist</i> , 2016, 211, 926-939.	3.5	72
1760	Draft Genome Sequence of Actinobaculum massiliense Strain FC3. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
1761	<i>Colletotrichum higginsianum</i> extracellular LysM proteins play dual roles in appressorial function and suppression of chitin-triggered plant immunity. <i>New Phytologist</i> , 2016, 211, 1323-1337.	3.5	155
1762	bioassayR: Cross-Target Analysis of Small Molecule Bioactivity. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1237-1242.	2.5	13

#	ARTICLE	IF	CITATIONS
1763	Analysis of the distribution and evolution of the <sc>ATP</sc>-dependent <sc>DNA</sc> ligases of bacteria delineates a distinct phylogenetic group <sc>L</sc>ig <sc>E</sc>™. Molecular Microbiology, 2016, 99, 274-290.	1.2	16
1764	Investigating polymorphisms by bioinformatics is a potential cost-effective method to screen for germline mutations in Chinese familial adenomatous polyposis patients. Oncology Letters, 2016, 12, 421-428.	0.8	1
1765	Molecular cloning, heterologous expression, and enzymatic characterization of lysoplasmalogen-specific phospholipase D from Thermocrispum sp.. FEBS Open Bio, 2016, 6, 1113-1130.	1.0	12
1766	Methuselah/Methuselah-like G protein-coupled receptors constitute an ancient metazoan gene family. Scientific Reports, 2016, 6, 21801.	1.6	24
1767	FAMSA: Fast and accurate multiple sequence alignment of huge protein families. Scientific Reports, 2016, 6, 33964.	1.6	92
1768	RNA-seq-based evaluation of bicolor tepal pigmentation in Asiatic hybrid lilies (Lilium spp.). BMC Genomics, 2016, 17, 611.	1.2	65
1769	A genome-wide analysis of the ASYMMETRIC LEAVES2/LATERAL ORGAN BOUNDARIES (AS2/LOB) gene family in barley (Hordeum vulgare L.). Journal of Zhejiang University: Science B, 2016, 17, 763-774.	1.3	22
1770	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. Scientific Reports, 2016, 6, 20915.	1.6	11
1771	Diversity of ABC transporter genes across the plant kingdom and their potential utility in biotechnology. BMC Biotechnology, 2016, 16, 47.	1.7	91
1772	Delta-proteobacterial SAR324 group in hydrothermal plumes on the South Mid-Atlantic Ridge. Scientific Reports, 2016, 6, 22842.	1.6	21
1773	Evolutionary Histories of Gene Families in Angiosperm Trees. Plant Genetics and Genomics: Crops and Models, 2016, , 121-137.	0.3	0
1774	Enhanced antimicrobial peptide-induced activity in the mollusc Toll-2 family through evolution via tandem Toll/interleukin-1 receptor. Royal Society Open Science, 2016, 3, 160123.	1.1	5
1775	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. DNA Research, 2017, 24, dsw049.	1.5	38
1776	Toxin inhibition in <i>C. crescentus</i> VapBC1 is mediated by a flexible pseudo-palindromic protein motif and modulated by DNA binding. Nucleic Acids Research, 2016, 45, gkw1266.	6.5	13
1777	Transcriptome analyses of the Dof-like gene family in grapevine reveal its involvement in berry, flower and seed development. Horticulture Research, 2016, 3, 16042.	2.9	25
1778	From Genomes to Phenotypes: TraitAr, the Microbial Trait Analyzer. MSystems, 2016, 1, .	1.7	102
1779	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
1780	A long noncoding RNA associated with susceptibility to celiac disease. Science, 2016, 352, 91-95.	6.0	211

#	ARTICLE	IF	CITATIONS
1781	The tertiary structures of porcine AhR and ARNT proteins and molecular interactions within the TCDD/AhR/ARNT complex. <i>Journal of Molecular Graphics and Modelling</i> , 2016, 67, 119-126.	1.3	1
1782	Vasohibins: new transglutaminase-like cysteine proteases possessing a non-canonical Cys-His-Ser catalytic triad. <i>Bioinformatics</i> , 2016, 32, 1441-1445.	1.8	35
1783	Experimental validation of in silico modelâ€redicted isocitrate dehydrogenase and phosphomannose isomerase from <i>D. ehalococcoides mccartyi</i> . <i>Microbial Biotechnology</i> , 2016, 9, 47-60.	2.0	1
1784	Delineation of Polypharmacology across the Human Structural Kinome Using a Functional Site Interaction Fingerprint Approach. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4326-4341.	2.9	39
1785	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	6.5	35
1786	Leptin receptor gene in the European sea bass (<i>Dicentrarchus labrax</i>): Cloning, phylogeny, tissue distribution and neuroanatomical organization. <i>General and Comparative Endocrinology</i> , 2016, 229, 100-111.	0.8	22
1787	Multidomain, Surface Layer-associated Glycoside Hydrolases Contribute to Plant Polysaccharide Degradation by <i>Caldicellulosiruptor</i> Species. <i>Journal of Biological Chemistry</i> , 2016, 291, 6732-6747.	1.6	44
1788	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. <i>Nucleic Acids Research</i> , 2016, 44, 3513-3533.	6.5	54
1789	Complete Genome Sequence of Methanogenic Archaeon ISO4-G1, a Member of the <i>Methanomassiliicoccales</i> , Isolated from a Sheep Rumen. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
1790	A comparative analysis of the "other roles" of transcriptional factors from pathogenic organisms. <i>Gene</i> , 2016, 586, 274-280.	1.0	1
1791	Genome- wide characterization of Nuclear Factor Y (NF-Y) gene family of sorghum [<i>Sorghum bicolor</i> (L.) Moench]: a bioinformatics approach. <i>Physiology and Molecular Biology of Plants</i> , 2016, 22, 33-49.	1.4	22
1792	Genome-wide analysis of the BES1 transcription factor family in Chinese cabbage (<i>Brassica rapa</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	35
1793	On the Entropy of Protein Families. <i>Journal of Statistical Physics</i> , 2016, 162, 1267-1293.	0.5	22
1794	Evaluation of Descriptor Algorithms of Biological Sequences and Distance Measures for the Intelligent Cluster Index (IClx). <i>Communications in Computer and Information Science</i> , 2016, , 434-448.	0.4	0
1795	DiiA is a novel dimorphic cell wall protein of <i>Streptococcus pneumoniae</i> involved in invasive disease. <i>Journal of Infection</i> , 2016, 73, 71-81.	1.7	6
1796	Characterization and mutagenesis of two novel ironâ€sulphur cluster pentonate dehydratases. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7549-7563.	1.7	27
1797	Homology-Based Annotation of Large Protein Datasets. <i>Methods in Molecular Biology</i> , 2016, 1415, 153-176.	0.4	0
1798	Gene expression analysis of disabled and re-induced isoprene emission by the tropical tree <i>Ficus septica</i> before and after cold ambient temperature exposure. <i>Tree Physiology</i> , 2016, 36, 873-882.	1.4	11

#	ARTICLE	IF	CITATIONS
1799	A Eukaryote without a Mitochondrial Organelle. <i>Current Biology</i> , 2016, 26, 1274-1284.	1.8	302
1800	Long-Term Warming Alters Carbohydrate Degradation Potential in Temperate Forest Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6518-6530.	1.4	68
1801	Polysaccharide utilisation loci of <i>Bacteroidetes</i> from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016, 18, 4456-4470.	1.8	56
1802	DEF: an automated dead-end filling approach based on quasi-endosymbiosis. <i>Bioinformatics</i> , 2017, 33, 405-413.	1.8	4
1803	De novo transcriptome assembly of mangosteen (<i>Garcinia mangostana</i> L.) fruit. <i>Genomics Data</i> , 2016, 10, 35-37.	1.3	9
1804	Protein-protein interaction and molecular dynamics analysis for identification of novel inhibitors in <i>Burkholderia cepacia</i> GG4. <i>Computational Biology and Chemistry</i> , 2016, 65, 80-90.	1.1	7
1805	A combined proteomic and transcriptomic analysis of slime secreted by the southern bottletail squid, <i>Sepiadarium austrinum</i> (Cephalopoda). <i>Journal of Proteomics</i> , 2016, 148, 170-182.	1.2	14
1806	Genomic identification, rapid evolution, and expression of <i>Argonaute</i> genes in the tilapia, <i>Oreochromis niloticus</i> . <i>Development Genes and Evolution</i> , 2016, 226, 339-348.	0.4	26
1807	Integrating metabolomics and transcriptomics data to discover a biocatalyst that can generate the amine precursors for alkalamide biosynthesis. <i>Plant Journal</i> , 2016, 88, 775-793.	2.8	17
1808	The protein inventory of <i>Clostridium difficile</i> grown in complex and minimal medium. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1068-1072.	0.8	36
1809	The conserved carboxyl domain of MorC, an inner membrane protein of <i>Aggregatibacter actinomycetemcomitans</i> , is essential for membrane function. <i>Molecular Oral Microbiology</i> , 2016, 31, 43-58.	1.3	9
1810	The obligate respiratory supercomplex from Actinobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1705-1714.	0.5	41
1811	Diverse gene functions in a soil mobilome. <i>Soil Biology and Biochemistry</i> , 2016, 101, 175-183.	4.2	24
1812	Mammalian cell entry (Mce) protein of <i>Leptospira interrogans</i> binds extracellular matrix components, plasminogen and β 2 integrin. <i>Microbiology and Immunology</i> , 2016, 60, 586-598.	0.7	15
1813	Genomics and expression analysis of DHHC-cysteine-rich domain S-acyl transferase protein family in apple. <i>Genes and Genomics</i> , 2016, 38, 671-684.	0.5	0
1814	High diversity of picornaviruses in rats from different continents revealed by deep sequencing. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	14
1815	Extensive complementarity between gene function prediction methods. <i>Bioinformatics</i> , 2016, 32, 3645-3653.	1.8	12
1816	Renew or die: The molecular mechanisms of peptidoglycan recycling and antibiotic resistance in Gram-negative pathogens. <i>Drug Resistance Updates</i> , 2016, 28, 91-104.	6.5	24

#	ARTICLE	IF	CITATIONS
1817	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016, 20, 357-367.	5.1	123
1818	Improved glycerol to ethanol conversion by <i>E. coli</i> using a metagenomic fragment isolated from an anaerobic reactor. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 1405-1416.	1.4	18
1819	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
1820	Identification and expression analysis of cytokinin response regulators in <i>Fragaria vesca</i> . <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	9
1821	Evolutionary analysis of the jacalin-related lectin family genes in 11 fishes. <i>Fish and Shellfish Immunology</i> , 2016, 56, 543-553.	1.6	11
1822	Genome sequence and comparative analysis of clavicipitaceous insect-pathogenic fungus <i>Aschersonia badia</i> with <i>Metarhizium</i> spp.. <i>BMC Genomics</i> , 2016, 17, 367.	1.2	12
1823	LRR-RLK family from two Citrus species: genome-wide identification and evolutionary aspects. <i>BMC Genomics</i> , 2016, 17, 623.	1.2	35
1824	First Comprehensive Proteome Analyses of Lysine Acetylation and Succinylation in Seedling Leaves of <i>Brachypodium distachyon</i> L.. <i>Scientific Reports</i> , 2016, 6, 31576.	1.6	62
1825	Characterization of long non-coding RNA transcriptome in high-energy diet induced nonalcoholic steatohepatitis minipigs. <i>Scientific Reports</i> , 2016, 6, 30709.	1.6	29
1826	Systematic identification and analysis of frequent gene fusion events in metabolic pathways. <i>BMC Genomics</i> , 2016, 17, 473.	1.2	13
1827	Application of Systems Biology to Neuroproteomics: The Path to Enhanced Theranostics in Traumatic Brain Injury. <i>Methods in Molecular Biology</i> , 2016, 1462, 139-155.	0.4	6
1828	Substrate specificity characterization for eight putative nudix hydrolases. Evaluation of criteria for substrate identification within the Nudix family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1810-1822.	1.5	10
1829	Structural and functional analyses of PolyProline-II helices in globular proteins. <i>Journal of Structural Biology</i> , 2016, 196, 414-425.	1.3	21
1830	Mammalian Fe-S proteins: definition of a consensus motif recognized by the co-chaperone HSC20. <i>Metallomics</i> , 2016, 8, 1032-1046.	1.0	29
1831	Improve homology search sensitivity of PacBio data by correcting frameshifts. <i>Bioinformatics</i> , 2016, 32, i529-i537.	1.8	12
1832	Adaptation of <i>Ustilago maydis</i> to extreme pH values: A transcriptomic analysis. <i>Journal of Basic Microbiology</i> , 2016, 56, 1222-1233.	1.8	10
1833	The Evolution of Olfactory Gene Families in <i>Drosophila</i> and the Genomic Basis of chemical-Ecological Adaptation in <i>Drosophila suzukii</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2297-2311.	1.1	76
1834	Reconfigurable Hardware Accelerator for Profile Hidden Markov Models. <i>Arabian Journal for Science and Engineering</i> , 2016, 41, 3267-3277.	1.1	7

#	ARTICLE	IF	CITATIONS
1835	Structural insight with mutational impact on tyrosinase and PKC- β interaction from Homo sapiens : Molecular modeling and docking studies for melanogenesis, albinism and increased risk for melanoma. <i>Gene</i> , 2016, 592, 99-109.	1.0	5
1836	Mutation Drivers of Immunological Responses to Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 789-798.	1.6	32
1837	Genomic location and expression analysis of expansin gene family reveals the evolutionary and functional significance in <i>Triticum aestivum</i> . <i>Genes and Genomics</i> , 2016, 38, 1021-1030.	0.5	12
1838	Perceptron ensemble of graph-based positive-unlabeled learning for disease gene identification. <i>Computational Biology and Chemistry</i> , 2016, 64, 263-270.	1.1	18
1839	Evolution of Protein Domain Repeats in Metazoa. <i>Molecular Biology and Evolution</i> , 2016, 33, 3170-3182.	3.5	41
1840	An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233.	1.6	278
1841	Computational analysis of translational readthrough proteins in <i>Drosophila</i> and yeast reveals parallels to alternative splicing. <i>Scientific Reports</i> , 2016, 6, 32142.	1.6	9
1842	A direct-sensing galactose chemoreceptor recently evolved in invasive strains of <i>Campylobacter jejuni</i> . <i>Nature Communications</i> , 2016, 7, 13206.	5.8	49
1843	Evolution of Enzyme Superfamilies: Comprehensive Exploration of Sequence-Function Relationships. <i>Biochemistry</i> , 2016, 55, 6375-6388.	1.2	56
1844	Frequent mutations in acetylation and ubiquitination sites suggest novel driver mechanisms of cancer. <i>Genome Medicine</i> , 2016, 8, 55.	3.6	51
1845	Characterisation of the immune compounds in koala milk using a combined transcriptomic and proteomic approach. <i>Scientific Reports</i> , 2016, 6, 35011.	1.6	25
1846	Analyses of Long Non-Coding RNA and mRNA profiling using RNA sequencing during the pre-implantation phases in pig endometrium. <i>Scientific Reports</i> , 2016, 6, 20238.	1.6	150
1847	Combining biophysical methods to analyze the disulfide bond in SH2 domain of C-terminal Src kinase. <i>Biophysics Reports</i> , 2016, 2, 33-43.	0.2	15
1848	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms. <i>Nature Communications</i> , 2016, 7, 11491.	5.8	207
1849	RCD1 homologues and their constituent WWE domain in plants: analysis of conservation through phylogeny methods. <i>Biologia (Poland)</i> , 2016, 71, 642-650.	0.8	3
1850	Computational Identification of Novel Genes: Current and Future Perspectives. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S39950.	1.0	32
1851	Survey of Genes Involved in Biosynthesis, Transport, and Signaling of Phytohormones with Focus on <i>Solanum lycopersicum</i> . <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38425.	1.0	21
1852	Genome-Wide Association Study for Nine Plant Architecture Traits in Sorghum. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0044.	1.6	67

#	ARTICLE	IF	CITATIONS
1853	Draft Genome Sequence of <i>Mycobacterium houstonense</i> Strain ATCC 49403 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
1854	Draft Genome Sequence of <i>Mycobacterium interjectum</i> Strain ATCC 51457 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
1855	Draft Genome Sequence of <i>Mycobacterium acapulcensis</i> Strain CSURP1424. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
1856	Assembling the <i>Setaria italica</i> L. Beauv. genome into nine chromosomes and insights into regions affecting growth and drought tolerance. <i>Scientific Reports</i> , 2016, 6, 35076.	1.6	10
1857	Complete Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Strain RM1285 Isolated from Packaged Chicken. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
1858	The complete genome sequence of the rumen methanogen <i>Methanobrevibacter millerae</i> SM9. <i>Standards in Genomic Sciences</i> , 2016, 11, 49.	1.5	15
1859	Implementation and comparison of kernel-based learning methods to predict metabolic networks. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2016, 5, 26.	1.2	5
1860	A common theme in extracellular fluids of beetles: extracellular superoxide dismutases crucial for balancing ROS in response to microbial challenge. <i>Scientific Reports</i> , 2016, 6, 24082.	1.6	17
1861	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	2.8	233
1862	Different evolutionary patterns of SNPs between domains and unassigned regions in human protein-coding sequences. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1127-1136.	1.0	2
1863	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. <i>BMC Bioinformatics</i> , 2016, 17, 150.	1.2	0
1864	Type VI secretion systems of human gut Bacteroidales segregate into three genetic architectures, two of which are contained on mobile genetic elements. <i>BMC Genomics</i> , 2016, 17, 58.	1.2	121
1865	Recovering complete and draft population genomes from metagenome datasets. <i>Microbiome</i> , 2016, 4, 8.	4.9	254
1866	The standard operating procedure of the DOE-JGI Metagenome Annotation Pipeline (MAP v.4). <i>Standards in Genomic Sciences</i> , 2016, 11, 17.	1.5	161
1867	Microbial Culturomics to Map Halophilic Bacterium in Human Gut: Genome Sequence and Description of <i>Oceanobacillus jeddahense</i> sp. nov.. <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 248-258.	1.0	11
1868	Towards synthesis of monoterpenes and derivatives using synthetic biology. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 37-43.	2.8	89
1869	Mechanisms of transcription factor evolution in Metazoa. <i>Nucleic Acids Research</i> , 2016, 44, 6287-6297.	6.5	60
1870	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2016, 19, 34-44.	0.4	22

#	ARTICLE	IF	CITATIONS
1871	Amplification and function analysis of N6-adenine-specific DNA methyltransferase gene in <i>Nilaparvata lugens</i> . <i>Journal of Integrative Agriculture</i> , 2016, 15, 591-599.	1.7	2
1872	De novo assembly of the blunt snout bream (<i>Megalobrama amblycephala</i>) gill transcriptome to identify ammonia exposure associated microRNAs and their targets. <i>Results in Immunology</i> , 2016, 6, 21-27.	2.2	12
1873	Computational identification and systematic classification of novel GRAS genes in <i>Isatis indigotica</i> . <i>Chinese Journal of Natural Medicines</i> , 2016, 14, 161-176.	0.7	9
1874	Characterisation of a novel enterobacteria phage, CAjan, isolated from rat faeces. <i>Archives of Virology</i> , 2016, 161, 2219-2226.	0.9	31
1875	Transcriptome sequencing based annotation and homologous evidence based scaffolding of <i>Anguilla japonica</i> draft genome. <i>BMC Genomics</i> , 2016, 17, 13.	1.2	9
1876	Genome-wide analysis of long non-coding RNAs at early stage of skin pigmentation in goats (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	139
1877	ChlamyNET: a <i>Chlamydomonas</i> gene co-expression network reveals global properties of the transcriptome and the early setup of key co-expression patterns in the green lineage. <i>BMC Genomics</i> , 2016, 17, 227.	1.2	45
1878	Red Sea Atlantis II brine pool nitrilase with unique thermostability profile and heavy metal tolerance. <i>BMC Biotechnology</i> , 2016, 16, 14.	1.7	19
1879	Transcriptome analysis reveals a ribosome constituents disorder involved in the RPL5 downregulated zebrafish model of Diamond-Blackfan anemia. <i>BMC Medical Genomics</i> , 2016, 9, 13.	0.7	32
1880	A <i>Colletotrichum graminicola</i> mutant deficient in the establishment of biotrophy reveals early transcriptional events in the maize anthracnose disease interaction. <i>BMC Genomics</i> , 2016, 17, 202.	1.2	33
1881	Comparative transcript profiling of resistant and susceptible peanut post-harvest seeds in response to aflatoxin production by <i>Aspergillus flavus</i> . <i>BMC Plant Biology</i> , 2016, 16, 54.	1.6	41
1882	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. <i>Standards in Genomic Sciences</i> , 2016, 11, 9.	1.5	2
1883	Cloning, characterization, and expression analysis of LGP2 cDNA from goose, <i>Anser cygnoides</i> . <i>Poultry Science</i> , 2016, 95, 2290-2296.	1.5	9
1884	Proteomic Identification of Putative MicroRNA394 Target Genes in <i>Arabidopsis thaliana</i> Identifies Major Latex Protein Family Members Critical for Normal Development. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2033-2047.	2.5	39
1885	Genome-Based Selection and Characterization of <i>Fusarium circinatum</i> -Specific Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 631-639.	0.8	14
1886	Why reinvent the wheel? Building new proteins based on ready-made parts. <i>Protein Science</i> , 2016, 25, 1179-1187.	3.1	33
1887	PhyloPro2.0: a database for the dynamic exploration of phylogenetically conserved proteins and their domain architectures across the Eukarya. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw013.	1.4	12
1888	<i>OsSIDP366</i> , a DUF1644 gene, positively regulates responses to drought and salt stresses in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 492-502.	4.1	54

#	ARTICLE	IF	CITATIONS
1889	Origin and mechanism of crassulacean acid metabolism in orchids as implied by comparative transcriptomics and genomics of the carbon fixation pathway. <i>Plant Journal</i> , 2016, 86, 175-185.	2.8	45
1890	Mutation screening of SCN2A in schizophrenia and identification of a novel loss-of-function mutation. <i>Psychiatric Genetics</i> , 2016, 26, 60-65.	0.6	45
1891	Unravelling the one-carbon metabolism of the acetogen <i>Sporomusa</i> strain <i>ScpA</i> by genome and proteome analysis. <i>Environmental Microbiology</i> , 2016, 18, 2843-2855.	1.8	25
1892	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. <i>Environmental Microbiology</i> , 2016, 18, 2825-2842.	1.8	72
1893	Functional annotation of introns in mitochondrial genome – a brief review. <i>Mitochondrial DNA</i> , 2016, 27, 811-814.	0.6	3
1894	Orphan Crops Browser: a bridge between model and orphan crops. <i>Molecular Breeding</i> , 2016, 36, 9.	1.0	18
1895	Continuous colorimetric screening assays for the detection of specific L- or D-amino acid transaminases in enzyme libraries. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 397-408.	1.7	10
1896	Quantitative metabolome, proteome and transcriptome analysis of midgut and fat body tissues in the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, and insights into pheromone biosynthesis. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 70, 170-183.	1.2	37
1897	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. <i>Plant Physiology</i> , 2016, 170, 1878-1894.	2.3	63
1898	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	6.5	21
1899	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. <i>ISME Journal</i> , 2016, 10, 1902-1914.	4.4	66
1900	ELM 2016 data update and new functionality of the eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2016, 44, D294-D300.	6.5	289
1901	HGTree: database of horizontally transferred genes determined by tree reconciliation. <i>Nucleic Acids Research</i> , 2016, 44, D610-D619.	6.5	45
1902	A functional genomics tool for the Pacific bluefin tuna: Development of a 44K oligonucleotide microarray from whole-genome sequencing data for global transcriptome analysis. <i>Gene</i> , 2016, 576, 603-609.	1.0	10
1903	Structures of replication initiation proteins from staphylococcal antibiotic resistance plasmids reveal protein asymmetry and flexibility are necessary for replication. <i>Nucleic Acids Research</i> , 2016, 44, 2417-2428.	6.5	22
1904	De novo analysis of transcriptome reveals genes associated with leaf abscission in sugarcane (<i>Saccharum officinarum</i> L.). <i>BMC Genomics</i> , 2016, 17, 195.	1.2	51
1905	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. <i>Nucleic Acids Research</i> , 2016, 44, D410-D414.	6.5	4
1906	Transmembrane START domain proteins: in silico identification, characterization and expression analysis under stress conditions in chickpea (<i>Cicer arietinum</i> L.). <i>Plant Signaling and Behavior</i> , 2016, 11, e992698.	1.2	8

#	ARTICLE	IF	CITATIONS
1907	The <i>Pseudomonas aeruginosa</i> PAO1 Two-Component Regulator CarSR Regulates Calcium Homeostasis and Calcium-Induced Virulence Factor Production through Its Regulatory Targets CarO and CarP. <i>Journal of Bacteriology</i> , 2016, 198, 951-963.	1.0	44
1908	Evolutionary distinctiveness of fatty acid and polyketide synthesis in eukaryotes. <i>ISME Journal</i> , 2016, 10, 1877-1890.	4.4	72
1909	New features of desiccation tolerance in the lichen photobiont <i>Trebouxia gelatinosa</i> are revealed by a transcriptomic approach. <i>Plant Molecular Biology</i> , 2016, 91, 319-339.	2.0	69
1910	Identification and characterization of Lateral Organ Boundaries Domain genes in mulberry, <i>Morus notabilis</i> . <i>Meta Gene</i> , 2016, 8, 44-50.	0.3	15
1911	Signaling via the CytoR/JAK/STAT/SOCS pathway: Emergence during evolution. <i>Molecular Immunology</i> , 2016, 71, 166-175.	1.0	27
1912	The mid-developmental transition and the evolution of animal body plans. <i>Nature</i> , 2016, 531, 637-641.	13.7	231
1913	First structure of archaeal branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> specific for L-amino acids and R-amines. <i>Extremophiles</i> , 2016, 20, 215-225.	0.9	28
1914	Exome sequencing reveals genetic differentiation due to high-altitude adaptation in the Tibetan cashmere goat (<i>Capra hircus</i>). <i>BMC Genomics</i> , 2016, 17, 122.	1.2	87
1915	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
1916	Knockdown of Five Genes Encoding Uncharacterized Proteins Inhibits <i>Entamoeba histolytica</i> Phagocytosis of Dead Host Cells. <i>Infection and Immunity</i> , 2016, 84, 1045-1053.	1.0	10
1917	Complete genome sequence and description of <i>Lactococcus garvieae</i> M14 isolated from Algerian fermented milk. <i>New Microbes and New Infections</i> , 2016, 10, 122-131.	0.8	9
1918	Systematic Analysis of Intracellular-targeting Antimicrobial Peptides, Bactenecin 7, Hybrid of Pleurocidin and Dermaseptin, Proline-Arginine-rich Peptide, and Lactoferricin B, by Using <i>Escherichia coli</i> Proteome Microarrays. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1837-1847.	2.5	55
1919	GprotPRED: Annotation of G α_1 , G α_2 and G α_3 subunits of G-proteins using profile Hidden Markov Models (pHMMs) and application to proteomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 435-440.	1.1	2
1920	Novel insights on ENTH domain-containing proteins in apicomplexan parasites. <i>Parasitology Research</i> , 2016, 115, 2191-2202.	0.6	3
1921	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. <i>Biotechnology Advances</i> , 2016, 34, 663-686.	6.0	30
1922	Transcript Abundance of Putative Lipid Phosphate Phosphatases During Development of <i>Trypanosoma brucei</i> in the Tsetse Fly. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 890-893.	0.6	4
1923	Transcriptome analysis reveals long noncoding RNAs involved in fiber development in cotton (<i>Gossypium arboreum</i>). <i>Science China Life Sciences</i> , 2016, 59, 164-171.	2.3	78
1924	Mte1 interacts with Mph1 and promotes crossover recombination and telomere maintenance. <i>Genes and Development</i> , 2016, 30, 700-717.	2.7	27

#	ARTICLE	IF	CITATIONS
1925	Comparative analysis of genome-wide Mlo gene family in <i>Cajanus cajan</i> and <i>Phaseolus vulgaris</i> . <i>Genetica</i> , 2016, 144, 229-241.	0.5	3
1926	Bacterial ferrous iron transport: the Feo system. <i>FEMS Microbiology Reviews</i> , 2016, 40, 273-298.	3.9	301
1927	The Female Post-Mating Response Requires Genes Expressed in the Secondary Cells of the Male Accessory Gland in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 202, 1029-1041.	1.2	61
1928	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	9.4	235
1929	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	6.5	5,391
1930	The role of the intestinal microbiota in type 1 diabetes mellitus. <i>Nature Reviews Endocrinology</i> , 2016, 12, 154-167.	4.3	335
1931	Detecting reliable non interacting proteins (NIPs) significantly enhancing the computational prediction of protein-protein interactions using machine learning methods. <i>Molecular BioSystems</i> , 2016, 12, 778-785.	2.9	5
1932	Recruitment of Factor H as a Novel Complement Evasion Strategy for Blood-Stage <i>Plasmodium falciparum</i> Infection. <i>Journal of Immunology</i> , 2016, 196, 1239-1248.	0.4	90
1933	Genome-wide analysis and expression patterns of ZF-HD transcription factors under different developmental tissues and abiotic stresses in Chinese cabbage. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1451-1464.	1.0	53
1934	Complete genome analysis of <i>Clostridium bornimense</i> strain M2/40T: A new acidogenic <i>Clostridium</i> species isolated from a mesophilic two-phase laboratory-scale biogas reactor. <i>Journal of Biotechnology</i> , 2016, 232, 38-49.	1.9	19
1935	Overexpression of lycopene β -cyclase gene from <i>Lycium chinense</i> confers tolerance to chilling stress in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2016, 576, 395-403.	1.0	24
1936	Genomic survey and expression analysis of DNA repair genes in the genus <i>Leptospira</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 703-722.	1.0	8
1937	Structural disorder: a tool for housekeeping proteins performing tissue-specific interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1930-1945.	2.0	4
1938	Using THz Spectroscopy, Evolutionary Network Analysis Methods, and MD Simulation to Map the Evolution of Allosteric Communication Pathways in c-Type Lysozymes. <i>Molecular Biology and Evolution</i> , 2016, 33, 40-61.	3.5	6
1939	Genome-wide identification and comparative analysis of the TUBBY-like protein gene family in maize. <i>Genes and Genomics</i> , 2016, 38, 25-36.	0.5	24
1940	Single-cell genomics of uncultivated deep-branching magnetotactic bacteria reveals a conserved set of magnetosome genes. <i>Environmental Microbiology</i> , 2016, 18, 21-37.	1.8	115
1941	Deciphering the cause of evolutionary variance within intrinsically disordered regions in human proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 233-249.	2.0	9
1942	Protein complex analysis: From raw protein lists to protein interaction networks. <i>Mass Spectrometry Reviews</i> , 2017, 36, 600-614.	2.8	22

#	ARTICLE	IF	CITATIONS
1943	Nucleoplasmin-like domain of FKBP39 from <i>Drosophila melanogaster</i> forms a tetramer with partly disordered tentacle-like C-terminal segments. <i>Scientific Reports</i> , 2017, 7, 40405.	1.6	7
1944	Mutations and interactions in human ER α and bZIP proteins: An in silico approach for cell signaling in breast oncology. <i>Gene</i> , 2017, 610, 90-102.	1.0	2
1945	Draft genome sequence of a human-associated isolate of <i>Haloferax alexandrinus</i> strain Arc-hr, an extremely halophilic archaea. <i>New Microbes and New Infections</i> , 2017, 15, 44-45.	0.8	10
1946	De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. <i>Scientific Reports</i> , 2017, 7, 40472.	1.6	18
1947	Molecular Dynamics Simulations for Deciphering the Structural Basis of Recognition of Pre-let-7 miRNAs by LIN28. <i>Biochemistry</i> , 2017, 56, 723-735.	1.2	5
1948	A comparative genomic analysis of putative pathogenicity genes in the host-specific sibling species <i>Colletotrichum graminicola</i> and <i>Colletotrichum sublineola</i> . <i>BMC Genomics</i> , 2017, 18, 67.	1.2	53
1949	Structural insight, mutation and interactions in human Beta-catenin and SOX17 protein: A molecular-level outlook for organogenesis. <i>Gene</i> , 2017, 610, 118-126.	1.0	7
1950	Binding of NADP ⁺ triggers an open-to-closed transition in a mycobacterial FabG β -ketoacyl-ACP reductase. <i>Biochemical Journal</i> , 2017, 474, 907-921.	1.7	12
1951	Predicting Beta Barrel Transmembrane Proteins Using HMMs. <i>Methods in Molecular Biology</i> , 2017, 1552, 43-61.	0.4	3
1952	Amino acid transporter SLC38A3 promotes metastasis of non-small cell lung cancer cells by activating PDK1. <i>Cancer Letters</i> , 2017, 393, 8-15.	3.2	38
1953	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
1954	High quality draft genome sequence of <i>Janthinobacterium psychrotolerans</i> sp. nov., isolated from a frozen freshwater pond. <i>Standards in Genomic Sciences</i> , 2017, 12, 8.	1.5	28
1955	Genome-wide identification and expression analysis of the GRAS family proteins in <i>Medicago truncatula</i> . <i>Acta Physiologiae Plantarum</i> , 2017, 39, 1.	1.0	20
1956	Genomic Sequence of <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> HS:19 Penner Serotype Reference Strain RM3420. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1957	Role of Modular Polyketide Synthases in the Production of Polyether Ladder Compounds in <i>Ciguatoxin</i> -Producing <i>Gambierdiscus polynesiensis</i> and <i>G. excentricus</i> (Dinophyceae). <i>Journal of Eukaryotic Microbiology</i> , 2017, 64, 691-706.	0.8	31
1958	Detection of putative polysaccharide biosynthesis genes in <i>Azospirillum brasilense</i> strains from serogroups I and II. <i>Russian Journal of Genetics</i> , 2017, 53, 39-48.	0.2	1
1959	Genome-wide analysis and expression patterns of the NAC transcription factor family in <i>Medicago truncatula</i> . <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 343-356.	1.4	40
1960	Lateral Gene Transfer in the Adaptation of the Anaerobic Parasite <i>Blastocystis</i> to the Gut. <i>Current Biology</i> , 2017, 27, 807-820.	1.8	94

#	ARTICLE	IF	CITATIONS
1961	The MiiA motif is a common marker present in polytopic surface proteins of oral and urinary tract invasive bacteria. <i>Infection, Genetics and Evolution</i> , 2017, 49, 283-292.	1.0	2
1962	Complete Annotated Genome Sequences of Three <i>Campylobacter jejuni</i> Strains Isolated from Naturally Colonized Farm-Raised Chickens. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
1963	QuickProbs 2: Towards rapid construction of high-quality alignments of large protein families. <i>Scientific Reports</i> , 2017, 7, 41553.	1.6	9
1964	Discovery of a novel oocyte-specific KrÄ½ppel-associated box domain-containing zinc finger protein required for early embryogenesis in cattle. <i>Mechanisms of Development</i> , 2017, 144, 103-112.	1.7	8
1965	Seasonal patterns in Arctic prasinophytes and inferred ecology of <i>Bathycoccus</i> unveiled in an Arctic winter metagenome. <i>ISME Journal</i> , 2017, 11, 1372-1385.	4.4	54
1966	Identification and functional analysis of the ICK gene family in maize. <i>Scientific Reports</i> , 2017, 7, 43818.	1.6	6
1967	Domain prediction with probabilistic directional context. <i>Bioinformatics</i> , 2017, 33, 2471-2478.	1.8	4
1968	Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to <i>Mycobacterium tuberculosis</i> . <i>BMC Bioinformatics</i> , 2017, 18, 201.	1.2	14
1969	Transcriptome analyses of differential gene expression in the bursa of Fabricius between Silky Fowl and White Leghorn. <i>Scientific Reports</i> , 2017, 7, 45959.	1.6	18
1970	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. <i>Scientific Reports</i> , 2017, 7, 46562.	1.6	6
1971	Genome-wide identification, characterization of the MADS-box gene family in Chinese jujube and their involvement in flower development. <i>Scientific Reports</i> , 2017, 7, 1025.	1.6	42
1972	Transcriptomic changes in an animal-bacterial symbiosis under modeled microgravity conditions. <i>Scientific Reports</i> , 2017, 7, 46318.	1.6	19
1973	ThreaDomEx: a unified platform for predicting continuous and discontinuous protein domains by multiple-threading and segment assembly. <i>Nucleic Acids Research</i> , 2017, 45, W400-W407.	6.5	25
1974	Transposable Element Misregulation Is Linked to the Divergence between Parental piRNA Pathways in <i>Drosophila</i> Hybrids. <i>Genome Biology and Evolution</i> , 2017, 9, 1450-1470.	1.1	26
1975	Identification of factors required for m ⁶ A mRNA methylation in <i>Arabidopsis</i> reveals a role for the conserved E3 ubiquitin ligase HAKAI. <i>New Phytologist</i> , 2017, 215, 157-172.	3.5	301
1976	Draft Genome Sequence of <i>Mycobacterium boenickei</i> CIP 107829. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
1977	Comparative transcriptomic analysis of <i>Gardnerella vaginalis</i> biofilms vs. planktonic cultures using RNA-seq. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 3.	2.9	66
1978	The s48/45 six-cysteine proteins: mediators of interaction throughout the <i>Plasmodium</i> life cycle. <i>International Journal for Parasitology</i> , 2017, 47, 409-423.	1.3	45

#	ARTICLE	IF	CITATIONS
1979	Identification of non-coding and coding RNAs in porcine endometrium. <i>Genomics</i> , 2017, 109, 43-50.	1.3	33
1980	Genomic Database Searching. <i>Methods in Molecular Biology</i> , 2017, 1525, 225-269.	0.4	2
1981	Loss of the <i>ssrA</i> genome island led to partial debromination in the PBDE respiring <i>Dehalococcoides mccartyi</i> strain GY50. <i>Environmental Microbiology</i> , 2017, 19, 2906-2915.	1.8	27
1982	Complete genome of a metabolically-diverse marine bacterium <i>Shewanella japonica</i> KCTC 22435 T. <i>Marine Genomics</i> , 2017, 35, 39-42.	0.4	3
1983	On patterns and re-use in bioinformatics databases. <i>Bioinformatics</i> , 2017, 33, 2731-2736.	1.8	6
1984	Protein contact prediction by using information theory. <i>Journal of the Korean Physical Society</i> , 2017, 70, 876-879.	0.3	3
1985	Genome-Wide Identification of Auxin Response Factor (ARF) Genes Family and its Tissue-Specific Prominent Expression in Pineapple (<i>Ananas comosus</i>). <i>Tropical Plant Biology</i> , 2017, 10, 86-96.	1.0	42
1986	In vitro and in silico characterization of metagenomic soil-derived cellulases capable of hydrolyzing oil palm empty fruit bunch. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2017, 15, 55-62.	2.1	8
1987	<i>Mycobacterium massilipolynesiensis</i> sp. nov., a rapidly-growing mycobacterium of medical interest related to <i>Mycobacterium phlei</i> . <i>Scientific Reports</i> , 2017, 7, 40443.	1.6	6
1988	The Landscape of Isoform Switches in Human Cancers. <i>Molecular Cancer Research</i> , 2017, 15, 1206-1220.	1.5	208
1989	Genome-wide identification and phylogenetic, comparative genomic, alternative splicing, and expression analyses of TCP genes in plants. <i>Plant Gene</i> , 2017, 12, 23-32.	1.4	6
1990	Perfecting prediction of mutational impact on the aggregation propensity of the <i>ALS</i> associated hnRNP2 prion-like protein. <i>FEBS Letters</i> , 2017, 591, 1966-1971.	1.3	13
1991	Crystal structures of $\hat{1}$ -carboxysome shell protein CcmP: ligand binding correlates with the closed or open central pore. <i>Journal of Experimental Botany</i> , 2017, 68, 3857-3867.	2.4	40
1992	Testing for the Occurrence of Selective Episodes During the Divergence of Otophysan Fishes: Insights from Mitogenomics. <i>Journal of Molecular Evolution</i> , 2017, 84, 162-173.	0.8	5
1993	Comparative genomics of <i>Vibrio campbellii</i> strains and core species of the <i>Vibrio Harveyi</i> clade. <i>Scientific Reports</i> , 2017, 7, 41394.	1.6	42
1994	Structural insights into ligand binding of PGRP1 splice variants in Chinese giant salamander (<i>Andrias</i>) Tj ETQq1 1 0.784314 rgBT /Ove 2017, 23, 135.	0.8	2
1996	Crystal Structure of the Extracellular Domain of the Human Dendritic Cell Surface Marker CD83. <i>Journal of Molecular Biology</i> , 2017, 429, 1227-1243.	2.0	11
1997	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins " extended Database. <i>Journal of Molecular Biology</i> , 2017, 429, 348-355.	2.0	85

#	ARTICLE	IF	CITATIONS
1998	The evolution of function within the Nudix homology clan. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 775-811.	1.5	53
1999	Curd development associated gene (CDAG1) in cauliflower (<i>Brassica oleracea</i> L. var. botrytis) could result in enlarged organ size and increased biomass. <i>Plant Science</i> , 2017, 254, 82-94.	1.7	13
2000	Carboxyl-terminal Tail-mediated Homodimerizations of Sphingomyelin Synthases Are Responsible for Efficient Export from the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2017, 292, 1122-1141.	1.6	8
2001	Dynein light chain family genes in 15 plant species: Identification, evolution and expression profiles. <i>Plant Science</i> , 2017, 254, 70-81.	1.7	14
2002	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. <i>Nature Communications</i> , 2017, 8, 1167.	5.8	40
2003	Whole-genome comparison of urinary pathogenic <i>Escherichia coli</i> and faecal isolates of UTI patients and healthy controls. <i>International Journal of Medical Microbiology</i> , 2017, 307, 497-507.	1.5	57
2004	Comparative transcriptome and histological analyses provide insights into the prenatal skin pigmentation in goat (<i>Capra hircus</i>). <i>Physiological Genomics</i> , 2017, 49, 703-711.	1.0	8
2005	Genomic characterization, phylogenetic analysis, and identification of virulence factors in <i>Aerococcus sanguinicola</i> and <i>Aerococcus urinae</i> strains isolated from infection episodes. <i>Microbial Pathogenesis</i> , 2017, 112, 327-340.	1.3	14
2006	Characterization of <i>Trypanosoma cruzi</i> MutY DNA glycosylase ortholog and its role in oxidative stress response. <i>Infection, Genetics and Evolution</i> , 2017, 55, 332-342.	1.0	6
2008	Oligo(<i>cis</i> -1,4-isoprene) aldehyde-oxidizing dehydrogenases of the rubber-degrading bacterium <i>Gordonia polyisoprenivorans</i> VH2. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7945-7960.	1.7	10
2009	THE PATTERN RECOGNITION OF PROBABILITY DISTRIBUTIONS OF AMINO ACIDS IN PROTEIN FAMILIES. , 2017, , 29-50.		1
2010	Both modular and single-domain Type I polyketide synthases are expressed in the brevetoxin-producing dinoflagellate, <i>Karenia brevis</i> (Dinophyceae). <i>Journal of Phycology</i> , 2017, 53, 1325-1339.	1.0	28
2011	Comparative transcriptomics reveal developmental turning points during embryogenesis of a hemimetabolous insect, the damselfly <i>Ischnura elegans</i> . <i>Scientific Reports</i> , 2017, 7, 13547.	1.6	24
2012	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	3.3	111
2013	Draft Genome Sequences of 25 <i>Listeria monocytogenes</i> Isolates Associated with Human Clinical Listeriosis in Ireland. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
2014	Active site gate of M32 carboxypeptidases illuminated by crystal structure and molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1406-1415.	1.1	8
2015	A Bacterial Multidomain NAD-Independent α -Lactate Dehydrogenase Utilizes Flavin Adenine Dinucleotide and Fe-S Clusters as Cofactors and Quinone as an Electron Acceptor for α -Lactate Oxidation. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	12
2016	Genome-wide identification and tissue-specific expression analysis of nucleotide binding site-leucine rich repeat gene family in <i>Cicer arietinum</i> (kabuli chickpea). <i>Genomics Data</i> , 2017, 14, 24-31.	1.3	16

#	ARTICLE	IF	CITATIONS
2017	Shear force-based genetic screen reveals negative regulators of cell adhesion and protrusive activity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7727-E7736.	3.3	19
2018	Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. Structure, 2017, 25, 1598-1610.e3.	1.6	105
2019	Metagenomics for Monitoring Environmental Biodiversity: Challenges, Progress, and Opportunities. Health Information Science, 2017, , 73-87.	0.3	2
2020	Genome reconstruction in <i>Cynara cardunculus</i> taxa gains access to chromosome-scale DNA variation. Scientific Reports, 2017, 7, 5617.	1.6	30
2021	Characterization of Phospholipid: Diacylglycerol Acyltransferases (PDATs) from <i>Camelina sativa</i> and Their Roles in Stress Responses. Biology Open, 2017, 6, 1024-1034.	0.6	31
2022	Isolation and characterization of a novel endo- β -1,4-glucanase from a metagenomic library of the black-goat rumen. Brazilian Journal of Microbiology, 2017, 48, 801-808.	0.8	22
2023	DnrI of <i>Streptomyces peucetius</i> binds to the resistance genes, <i>drrAB</i> and <i>drrC</i> but is activated by daunorubicin. Journal of Basic Microbiology, 2017, 57, 862-872.	1.8	7
2024	Draft Genome Sequence of <i>Mycobacterium colombiense</i> . Genome Announcements, 2017, 5, .	0.8	0
2025	TbIRK is a signature sequence free potassium channel from <i>Trypanosoma brucei</i> locating to acidocalcisomes. Scientific Reports, 2017, 7, 656.	1.6	13
2026	Predicting the functional consequences of non-synonymous single nucleotide polymorphisms in IL8 gene. Scientific Reports, 2017, 7, 6525.	1.6	75
2027	Using RNA sequencing to identify putative competing endogenous RNAs (ceRNAs) potentially regulating fat metabolism in bovine liver. Scientific Reports, 2017, 7, 6396.	1.6	65
2028	ET&C Best Paper of 2016. Environmental Toxicology and Chemistry, 2017, 36, 1693-1694.	2.2	0
2029	In silico characterization of tandem repeats in <i>Trichophyton rubrum</i> and related dermatophytes provides new insights into their role in pathogenesis. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	4
2030	Long noncoding RNAs that respond to <i>Fusarium oxysporum</i> infection in 'Cavendish' banana (<i>Musa</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.6	22
2031	Genomic assessment in <i>Lactobacillus plantarum</i> links the butyrogenic pathway with glutamine metabolism. Scientific Reports, 2017, 7, 15975.	1.6	25
2033	Complete Genome Sequences of <i>Vibrio cholerae</i> -Specific Bacteriophages 24 and X29. Genome Announcements, 2017, 5, .	0.8	6
2034	What Defines the 'Kingdom' Fungi?. Microbiology Spectrum, 2017, 5, .	1.2	59
2035	Massive expansion and differential evolution of small heat shock proteins with wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.6	17

#	ARTICLE	IF	CITATIONS
2036	Long noncoding RNA expression profile changes associated with dietary energy in the sheep testis during sexual maturation. <i>Scientific Reports</i> , 2017, 7, 5180.	1.6	51
2037	The marine sulfate reducer <i>Desulfobacterium autotrophicum</i> HRM2 can switch between low and high apparent half-saturation constants for dissimilatory sulfate reduction. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	24
2038	Transcriptomic profiling of <i>Melilotus albus</i> near-isogenic lines contrasting for coumarin content. <i>Scientific Reports</i> , 2017, 7, 4577.	1.6	21
2039	Insecticide resistance and resistance mechanisms in bed bugs, <i>Cimex</i> spp. (Hemiptera: Cimicidae). <i>Parasites and Vectors</i> , 2017, 10, 318.	1.0	159
2040	In silico approach to designing rational metagenomic libraries for functional studies. <i>BMC Bioinformatics</i> , 2017, 18, 267.	1.2	19
2041	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	1.2	33
2042	Genome-wide analysis of UDP-glycosyltransferase super family in <i>Brassica rapa</i> and <i>Brassica oleracea</i> reveals its evolutionary history and functional characterization. <i>BMC Genomics</i> , 2017, 18, 474.	1.2	54
2043	Complete genome sequence of <i>Pseudoalteromonas</i> phage vB_PspS-H40/1 (formerly H40/1) that infects <i>Pseudoalteromonas</i> sp. strain H40 and is used as biological tracer in hydrological transport studies. <i>Standards in Genomic Sciences</i> , 2017, 12, 20.	1.5	8
2044	Lipidomics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	10
2045	Virus-host relationships of marine single-celled eukaryotes resolved from metatranscriptomics. <i>Nature Communications</i> , 2017, 8, 16054.	5.8	100
2046	Computational Functional Analysis of Lipid Metabolic Enzymes. <i>Methods in Molecular Biology</i> , 2017, 1609, 195-216.	0.4	2
2047	Discovery of a novel insecticidal protein from <i>Chromobacterium piscinae</i> , with activity against Western Corn Rootworm, <i>Diabrotica virgifera virgifera</i> . <i>Journal of Invertebrate Pathology</i> , 2017, 142, 34-43.	1.5	25
2048	Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. <i>Indian Journal of Microbiology</i> , 2017, 57, 23-38.	1.5	21
2049	Genome-wide identification and expression analysis of sulphate transporter (SULTR) genes under sulfur deficiency in <i>Brachypodium distachyon</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 263-273.	0.9	5
2050	Isolation and characterization of a novel glycosyl hydrolase family 74 (GH74) cellulase from the black goat rumen metagenomic library. <i>Folia Microbiologica</i> , 2017, 62, 175-181.	1.1	19
2051	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by high-depth physical mapping and short-read DNA sequencing strategies. <i>Plant Journal</i> , 2017, 89, 617-635.	2.8	115
2052	Structural and functional annotation of human FAM26F: A multifaceted protein having a critical role in the immune system. <i>Gene</i> , 2017, 597, 66-75.	1.0	20
2053	Overexpression of PSK1, a SKP1-like gene homologue, from <i>Paeonia suffruticosa</i> , confers salinity tolerance in <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2017, 36, 151-162.	2.8	20

#	ARTICLE	IF	CITATIONS
2054	Genome-wide identification, characterisation and expression profiles of calcium-dependent protein kinase genes in barley (<i>Hordeum vulgare</i> L.). <i>Journal of Applied Genetics</i> , 2017, 58, 11-22.	1.0	17
2055	Thiol oxidation of hemolymph proteins in oysters <i>Crassostrea brasiliana</i> as markers of oxidative damage induced by urban sewage exposure. <i>Environmental Toxicology and Chemistry</i> , 2017, 36, 1833-1845.	2.2	9
2056	Draft genome sequence of pectic polysaccharide-degrading moderate thermophilic bacterium <i>Geobacillus thermodenitrificans</i> DSM 101594. <i>Brazilian Journal of Microbiology</i> , 2017, 48, 7-8.	0.8	6
2057	High-throughput metagenomic analysis of petroleum-contaminated soil microbiome reveals the versatility in xenobiotic aromatics metabolism. <i>Journal of Environmental Sciences</i> , 2017, 56, 25-35.	3.2	50
2058	Alternative Splicing May Not Be the Key to Proteome Complexity. <i>Trends in Biochemical Sciences</i> , 2017, 42, 98-110.	3.7	277
2059	Characterization of the <i>Xylella fastidiosa</i> PD1311 gene mutant and its suppression of Pierce's disease on grapevines. <i>Molecular Plant Pathology</i> , 2017, 18, 684-694.	2.0	8
2060	Metagenomic analysis reveals unusually high incidence of proteorhodopsin genes in the ultraoligotrophic <i>E</i> astern <i>M</i> editerranean <i>S</i> ea. <i>Environmental Microbiology</i> , 2017, 19, 1077-1090.	1.8	31
2061	A metagenome-derived thermostable β -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. <i>Scientific Reports</i> , 2017, 7, 17306.	1.6	15
2062	Complete Genome Sequences of Seven <i>Vibrio cholerae</i> Phages Isolated in China. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
2063	Genome-Based Analyses of Six Hexacorallian Species Reject the "Naked Coral" Hypothesis. <i>Genome Biology and Evolution</i> , 2017, 9, 2626-2634.	1.1	8
2064	De novo genome assembly and annotation of Australia's largest freshwater fish, the Murray cod (<i>Maccullochella peelii</i>), from Illumina and Nanopore sequencing read. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	57
2065	9 Delivery of iron-sulfur clusters to recipient proteins: the role of chaperone and cochaperone proteins. , 2017, , 205-226.		1
2066	What Defines the "Kingdom" Fungi?. , 2017, , 57-77.		6
2067	Transcriptome-Wide Identification, Classification, and Characterization of AP2/ERF Family Genes in the Desert Moss <i>Syntrichia caninervis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 262.	1.7	25
2068	A Transcriptomics and Comparative Genomics Analysis Reveals Gene Families with a Role in Body Plan Complexity. <i>Frontiers in Plant Science</i> , 2017, 8, 869.	1.7	5
2069	Evolution of Daily Gene Co-expression Patterns from Algae to Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 1217.	1.7	26
2070	Comparative Genomics of <i>Ralstonia solanacearum</i> Identifies Candidate Genes Associated with Cool Virulence. <i>Frontiers in Plant Science</i> , 2017, 8, 1565.	1.7	25
2071	Metagenomic Analysis of a Complex Community Present in Pond Sediment. <i>Journal of Genomics</i> , 2017, 5, 36-47.	0.6	12

#	ARTICLE	IF	CITATIONS
2072	The purplish bifurcate mussel <i>Mytilisepta virgata</i> gene expression atlas reveals a remarkable tissue functional specialization. <i>BMC Genomics</i> , 2017, 18, 590.	1.2	32
2073	A Transcriptome Survey Spanning Life Stages and Sexes of the Harlequin Bug, <i>Murgantia histrionica</i> . <i>Insects</i> , 2017, 8, 55.	1.0	20
2074	Integrated analysis of coding genes and non-coding RNAs during hair follicle cycle of cashmere goat (<i>Capra hircus</i>). <i>BMC Genomics</i> , 2017, 18, 767.	1.2	119
2075	Genome-Wide Analysis Reveals Extensive Changes in LncRNAs during Skeletal Muscle Development in Hu Sheep. <i>Genes</i> , 2017, 8, 191.	1.0	41
2076	c-di-AMP: An Essential Molecule in the Signaling Pathways that Regulate the Viability and Virulence of Gram-Positive Bacteria. <i>Genes</i> , 2017, 8, 197.	1.0	97
2077	Hybrid Sequencing of Full-Length cDNA Transcripts of Stems and Leaves in <i>Dendrobium officinale</i> . <i>Genes</i> , 2017, 8, 257.	1.0	20
2078	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	2.8	121
2079	Genome-Wide Analysis Suggests the Relaxed Purifying Selection Affect the Evolution of WOX Genes in <i>Pyrus bretschneideri</i> , <i>Prunus persica</i> , <i>Prunus mume</i> , and <i>Fragaria vesca</i> . <i>Frontiers in Genetics</i> , 2017, 8, 78.	1.1	68
2080	A Preliminary List of Horizontally Transferred Genes in Prokaryotes Determined by Tree Reconstruction and Reconciliation. <i>Frontiers in Genetics</i> , 2017, 8, 112.	1.1	11
2081	Identification of New Features from Known Bacterial Protective Vaccine Antigens Enhances Rational Vaccine Design. <i>Frontiers in Immunology</i> , 2017, 8, 1382.	2.2	25
2082	In silico Prediction, in vitro Antibacterial Spectrum, and Physicochemical Properties of a Putative Bacteriocin Produced by <i>Lactobacillus rhamnosus</i> Strain L156.4. <i>Frontiers in Microbiology</i> , 2017, 8, 876.	1.5	29
2083	Genome-Wide Analyses Reveal Genes Subject to Positive Selection in <i>Pasteurella multocida</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 961.	1.5	36
2084	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	1.5	15
2085	The Different Faces of Rolling-Circle Replication and Its Multifunctional Initiator Proteins. <i>Frontiers in Microbiology</i> , 2017, 8, 2353.	1.5	82
2086	Niche Partitioning of the N Cycling Microbial Community of an Offshore Oxygen Deficient Zone. <i>Frontiers in Microbiology</i> , 2017, 8, 2384.	1.5	60
2087	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and <i>Brassica</i> species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	1.2	37
2088	Transcriptome Analysis of <i>Taxillus chinensis</i> (DC.) Danser Seeds in Response to Water Loss. <i>PLoS ONE</i> , 2017, 12, e0169177.	1.1	31
2089	Characterisation and genome sequence of the lytic <i>Acinetobacter baumannii</i> bacteriophage vB_AbaS_Loki. <i>PLoS ONE</i> , 2017, 12, e0172303.	1.1	26

#	ARTICLE	IF	CITATIONS
2090	RNA-Seq de novo assembly and differential transcriptome analysis of the nematode <i>Ascaridia galli</i> in relation to in vivo exposure to flubendazole. <i>PLoS ONE</i> , 2017, 12, e0185182.	1.1	11
2091	Ensemble-based modeling and rigidity decomposition of allosteric interaction networks and communication pathways in cyclin-dependent kinases: Differentiating kinase clients of the Hsp90-Cdc37 chaperone. <i>PLoS ONE</i> , 2017, 12, e0186089.	1.1	17
2092	Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of <i>Malassezia sympodialis</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkx006.	6.5	47
2093	A highly specific phage defense system is a conserved feature of the <i>Vibrio cholerae</i> mobilome. <i>PLoS Genetics</i> , 2017, 13, e1006838.	1.5	101
2094	B-BOX genes: genome-wide identification, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>BMC Plant Biology</i> , 2017, 17, 156.	1.6	56
2095	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	1.7	238
2096	Whole transcriptome RNA-Seq analysis reveals extensive cell type-specific compartmentalization in <i>Volvox carteri</i> . <i>BMC Biology</i> , 2017, 15, 111.	1.7	19
2097	Viral communities of the human gut: metagenomic analysis of composition and dynamics. <i>Mobile DNA</i> , 2017, 8, 12.	1.3	119
2098	Constructing an integrated gene similarity network for the identification of disease genes. <i>Journal of Biomedical Semantics</i> , 2017, 8, 32.	0.9	24
2099	Perturbed human sub-networks by <i>Fusobacterium nucleatum</i> candidate virulence proteins. <i>Microbiome</i> , 2017, 5, 89.	4.9	27
2100	Differential gene expression in response to <i>Fusarium oxysporum</i> infection in resistant and susceptible genotypes of flax (<i>Linum usitatissimum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 253.	1.6	61
2101	A sensitive short read homology search tool for paired-end read sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 414.	1.2	3
2102	LiverWiki: a wiki-based database for human liver. <i>BMC Bioinformatics</i> , 2017, 18, 452.	1.2	4
2103	A dual transcript-discovery approach to improve the delimitation of gene features from RNA-seq data in the chicken model. <i>Biology Open</i> , 2018, 7, .	0.6	7
2105	Gene expression and ultrastructure of meso- and thermophilic methanotrophic consortia. <i>Environmental Microbiology</i> , 2018, 20, 1651-1666.	1.8	90
2106	Genome-wide identification and analysis of elongase of very long chain fatty acid genes in the silkworm, <i>Bombyx mori</i> . <i>Genome</i> , 2018, 61, 167-176.	0.9	14
2107	A biallelic <i>ANTXR1</i> variant expands the anthrax toxin receptor associated phenotype to tooth agenesis. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1015-1022.	0.7	11
2108	Phylogenetic spread of sequence data affects fitness of SOD1 consensus enzymes: Insights from sequence statistics and structural analyses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 609-620.	1.5	6

#	ARTICLE	IF	CITATIONS
2109	TMEM132: an ancient architecture of cohesin and immunoglobulin domains define a new family of neural adhesion molecules. <i>Bioinformatics</i> , 2018, 34, 721-724.	1.8	38
2110	Genome-wide identification and expression analysis of GRAS family transcription factors in tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2018, 8, 3949.	1.6	62
2111	Comprehensive Redox Profiling of the Thiol Proteome of <i>Clostridium difficile</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1035-1046.	2.5	21
2112	Systematic analysis and comparison of the PHD-Finger gene family in Chinese pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 519-531.	1.4	21
2113	The <i>Gastrodia elata</i> genome provides insights into plant adaptation to heterotrophy. <i>Nature Communications</i> , 2018, 9, 1615.	5.8	170
2114	Sporulation capability and amylosome conservation among diverse human colonic and rumen isolates of the keystone starch-degrader <i>Ruminococcus bromii</i> . <i>Environmental Microbiology</i> , 2018, 20, 324-336.	1.8	79
2115	Proteomic approach and expression analysis revealed the differential expression of predicted leptospiral proteases capable of ECM degradation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 712-721.	1.1	7
2116	Genome-wide Identification and Expression Analysis of the TRK Gene Family in <i>Aspergillus oryzae</i> . , 2018, , ,		0
2117	Identification and characterization of long non-coding RNAs involved in the formation and development of poplar adventitious roots. <i>Industrial Crops and Products</i> , 2018, 118, 334-346.	2.5	66
2118	Recurrent acquisition of cytosine methyltransferases into eukaryotic retrotransposons. <i>Nature Communications</i> , 2018, 9, 1341.	5.8	42
2119	A resource for sustainable management: De novo assembly and annotation of the liver transcriptome of the Atlantic chub mackerel, <i>Scomber colias</i> . <i>Data in Brief</i> , 2018, 18, 276-284.	0.5	7
2120	Comparative and evolutionary analysis of the 14-3-3 family genes in eleven fishes. <i>Gene</i> , 2018, 662, 76-82.	1.0	12
2121	Exploration and exploitation of the environment for novel specialized metabolites. <i>Current Opinion in Biotechnology</i> , 2018, 50, 206-213.	3.3	32
2122	Transcriptomic profiling reveals pigment regulation during peanut testa development. <i>Plant Physiology and Biochemistry</i> , 2018, 125, 116-125.	2.8	15
2123	Novel global effector mining from the transcriptome of early life stages of the soybean cyst nematode <i>Heterodera glycines</i> . <i>Scientific Reports</i> , 2018, 8, 2505.	1.6	31
2124	Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. <i>Nature Communications</i> , 2018, 9, 448.	5.8	146
2125	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. <i>Mycology</i> , 2018, 9, 59-69.	2.0	12
2126	Significance of dark CO ₂ fixation in arctic soils. <i>Soil Biology and Biochemistry</i> , 2018, 119, 11-21.	4.2	58

#	ARTICLE	IF	CITATIONS
2127	Insights from Ion Binding Site Network Analysis into Evolution and Functions of Proteins. <i>Molecular Informatics</i> , 2018, 37, e1700144.	1.4	4
2128	Genome sequence and description of <i>Haloferax massiliense</i> sp. nov., a new halophilic archaeon isolated from the human gut. <i>Extremophiles</i> , 2018, 22, 485-498.	0.9	14
2129	Novel Isoforms of N16 and N19 Families Implicated for the Nacreous Layer Formation in the Pearl Oyster <i>Pinctada fucata</i> . <i>Marine Biotechnology</i> , 2018, 20, 155-167.	1.1	5
2130	Function, distribution, and annotation of characterized cellulases, xylanases, and chitinases from CAZy. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1629-1637.	1.7	109
2131	Complete Genome Sequence of <i>Bacillus methylotrophicus</i> Strain NKG-1, Isolated from the Changbai Mountains, China. <i>Genome Announcements</i> , 2018, 6, .	0.8	7
2132	Genome-wide searches and molecular analyses highlight the unique evolutionary path of flavone synthase I (FNSI) in Apiaceae. <i>Genome</i> , 2018, 61, 103-109.	0.9	7
2133	A Practical Guide for Comparative Genomics of Mobile Genetic Elements in Prokaryotic Genomes. <i>Methods in Molecular Biology</i> , 2018, 1704, 213-242.	0.4	15
2134	CRISPR Screens Uncover Genes that Regulate Target Cell Sensitivity to the Morphogen Sonic Hedgehog. <i>Developmental Cell</i> , 2018, 44, 113-129.e8.	3.1	95
2135	Interactome INSIDER: a structural interactome browser for genomic studies. <i>Nature Methods</i> , 2018, 15, 107-114.	9.0	133
2136	Comparative transcriptomic analysis of two <i>Vicia sativa</i> L. varieties with contrasting responses to cadmium stress reveals the important role of metal transporters in cadmium tolerance. <i>Plant and Soil</i> , 2018, 423, 241-255.	1.8	34
2137	Characteristics of a PHD Finger Subtype. <i>Biochemistry</i> , 2018, 57, 525-539.	1.2	11
2138	Identification and characterization of the BZR transcription factor family and its expression in response to abiotic stresses in <i>Zea mays</i> L.. <i>Plant Growth Regulation</i> , 2018, 84, 423-436.	1.8	68
2139	Identification of a novel botulinum neurotoxin gene cluster in <i>Enterococcus</i> . <i>FEBS Letters</i> , 2018, 592, 310-317.	1.3	82
2140	The role of introns in the conservation of the metabolic genes of <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2018, 110, 310-317.	1.3	30
2141	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 172-174.	9.4	156
2142	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. <i>Scientific Reports</i> , 2018, 8, 85.	1.6	99
2143	PlanNET: homology-based predicted interactome for multiple planarian transcriptomes. <i>Bioinformatics</i> , 2018, 34, 1016-1023.	1.8	19
2144	A novel galactolipase from a green microalga <i>Chlorella kessleri</i> : purification, characterization, molecular cloning, and heterologous expression. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 1711-1723.	1.7	2

#	ARTICLE	IF	CITATIONS
2145	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. <i>BMC Systems Biology</i> , 2018, 12, 13.	3.0	1
2146	Formation of chimeric genes with essential functions at the origin of eukaryotes. <i>BMC Biology</i> , 2018, 16, 30.	1.7	19
2147	A novel chimaeric flocculation protein enhances flocculation in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2018, 6, 49-55.	1.9	3
2148	Functional Prediction of Hypothetical Transcription Factors of <i>Escherichia coli</i> K-12 Based on Expression Data. <i>Computational and Structural Biotechnology Journal</i> , 2018, 16, 157-166.	1.9	6
2149	Genome-wide identification, putative functionality and interactions between lncRNAs and miRNAs in Brassica species. <i>Scientific Reports</i> , 2018, 8, 4960.	1.6	37
2150	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain 3519A. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
2151	Complete Genome Sequence of <i>Mycobacterium</i> sp. Strain 4858. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
2152	Sequence- and structure-based analysis of proteins involved in miRNA biogenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 139-151.	2.0	5
2153	Genomewide analysis of the lateral organ boundaries domain gene family in <i>Eucalyptus grandis</i> reveals members that differentially impact secondary growth. <i>Plant Biotechnology Journal</i> , 2018, 16, 124-136.	4.1	44
2154	Three-dimensional structures of Lipoproteins from <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 692-704.	1.5	11
2155	Sex determination and differentiation genes in a functional hermaphrodite scallop, <i>Nodipecten subnodosus</i> . <i>Marine Genomics</i> , 2018, 37, 161-175.	0.4	16
2156	On the Early Evolution of Catabolic Pathways: A Comparative Genomics Approach. I. The Cases of Glucose, Ribose, and the Nucleobases Catabolic Routes. <i>Journal of Molecular Evolution</i> , 2018, 86, 27-46.	0.8	9
2157	Genome-wide identification and cadmium induced expression profiling of sulfate transporter (SULTR) genes in sorghum (<i>Sorghum bicolor</i> L.). <i>BioMetals</i> , 2018, 31, 91-105.	1.8	16
2158	Gene expression profile and long non-coding RNA analysis, using RNA-Seq, in chicken embryonic fibroblast cells infected by avian leukosis virus J. <i>Archives of Virology</i> , 2018, 163, 639-647.	0.9	15
2159	Deciphering the tRNA-dependent lipid aminoacylation systems in bacteria: Novel components and structural advances. <i>RNA Biology</i> , 2018, 15, 480-491.	1.5	22
2160	Transcriptomic Characterization of the South American Freshwater Stingray <i>Potamotrygon motoro</i> Venom Apparatus. <i>Toxins</i> , 2018, 10, 544.	1.5	13
2161	Improving Standard Progressive Multiple Sequence Alignment by Using Multithreading Techniques. , 2018, , .		0
2162	A new insight into the evolution and functional divergence of <i>FRK</i> genes in <i>Pyrus bretschneideri</i> . <i>Royal Society Open Science</i> , 2018, 5, 171463.	1.1	6

#	ARTICLE	IF	CITATIONS
2163	Draft Genome Sequence of <i>Paucibacter aquatile</i> CR182 ^T , a Strain with Antimicrobial Activity Isolated from Freshwater of Nakdong River in South Korea. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
2164	Isolation of A Novel <i>Bacillus thuringiensis</i> Phage Representing A New Phage Lineage and Characterization of Its Endolysin. <i>Viruses</i> , 2018, 10, 611.	1.5	14
2165	Complete Genome Sequence of the <i>Arcobacter molluscorum</i> Type Strain LMG 25693. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	6
2166	Combining bioinformatics, cheminformatics, functional genomics and whole organism approaches for identifying epigenetic drug targets in <i>Schistosoma mansoni</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 559-570.	1.4	34
2167	Identification, Classification, and Functional Analysis of AP2/ERF Family Genes in the Desert Moss <i>Bryum argenteum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3637.	1.8	21
2168	Fungi between extremotolerance and opportunistic pathogenicity on humans. <i>Fungal Diversity</i> , 2018, 93, 195-213.	4.7	73
2169	An Integrative Approach to Virus-Host Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2018, 1819, 175-196.	0.4	5
2170	Dissecting the Repertoire of DNA-Binding Transcription Factors of the Archaeon <i>Pyrococcus furiosus</i> DSM 3638. <i>Life</i> , 2018, 8, 40.	1.1	5
2171	Complete Genome Sequence of the <i>Arcobacter suis</i> Type Strain LMG 26152. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
2172	Complete Genome Sequence of the <i>Arcobacter skirrowii</i> Type Strain LMG 6621. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
2173	Evolutionary Evidence of Algal Polysaccharide Degradation Acquisition by <i>Pseudoalteromonas carrageenovora</i> 9T to Adapt to Macroalgal Niches. <i>Frontiers in Microbiology</i> , 2018, 9, 2740.	1.5	54
2174	Characterization of the Ubiquitin C-Terminal Hydrolase and Ubiquitin-Specific Protease Families in Rice (<i>Oryza sativa</i>). <i>Frontiers in Plant Science</i> , 2018, 9, 1636.	1.7	22
2175	Comparative Analysis of the Nodule Transcriptomes of <i>Ceanothus thrysiflorus</i> (Rhamnaceae, Rosales) and <i>Datisca glomerata</i> (Datisceae, Cucurbitales). <i>Frontiers in Plant Science</i> , 2018, 9, 1629.	1.7	12
2176	A two-level model for the role of complex and young genes in the formation of organism complexity and new insights into the relationship between evolution and development. <i>EvoDevo</i> , 2018, 9, 22.	1.3	12
2177	Draft Genome Sequence of <i>Deinococcus koreensis</i> SJW1-2 ^T , a Gamma Radiation-Resistant Bacterium Isolated from River Water. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
2178	Multiple paralogues of $\hat{\pm}$ -SNAP in <i>Giardia lamblia</i> exhibit independent subcellular localization and redistribution during encystation and stress. <i>Parasites and Vectors</i> , 2018, 11, 539.	1.0	3
2179	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 283-293.	3.0	19
2180	DREB2 (dehydration-responsive element-binding protein 2) type transcription factor in sorghum (<i>Sorghum bicolor</i>): genome-wide identification, characterization and expression profiles under cadmium and salt stresses. <i>3 Biotech</i> , 2018, 8, 426.	1.1	28

#	ARTICLE	IF	CITATIONS
2181	Identifying Drivers of Parallel Evolution: A Regression Model Approach. <i>Genome Biology and Evolution</i> , 2018, 10, 2801-2812.	1.1	19
2182	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21
2183	Genome-Wide Analysis of Glycine soja Response Regulator GsRR Genes Under Alkali and Salt Stresses. <i>Frontiers in Plant Science</i> , 2018, 9, 1306.	1.7	7
2184	Staying alive: growth and survival of <i>Bifidobacterium animalis</i> subsp. <i>animalis</i> under in vitro and in vivo conditions. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10645-10663.	1.7	3
2185	Using transcriptomics to enable a plethodontid salamander (<i>Bolitoglossa ramosi</i>) for limb regeneration research. <i>BMC Genomics</i> , 2018, 19, 704.	1.2	20
2186	Genomic comparison of <i>Trypanosoma conorhini</i> and <i>Trypanosoma rangeli</i> to <i>Trypanosoma cruzi</i> strains of high and low virulence. <i>BMC Genomics</i> , 2018, 19, 770.	1.2	14
2187	Refining cellular pathway models using an ensemble of heterogeneous data sources. <i>Annals of Applied Statistics</i> , 2018, 12, .	0.5	1
2188	Deciphering the structure of the condensin protein complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11911-11916.	3.3	15
2189	Genetic Evidence Supporting the Role of the Calcium Channel, CACNA1S, in Tooth Cusp and Root Patterning. <i>Frontiers in Physiology</i> , 2018, 9, 1329.	1.3	10
2190	In silico approach to identify non-synonymous SNPs with highest predicted deleterious effect on protein function in human obesity related gene, neuronal growth regulator 1 (NEGR1). <i>3 Biotech</i> , 2018, 8, 466.	1.1	9
2191	Flexibility and constraint: Evolutionary remodeling of the sporulation initiation pathway in Firmicutes. <i>PLoS Genetics</i> , 2018, 14, e1007470.	1.5	13
2192	Draft Genome Sequence of <i>Mycobacterium setense</i> CSUR47. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
2193	Global Transcriptome Analyses Reveal Differentially Expressed Genes of Six Organs and Putative Genes Involved in (Iso)flavonoid Biosynthesis in <i>Belamcanda chinensis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1160.	1.7	9
2194	Genome-Wide Identification and Functional Prediction of Novel Drought-Responsive lncRNAs in <i>Pyrus betulifolia</i> . <i>Genes</i> , 2018, 9, 311.	1.0	27
2195	A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. <i>Microbiome</i> , 2018, 6, 149.	4.9	41
2196	Molecular Signal Integration of Aging and Diabetes Mellitus. , 2018, , .		0
2197	Identification of transposons near predicted lncRNA and mRNA pools of <i>Prunus mume</i> using an integrative transposable element database constructed from Rosaceae plant genomes. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1301-1316.	1.0	3
2198	Floral pigmentation pattern in Oriental hybrid lily (<i>Lilium</i> spp.) cultivar "Dizzy"™ is caused by transcriptional regulation of anthocyanin biosynthesis genes. <i>Journal of Plant Physiology</i> , 2018, 228, 85-91.	1.6	21

#	ARTICLE	IF	CITATIONS
2199	High pCO ₂ -induced exopolysaccharide-rich ballasted aggregates of planktonic cyanobacteria could explain Paleoproterozoic carbon burial. <i>Nature Communications</i> , 2018, 9, 2116.	5.8	19
2200	Introgression and gene family contraction drive the evolution of lifestyle and host shifts of hypocrealean fungi. <i>Mycology</i> , 2018, 9, 176-188.	2.0	35
2201	Sequential search leads to faster, more efficient fragment-based <i>de novo</i> protein structure prediction. <i>Bioinformatics</i> , 2018, 34, 1132-1140.	1.8	12
2202	Discovery and Sequence Analysis of Four Deltacoronaviruses from Birds in the Middle East Reveal Interspecies Jumping with Recombination as a Potential Mechanism for Avian-to-Avian and Avian-to-Mammalian Transmission. <i>Journal of Virology</i> , 2018, 92, .	1.5	62
2203	Transcriptome analysis reveals the genetic foundation for the dynamics of starch and lipid production in <i>Ettlia oleoabundans</i> . <i>Algal Research</i> , 2018, 33, 142-155.	2.4	21
2204	Cellulases. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	1
2205	Discovery of Novel Cellulases Using Proteomic Strategies. <i>Methods in Molecular Biology</i> , 2018, 1796, 103-113.	0.4	1
2206	Evolutionary and expression analysis of <i>Vitis vinifera</i> OFP gene family. <i>Plant Systematics and Evolution</i> , 2018, 304, 995-1008.	0.3	5
2207	Early metazoan cell type diversity and the evolution of multicellular gene regulation. <i>Nature Ecology and Evolution</i> , 2018, 2, 1176-1188.	3.4	226
2208	Gene family innovation, conservation and loss on the animal stem lineage. <i>ELife</i> , 2018, 7, .	2.8	149
2209	The first Illumina-based <i>de novo</i> transcriptome analysis and molecular marker development in Napier grass (<i>Pennisetum purpureum</i>). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	42
2210	Local and Systemic Effect of Cytokinins on Soybean Nodulation and Regulation of Their Isopentenyl Transferase (IPT) Biosynthesis Genes Following Rhizobia Inoculation. <i>Frontiers in Plant Science</i> , 2018, 9, 1150.	1.7	41
2211	Insights into Avian Incomplete Dosage Compensation: Sex-Biased Gene Expression Coevolves with Sex Chromosome Degeneration in the Common Whitethroat. <i>Genes</i> , 2018, 9, 373.	1.0	13
2212	Acquisition of MACPF domain-encoding genes is the main contributor to LPS glycan diversity in gut <i>Bacteroides</i> species. <i>ISME Journal</i> , 2018, 12, 2919-2928.	4.4	17
2213	Transcriptome Reveals Long Non-coding RNAs and mRNAs Involved in Primary Wool Follicle Induction in Carpet Sheep Fetal Skin. <i>Frontiers in Physiology</i> , 2018, 9, 446.	1.3	72
2214	A Suppressor/Avirulence Gene Combination in <i>Hyaloperonospora arabidopsidis</i> Determines Race Specificity in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 265.	1.7	14
2215	Molecular Mechanisms of Acclimatization to Phosphorus Starvation and Recovery Underlying Full-Length Transcriptome Profiling in Barley (<i>Hordeum vulgare</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 500.	1.7	57
2216	Altered Expression of the Malate-Permeable Anion Channel OsALMT4 Reduces the Growth of Rice Under Low Radiance. <i>Frontiers in Plant Science</i> , 2018, 9, 542.	1.7	10

#	ARTICLE	IF	CITATIONS
2217	The Genome of a Thermo Tolerant, Pathogenic Albino <i>Aspergillus fumigatus</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1827.	1.5	12
2218	Characterization of long non-coding RNA and messenger RNA profiles in follicular fluid from mature and immature ovarian follicles of healthy women and women with polycystic ovary syndrome. <i>Human Reproduction</i> , 2018, 33, 1735-1748.	0.4	65
2219	Identification of likely pathogenic and known variants in TSPEAR, LAMB3, BCOR, and WNT10A in four Turkish families with tooth agenesis. <i>Human Genetics</i> , 2018, 137, 689-703.	1.8	24
2220	Functional characterisation of the actin-depolymerising factor from the apicomplexan <i>Neospora caninum</i> (NcADF). <i>Molecular and Biochemical Parasitology</i> , 2018, 224, 26-36.	0.5	2
2221	Genome-wide analysis of differentially expressed profiles of mRNAs, lncRNAs and circRNAs during <i>Cryptosporidium baileyi</i> infection. <i>BMC Genomics</i> , 2018, 19, 356.	1.2	26
2222	Antisense and yet sensitive: Copy number control of rolling circle replicating plasmids by small RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1500.	3.2	6
2223	Metagenomic Approaches to Investigate the Contribution of the Vineyard Environment to the Quality of Wine Fermentation: Potentials and Difficulties. <i>Frontiers in Microbiology</i> , 2018, 9, 991.	1.5	90
2224	Profiling of Long Non-coding RNAs and mRNAs by RNA-Sequencing in the Hippocampi of Adult Mice Following Propofol Sedation. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 91.	1.4	9
2225	Characterization of a novel phage infecting the pathogenic multidrug-resistant <i>Bacillus cereus</i> and functional analysis of its endolysin. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7901-7912.	1.7	26
2226	The ALMT Gene Family Performs Multiple Functions in Plants. <i>Agronomy</i> , 2018, 8, 20.	1.3	19
2227	Genome Wide Identification, Evolutionary, and Expression Analysis of VQ Genes from Two <i>Pyrus</i> Species. <i>Genes</i> , 2018, 9, 224.	1.0	16
2228	Genome-Wide Analysis of Long Non-Coding RNAs in Potato and Their Potential Role in Tuber Sprouting Process. <i>International Journal of Molecular Sciences</i> , 2018, 19, 101.	1.8	22
2229	PhcrTx2, a New Crab-Paralyzing Peptide Toxin from the Sea Anemone <i>Phymanthus crucifer</i> . <i>Toxins</i> , 2018, 10, 72.	1.5	7
2230	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	1.5	37
2231	Comparative and Expression Analysis of Ubiquitin Conjugating Domain-Containing Genes in Two <i>Pyrus</i> Species. <i>Cells</i> , 2018, 7, 77.	1.8	24
2232	Differentially expressed genes in hemocytes of <i>Litopenaeus vannamei</i> challenged with <i>Vibrio parahaemolyticus</i> AHPND (VPAHPND) and VPAHPND toxin. <i>Fish and Shellfish Immunology</i> , 2018, 81, 284-296.	1.6	36
2233	Characterization of esterase activity from an <i>Acetomicrobium hydrogeniformans</i> enzyme with high structural stability in extreme conditions. <i>Extremophiles</i> , 2018, 22, 781-793.	0.9	10
2234	Deep Sequencing-Based Transcriptome Profiling Reveals Avian Interferon-Stimulated Genes and Provides Comprehensive Insight into Newcastle Disease Virus-Induced Host Responses. <i>Viruses</i> , 2018, 10, 162.	1.5	25

#	ARTICLE	IF	CITATIONS
2235	Genome-wide identification and characterization of mRNAs and lncRNAs involved in cold stress in the wild banana (<i>Musa itinerans</i>). PLoS ONE, 2018, 13, e0200002.	1.1	61
2236	Genome-wide expert annotation of the epigenetic machinery of the plant-parasitic nematodes <i>Meloidogyne</i> spp., with a focus on the asexually reproducing species. BMC Genomics, 2018, 19, 321.	1.2	18
2237	Acyl-CoA-binding protein family members in laticifers are possibly involved in lipid and latex metabolism of <i>Hevea brasiliensis</i> (the Para rubber tree). BMC Genomics, 2018, 19, 5.	1.2	8
2238	The aquatic animals TM transcriptome resource for comparative functional analysis. BMC Genomics, 2018, 19, 103.	1.2	5
2239	Improving conditional random field model for prediction of protein-RNA residue-base contacts. Quantitative Biology, 2018, 6, 155-162.	0.3	1
2240	Identification of lncRNAs and Their Functional Network Associated with Chemoresistance in SW1990/GZ Pancreatic Cancer Cells by RNA Sequencing. DNA and Cell Biology, 2018, 37, 839-849.	0.9	25
2241	Transcriptome sequencing to detect the potential role of long non-coding RNAs in bovine mammary gland during the dry and lactation period. BMC Genomics, 2018, 19, 605.	1.2	54
2243	Comparative analysis of the tetraspanin gene family in six teleost fishes. Fish and Shellfish Immunology, 2018, 82, 432-441.	1.6	9
2244	Differential expression of lncRNAs and predicted target genes in normal mouse melanocytes and B16 cells. Experimental Dermatology, 2018, 27, 1230-1236.	1.4	8
2245	Tangled history of a multigene family: The evolution of ISOPENTENYLTRANSFERASE genes. PLoS ONE, 2018, 13, e0201198.	1.1	25
2246	Essential Gene Clusters Identified in <i>Stenotrophomonas</i> MB339 for Multiple Metal/Antibiotic Resistance and Xenobiotic Degradation. Current Microbiology, 2018, 75, 1484-1492.	1.0	16
2247	Genome-wide identification, evolution, and expression analysis of the <i>KT/HAK/KUP</i> family in pear. Genome, 2018, 61, 755-765.	0.9	25
2248	Tracking gene expression and oxidative damage of O ₂ -stressed <i>Clostridioides difficile</i> by a multi-omics approach. Anaerobe, 2018, 53, 94-107.	1.0	21
2249	±-Adducin nsSNPs affect mRNA secondary structure, protein modification and stability. Meta Gene, 2018, 17, 153-162.	0.3	7
2250	Learning Effective Molecular Models from Experimental Observables. Journal of Chemical Theory and Computation, 2018, 14, 3849-3858.	2.3	34
2251	Phylogenetic Analysis of Protein Family. Methods in Molecular Biology, 2018, 1775, 267-275.	0.4	9
2252	Cwp19 Is a Novel Lytic Transglycosylase Involved in Stationary-Phase Autolysis Resulting in Toxin Release in <i>Clostridium difficile</i> . MBio, 2018, 9, .	1.8	60
2253	Transcriptome profiling with focus on potential key genes for wing development and evolution in <i>Megalopterus caeruleus</i> , the damselfly species with the world's largest wings. PLoS ONE, 2018, 13, e0189898.	1.1	4

#	ARTICLE	IF	CITATIONS
2254	Dicer-like and RNA-dependent RNA polymerase gene family identification and annotation in the cultivated <i>Solanum tuberosum</i> and its wild relative <i>S. commersonii</i> . <i>Planta</i> , 2018, 248, 729-743.	1.6	24
2255	De novo transcriptome assembly and functional annotation of the southern rock lobster (<i>Jasus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 0.4 9		
2256	<i>In silico</i> functional and tumor suppressor role of hypothetical protein PCNXL2 with regulation of the Notch signaling pathway. <i>RSC Advances</i> , 2018, 8, 21414-21430.	1.7	7
2257	Application of Computation in the Biosynthesis of Phytochemicals. , 2018, , 255-276.		0
2258	Comprehensive search for accessory proteins encoded with archaeal and bacterial type III CRISPR- <i>cas</i> gene cassettes reveals 39 new <i>cas</i> gene families. <i>RNA Biology</i> , 2019, 16, 530-542.	1.5	97
2259	3gClust: Human Protein Cluster Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1-1.	1.9	6
2260	Effusion: prediction of protein function from sequence similarity networks. <i>Bioinformatics</i> , 2019, 35, 442-451.	1.8	12
2261	Biomolecular Structures: Prediction, Identification and Analyses. , 2019, , 504-534.		2
2262	Combination of label-free quantitative proteomics and transcriptomics reveals intraspecific venom variation between the two strains of <i>Tetrastichus brontispae</i> , a parasitoid of two invasive beetles. <i>Journal of Proteomics</i> , 2019, 192, 37-53.	1.2	18
2263	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	1.5	45
2264	The Oxyomonad Genome Displays Canonical Eukaryotic Complexity in the Absence of a Mitochondrion. <i>Molecular Biology and Evolution</i> , 2019, 36, 2292-2312.	3.5	49
2265	Bioinorganics and Wound Healing. <i>Advanced Healthcare Materials</i> , 2019, 8, e1900764.	3.9	80
2266	CasPDB: an integrated and annotated database for Cas proteins from bacteria and archaea. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	8
2267	Comprehensive Analysis of LncRNA Reveals the Temporal-Specific Module of Goat Skeletal Muscle Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3950.	1.8	25
2268	Development and Genome Sequencing of a Laboratory-Inbred Miniature Pig Facilitates Study of Human Diabetic Disease. <i>IScience</i> , 2019, 19, 162-176.	1.9	31
2269	Transcriptome Landscape Variation in the Genus <i>Thymus</i> . <i>Genes</i> , 2019, 10, 620.	1.0	11
2270	Transcriptome analysis and codominant markers development in caper, a drought tolerant orphan crop with medicinal value. <i>Scientific Reports</i> , 2019, 9, 10411.	1.6	23
2271	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	1.6	37

#	ARTICLE	IF	CITATIONS
2272	Induction of vitellogenesis in female banana shrimp, <i>Fenneropenaeus merguensis</i> by leucine-tyrosine-arginine motif-containing protein 5 (LYRM5). <i>Aquaculture</i> , 2019, 512, 734292.	1.7	0
2273	Integrative analysis reveals evolutionary patterns and potential functions of SWEET transporters in Euphorbiaceae. <i>International Journal of Biological Macromolecules</i> , 2019, 139, 1-11.	3.6	29
2274	De novo genome assembly of the endangered <i>Acer yangbiense</i> , a plant species with extremely small populations endemic to Yunnan Province, China. <i>GigaScience</i> , 2019, 8, .	3.3	42
2275	Lack of long-term acclimation in Antarctic encrusting species suggests vulnerability to warming. <i>Nature Communications</i> , 2019, 10, 3383.	5.8	21
2276	<p>Long noncoding RNA THAP9-AS1 is induced by Helicobacter pylori and promotes cell growth and migration of gastric cancer<p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 6653-6663.	1.0	35
2277	The mixed liver and heart transcriptome dataset of the New Zealand brushtail possum, <i>Trichosurus vulpecula</i> . <i>Data in Brief</i> , 2019, 27, 104577.	0.5	1
2278	Complete genome sequence of the novel phage vB_BthS-HD29phi infecting <i>Bacillus thuringiensis</i> . <i>Archives of Virology</i> , 2019, 164, 3089-3093.	0.9	2
2279	RFQAmode: Random Forest Quality Assessment to identify a predicted protein structure in the correct fold. <i>PLoS ONE</i> , 2019, 14, e0218149.	1.1	3
2280	A Novel Control Strategy for Shunt Active Power Filter Based on Gray Prediction and Optimal Voltage Vector. <i>IOP Conference Series: Earth and Environmental Science</i> , 0, 252, 032217.	0.2	1
2281	Essentials of Bioinformatics, Volume III. , 2019, , .		0
2282	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. <i>Scientific Reports</i> , 2019, 9, 15884.	1.6	34
2283	Identification of lncRNAs by RNA Sequencing Analysis During in Vivo Pre-Implantation Developmental Transformation in the Goat. <i>Frontiers in Genetics</i> , 2019, 10, 1040.	1.1	10
2284	Transcriptome-Based Identification and Molecular Evolution of the Cytochrome P450 Genes and Expression Profiling under Dimethoate Treatment in Amur Stickleback (<i>Pungitius sinensis</i>). <i>Animals</i> , 2019, 9, 873.	1.0	6
2285	Small RNA inhibits infection by downy mildew pathogen <i>Hyaloperonospora arabidopsidis</i>. <i>Molecular Plant Pathology</i> , 2019, 20, 1523-1534.	2.0	28
2286	Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	80
2287	Measuring the impact of gene prediction on gene loss estimates in Eukaryotes by quantifying falsely inferred absences. <i>PLoS Computational Biology</i> , 2019, 15, e1007301.	1.5	43
2288	Proteomics and Docking Study Targeting Penicillin-Binding Protein and Penicillin-Binding Protein2a of Methicillin-Resistant <i>Staphylococcus aureus</i> Strain SO-1977 Isolated from Sudan. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431986494.	0.6	14
2289	The VirAnnot Pipeline: A Resource for Automated Viral Diversity Estimation and Operational Taxonomy Units Assignment for Virome Sequencing Data. <i>Phytobiomes Journal</i> , 2019, 3, 256-259.	1.4	26

#	ARTICLE	IF	CITATIONS
2290	Genome-Wide Analysis of the YABBY Gene Family in Grapevine and Functional Characterization of VvYABBY4. <i>Frontiers in Plant Science</i> , 2019, 10, 1207.	1.7	37
2291	Genome-wide identification and expression analysis of the <i>VQ</i> gene family in soybean (<i>Glycine</i> Tj ETQq1 1.0.784314 rgBT / Dv). <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	1.7	13
2292	Hybrid Genome Assembly of a Neotropical Mutualistic Ant. <i>Genome Biology and Evolution</i> , 2019, 11, 2306-2311.	1.1	11
2293	Finding New Cell Wall Regulatory Genes in <i>Populus trichocarpa</i> Using Multiple Lines of Evidence. <i>Frontiers in Plant Science</i> , 2019, 10, 1249.	1.7	13
2294	Hexa-Longin domain scaffolds for inter-Rab signalling. <i>Bioinformatics</i> , 2020, 36, 990-993.	1.8	5
2295	ABC-F proteins in mRNA translation and antibiotic resistance. <i>Research in Microbiology</i> , 2019, 170, 435-447.	1.0	27
2296	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	5.8	112
2297	Integrative Analysis of the Core Fruit Lignification Toolbox in Pear Reveals Targets for Fruit Quality Bioengineering. <i>Biomolecules</i> , 2019, 9, 504.	1.8	28
2298	Genome sequence of <i>Malania oleifera</i> , a tree with great value for nervonic acid production. <i>GigaScience</i> , 2019, 8, .	3.3	36
2299	Comprehensive transcriptional profiling of porcine brain aging. <i>Gene</i> , 2019, 693, 1-9.	1.0	12
2300	Significant abundance of configurations of coding variants in diploid human genomes. <i>Nucleic Acids Research</i> , 2019, 47, 2981-2995.	6.5	5
2301	The Genetic Structures of an Extensively Drug Resistant (XDR) <i>Klebsiella pneumoniae</i> and Its Plasmids. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 446.	1.8	28
2302	Genomic Signals of Adaptation towards Mutualism and Sociality in Two Ambrosia Beetle Complexes. <i>Life</i> , 2019, 9, 2.	1.1	5
2303	The landscape of transposable elements and satellite DNAs in the genome of a dioecious plant spinach (<i>Spinacia oleracea</i> L.). <i>Mobile DNA</i> , 2019, 10, 3.	1.3	37
2304	Comparison of fertile and sterile male gametogenesis in <i>Cryptomeria japonica</i> D. Don. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	7
2305	lncRNA profile of <i>Apis mellifera</i> and its possible role in behavioural transition from nurses to foragers. <i>BMC Genomics</i> , 2019, 20, 393.	1.2	37
2306	A genome-wide approach to the comprehensive analysis of GASA gene family in <i>Glycine max</i> . <i>Plant Molecular Biology</i> , 2019, 100, 607-620.	2.0	42
2308	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 18.	1.0	12

#	ARTICLE	IF	CITATIONS
2309	Comparative physiology and transcriptome analysis allows for identification of lncRNAs imparting tolerance to drought stress in autotetraploid cassava. <i>BMC Genomics</i> , 2019, 20, 514.	1.2	25
2310	Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family. <i>Genome Research</i> , 2019, 29, 1277-1286.	2.4	19
2311	Heterologous Microcompartment Assembly in <i>Bacillaceae</i> : Establishing the Components Necessary for Scaffold Formation. <i>ACS Synthetic Biology</i> , 2019, 8, 1642-1654.	1.9	9
2312	A survey of transcriptome complexity using PacBio single-molecule real-time analysis combined with Illumina RNA sequencing for a better understanding of ricinoleic acid biosynthesis in <i>Ricinus communis</i> . <i>BMC Genomics</i> , 2019, 20, 456.	1.2	25
2313	Structural, functional, and evolutionary analysis of late embryogenesis abundant proteins (LEA) in <i>Triticum aestivum</i> : A detailed molecular level biochemistry using in silico approach. <i>Computational Biology and Chemistry</i> , 2019, 82, 9-24.	1.1	18
2314	Identification of lncRNAs Responsive to Infection by <i>Plasmodiophora brassicae</i> in Clubroot-Susceptible and -Resistant <i>Brassica napus</i> Lines Carrying Resistance Introgressed from Rutabaga. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1360-1377.	1.4	24
2315	Comprehensive Genomic Survey, Characterization and Expression Analysis of the HECT Gene Family in <i>Brassica rapa</i> L. and <i>Brassica oleracea</i> L.. <i>Genes</i> , 2019, 10, 400.	1.0	15
2316	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27
2317	Integrative Analyses of Long Non-coding RNA and mRNA Involved in Piglet Ileum Immune Response to <i>Clostridium perfringens</i> Type C Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 130.	1.8	40
2318	Transcriptomics Analysis Reveals New Insights into the Roles of Notch1 Signaling on Macrophage Polarization. <i>Scientific Reports</i> , 2019, 9, 7999.	1.6	23
2319	Mutation of a bHLH transcription factor allowed almond domestication. <i>Science</i> , 2019, 364, 1095-1098.	6.0	116
2320	Long non-coding RNA and MicroRNA profiling provides comprehensive insight into non-coding RNA involved host immune responses in ALVJ-infected chicken primary macrophage. <i>Developmental and Comparative Immunology</i> , 2019, 100, 103414.	1.0	10
2321	Structural and immunological characterization of a new nucleotidyltransferase-like antigen from <i>Paracoccidioides brasiliensis</i> . <i>Molecular Immunology</i> , 2019, 112, 151-162.	1.0	5
2322	HOT or not: examining the basis of high-occupancy target regions. <i>Nucleic Acids Research</i> , 2019, 47, 5735-5745.	6.5	41
2323	Whirly (Why) transcription factors in tomato (<i>Solanum lycopersicum</i> L.): genome-wide identification and transcriptional profiling under drought and salt stresses. <i>Molecular Biology Reports</i> , 2019, 46, 4139-4150.	1.0	13
2324	Comparative Analysis of the aquaporin Gene Family in 12 Fish Species. <i>Animals</i> , 2019, 9, 233.	1.0	14
2325	An annual cycle of gene regulation in the red-legged salamander mental gland: from hypertrophy to expression of rapidly evolving pheromones. <i>BMC Developmental Biology</i> , 2019, 19, 10.	2.1	7
2326	Expression, purification, and subcellular localization of phospholipase C in <i>Dunaliella salina</i> . <i>Journal of Oceanology and Limnology</i> , 2019, 37, 1363-1371.	0.6	0

#	ARTICLE	IF	CITATIONS
2327	An Integrated Analysis of Cashmere Fineness lncRNAs in Cashmere Goats. <i>Genes</i> , 2019, 10, 266.	1.0	26
2328	In silico characterisation and functional validation of chilling tolerant divergence 1 (COLD1) gene in monocots during abiotic stress. <i>Functional Plant Biology</i> , 2019, 46, 524.	1.1	8
2329	Identification and characterization of pineapple leaf lncRNAs in crassulacean acid metabolism (CAM) photosynthesis pathway. <i>Scientific Reports</i> , 2019, 9, 6658.	1.6	17
2330	Prevalence and Diversity Analysis of Candidate Prophages to Provide An Understanding on Their Roles in <i>Bacillus Thuringiensis</i> . <i>Viruses</i> , 2019, 11, 388.	1.5	17
2331	Key genes differential expressions and pathway involved in salt and water-deprivation stresses for renal cortex in camel. <i>BMC Molecular Biology</i> , 2019, 20, 11.	3.0	6
2332	Comparative analysis of the root and leaf transcriptomes in <i>Chelidonium majus</i> L.. <i>PLoS ONE</i> , 2019, 14, e0215165.	1.1	13
2333	Transcriptome analysis reveals downregulation of virulence-associated genes expression in a low virulence <i>Verticillium dahliae</i> strain. <i>Archives of Microbiology</i> , 2019, 201, 927-941.	1.0	23
2334	Aurora kinase protein family in <i>Trypanosoma cruzi</i> : Novel role of an AUK-B homologue in kinetoplast replication. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007256.	1.3	14
2335	<i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> genomes provide insights into the origin and evolution of allotetraploid cotton. <i>Nature Genetics</i> , 2019, 51, 739-748.	9.4	568
2336	Characterization of an <i>Arabidopsis thaliana</i> DUF761-containing protein with a potential role in development and defense responses. <i>Theoretical and Experimental Plant Physiology</i> , 2019, 31, 303-316.	1.1	13
2337	Transcriptomic Analysis of Coding Genes and Non-Coding RNAs Reveals Complex Regulatory Networks Underlying the Black Back and White Belly Coat Phenotype in Chinese Wuzhishan Pigs. <i>Genes</i> , 2019, 10, 201.	1.0	6
2338	A new chromatographic approach to analyze methylproteome with enhanced lysine methylation identification performance. <i>Analytica Chimica Acta</i> , 2019, 1068, 111-119.	2.6	13
2339	Diversified secondary metabolite biosynthesis gene repertoire revealed in symbiotic dinoflagellates. <i>Scientific Reports</i> , 2019, 9, 1204.	1.6	21
2340	Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). <i>PLoS ONE</i> , 2019, 14, e0211043.	1.1	5
2341	From the Amazon: A comprehensive liver transcriptome dataset of the teleost fish tambaqui, <i>Colossoma macropomum</i> . <i>Data in Brief</i> , 2019, 23, 103751.	0.5	3
2342	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea <i>Geoglobus acetivorans</i> and <i>Archaeoglobus fulgidus</i> : Biochemical and Structural Characterization. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 7.	2.0	26
2343	Genome-wide identification of Lysin-Motif Receptor-Like Kinase (LysM-RLK) gene family in <i>Brachypodium distachyon</i> and docking analysis of chitin/LYK binding. <i>Physiological and Molecular Plant Pathology</i> , 2019, 106, 217-225.	1.3	19
2344	A genome-wide analysis of coatomer protein (COP) subunits of apicomplexan parasites and their evolutionary relationships. <i>BMC Genomics</i> , 2019, 20, 98.	1.2	5

#	ARTICLE	IF	CITATIONS
2345	Flax (<i>Linum usitatissimum</i> L.) response to non-optimal soil acidity and zinc deficiency. <i>BMC Plant Biology</i> , 2019, 19, 54.	1.6	28
2346	Impact of a bathing tradition on shared gut microbes among Japanese families. <i>Scientific Reports</i> , 2019, 9, 4380.	1.6	16
2347	LncRNA/circRNA/miRNA/mRNA networks regulate the development of root and shoot meristems of <i>Populus</i> . <i>Industrial Crops and Products</i> , 2019, 133, 333-347.	2.5	51
2348	Horizontal gene transfer in human-associated microorganisms inferred by phylogenetic reconstruction and reconciliation. <i>Scientific Reports</i> , 2019, 9, 5953.	1.6	55
2349	The genome of the arapaima (<i>Arapaima gigas</i>) provides insights into gigantism, fast growth and chromosomal sex determination system. <i>Scientific Reports</i> , 2019, 9, 5293.	1.6	25
2350	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , 2019, 21, 2148-2170.	1.8	15
2351	Flowering plant immune repertoires expand under mycorrhizal symbiosis. <i>Plant Direct</i> , 2019, 3, e00125.	0.8	2
2352	Distribution, diversity and functional dissociation of the mac genes in marine biofilms. <i>Biofouling</i> , 2019, 35, 230-243.	0.8	9
2353	Metacaspase gene family in Rosaceae genomes: Comparative genomic analysis and their expression during pear pollen tube and fruit development. <i>PLoS ONE</i> , 2019, 14, e0211635.	1.1	9
2354	Structure-function characterization of an insecticidal protein GNIP1Aa, a member of an MACPF and Î ² -tripod families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2897-2906.	3.3	19
2355	Bifunctional Chloroplastic DJ-1B from <i>Arabidopsis thaliana</i> is an Oxidation-Robust Holdase and a Glyoxalase Sensitive to H ₂ O ₂ . <i>Antioxidants</i> , 2019, 8, 8.	2.2	17
2356	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 944-956.	2.2	27
2357	Novel Insights reveal Anti-microbial Gene Regulation of Piglet Intestine Immune in response to <i>Clostridium perfringens</i> Infection. <i>Scientific Reports</i> , 2019, 9, 1963.	1.6	14
2358	Genome-Wide Identification of Trihelix Genes in Moso Bamboo (<i>Phyllostachys edulis</i>) and Their Expression in Response to Abiotic Stress. <i>Journal of Plant Growth Regulation</i> , 2019, 38, 1127-1140.	2.8	9
2359	Linking gene expression and oenological traits: Comparison between <i>Torulaspora delbrueckii</i> and <i>Saccharomyces cerevisiae</i> strains. <i>International Journal of Food Microbiology</i> , 2019, 294, 42-49.	2.1	27
2360	Hydrogenotrophic methanogenesis in archaeal phylum Verstraetearchaeota reveals the shared ancestry of all methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5037-5044.	3.3	187
2361	The <i>Galleria mellonella</i> Hologenome Supports Microbiota-Independent Metabolism of Long-Chain Hydrocarbon Beeswax. <i>Cell Reports</i> , 2019, 26, 2451-2464.e5.	2.9	103
2362	The Genome Sequence of the Eastern Woodchuck (<i>Marmota monax</i>) – A Preclinical Animal Model for Chronic Hepatitis B. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3943-3952.	0.8	13

#	ARTICLE	IF	CITATIONS
2363	Evaluating Precision and Recall through the Utility of msTALI via an Active Site Study on Fold Families. , 2019, , .		0
2364	Hybrid de novo whole-genome assembly and annotation of the model tapeworm <i>Hymenolepis diminuta</i> . <i>Scientific Data</i> , 2019, 6, 302.	2.4	21
2365	Complete Genome Sequence of <i>Phreatobacter</i> sp. Strain NMCR1094, a Formate-Utilizing Bacterium Isolated from a Freshwater Stream. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
2366	5. Metagenomics of extreme environments: methods and applications. , 2019, , 93-126.		0
2367	Cyberbiosecurity Challenges of Pathogen Genome Databases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 106.	2.0	17
2368	The Endophytic Fungus <i>Chaetomium cupreum</i> Regulates Expression of Genes Involved in the Tolerance to Metals and Plant Growth Promotion in <i>Eucalyptus globulus</i> Roots. <i>Microorganisms</i> , 2019, 7, 490.	1.6	28
2369	The transcriptomic signature of low aggression in honey bees resembles a response to infection. <i>BMC Genomics</i> , 2019, 20, 1029.	1.2	11
2370	Clinical Spectrum and Functional Consequences Associated with Bi-Allelic Pathogenic PNPT1 Variants. <i>Journal of Clinical Medicine</i> , 2019, 8, 2020.	1.0	16
2371	Dynamic Changes of DNA Methylation and Transcriptome Expression in Porcine Ovaries during Aging. <i>BioMed Research International</i> , 2019, 2019, 1-15.	0.9	9
2372	The Transcription Factor Aabzip9 Positively Regulates the Biosynthesis of Artemisinin in <i>Artemisia annua</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1294.	1.7	14
2373	Molecular Characterization and Expression Analysis of MYB Transcription Factors Involved in the Glucosinolate Pathway in Chinese Cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Agronomy</i> , 2019, 9, 807.	1.3	4
2374	Comparative transcriptome analysis of TUCPs in <i>Gossypium hirsutum</i> Ligon-lintless-1 mutant and their proposed functions in cotton fiber development. <i>Molecular Genetics and Genomics</i> , 2019, 294, 23-34.	1.0	5
2375	Genome-wide identification of citrus <i>CAMTA</i> genes and their expression analysis under stress and hormone treatments. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 331-340.	0.9	16
2376	An important resource for understanding bio-adhesion mechanisms: Cement gland transcriptomes of two goose barnacles, <i>Pollicipes pollicipes</i> and <i>Lepas anatifera</i> (Cirripedia, Thoracica). <i>Marine Genomics</i> , 2019, 45, 16-20.	0.4	11
2377	Identification of O-acetylserine(thiol)lyase (OASTL) genes in sorghum (<i>Sorghum bicolor</i>) and gene expression analysis under cadmium stress. <i>Molecular Biology Reports</i> , 2019, 46, 343-354.	1.0	9
2378	Gene expression changes elicited by a parasitic B chromosome in the grasshopper <i>Eyprepocnemis plorans</i> are consistent with its phenotypic effects. <i>Chromosoma</i> , 2019, 128, 53-67.	1.0	15
2379	Methods to Study Long Noncoding RNA Expression and Dynamics in Zebrafish Using RNA Sequencing. <i>Methods in Molecular Biology</i> , 2019, 1912, 77-110.	0.4	1
2380	How crickets become freeze tolerant: The transcriptomic underpinnings of acclimation in <i>Gryllus veletis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 55-66.	0.4	18

#	ARTICLE	IF	CITATIONS
2381	Cross-strand disulfides in the hydrogen bonding site of antiparallel β -sheet (aCSDhs): Forbidden disulfides that are highly strained, easily broken. <i>Protein Science</i> , 2019, 28, 239-256.	3.1	4
2382	Differentially Expressed lncRNAs After the Activation of Primordial Follicles in Mouse. <i>Reproductive Sciences</i> , 2019, 26, 1094-1104.	1.1	7
2383	Molecular Adaptations of Bacterial Mercuric Reductase to the Hypersaline Kebrit Deep in the Red Sea. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	7
2384	Whole transcriptome sequencing reveals biologically significant RNA markers and related regulating biological pathways in cardiomyocyte hypertrophy induced by high glucose. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1018-1027.	1.2	26
2385	Genome-wide differential expression of long noncoding RNAs and mRNAs in ovarian follicles of two different chicken breeds. <i>Genomics</i> , 2019, 111, 1395-1403.	1.3	26
2386	Identification and characterization of long non-coding RNA in prenatal and postnatal skeletal muscle of sheep. <i>Genomics</i> , 2019, 111, 133-141.	1.3	15
2387	HMMCAS: A Web Tool for the Identification and Domain Annotations of CAS Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1313-1315.	1.9	43
2388	Deleterious Non-Synonymous Single Nucleotide Polymorphism Predictions on Human Transcription Factors. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 327-333.	1.9	4
2389	Screening and evaluating of long non-coding RNAs in prenatal and postnatal pituitary gland of sheep. <i>Genomics</i> , 2020, 112, 934-942.	1.3	19
2390	Comprehensive Analysis of Wall-Associated Kinase Genes and Their Expression Under Abiotic and Biotic Stress in Chinese Cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>). <i>Journal of Plant Growth Regulation</i> , 2020, 39, 72-86.	2.8	13
2391	Genome-wide identification and expression analysis of two component system genes in <i>Cicer arietinum</i> . <i>Genomics</i> , 2020, 112, 1371-1383.	1.3	26
2392	Genome-wide analysis of long noncoding RNA and mRNA profiles in PRRSV-infected porcine alveolar macrophages. <i>Genomics</i> , 2020, 112, 1879-1888.	1.3	9
2393	Evolution of DNA Methylome Diversity in Eukaryotes. <i>Journal of Molecular Biology</i> , 2020, 432, 1687-1705.	2.0	82
2394	Machine learning techniques for protein function prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 397-413.	1.5	90
2395	Systematically Scrutinizing the Impact of Substitution Sites on Thermostability and Detergent Tolerance for <i>Bacillus subtilis</i> Lipase A. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1568-1584.	2.5	21
2396	PhoH2 proteins couple RNA helicase and RNase activities. <i>Protein Science</i> , 2020, 29, 883-892.	3.1	10
2397	Comprehensive genomic analysis of the DUF4228 gene family in land plants and expression profiling of ATDUF4228 under abiotic stresses. <i>BMC Genomics</i> , 2020, 21, 12.	1.2	25
2398	Residual Participation and Thermodynamic Stability Due to Molecular Interactions in IL11, IL11R β and Cp130 from <i>Homo sapiens</i> : An In Silico Outlook for IL11 as a Therapeutic Remedy. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2009-2020.	0.9	3

#	ARTICLE	IF	CITATIONS
2399	Dataset on the formation of Thioredoxin interacting protein (Txnip) containing redox sensitive high molecular weight nucleoprotein complexes. Data in Brief, 2020, 28, 104893.	0.5	1
2400	Characterization and genome sequencing of a novel T7-like lytic phage, kpssk3, infecting carbapenem-resistant <i>Klebsiella pneumoniae</i> . Archives of Virology, 2020, 165, 97-104.	0.9	25
2401	Comparative transcriptomic analysis reveals novel insights into the response to Cr(VI) exposure in Cr(VI) tolerant ectomycorrhizal fungi <i>Pisolithus</i> sp. 1 LS-2017. Ecotoxicology and Environmental Safety, 2020, 188, 109935.	2.9	10
2402	Comparative genome and transcriptome analysis of the nematode-trapping fungus <i>Duddingtonia flagrans</i> reveals high pathogenicity during nematode infection. Biological Control, 2020, 143, 104159.	1.4	6
2403	Systematic Characterization of Long Non-Coding RNAs and Their Responses to Drought Stress in Dongxiang Wild Rice. Rice Science, 2020, 27, 21-31.	1.7	25
2404	Esterase is a powerful tool for the biodegradation of pyrethroid insecticides. Chemosphere, 2020, 244, 125507.	4.2	148
2405	A computational framework to explore large-scale biosynthetic diversity. Nature Chemical Biology, 2020, 16, 60-68.	3.9	569
2406	Transcriptomic and Epigenomic Dynamics of Honey Bees in Response to Lethal Viral Infection. Frontiers in Genetics, 2020, 11, 566320.	1.1	16
2407	Genome-Wide Identification and Characterization of <i>Fusarium graminearum</i> -Responsive lncRNAs in <i>Triticum aestivum</i> . Genes, 2020, 11, 1135.	1.0	4
2408	Molecular evolutionary and structural analysis of human UCHL1 gene demonstrates the relevant role of intragenic epistasis in Parkinson's disease and other neurological disorders. BMC Evolutionary Biology, 2020, 20, 130.	3.2	7
2409	Identification and characterization of long non-coding RNAs regulating flavonoid biosynthesis in <i>Ginkgo biloba</i> leaves. Industrial Crops and Products, 2020, 158, 112980.	2.5	18
2410	Hidden in plain sight: Systematic investigation of Leucine-rich repeat containing genes unveil the their regulatory network in response to <i>Fusarium</i> wilt in tung tree. International Journal of Biological Macromolecules, 2020, 163, 1759-1767.	3.6	10
2411	RNA-seq reveals the salt tolerance of <i>Ipomoea pes-caprae</i> , a wild relative of sweet potato. Journal of Plant Physiology, 2020, 255, 153276.	1.6	17
2412	Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell Systems, 2020, 11, 402-411.e4.	2.9	121
2413	To gel or not to gel: differential expression of carrageenan-related genes between the gametophyte and tetrasporophyte life cycle stages of the red alga <i>Chondrus crispus</i> . Scientific Reports, 2020, 10, 11498.	1.6	24
2414	Computational identification of receptor-like kinases (RLK) and receptor-like proteins (RLP) in legumes. BMC Genomics, 2020, 21, 459.	1.2	16
2415	De novo transcriptome assembly and data for the blue-winged teal (<i>Spatula discors</i>). Data in Brief, 2020, 30, 105380.	0.5	2
2416	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. ISME Journal, 2020, 14, 2907-2922.	4.4	51

#	ARTICLE	IF	CITATIONS
2417	Long noncoding RNA MARL regulates antiviral responses through suppression miR-122-dependent MAVS downregulation in lower vertebrates. <i>PLoS Pathogens</i> , 2020, 16, e1008670.	2.1	65
2418	Liver transcriptome resources of four commercially exploited teleost species. <i>Scientific Data</i> , 2020, 7, 214.	2.4	4
2419	Whole genome resequencing of four Italian sweet pepper landraces provides insights on sequence variation in genes of agronomic value. <i>Scientific Reports</i> , 2020, 10, 9189.	1.6	18
2420	Transcriptome Analysis Reveals the Potential Role of Long Non-coding RNAs in Mammary Gland of Yak During Lactation and Dry Period. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 579708.	1.8	9
2421	Understanding the relationship between viral infections and trace elements from a metallomics perspective: implications for COVID-19. <i>Metallomics</i> , 2020, 12, 1912-1930.	1.0	21
2422	Chorismate mutase and isochorismatase, two potential effectors of the migratory nematode <i>Hirschmanniella oryzae</i> , increase host susceptibility by manipulating secondary metabolite content of rice. <i>Molecular Plant Pathology</i> , 2020, 21, 1634-1646.	2.0	12
2423	Major SCP/TAPS protein expansion in <i>Lucilia cuprina</i> is associated with novel tandem array organisation and domain architecture. <i>Parasites and Vectors</i> , 2020, 13, 598.	1.0	1
2424	Genome-Wide Analysis Reveals Changes in Long Noncoding RNAs in the Differentiation of Canine BMSCs into Insulin-Producing Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5549.	1.8	5
2425	Molecular Evolution and Characterization of Fish Stathmin Genes. <i>Animals</i> , 2020, 10, 1328.	1.0	2
2426	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7
2427	Functional Insight of Nitric-Oxide Induced DUF Genes in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 1041.	1.7	24
2428	De novo transcriptome assembly and functional annotation for Y-organs of the blue crab (<i>Callinectes</i>) Tj ETQq1 1 0.784314 rgBT /Ove Endocrinology, 2020, 298, 113567.	0.8	7
2429	HAK/KUP/KT family potassium transporter genes are involved in potassium deficiency and stress responses in tea plants (<i>Camellia sinensis</i> L.): expression and functional analysis. <i>BMC Genomics</i> , 2020, 21, 556.	1.2	27
2430	Evolutionary Remodeling of the Cell Envelope in Bacteria of the Planctomycetes Phylum. <i>Genome Biology and Evolution</i> , 2020, 12, 1528-1548.	1.1	13
2431	“Mind the Gap” Hi-C Technology Boosts Contiguity of the Globe Artichoke Genome in Low-Recombination Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3557-3564.	0.8	12
2432	Transcriptomic data on the transgenerational exposure of the keystone amphipod <i>Gammarus locusta</i> to simvastatin. <i>Data in Brief</i> , 2020, 32, 106248.	0.5	7
2433	Identification of Putative Non-Substrate-Based XT-I Inhibitors by Natural Product Library Screening. <i>Biomolecules</i> , 2020, 10, 1467.	1.8	8
2434	Streamlined and Abundant Bacterioplankton Thrive in Functional Cohorts. <i>MSystems</i> , 2020, 5, .	1.7	8

#	ARTICLE	IF	CITATIONS
2435	Genome-Wide Characterization and Expression of Two-Component System Genes in Cytokinin-Regulated Gall Formation in <i>Zizania latifolia</i> . <i>Plants</i> , 2020, 9, 1409.	1.6	14
2436	The Infant-Derived <i>Bifidobacterium bifidum</i> Strain CNCM I-4319 Strengthens Gut Functionality. <i>Microorganisms</i> , 2020, 8, 1313.	1.6	10
2437	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. <i>Scientific Reports</i> , 2020, 10, 14453.	1.6	27
2438	Consistency of the Tools That Predict the Impact of Single Nucleotide Variants (SNVs) on Gene Functionality: The BRCA1 Gene. <i>Biomolecules</i> , 2020, 10, 475.	1.8	0
2439	Bioinformatics approach to understand nature's unified mechanism of stereo-divergent synthesis of isoprenoid skeletons. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 142.	1.7	2
2440	Multiple Intraspecific Variations of Mitochondrial Genomes in the Green-Tide Forming Alga, <i>Ulva compressa</i> Linnaeus (Ulvophyceae, Chlorophyta). <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
2441	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	6.0	302
2442	Characterization and molecular evolution of claudin genes in the <i>Pungitius sinensis</i> . <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2020, 190, 749-759.	0.7	2
2443	Molecular characterisation and expression analysis of NAC transcription factor genes in wild <i>Medicago falcata</i> under abiotic stresses. <i>Functional Plant Biology</i> , 2020, 47, 327.	1.1	2
2444	Large-scale tethered function assays identify factors that regulate mRNA stability and translation. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 989-1000.	3.6	51
2445	Omics approaches for conservation biology research on the bivalve <i>Chamelea gallina</i> . <i>Scientific Reports</i> , 2020, 10, 19177.	1.6	9
2446	Localized effect of treated wastewater effluent on the resistome of an urban watershed. <i>GigaScience</i> , 2020, 9, .	3.3	21
2447	Classification and Computational Analysis of <i>Arabidopsis thaliana</i> Sperm Cell-Specific F-Box Protein Gene 3p.AtFBP113. <i>Frontiers in Genetics</i> , 2020, 11, 609668.	1.1	2
2448	Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. <i>BMC Biology</i> , 2020, 18, 139.	1.7	17
2449	Changing Expression Profiles of Messenger RNA, MicroRNA, Long Non-coding RNA, and Circular RNA Reveal the Key Regulators and Interaction Networks of Competing Endogenous RNA in Pulmonary Fibrosis. <i>Frontiers in Genetics</i> , 2020, 11, 558095.	1.1	9
2450	Genomic and transcriptomic landscapes and evolutionary dynamics of molluscan glycoside hydrolase families with implications for algae-feeding biology. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2744-2756.	1.9	2
2451	Zn-CysHis Protein Factor Families: Role of Electrostatic Interaction of Zn-Domains in Factor Functions. <i>Molecular Biology</i> , 2020, 54, 157-162.	0.4	0
2452	The genome of Mekong tiger perch (<i>Datnioides undecimradiatus</i>) provides insights into the phylogenetic position of Lobotiformes and biological conservation. <i>Scientific Reports</i> , 2020, 10, 8164.	1.6	3

#	ARTICLE	IF	CITATIONS
2453	Segmental Translocation Contributed to the Origin of the Brassica S-locus. Horticultural Plant Journal, 2020, 6, 167-178.	2.3	8
2454	A Novel Computational Approach for Identifying Essential Proteins From Multiplex Biological Networks. Frontiers in Genetics, 2020, 11, 343.	1.1	6
2455	Ginkgo biloba Seeds. , 2020, , 241-254.		1
2456	The N ¹ -Methyladenosine Methylome of Petunia mRNA. Plant Physiology, 2020, 183, 1710-1724.	2.3	31
2457	Genomic and transcriptomic analyses in Drosophila suggest that the ecdysteroid kinase-like (EckL) gene family encodes the "detoxification-by-phosphorylation" enzymes of insects. Insect Biochemistry and Molecular Biology, 2020, 123, 103429.	1.2	24
2458	Comparative genome analysis on intraspecific evolution and nitrogen fixation of Leptospirillum ferriphilum isolates. Transactions of Nonferrous Metals Society of China, 2020, 30, 1635-1646.	1.7	4
2459	Basic Helix-Loop-Helix (bHLH) transcription factor family in Yellow horn (Xanthoceras sorbifolia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50 patterns. International Journal of Biological Macromolecules, 2020, 160, 711-723.	3.6	17
2460	Shifting evolutionary sands: transcriptome characterization of the Aptostichus atomarius species complex. BMC Evolutionary Biology, 2020, 20, 68.	3.2	1
2461	Genetic and functional diversification of chemosensory pathway receptors in mosquito-borne filarial nematodes. PLoS Biology, 2020, 18, e3000723.	2.6	33
2462	Genome-Wide Detection of Key Genes and Epigenetic Markers for Chicken Fatty Liver. International Journal of Molecular Sciences, 2020, 21, 1800.	1.8	11
2463	Comparative Genomic Analysis Confirms Five Genetic Populations of the Select Agent, Rathayibacter toxicus. Microorganisms, 2020, 8, 366.	1.6	3
2464	Identification of tissue-specific and cold-responsive lncRNAs in Medicago truncatula by high-throughput RNA sequencing. BMC Plant Biology, 2020, 20, 99.	1.6	29
2465	The CRISPR-Cas systems were selectively inactivated during evolution of Bacillus cereus group for adaptation to diverse environments. ISME Journal, 2020, 14, 1479-1493.	4.4	32
2466	Genome-wide analysis of glutathione S-transferase gene family in G. max. Biologia (Poland), 2020, 75, 1691-1705.	0.8	9
2467	Improved hybrid de novo genome assembly and annotation of African wild rice, Oryza longistaminata, from Illumina and PacBio sequencing reads. Plant Genome, 2020, 13, e20001.	1.6	15
2468	First draft genome for the sand-hopper Trinorchestia longiramus. Scientific Data, 2020, 7, 85.	2.4	8
2469	Targeted assemblies of cas1 suggest CRISPR-Cas™s response to soil warming. ISME Journal, 2020, 14, 1651-1662.	4.4	6
2470	Bioinformatics analysis of genes of Streptomyces xinghaiensis (fradiae) ATCC 19609 with a focus on mutations conferring resistance to oligomycin A and its derivatives. Journal of Global Antimicrobial Resistance, 2020, 22, 47-53.	0.9	5

#	ARTICLE	IF	CITATIONS
2471	Screening of drought-resistance related genes and analysis of promising regulatory pathway in camel renal medulla. <i>Genomics</i> , 2020, 112, 2633-2639.	1.3	4
2472	Integrative analysis of the RNA interference toolbox in two Salicaceae willow species, and their roles in stress response in poplar (<i>Populus trichocarpa</i> Torr. & Gray). <i>International Journal of Biological Macromolecules</i> , 2020, 162, 1127-1139.	3.6	9
2473	Long Noncoding RNA Expression Profiling During the Neuronal Differentiation of Glial Precursor Cells from Rat Dorsal Root Ganglia. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 356-373.	1.4	2
2474	Structure of LINC00511 siRNA conjugated nanobubbles and improvement of cisplatin sensitivity on triple negative breast cancer. <i>FASEB Journal</i> , 2020, 34, 9713-9726.	0.2	28
2475	Transcriptomic and functional analyses uncover the regulatory role of lncRNA000170 in tomato multicellular trichome formation. <i>Plant Journal</i> , 2020, 104, 18-29.	2.8	16
2476	Evidence from ileum and liver transcriptomes of resistance to high-salt and water-deprivation conditions in camel. <i>Zoological Letters</i> , 2020, 6, 8.	0.7	4
2477	Transcriptomic Analysis of Liver Tissue in Fat Greenling (<i>Hexagrammos otakii</i>) Exposed to Elevated Ambient Ammonia. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
2478	A Chinese White Pear (<i>Pyrus bretschneideri</i>) BZR Gene PbBZR1 Act as a Transcriptional Repressor of Lignin Biosynthetic Genes in Fruits. <i>Frontiers in Plant Science</i> , 2020, 11, 1087.	1.7	16
2479	Insight into Evolution and Conservation Patterns of B1-Subfamily Members of GPCR. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 2505-2517.	0.9	3
2480	Analysis of two Mexican <i>Pectobacterium brasiliense</i> strains reveals an inverted relationship between c-di-GMP levels with exopolysaccharide production and swarming motility. <i>Microbiological Research</i> , 2020, 235, 126427.	2.5	7
2481	Analysis of pituitary transcriptomics indicates that lncRNAs are involved in the regulation of sheep estrus. <i>Functional and Integrative Genomics</i> , 2020, 20, 563-573.	1.4	11
2482	Genome-wide identification and characterization of novel long non-coding RNA in Ruminal tissue affected with sub-acute Ruminal acidosis from Holstein cattle. <i>Veterinary Research Communications</i> , 2020, 44, 19-27.	0.6	5
2483	Domain-mediated interactions for protein subfamily identification. <i>Scientific Reports</i> , 2020, 10, 264.	1.6	2
2484	Crystal structure of Alr1298, a pentapeptide repeat protein from the cyanobacterium <i>Nostoc</i> sp. PCC 7120, determined at 2.1 Å... resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1143-1153.	1.5	7
2485	High-throughput transcriptome analysis reveals potentially important relationships between lncRNAs and genes in broilers affected by Valgus-varus Deformity (<i>Gallus gallus</i>). <i>Gene</i> , 2020, 743, 144511.	1.0	8
2486	The first glimpse of the endometrial microbiota in early pregnancy. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, 296-305.	0.7	40
2487	Phylogenomics changes our understanding about earwig evolution. <i>Systematic Entomology</i> , 2020, 45, 516-526.	1.7	15
2488	Paralogization and New Protein Architectures in Planctomycetes Bacteria with Complex Cell Structures. <i>Molecular Biology and Evolution</i> , 2020, 37, 1020-1040.	3.5	6

#	ARTICLE	IF	CITATIONS
2489	Genome-wide analysis of mRNAs and lncRNAs in <i>Mycoplasma bovis</i> infected and non-infected bovine mammary gland tissues. <i>Molecular and Cellular Probes</i> , 2020, 50, 101512.	0.9	17
2490	Subchromosome-Scale Nuclear and Complete Mitochondrial Genome Characteristics of <i>Morchella crassipes</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 483.	1.8	27
2491	A comparative gene co-expression analysis using self-organizing maps on two congener filmy ferns identifies specific desiccation tolerance mechanisms associated to their microhabitat preference. <i>BMC Plant Biology</i> , 2020, 20, 56.	1.6	17
2492	Effects of Castration on miRNA, lncRNA, and mRNA Profiles in Mice Thymus. <i>Genes</i> , 2020, 11, 147.	1.0	8
2493	Draft Genome of the Asian Buffalo Leech <i>Hirudinaria manillensis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 1321.	1.1	11
2494	Genome-wide identification of long non-coding RNAs and circular RNAs reveal their ceRNA networks in response to cucumber green mottle mosaic virus infection in watermelon. <i>Archives of Virology</i> , 2020, 165, 1177-1190.	0.9	41
2495	The transcriptome of the newt <i>Cynops orientalis</i> provides new insights into evolution and function of sexual gene networks in sarcopterygians. <i>Scientific Reports</i> , 2020, 10, 5445.	1.6	11
2496	Evolution and domestication of Tc1/mariner transposons in the genome of African coelacanth (<i>Latimeria chalumnae</i>). <i>Genome</i> , 2020, 63, 375-386.	0.9	1
2497	Two-Level Protein Methylation Prediction using structure model-based features. <i>Scientific Reports</i> , 2020, 10, 6008.	1.6	7
2498	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.	3.1	60
2499	Identification and evolutionary analysis of the nucleolar proteome of <i>Giardia lamblia</i> . <i>BMC Genomics</i> , 2020, 21, 269.	1.2	7
2500	Transcriptomic analysis of polyketide synthases in a highly ciguatoxic dinoflagellate, <i>Gambierdiscus polynesiensis</i> and low toxicity <i>Gambierdiscus pacificus</i> , from French Polynesia. <i>PLoS ONE</i> , 2020, 15, e0231400.	1.1	14
2501	ABC translation factors: from antibiotic resistance to immune response. <i>FEBS Letters</i> , 2021, 595, 675-706.	1.3	25
2502	Global profiling of lncRNAs-miRNAs-mRNAs reveals differential expression of coding genes and non-coding RNAs in the lung of beagle dogs at different stages of <i>Toxocara canis</i> infection. <i>International Journal for Parasitology</i> , 2021, 51, 49-61.	1.3	13
2503	High quality genome of <i>Erigeron breviscapus</i> provides a reference for herbal plants in Asteraceae. <i>Molecular Ecology Resources</i> , 2021, 21, 153-169.	2.2	21
2504	A chromosome-level genome assembly of the woolly apple aphid, <i>Eriosoma lanigerum</i> Hausmann (Hemiptera: Aphididae). <i>Molecular Ecology Resources</i> , 2021, 21, 316-326.	2.2	28
2505	Comprehensive identification and analyses of the Hsf gene family in the whole-genome of three Apiaceae species. <i>Horticultural Plant Journal</i> , 2021, 7, 457-468.	2.3	15
2506	Molecular mechanism of Chinese alligator (<i>Alligator sinensis</i>) adapting to hibernation. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2021, 336, 32-49.	0.6	7

#	ARTICLE	IF	CITATIONS
2507	Genome-wide characterization and expression analysis of HAK K ⁺ transport family in Ipomoea. 3 Biotech, 2021, 11, 3.	1.1	13
2508	The profile secretion of <i>Aspergillus clavatus</i> : Different pre-treatments of sugarcane bagasse distinctly induces holocellulases for the lignocellulosic biomass conversion into sugar. Renewable Energy, 2021, 165, 748-757.	4.3	13
2509	Characterization and analysis of the transcriptome in <i>Opisina arenosella</i> from different developmental stages using single-molecule real-time transcript sequencing and RNA-seq. International Journal of Biological Macromolecules, 2021, 169, 216-227.	3.6	10
2510	Human SIRT1 Multispecificity Is Modulated by Active-Site Vicinity Substitutions during Natural Evolution. Molecular Biology and Evolution, 2021, 38, 545-556.	3.5	5
2511	Gene expression during bacterivorous growth of a widespread marine heterotrophic flagellate. ISME Journal, 2021, 15, 154-167.	4.4	13
2512	Metagenomics of Plant Rhizosphere and Endophytic Association: Concepts and Applications. Rhizosphere Biology, 2021, , 275-291.	0.4	0
2513	Transcriptome characterization and generation of marker resource for Himalayan vulnerable species, <i>Ulmus wallichiana</i> . Molecular Biology Reports, 2021, 48, 721-729.	1.0	3
2514	Transcriptome profiling of <i>Stevia rebaudiana</i> MS007 revealed genes involved in flower development. Turkish Journal of Biology, 2021, 45, 314-322.	2.1	2
2516	AhR and Cancer: From Gene Profiling to Targeted Therapy. International Journal of Molecular Sciences, 2021, 22, 752.	1.8	42
2517	RNA-sequencing indicates high hemocyanin expression as a key strategy for cold adaptation in the Antarctic amphipod <i>Eusirus cf. giganteus</i> clade g3. Biocell, 2021, 45, 1611-1619.	0.4	5
2518	Genome Recovery, Functional Profiling, and Taxonomic Classification from Metagenomes. Methods in Molecular Biology, 2021, 2242, 153-172.	0.4	2
2519	The microbiome of deep-sea fish reveals new microbial species and a sparsity of antibiotic resistance genes. Gut Microbes, 2021, 13, 1-13.	4.3	19
2520	Screening and Analysis of Key lncRNA and miRNA Affecting the Occurrence and Proliferation of Human Glioma Cells. Asian Case Reports in Oncology, 2021, 10, 1-23.	0.0	0
2521	Integrated analysis of lncRNA and mRNA transcriptomes reveals the potential regulatory role of lncRNA in kiwifruit ripening and softening. Scientific Reports, 2021, 11, 1671.	1.6	17
2522	Genetics, molecular biomarkers, and artificial intelligence to improve diagnostic and prognostic efficacy. , 2021, , 167-176.		0
2523	The C-terminal loop of <i>Arabidopsis thaliana</i> guanosine deaminase is essential to catalysis. Chemical Communications, 2021, 57, 9748-9751.	2.2	2
2524	Identification, characterization and functional analysis of grape (<i>Vitis vinifera</i> L.) mitochondrial transcription termination factor (mTERF) genes in responding to biotic stress and exogenous phytohormone. BMC Genomics, 2021, 22, 136.	1.2	9
2525	Evolution of frustrated and stabilising contacts in reconstructed ancient proteins. European Biophysics Journal, 2021, 50, 699-712.	1.2	1

#	ARTICLE	IF	CITATIONS
2527	Comparative genomics reveals broad genetic diversity, extensive recombination and nascent ecological adaptation in <i>Micrococcus luteus</i> . <i>BMC Genomics</i> , 2021, 22, 124.	1.2	15
2528	<i>Brassica carinata</i> genome characterization clarifies U TM s triangle model of evolution and polyploidy in <i>Brassica</i> . <i>Plant Physiology</i> , 2021, 186, 388-406.	2.3	75
2529	Genome-wide identification of the SOD gene family and expression analysis under drought and salt stress in barley. <i>Plant Growth Regulation</i> , 2021, 94, 49-60.	1.8	33
2530	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. <i>ISME Journal</i> , 2021, 15, 807-817.	4.4	28
2531	Multiple putative methemoglobin reductases in <i>C. reinhardtii</i> may support enzymatic functions for its multiple hemoglobins. <i>International Journal of Biological Macromolecules</i> , 2021, 171, 465-479.	3.6	3
2532	Choanoflagellates and the ancestry of neurosecretory vesicles. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20190759.	1.8	17
2533	Variation in Parasitoid Virulence of <i>Tetrastichus brontispae</i> during the Targeting of Two Host Beetles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3581.	1.8	2
2534	Metagenomic Analysis of Microbial Community Affiliated with Termitarium Reveals High Lignocellulolytic Potential. <i>Current Microbiology</i> , 2021, 78, 1551-1565.	1.0	0
2535	Primary Metabolism co-Opted for Defensive Chemical Production in the Carabid Beetle, <i>Harpalus pensylvanicus</i> . <i>Journal of Chemical Ecology</i> , 2021, 47, 334-349.	0.9	0
2536	Characterization and Full Genome Sequence of Novel KPP-5 Lytic Phage against <i>Klebsiella pneumoniae</i> Responsible for Recalcitrant Infection. <i>Biomedicines</i> , 2021, 9, 342.	1.4	18
2537	Resequencing and SNP discovery of <i>Amur ide</i> (<i>Leuciscus waleckii</i>) provides insights into local adaptations to extreme environments. <i>Scientific Reports</i> , 2021, 11, 5064.	1.6	15
2538	An Overview of Antennal Esterases in Lepidoptera. <i>Frontiers in Physiology</i> , 2021, 12, 643281.	1.3	14
2541	XlinkCyNET: A Cytoscape Application for Visualization of Protein Interaction Networks Based on Cross-Linking Mass Spectrometry Identifications. <i>Journal of Proteome Research</i> , 2021, 20, 1943-1950.	1.8	8
2542	Bet v 1 potential allergens are involved in anthracnose resistance of strawberry varieties. <i>Journal of Berry Research</i> , 2021, 11, 21-32.	0.7	5
2543	Topological Analysis for Sequence Variability: Case Study on more than 2K SARS-CoV-2 sequences of COVID-19 infected 54 countries in comparison with SARS-CoV-1 and MERS-CoV. <i>Infection, Genetics and Evolution</i> , 2021, 88, 104708.	1.0	6
2544	A Roadmap for Genome-Based Phage Taxonomy. <i>Viruses</i> , 2021, 13, 506.	1.5	268
2545	Rational Design of Adenylate Kinase Thermostability through Coevolution and Sequence Divergence Analysis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2768.	1.8	5
2546	Functional long non-coding and circular RNAs in zebrafish. <i>Briefings in Functional Genomics</i> , 2021, , .	1.3	4

#	ARTICLE	IF	CITATIONS
2547	Composition and function of ciliary inner dynein arm subunits studied in <i>Chlamydomonas reinhardtii</i> . Cytoskeleton, 2021, 78, 77-96.	1.0	19
2548	Genome-resolved metagenomics using environmental and clinical samples. Briefings in Bioinformatics, 2021, 22, .	3.2	18
2549	The genetic variation landscape of African swine fever virus reveals frequent positive selection and adaptive flexibility. Transboundary and Emerging Diseases, 2021, 68, 2703-2721.	1.3	10
2550	Genome-wide comparative analysis of long-chain acyl-CoA synthetases (LACSs) gene family: A focus on identification, evolution and expression profiling related to lipid synthesis. Plant Physiology and Biochemistry, 2021, 161, 1-11.	2.8	43
2552	Characterization of putative salinity-responsive biomarkers in olive (<i>Olea europaea</i> L.). Plant Genetic Resources: Characterisation and Utilisation, 2021, 19, 133-143.	0.4	2
2553	Transcriptome analysis of the liver of <i>Eospalax fontanierii</i> under hypoxia. PeerJ, 2021, 9, e11166.	0.9	3
2554	Whole transcriptome sequencing and integrated network analysis elucidates the effects of 3,8-Di-O-methylelagic acid 2-O-glucoside derived from <i>Sanguisorba officinalis</i> L., a novel differentiation inducer on erythroleukemia cells. Pharmacological Research, 2021, 166, 105491.	3.1	7
2555	Structure and Expression Analysis of Sucrose Phosphate Synthase, Sucrose Synthase and Invertase Gene Families in <i>Solanum lycopersicum</i> . International Journal of Molecular Sciences, 2021, 22, 4698.	1.8	28
2556	Tissue-specific regulatory mechanism of lncRNAs and methylation in sheep adipose and muscle induced by <i>Allium mongolicum</i> Regel extracts. Scientific Reports, 2021, 11, 9186.	1.6	8
2557	Transcriptome-based metabolic profiling of flavonoids in <i>Agave lechuguilla</i> waste biomass. Plant Science, 2021, 305, 110748.	1.7	12
2558	Reboot: a straightforward approach to identify genes and splicing isoforms associated with cancer patient prognosis. NAR Cancer, 2021, 3, zcab024.	1.6	8
2559	Chloroplast Genomes of the Green-Tide Forming Alga <i>Ulva compressa</i> : Comparative Chloroplast Genomics in the Genus <i>Ulva</i> (Ulvophyceae, Chlorophyta). Frontiers in Marine Science, 2021, 8, .	1.2	10
2561	A Primer on the Analysis of High-Throughput Sequencing Data for Detection of Plant Viruses. Microorganisms, 2021, 9, 841.	1.6	36
2563	Molecular evidence of the avocado defense response to <i>Fusarium kuroshium</i> infection: a deep transcriptome analysis using RNA-Seq. PeerJ, 2021, 9, e11215.	0.9	10
2564	Intrinsically Disordered Proteins as Regulators of Transient Biological Processes and as Untapped Drug Targets. Molecules, 2021, 26, 2118.	1.7	13
2566	Draft Genome Sequence of <i>Deefgea</i> sp. Strain CFH1-16, Isolated from the Intestine of the Freshwater Fish <i>Hypomesus nipponensis</i> . Microbiology Resource Announcements, 2021, 10, .	0.3	1
2567	Deciphering the roles of leucine-rich repeat receptor-like protein kinases (LRR-RLKs) in response to <i>Fusarium wilt</i> in the <i>Vernicia fordii</i> (Tung tree). Phytochemistry, 2021, 185, 112686.	1.4	12
2568	A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. Cell, 2021, 184, 2973-2987.e18.	13.5	111

#	ARTICLE	IF	CITATIONS
2569	Transcriptome analysis reveals potential function of long non-coding RNAs in 20-hydroxyecdysone regulated autophagy in <i>Bombyx mori</i> . <i>BMC Genomics</i> , 2021, 22, 374.	1.2	12
2570	The Subcellular Proteome of a Planctomycetes Bacterium Shows That Newly Evolved Proteins Have Distinct Fractionation Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 643045.	1.5	8
2571	CBP/p300 homologs CBP2 and CBP3 play distinct roles in planarian stem cell function. <i>Developmental Biology</i> , 2021, 473, 130-143.	0.9	15
2572	Enterococcal PrgU Provides Additional Regulation of Pheromone-Inducible Conjugative Plasmids. <i>MSphere</i> , 2021, 6, e0026421.	1.3	4
2573	Identification and Analysis of Long Non-coding RNAs in <i>Leuciscus waleckii</i> Adapted to Highly Alkaline Conditions. <i>Frontiers in Physiology</i> , 2021, 12, 665268.	1.3	11
2574	Characterization of the role of esterases in the biodegradation of organophosphate, carbamate, and pyrethroid pesticides. <i>Journal of Hazardous Materials</i> , 2021, 411, 125026.	6.5	115
2575	Gapless indica rice genome reveals synergistic contributions of active transposable elements and segmental duplications to rice genome evolution. <i>Molecular Plant</i> , 2021, 14, 1745-1756.	3.9	50
2577	<i>Toxocara canis</i> Infection Alters lncRNA and mRNA Expression Profiles of Dog Bone Marrow. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 688128.	1.8	5
2578	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 660052.	1.5	20
2579	Network-based visualisation reveals new insights into transposable element diversity. <i>Molecular Systems Biology</i> , 2021, 17, e9600.	3.2	2
2580	Zetaproteobacteria Pan-Genome Reveals Candidate Gene Cluster for Twisted Stalk Biosynthesis and Export. <i>Frontiers in Microbiology</i> , 2021, 12, 679409.	1.5	9
2581	Production of Glucose 6-Phosphate From a Cellulosic Feedstock in a One Pot Multi-Enzyme Synthesis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 678038.	2.0	1
2582	Enhanced mutualistic symbiosis between soil phages and bacteria with elevated chromium-induced environmental stress. <i>Microbiome</i> , 2021, 9, 150.	4.9	67
2583	The landscape and biological relevance of aberrant alternative splicing events in esophageal squamous cell carcinoma. <i>Oncogene</i> , 2021, 40, 4184-4197.	2.6	8
2584	Identification and Comparative Analysis of Long Non-coding RNAs in High- and Low-Fecundity Goat Ovaries During Estrus. <i>Frontiers in Genetics</i> , 2021, 12, 648158.	1.1	4
2585	Trajectories of Homoeolog-Specific Expression in Allotetraploid <i>Tragopogon castellanus</i> Populations of Independent Origins. <i>Frontiers in Plant Science</i> , 2021, 12, 679047.	1.7	3
2586	Comparative genomic analysis of <i>Escherichia coli</i> isolates from cases of bovine clinical mastitis identifies nine specific pathotype marker genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
2587	<i>Trichoderma reesei</i> ACE4, a Novel Transcriptional Activator Involved in the Regulation of Cellulase Genes during Growth on Cellulose. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0059321.	1.4	20

#	ARTICLE	IF	CITATIONS
2588	A Transcriptome-Wide Isoform Landscape of Melanocytic Nevi and Primary Melanomas Identifies Gene Isoforms Associated with Malignancy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7165.	1.8	7
2589	Genome-wide analysis of the B3 transcription factors reveals that RcABI3/VP1 subfamily plays important roles in seed development and oil storage in castor bean (<i>Ricinus communis</i>). <i>Plant Diversity</i> , 2022, 44, 201-212.	1.8	8
2590	Genome-wide identification and analysis of the YABBY gene family in Moso Bamboo (<i>Phyllostachys</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.9	9
2591	Comprehensive Analysis of the Expression Profiles of Hepatic lncRNAs in the Mouse Model of Alcoholic Liver Disease. <i>Frontiers in Pharmacology</i> , 2021, 12, 709287.	1.6	6
2593	Lactic Acid Bacteria Diversity and Characterization of Probiotic Candidates in Fermented Meats. <i>Foods</i> , 2021, 10, 1519.	1.9	23
2594	Transcriptome analysis of messenger RNA and long noncoding RNA related to different developmental stages of tail adipose tissues of sunite sheep. <i>Food Science and Nutrition</i> , 2021, 9, 5722-5734.	1.5	7
2595	Potential stress tolerance roles of barley germins and GLPs. <i>Development Genes and Evolution</i> , 2021, 231, 109-118.	0.4	3
2596	Integrative overview of IFITMs family based on Bioinformatics analysis. <i>Intractable and Rare Diseases Research</i> , 2021, 10, 165-172.	0.3	6
2597	Data on the first functionally-annotated de novo transcriptome assembly for North American flying squirrels (genus <i>Glaucomys</i>). <i>Data in Brief</i> , 2021, 37, 107267.	0.5	1
2599	Comparison of mouse models reveals a molecular distinction between psychotic illness in PWS and schizophrenia. <i>Translational Psychiatry</i> , 2021, 11, 433.	2.4	5
2600	Gene expression profile and long noncoding RNA analysis in <i>Candida albicans</i> insoluble Î2-glucan-stimulated CD14+ monocytes and THP-1 cells. <i>Microbial Pathogenesis</i> , 2021, 157, 104963.	1.3	3
2601	Chromosome-scale assembly and evolution of the tetraploid <i>Salvia splendens</i> (Lamiaceae) genome. <i>Horticulture Research</i> , 2021, 8, 177.	2.9	27
2602	Whole-Genome and Transcriptome Sequencing of <i>Phlebopus portentosus</i> Reveals Its Associated Ectomycorrhizal Niche and Conserved Pathways Involved in Fruiting Body Development. <i>Frontiers in Microbiology</i> , 2021, 12, 732458.	1.5	8
2603	The GRAS gene family and its roles in seed development in litchi (<i>Litchi chinensis</i> Sonn). <i>BMC Plant Biology</i> , 2021, 21, 423.	1.6	8
2604	Comprehensive Assessment of the Relationship Between Site ² Specificity and Helix Î±2 in the Erbin PDZ Domain. <i>Journal of Molecular Biology</i> , 2021, 433, 167115.	2.0	0
2605	Genome sequencing and identification of cellulase genes in <i>Bacillus paralicheniformis</i> strains from the Red Sea. <i>BMC Microbiology</i> , 2021, 21, 254.	1.3	10
2606	De Novo Transcriptome Assembly, Functional Annotation, and Transcriptome Dynamics Analyses Reveal Stress Tolerance Genes in Mangrove Tree (<i>Bruguiera gymnorhiza</i>). <i>International Journal of Molecular Sciences</i> , 2021, 22, 9874.	1.8	3
2607	The genome sequence provides insights into salt tolerance of <i>Achnatherum splendens</i> (Gramineae), a constructive species of alkaline grassland. <i>Plant Biotechnology Journal</i> , 2022, 20, 116-128.	4.1	18

#	ARTICLE	IF	CITATIONS
2608	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. <i>IScience</i> , 2021, 24, 103081.	1.9	9
2609	Structure and substrate specificity determinants of NfnB, a dinitroaniline herbicide-catabolizing nitroreductase from <i>Sphingopyxis</i> sp. strain HMH. <i>Journal of Biological Chemistry</i> , 2021, 297, 101143.	1.6	6
2610	Genomic analysis of the carboxylesterase family in the salmon louse (<i>Lepeophtheirus salmonis</i>). <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2021, 248, 109095.	1.3	1
2611	Comprehensive analysis of miRNA-mRNA/lncRNA during gonadal development of triploid female rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Genomics</i> , 2021, 113, 3533-3543.	1.3	10
2612	Polyketide synthase genes and molecular trade-offs in the ichthyotoxic species <i>Prymnesium parvum</i> . <i>Science of the Total Environment</i> , 2021, 795, 148878.	3.9	10
2613	Genome-wide transcriptome profiling and characterization of mannuronan C5-epimerases in <i>Saccharina japonica</i> . <i>Algal Research</i> , 2021, 60, 102491.	2.4	6
2614	The Draft Genome Sequence of a New Land-Hopper <i>Platorchestia hallaensis</i> . <i>Frontiers in Genetics</i> , 2020, 11, 621301.	1.1	1
2615	Genome-Wide Identification and Comparative Analysis of ARF Family Genes in Three Apiaceae Species. <i>Frontiers in Genetics</i> , 2020, 11, 590535.	1.1	9
2616	Fluoxetine ameliorates depressive symptoms by regulating lncRNA expression in the mouse hippocampus. <i>Zoological Research</i> , 2021, 42, 28-42.	0.9	10
2618	Comparative analysis of the <i>TCP</i> gene family in celery, coriander and carrot (family) Tj ETQq1 1 0.784314 rgBT /Overbo 0,2 9		
2620	Configuration of Hidden Markov Models. , 2014, , 143-152.		1
2621	Target Selection for Structural Genomics of Infectious Diseases. <i>Methods in Molecular Biology</i> , 2014, 1140, 35-51.	0.4	1
2622	Structural Studies of TSPO, a Mitochondrial Membrane Protein. , 2014, , 393-421.		6
2623	GENCODE Pseudogenes. <i>Methods in Molecular Biology</i> , 2014, 1167, 129-155.	0.4	29
2624	Approaches for Classifying DNA Variants Found by Sanger Sequencing in a Medical Genetics Laboratory. <i>Methods in Molecular Biology</i> , 2014, 1168, 227-250.	0.4	3
2625	De Novo Membrane Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2015, 1215, 331-350.	0.4	7
2626	Discovering Essential Domains in Essential Genes. <i>Methods in Molecular Biology</i> , 2015, 1279, 235-245.	0.4	1
2627	Computational Prediction of Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2015, 1278, 57-75.	0.4	37

#	ARTICLE	IF	CITATIONS
2628	Functional Annotation of Rare Genetic Variants. , 2015, , 57-70.		2
2629	Computational Analysis of Virus-Host Interactomes. <i>Methods in Molecular Biology</i> , 2013, 1064, 115-130.	0.4	3
2630	Xylem Sap Proteomics. <i>Methods in Molecular Biology</i> , 2014, 1072, 391-405.	0.4	11
2631	MAFFT: Iterative Refinement and Additional Methods. <i>Methods in Molecular Biology</i> , 2014, 1079, 131-146.	0.4	397
2632	Bioinformatics Identification of Coevolving Residues. <i>Methods in Molecular Biology</i> , 2014, 1123, 223-243.	0.4	3
2633	Bioinformatics and Medicinal Plant Research: Current Scenario. , 2019, , 141-157.		1
2635	Antigens and Epitopes. , 2016, , 125-143.		1
2636	Efficient Sequence Regression by Learning Linear Models in All-Subsequence Space. <i>Lecture Notes in Computer Science</i> , 2017, , 37-52.	1.0	1
2637	Crop Genome Annotation: A Case Study for the Brassica rapa Genome. <i>Compendium of Plant Genomes</i> , 2015, , 53-64.	0.3	1
2639	Identifying Driver Mutations in Cancer. <i>Translational Bioinformatics</i> , 2013, , 33-56.	0.0	4
2640	Distribution of MACPF/CDC Proteins. <i>Sub-Cellular Biochemistry</i> , 2014, 80, 7-30.	1.0	38
2641	The Evolution of Transcriptional Regulation in the Viridiplantae and its Correlation with Morphological Complexity. <i>Advances in Marine Genomics</i> , 2015, , 301-333.	1.2	23
2642	Structural and Functional Characterization of Arabidopsis thaliana WW Domain Containing Protein F4JC80. <i>SpringerBriefs in Applied Sciences and Technology</i> , 2015, , 25-39.	0.2	3
2643	Systematic analysis of the OFP genes in six Rosaceae genomes and their roles in stress response in Chinese pear (<i>Pyrus bretschneideri</i>). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2085-2094.	1.4	8
2644	Unraveling the Genetic Complexities in Gene Set of Sugarcane Red Rot Pathogen <i>Colletotrichum falcatum</i> Through Transcriptomic Approach. <i>Sugar Tech</i> , 2017, 19, 604-615.	0.9	22
2645	MicroRNA and mRNA interactions coordinate the immune response in non-lethal heat stressed <i>Litopenaeus vannamei</i> against AHPND-causing <i>Vibrio parahaemolyticus</i> . <i>Scientific Reports</i> , 2020, 10, 787.	1.6	19
2646	Phospholipid ebb and flow makes mitochondria go. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	63
2647	A New Dinoflagellate Genome Illuminates a Conserved Gene Cluster Involved in Sunscreen Biosynthesis. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	31

#	ARTICLE	IF	CITATIONS
2648	Polysaccharide utilization loci and nutritional specialization in a dominant group of butyrate-producing human colonic Firmicutes. <i>Microbial Genomics</i> , 2016, 2, e000043.	1.0	162
2649	Genome mining of fungal lipid-degrading enzymes for industrial applications. <i>Microbiology (United Kingdom)</i> , 2016, 156, 1143-1153.	0.7	33
2667	A challenging interpretation of a hexagonally layered protein structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 203-208.	2.5	4
2669	ProfileGrids solve the large alignment visualization problem: influenza hemagglutinin example. <i>F1000Research</i> , 0, 2, 2.	0.8	5
2670	PanFunPro: PAN-genome analysis based on FUNctional PROfiles. <i>F1000Research</i> , 0, 2, 265.	0.8	17
2671	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. <i>F1000Research</i> , 2014, 3, 47.	0.8	11
2672	HeatMapView: interactive display of 2D data in biology. <i>F1000Research</i> , 2014, 3, 48.	0.8	17
2673	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	0.9	114
2674	Evolutionary analysis of the most polymorphic gene family in <i>falciparum</i> malaria. <i>Wellcome Open Research</i> , 2019, 4, 193.	0.9	64
2675	The Structural Basis of Coenzyme A Recycling in a Bacterial Organelle. <i>PLoS Biology</i> , 2016, 14, e1002399.	2.6	40
2676	Alternative Protein-Protein Interfaces Are Frequent Exceptions. <i>PLoS Computational Biology</i> , 2012, 8, e1002623.	1.5	26
2677	Application of Rigidity Theory to the Thermostabilization of Lipase A from <i>Bacillus subtilis</i> . <i>PLoS Computational Biology</i> , 2016, 12, e1004754.	1.5	48
2678	Learning causal networks with latent variables from multivariate information in genomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005662.	1.5	28
2679	Contact- and Protein Transfer-Dependent Stimulation of Assembly of the Gliding Motility Machinery in <i>Myxococcus xanthus</i> . <i>PLoS Genetics</i> , 2015, 11, e1005341.	1.5	49
2680	Human IgG1 Responses to Surface Localised <i>Schistosoma mansoni</i> Ly6 Family Members Drop following Praziquantel Treatment. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003920.	1.3	17
2681	NMR Structure of Lipoprotein YxeF from <i>Bacillus subtilis</i> Reveals a Calycin Fold and Distant Homology with the Lipocalin Blc from <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2012, 7, e37404.	1.1	6
2682	Cofactor Binding Protects Flavodoxin against Oxidative Stress. <i>PLoS ONE</i> , 2012, 7, e41363.	1.1	9
2683	Relating the Disease Mutation Spectrum to the Evolution of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR). <i>PLoS ONE</i> , 2012, 7, e42336.	1.1	12

#	ARTICLE	IF	CITATIONS
2684	FunSAV: Predicting the Functional Effect of Single Amino Acid Variants Using a Two-Stage Random Forest Model. PLoS ONE, 2012, 7, e43847.	1.1	43
2685	ThioFinder: A Web-Based Tool for the Identification of Thiopeptide Gene Clusters in DNA Sequences. PLoS ONE, 2012, 7, e45878.	1.1	51
2686	Metagenomic Analysis of the Microbiota from the Crop of an Invasive Snail Reveals a Rich Reservoir of Novel Genes. PLoS ONE, 2012, 7, e48505.	1.1	62
2687	Bioinformatic Analysis of Epigenetic and MicroRNA Mediated Regulation of Drought Responsive Genes in Rice. PLoS ONE, 2012, 7, e49331.	1.1	41
2688	Simultaneous RNA-Seq Analysis of a Mixed Transcriptome of Rice and Blast Fungus Interaction. PLoS ONE, 2012, 7, e49423.	1.1	242
2689	Differential Expression of In Vivo and In Vitro Protein Profile of Outer Membrane of <i>Acidovorax avenae</i> Subsp. <i>avenae</i> . PLoS ONE, 2012, 7, e49657.	1.1	22
2690	The Duplicated Genes Database: Identification and Functional Annotation of Co-Localised Duplicated Genes across Genomes. PLoS ONE, 2012, 7, e50653.	1.1	54
2691	Lack of RsmA-Mediated Control Results in Constant Hypervirulence, Cell Elongation, and Hyperflagellation in <i>Pectobacterium wasabiae</i> . PLoS ONE, 2013, 8, e54248.	1.1	19
2692	Massive-Scale Gene Co-Expression Network Construction and Robustness Testing Using Random Matrix Theory. PLoS ONE, 2013, 8, e55871.	1.1	49
2693	A Genome-Wide Analysis of the LBD (LATERAL ORGAN BOUNDARIES Domain) Gene Family in <i>Malus domestica</i> with a Functional Characterization of MdLBD11. PLoS ONE, 2013, 8, e57044.	1.1	49
2694	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. PLoS ONE, 2013, 8, e57848.	1.1	6
2695	Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. PLoS ONE, 2013, 8, e59361.	1.1	44
2696	New Putative Chloroplast Vesicle Transport Components and Cargo Proteins Revealed Using a Bioinformatics Approach: An Arabidopsis Model. PLoS ONE, 2013, 8, e59898.	1.1	42
2697	Transcriptional Changes of the Root-Knot Nematode <i>Meloidogyne incognita</i> in Response to <i>Arabidopsis thaliana</i> Root Signals. PLoS ONE, 2013, 8, e61259.	1.1	45
2698	CLCAs - A Family of Metalloproteases of Intriguing Phylogenetic Distribution and with Cases of Substituted Catalytic Sites. PLoS ONE, 2013, 8, e62272.	1.1	19
2699	Biochemical Characterization of Hypothetical Proteins from <i>Helicobacter pylori</i> . PLoS ONE, 2013, 8, e66605.	1.1	16
2700	The <i>Myxococcus xanthus</i> Two-Component System CorSR Regulates Expression of a Gene Cluster Involved in Maintaining Copper Tolerance during Growth and Development. PLoS ONE, 2013, 8, e68240.	1.1	13
2701	Identification of Immunity Related Genes to Study the <i>Physalis peruviana</i> "Fusarium oxysporum" Pathosystem. PLoS ONE, 2013, 8, e68500.	1.1	30

#	ARTICLE	IF	CITATIONS
2702	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast <i>Hortaea werneckii</i> . PLoS ONE, 2013, 8, e71328.	1.1	96
2703	Cross-Link Guided Molecular Modeling with ROSETTA. PLoS ONE, 2013, 8, e73411.	1.1	144
2704	Î²-Propeller Blades as Ancestral Peptides in Protein Evolution. PLoS ONE, 2013, 8, e77074.	1.1	77
2705	Inference of Gene-Phenotype Associations via Protein-Protein Interaction and Orthology. PLoS ONE, 2013, 8, e77478.	1.1	9
2706	Functional and Genomic Analyses of Alpha-Solenoid Proteins. PLoS ONE, 2013, 8, e79894.	1.1	26
2707	Plasmids of Carotenoid-Producing <i>Paracoccus</i> spp. (Alphaproteobacteria) - Structure, Diversity and Evolution. PLoS ONE, 2013, 8, e80258.	1.1	24
2708	The Venom Gland Transcriptome of <i>Latrodectus tredecimguttatus</i> Revealed by Deep Sequencing and cDNA Library Analysis. PLoS ONE, 2013, 8, e81357.	1.1	60
2709	Rbt1 Protein Domains Analysis in <i>Candida albicans</i> Brings Insights into Hyphal Surface Modifications and Rbt1 Potential Role during Adhesion and Biofilm Formation. PLoS ONE, 2013, 8, e82395.	1.1	26
2710	New Insights into the Phylogeny and Molecular Classification of Nicotinamide Mononucleotide Deamidases. PLoS ONE, 2013, 8, e82705.	1.1	7
2711	Genome-Wide Identification, Phylogeny, Evolution and Expression Patterns of AP2/ERF Genes and Cytokinin Response Factors in <i>Brassica rapa</i> ssp. <i>pekinensis</i> . PLoS ONE, 2013, 8, e83444.	1.1	38
2712	MIDDAS-M: Motif-Independent De Novo Detection of Secondary Metabolite Gene Clusters through the Integration of Genome Sequencing and Transcriptome Data. PLoS ONE, 2013, 8, e84028.	1.1	106
2713	Functional Annotation of Conserved Hypothetical Proteins from <i>Haemophilus influenzae</i> Rd KW20. PLoS ONE, 2013, 8, e84263.	1.1	93
2714	Bioinformatics Analysis of Bacterial Annexins – Putative Ancestral Relatives of Eukaryotic Annexins. PLoS ONE, 2014, 9, e85428.	1.1	14
2715	Non-Redundant Unique Interface Structures as Templates for Modeling Protein Interactions. PLoS ONE, 2014, 9, e86738.	1.1	66
2716	Silencing Motifs in the Clr2 Protein from Fission Yeast, <i>Schizosaccharomyces pombe</i> . PLoS ONE, 2014, 9, e86948.	1.1	8
2717	Comparative Genomic Analysis Reveals 2-Oxoacid Dehydrogenase Complex Lipoylation Correlation with Aerobiosis in Archaea. PLoS ONE, 2014, 9, e87063.	1.1	3
2718	Identification of a Fungi-Specific Lineage of Protein Kinases Closely Related to Tyrosine Kinases. PLoS ONE, 2014, 9, e89813.	1.1	22
2719	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. PLoS ONE, 2014, 9, e90574.	1.1	86

#	ARTICLE	IF	CITATIONS
2720	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. PLoS ONE, 2014, 9, e91172.	1.1	206
2721	Extensive Microbial and Functional Diversity within the Chicken Cecal Microbiome. PLoS ONE, 2014, 9, e91941.	1.1	359
2722	Fast and Accurate Multivariate Gaussian Modeling of Protein Families: Predicting Residue Contacts and Protein-Interaction Partners. PLoS ONE, 2014, 9, e92721.	1.1	127
2723	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
2724	Genome-Wide Identification, Evolution and Expression Analysis of mTERF Gene Family in Maize. PLoS ONE, 2014, 9, e94126.	1.1	48
2725	Proteomic Analysis of Cattle Tick Rhipicephalus (Boophilus) microplus Saliva: A Comparison between Partially and Fully Engorged Females. PLoS ONE, 2014, 9, e94831.	1.1	165
2726	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PiO2Bp S-SAD Crystal Structure. PLoS ONE, 2014, 9, e94981.	1.1	4
2727	Phylogenetic Analysis of the Endoribonuclease Dicer Family. PLoS ONE, 2014, 9, e95350.	1.1	24
2728	Calponin-Like Chd64 Is Partly Disordered. PLoS ONE, 2014, 9, e96809.	1.1	10
2729	Structure-Based Computational Study of Two Disease Resistance Gene Homologues (Hm1 and Hm2) in Maize (Zea mays L.) with Implications in Plant-Pathogen Interactions. PLoS ONE, 2014, 9, e97852.	1.1	28
2730	Genome-Wide Survey and Expression Analysis of Calcium-Dependent Protein Kinase in Gossypium raimondii. PLoS ONE, 2014, 9, e98189.	1.1	77
2731	BioAssemblyModeler (BAM): User-Friendly Homology Modeling of Protein Homo- and Heterooligomers. PLoS ONE, 2014, 9, e98309.	1.1	16
2732	Tissue-Specific Transcript Profiling for ABC Transporters in the Sequestering Larvae of the Phytophagous Leaf Beetle Chrysomela populi. PLoS ONE, 2014, 9, e98637.	1.1	37
2733	Mapping B-Cell Epitopes for the Peroxidoxin of Leishmania (Viannia) braziliensis and Its Potential for the Clinical Diagnosis of Tegumentary and Visceral Leishmaniasis. PLoS ONE, 2014, 9, e99216.	1.1	34
2734	Genome-Wide Analysis of the NADK Gene Family in Plants. PLoS ONE, 2014, 9, e101051.	1.1	37
2735	Establishing an In Vivo Assay System to Identify Components Involved in Environmental RNA Interference in the Western Corn Rootworm. PLoS ONE, 2014, 9, e101661.	1.1	72
2736	Redox Proteomics Changes in the Fungal Pathogen Trichosporon asahii on Arsenic Exposure: Identification of Protein Responses to Metal-Induced Oxidative Stress in an Environmentally-Sampled Isolate. PLoS ONE, 2014, 9, e102340.	1.1	18
2737	Phage Orf Family Recombinases: Conservation of Activities and Involvement of the Central Channel in DNA Binding. PLoS ONE, 2014, 9, e102454.	1.1	7

#	ARTICLE	IF	CITATIONS
2738	Genomes and Transcriptomes of Partners in Plant-Fungal- Interactions between Canola (Brassica) Tj ETQq0 0 0 rgBT /Overlock, 10 Tf 50 7	1.1	78
2739	Frequent Loss and Alteration of the MOXD2 Gene in Catarrhines and Whales: A Possible Connection with the Evolution of Olfaction. PLoS ONE, 2014, 9, e104085.	1.1	7
2740	Contrasting Metabolism in Perenniating Structures of Upland and Lowland Switchgrass Plants Late in the Growing Season. PLoS ONE, 2014, 9, e105138.	1.1	20
2741	Comparative Analysis of Functional Metagenomic Annotation and the Mappability of Short Reads. PLoS ONE, 2014, 9, e105776.	1.1	58
2742	Fast and Accurate Discovery of Degenerate Linear Motifs in Protein Sequences. PLoS ONE, 2014, 9, e106081.	1.1	12
2743	A Toolkit for ARB to Integrate Custom Databases and Externally Built Phylogenies. PLoS ONE, 2015, 10, e0109277.	1.1	1
2744	Computational and Experimental Characterization of dVHL Establish a Drosophila Model of VHL Syndrome. PLoS ONE, 2014, 9, e109864.	1.1	1
2745	Metagenomic Insights into the RDX-Degrading Potential of the Ovine Rumen Microbiome. PLoS ONE, 2014, 9, e110505.	1.1	13
2746	Acanthamoeba castellanii STAT Protein. PLoS ONE, 2014, 9, e111345.	1.1	6
2747	The pCri System: A Vector Collection for Recombinant Protein Expression and Purification. PLoS ONE, 2014, 9, e112643.	1.1	24
2748	Genome-Wide Investigation and Expression Profiling of AP2/ERF Transcription Factor Superfamily in Foxtail Millet (Setaria italica L.). PLoS ONE, 2014, 9, e113092.	1.1	148
2749	Whole-Transcriptome Survey of the Putative ATP-Binding Cassette (ABC) Transporter Family Genes in the Latex-Producing Laticifers of Hevea brasiliensis. PLoS ONE, 2015, 10, e0116857.	1.1	20
2750	Quality Control Test for Sequence-Phenotype Assignments. PLoS ONE, 2015, 10, e0118288.	1.1	2
2751	Exome Analysis Reveals Differentially Mutated Gene Signatures of Stage, Grade and Subtype in Breast Cancers. PLoS ONE, 2015, 10, e0119383.	1.1	19
2752	Analysis and Prediction of the Critical Regions of Antimicrobial Peptides Based on Conditional Random Fields. PLoS ONE, 2015, 10, e0119490.	1.1	30
2753	Genome-Wide Analysis of the AP2/ERF Transcription Factors Family and the Expression Patterns of DREB Genes in Moso Bamboo (Phyllostachys edulis). PLoS ONE, 2015, 10, e0126657.	1.1	96
2754	Phylogenetic Co-Occurrence of ExoR, ExoS, and ChvI, Components of the RSI Bacterial Invasion Switch, Suggests a Key Adaptive Mechanism Regulating the Transition between Free-Living and Host-Invading Phases in Rhizobiales. PLoS ONE, 2015, 10, e0135655.	1.1	23
2755	The Prediction and Validation of Small CDSs Expand the Gene Repertoire of the Smallest Known Eukaryotic Genomes. PLoS ONE, 2015, 10, e0139075.	1.1	3

#	ARTICLE	IF	CITATIONS
2756	Rice-Infecting <i>Pseudomonas</i> Genomes Are Highly Accessorized and Harbor Multiple Putative Virulence Mechanisms to Cause Sheath Brown Rot. <i>PLoS ONE</i> , 2015, 10, e0139256.	1.1	10
2757	COGNIZER: A Framework for Functional Annotation of Metagenomic Datasets. <i>PLoS ONE</i> , 2015, 10, e0142102.	1.1	87
2758	Late Embryogenesis Abundant (LEA) Constitutes a Large and Diverse Family of Proteins Involved in Development and Abiotic Stress Responses in Sweet Orange (<i>Citrus sinensis</i> L. Osb.). <i>PLoS ONE</i> , 2015, 10, e0145785.	1.1	90
2759	Chamber Specific Gene Expression Landscape of the Zebrafish Heart. <i>PLoS ONE</i> , 2016, 11, e0147823.	1.1	24
2760	An Approach to Function Annotation for Proteins of Unknown Function (PUFs) in the Transcriptome of Indian Mulberry. <i>PLoS ONE</i> , 2016, 11, e0151323.	1.1	40
2761	Genome-Wide Analysis of Long Noncoding RNAs and Their Responses to Drought Stress in Cotton (<i>Gossypium hirsutum</i> L.). <i>PLoS ONE</i> , 2016, 11, e0156723.	1.1	109
2762	Draft Genomes of <i>Anopheles cracens</i> and <i>Anopheles maculatus</i> : Comparison of Simian Malaria and Human Malaria Vectors in Peninsular Malaysia. <i>PLoS ONE</i> , 2016, 11, e0157893.	1.1	8
2763	Functional Comparison of Bacteria from the Human Gut and Closely Related Non-Gut Bacteria Reveals the Importance of Conjugation and a Paucity of Motility and Chemotaxis Functions in the Gut Environment. <i>PLoS ONE</i> , 2016, 11, e0159030.	1.1	9
2764	Machine Learning of Protein Interactions in Fungal Secretory Pathways. <i>PLoS ONE</i> , 2016, 11, e0159302.	1.1	7
2765	Characterization of Toxin Complex Gene Clusters and Insect Toxicity of Bacteria Representing Four Subgroups of <i>Pseudomonas fluorescens</i> . <i>PLoS ONE</i> , 2016, 11, e0161120.	1.1	43
2766	Genome-Wide Analysis of APETALA2/Ethylene-Responsive Factor (AP2/ERF) Gene Family in Barley (<i>Hordeum vulgare</i> L.). <i>PLoS ONE</i> , 2016, 11, e0161322.	1.1	108
2767	Large-scale bioactivity analysis of the small-molecule assayed proteome. <i>PLoS ONE</i> , 2017, 12, e0171413.	1.1	4
2768	Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom <i>Thalassiosira oceanica</i> . <i>PLoS ONE</i> , 2017, 12, e0181753.	1.1	24
2769	The role of core and accessory type IV pilus genes in natural transformation and twitching motility in the bacterium <i>Acinetobacter baylyi</i> . <i>PLoS ONE</i> , 2017, 12, e0182139.	1.1	43
2770	Insight into cordycepin biosynthesis of <i>Cordyceps militaris</i> : Comparison between a liquid surface culture and a submerged culture through transcriptomic analysis. <i>PLoS ONE</i> , 2017, 12, e0187052.	1.1	29
2771	Tpc1 is an important Zn(II)2Cys6 transcriptional regulator required for polarized growth and virulence in the rice blast fungus. <i>PLoS Pathogens</i> , 2017, 13, e1006516.	2.1	56
2772	Large-scale survey and database of high affinity ligands for peptide recognition modules. <i>Molecular Systems Biology</i> , 2020, 16, e9310.	3.2	22
2773	LncRNA mediated regulation of aging pathways in <i>Drosophila melanogaster</i> during dietary restriction. <i>Aging</i> , 2016, 8, 2182-2203.	1.4	36

#	ARTICLE	IF	CITATIONS
2774	Functional lncRNA-miRNA-mRNA networks in rabbit carotid atherosclerosis. <i>Aging</i> , 2020, 12, 2798-2813.	1.4	12
2775	LncRNA and mRNA profiling during activation of tilapia macrophages by HSP70 and <i>Streptococcus agalactiae</i> antigen. <i>Oncotarget</i> , 2017, 8, 98455-98470.	0.8	22
2776	Functional characterization of a short peptidoglycan recognition protein from Chinese giant salamander (<i>Andrias davidianus</i>). <i>Oncotarget</i> , 2017, 8, 99323-99335.	0.8	10
2777	Comprehensive transcriptional landscape of porcine cardiac and skeletal muscles reveals differences of aging. <i>Oncotarget</i> , 2018, 9, 1524-1541.	0.8	41
2778	Novel HER3/MUC4 oncogenic signaling aggravates the tumorigenic phenotypes of pancreatic cancer cells. <i>Oncotarget</i> , 2015, 6, 21085-21099.	0.8	31
2779	Exploring Proteomic Drug Targets, Therapeutic Strategies and Protein - Protein Interactions in Cancer: Mechanistic View. <i>Current Cancer Drug Targets</i> , 2019, 19, 430-448.	0.8	10
2780	Next-generation sequencing to elucidate adaptive stress response and plantaricin genes among <i>Lactobacillus plantarum</i> strains. <i>Future Microbiology</i> , 2020, 15, 333-348.	1.0	8
2781	Investigating the natural resistance of blackfoot p-a-%KERN_ERR%ua <i>Haliotis iris</i> to abalone viral ganglioneuritis using whole transcriptome analysis. <i>Diseases of Aquatic Organisms</i> , 2019, 135, 107-119.	0.5	7
2782	The gene repertoire of <i>Pythium porphyrae</i> (Oomycota) suggests an adapted plant pathogen tackling red algae. <i>Algae</i> , 2020, 35, 133-144.	0.9	4
2783	SFannotation: A Simple and Fast Protein Function Annotation System. <i>Genomics and Informatics</i> , 2014, 12, 76.	0.4	1
2784	A classification scoring schema to validate protein interactors. <i>Bioinformatics</i> , 2012, 8, 34-39.	0.2	15
2785	Domain analyses of Usher syndrome causing Clarin-1 and GPR98 protein models. <i>Bioinformatics</i> , 2014, 10, 491-495.	0.2	2
2786	A structural model of the active ribosome-bound membrane protein insertase YidC. <i>ELife</i> , 2014, 3, e03035.	2.8	69
2787	Ecology and evolution of viruses infecting uncultivated SUPO5 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , 2014, 3, e03125.	2.8	186
2788	CED-3 caspase acts with miRNAs to regulate non-apoptotic gene expression dynamics for robust development in <i>C. elegans</i> . <i>ELife</i> , 2014, 3, e04265.	2.8	43
2789	Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of <i>Albugo candida</i> , a generalist parasite. <i>ELife</i> , 2015, 4, .	2.8	71
2790	YcgC represents a new protein deacetylase family in prokaryotes. <i>ELife</i> , 2015, 4, .	2.8	52
2791	Many lncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. <i>ELife</i> , 2015, 4, e08890.	2.8	439

#	ARTICLE	IF	CITATIONS
2792	Complex transcriptional regulation and independent evolution of fungal-like traits in a relative of animals. <i>ELife</i> , 2015, 4, e08904.	2.8	59
2793	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	2.8	26
2794	The genetic factors of bilaterian evolution. <i>ELife</i> , 2020, 9, .	2.8	44
2795	Isolation and transcriptomic analysis of <i>Anopheles gambiae</i> oenocytes enables the delineation of hydrocarbon biosynthesis. <i>ELife</i> , 2020, 9, .	2.8	20
2796	Structure of the bacterial ribosome at 2 Å... resolution. <i>ELife</i> , 2020, 9, .	2.8	151
2797	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020, 9, .	2.8	25
2798	Perilipin-related protein regulates lipid metabolism in <i>C. elegans</i> . <i>PeerJ</i> , 2015, 3, e1213.	0.9	25
2799	Amino-acid site variability among natural and designed proteins. <i>PeerJ</i> , 2013, 1, e211.	0.9	18
2800	Genome-wide identification and characterization of WRKY gene family in <i>Salix suchowensis</i> . <i>PeerJ</i> , 2016, 4, e2437.	0.9	52
2801	Genomic and transcriptomic resources for assassin flies including the complete genome sequence of <i>Proctacanthus coquilletti</i> (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. <i>PeerJ</i> , 2017, 5, e2951.	0.9	23
2802	DoReMi: context-based prioritization of linear motif matches. <i>PeerJ</i> , 2014, 2, e315.	0.9	6
2803	A Profile Hidden Markov Model to investigate the distribution and frequency of LanB-encoding lantibiotic modification genes in the human oral and gut microbiome. <i>PeerJ</i> , 2017, 5, e3254.	0.9	24
2804	Genome-wide analysis suggests high level of microsynteny and purifying selection affect the evolution of <i>EIN3/EIL</i> family in Rosaceae. <i>PeerJ</i> , 2017, 5, e3400.	0.9	16
2805	Characterisation of the horse transcriptome from immunologically active tissues. <i>PeerJ</i> , 2014, 2, e382.	0.9	6
2806	Integration of lncRNA-miRNA-mRNA reveals novel insights into oviposition regulation in honey bees. <i>PeerJ</i> , 2017, 5, e3881.	0.9	49
2807	Genome-wide characterization and expression profiling of <i>NAC</i> transcription factor genes under abiotic stresses in radish (<i>Raphanus sativus</i> L.). <i>PeerJ</i> , 2017, 5, e4172.	0.9	20
2808	Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse <i>Peromyscus eremicus</i> . <i>PeerJ</i> , 2014, 2, e642.	0.9	34
2809	Comprehensive transcriptional profiling of aging porcine liver. <i>PeerJ</i> , 2019, 7, e6949.	0.9	6

#	ARTICLE	IF	CITATIONS
2810	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. PeerJ, 2015, 3, e740.	0.9	157
2811	Functions of intrinsically disordered proteins through evolutionary lenses. Progress in Molecular Biology and Translational Science, 2021, 183, 45-74.	0.9	10
2812	Chitinase Chit62J4 Essential for Chitin Processing by Human Microbiome Bacterium Clostridium paraputrificum J4. Molecules, 2021, 26, 5978.	1.7	5
2813	Sequence Engineering of an Aspergillus niger Tannase to Produce in Pichia pastoris a Single-Chain Enzyme with High Specific Activity. Molecular Biotechnology, 2022, 64, 388-400.	1.3	1
2814	A Genomic Survey of Mayetiola destructor Mobilome Provides New Insights into the Evolutionary History of Transposable Elements in the Cecidomyiid Midges. PLoS ONE, 2021, 16, e0257996.	1.1	6
2815	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. IScience, 2021, 24, 103324.	1.9	25
2816	Comparative Transcriptome Sequencing of Taro Corm Development With a Focus on the Starch and Sucrose Metabolism Pathway. Frontiers in Genetics, 2021, 12, 771081.	1.1	5
2817	Identification of GROWTH-REGULATING FACTOR transcription factors in lettuce (Lactuca sativa) genome and functional analysis of LsaGRF5 in leaf size regulation. BMC Plant Biology, 2021, 21, 485.	1.6	20
2819	Abberent expression analysis of LMNA gene in hutchinson-gilford progeria syndrome. Bioinformation, 2012, 8, 221-224.	0.2	1
2821	Data Fusion with Optimized Block Kernels in LS-SVM for Protein Classification. Engineering, 2013, 05, 223-236.	0.4	1
2822	ILP Characterization of 3D Protein-Binding Sites and FCA-Based Interpretation. Communications in Computer and Information Science, 2013, , 84-100.	0.4	0
2823	METAREP, Overview. , 2013, , 1-17.		0
2824	In Silico Analysis of the CST6 Tumor Suppressor Gene. International Journal of Systems Biology and Biomedical Technologies, 2013, 2, 42-58.	0.2	1
2825	Bioinformatic Methods and Resources for Neuroscience Research. Springer Protocols, 2014, , 453-463.	0.1	0
2826	Analysis of Biological Sequences. , 2014, , 249-253.		0
2827	Predicting residue contacts for protein-protein interactions by integration of multiple information. Journal of Biomedical Science and Engineering, 2014, 07, 28-37.	0.2	0
2828	Using Sequence Information to Identify Motifs. , 2014, , 1-6.		0
2829	Novel Inorganic Pyrophosphatase from Soil Metagenomic and Family and Subfamily Prediction. Open Journal of Applied Sciences, 2014, 04, 68-75.	0.2	1

#	ARTICLE	IF	CITATIONS
2830	In Silico Investigation of Cancer Using Publicly Available Data. , 2014, , 327-351.		0
2831	FeatureViewer, a BioJS component for visualization of position-based annotations in protein sequences. F1000Research, 2014, 3, 47.	0.8	8
2832	treeWidget: a BioJS component to visualise phylogenetic trees. F1000Research, 0, 3, 49.	0.8	1
2833	"Diabetes Associated Genes from the Dark Matter of the Human Proteome". MOJ Proteomics & Bioinformatics, 2014, 1, .	0.1	6
2834	Role of 2-Oxoglutarate-Dependent Oxygenases in Flavonoid Metabolism. 2-Oxoglutarate-Dependent Oxygenases, 2015, , 350-366.	0.8	1
2836	An Optimized In Silico Neuroinformatics Approach. Advances in Computational Intelligence and Robotics Book Series, 2016, , 802-820.	0.4	0
2837	Grundlagen natürlicher Allergene. , 2016, , 177-191.		0
2838	In Silico Perspective into Interactions and Mutations in Human TLR4 and Ebola Glycoprotein. Advances in Medical Technologies and Clinical Practice Book Series, 2016, , 209-231.	0.3	0
2839	Overview of Cellular Computing-Basic Principles and Applications. Advances in Computational Intelligence and Robotics Book Series, 2016, , 637-662.	0.4	0
2853	Sequence Information to Identify Motifs. , 2018, , 1121-1126.		0
2856	Domain-Based Approaches to Prediction and Analysis of Protein-Protein Interactions. , 2019, , 406-427.		0
2857	Comparative Analyses of 35 Marine Mammal Genomes Provide Insights into the Evolution of Aquatic Life. SSRN Electronic Journal, 0, , .	0.4	0
2858	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
2859	Alternative Splicing. , 2019, , 1-8.		0
2873	Genome-Wide Analysis of the Pectin Methylesterase Gene Family in Potato. Potato Research, 2021, 64, 1-19.	1.2	6
2874	Comparative RNA-Seq Analysis Reveals Potentially Resistance-Related Genes in Response to Bacterial Canker of Tomato. Genes, 2021, 12, 1745.	1.0	5
2875	GFICLEE: ultrafast tree-based phylogenetic profile method inferring gene function at the genomic-wide level. BMC Genomics, 2021, 22, 774.	1.2	2
2876	Esterases as emerging biocatalysts: Mechanistic insights, genomic and metagenomic, immobilization, and biotechnological applications. Biotechnology and Applied Biochemistry, 2022, 69, 2176-2194.	1.4	9

#	ARTICLE	IF	CITATIONS
2877	Transcriptome Analysis of Testicular Aging in Mice. <i>Cells</i> , 2021, 10, 2895.	1.8	16
2878	Pneumococcal Extracellular Serine Proteases: Molecular Analysis and Impact on Colonization and Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 763152.	1.8	4
2882	Unravelling neurological disorders through metallomics-based approaches. <i>Metallomics</i> , 2020, 12, 1878-1896.	1.0	7
2883	Overview of Cellular Computing-Basic Principles and Applications. , 2020, , 1895-1920.		0
2885	Transcriptomic Profile of the Cockle <i>Cerastoderma edule</i> Exposed to Seasonal Diarrhetic Shellfish Toxin Contamination. <i>Toxins</i> , 2021, 13, 784.	1.5	3
2886	The First De Novo Transcriptome Assembly and Transcriptomic Dynamics of the Mangrove Tree <i>Rhizophora stylosa</i> Griff. (Rhizophoraceae). <i>International Journal of Molecular Sciences</i> , 2021, 22, 11964.	1.8	5
2890	Screening of genes coupled to heat response in Mongolian and Dorper sheep breeds. <i>Biologia (Poland)</i> , 2021, 76, 949.	0.8	1
2891	Identification of lncRNAs in response to infection by <i>Plasmodiophora brassicae</i> in <i>Brassica napus</i> and development of lncRNA-based SSR markers. <i>Genome</i> , 2021, 64, 1-20.	0.9	16
2892	Using BioBin to explore rare variant population stratification. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 332-43.	0.7	11
2893	Genome Wide Analysis of Heat Shock Proteins. <i>Iranian Journal of Biotechnology</i> , 2020, 18, e2529.	0.3	1
2894	Advances in the Regulation of Epidermal Cell Development by C2H2 Zinc Finger Proteins in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 754512.	1.7	2
2895	Long Non-Coding RNAs profiling in pathogenesis of <i>Verticillium dahliae</i> : New insights in the host-pathogen interaction. <i>Plant Science</i> , 2022, 314, 111098.	1.7	6
2896	The male and female gonad transcriptome of the edible sea urchin, <i>Paracentrotus lividus</i> : Identification of sex-related and lipid biosynthesis genes. <i>Aquaculture Reports</i> , 2022, 22, 100936.	0.7	6
2897	Advances in the Regulation of Epidermal Cell Development by C2H2 Zinc Finger Proteins in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 754512.	1.7	16
2898	Review of Insecticide Resistance and Its Underlying Mechanisms in <i>Tribolium castaneum</i> , 0, , .		2
2899	High Genomic Identity between Clinical and Environmental Strains of <i>Herbaspirillum frisingense</i> Suggests Pre-Adaptation to Different Hosts and Intrinsic Resistance to Multiple Drugs. <i>Antibiotics</i> , 2021, 10, 1409.	1.5	3
2900	Comprehensive Comparative Analysis of the GATA Transcription Factors in Four Rosaceae Species and Phytohormonal Response in Chinese Pear (<i>Pyrus bretschneideri</i>) Fruit. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12492.	1.8	21
2902	Phenotypic Screening of Molecular Docking Enriched Chemical Libraries from Targets Identified in Ischemic Stroke Genome Data by Network-Based Method. <i>Journal of Healthcare Engineering</i> , 2021, 2021, 1-9.	1.1	0

#	ARTICLE	IF	CITATIONS
2903	Genome-Wide Identification and Characterization of Soybean GmLOR Gene Family and Expression Analysis in Response to Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12515.	1.8	4
2904	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
2905	Identification and functional annotation of hypothetical proteins of uropathogenic <i>Escherichia coli</i> strain CFT073 towards designing antimicrobial drug targets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 14084-14095.	2.0	4
2906	Two-Component System Genes in <i>Sorghum bicolor</i> : Genome-Wide Identification and Expression Profiling in Response to Environmental Stresses. <i>Frontiers in Genetics</i> , 2021, 12, 794305.	1.1	15
2907	Accurate expression quantification from nanopore direct RNA sequencing with NanoCount. <i>Nucleic Acids Research</i> , 2022, 50, e19-e19.	6.5	44
2908	An Exploration of Non-Coding RNAs in Extracellular Vesicles Delivered by Swine Anterior Pituitary. <i>Frontiers in Genetics</i> , 2021, 12, 772753.	1.1	3
2909	<i>Muribaculaceae</i> Genomes Assembled from Metagenomes Suggest Genetic Drivers of Differential Response to Acarbose Treatment in Mice. <i>MSphere</i> , 2021, 6, e0085121.	1.3	53
2910	Identification of discriminative gene-level and protein-level features associated with pathogenic gain-of-function and loss-of-function variants. <i>American Journal of Human Genetics</i> , 2021, 108, 2301-2318.	2.6	21
2912	The <i>espD</i> full gene as a potential biomarker in active pulmonary tuberculosis. <i>International Journal of Mycobacteriology</i> , 2021, 10, 421.	0.3	0
2914	Evolutionary Ecology of Natural <i>Comammox Nitrospira</i> Populations. <i>MSystems</i> , 2022, 7, e0113921.	1.7	14
2915	Building an embryo: An auxin gene toolkit for zygotic and somatic embryogenesis in Brazilian pine. <i>Gene</i> , 2022, 817, 146168.	1.0	3
2916	Characterization of XR_311113.2 as a MicroRNA Sponge for Pre-ovulatory Ovarian Follicles of Goats via Long Noncoding RNA Profile and Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 760416.	1.1	1
2917	The genome of low-chill Chinese plum 'Sanyueli' (<i>Prunus salicina</i> Lindl.) provides insights into the regulation of the chilling requirement of flower buds. <i>Molecular Ecology Resources</i> , 2022, 22, 1919-1938.	2.2	11
2918	Epigenomic and transcriptomic analyses reveal differences between low-grade inflammation and severe exhaustion in LPS-challenged murine monocytes. <i>Communications Biology</i> , 2022, 5, 102.	2.0	20
2919	Carbohydrate active enzymes (CAZy) regulate cellulolytic and pectinolytic enzymes in <i>Colletotrichum falcatum</i> causing red rot in sugarcane. <i>3 Biotech</i> , 2022, 12, 48.	1.1	5
2920	Chromosome-level genome assembly of the shuttles hopppfish, <i>Periophthalmus modestus</i> . <i>GigaScience</i> , 2022, 11, .	3.3	4
2921	Novel insights into water-deficit-responsive mRNAs and lncRNAs during fiber development in <i>Gossypium hirsutum</i> . <i>BMC Plant Biology</i> , 2022, 22, 6.	1.6	1
2922	Comparative transcriptomics reveal tissue level specialization towards diet in prickleback fishes. <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2022, 192, 275-295.	0.7	10

#	ARTICLE	IF	CITATIONS
2923	Habitat Adaptation Drives Speciation of a <i>Streptomyces</i> Species with Distinct Habitats and Disparate Geographic Origins. <i>MBio</i> , 2022, 13, e0278121.	1.8	15
2924	<i>Schistosoma mansoni</i> \pm -N-acetylgalactosaminidase (SmNAGAL) regulates coordinated parasite movement and egg production. <i>PLoS Pathogens</i> , 2022, 18, e1009828.	2.1	14
2926	Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. <i>BMC Genomics</i> , 2022, 23, 42.	1.2	11
2927	Characterization of a Group of UDP-Glycosyltransferases Involved in the Biosynthesis of Triterpenoid Saponins of <i>Panax notoginseng</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 770-779.	1.9	16
2928	Functional and genomic comparative study of the bitter taste receptor family TAS2R: Insight into the role of human TAS2R5. <i>FASEB Journal</i> , 2022, 36, e22175.	0.2	4
2929	Identification of sodium homeostasis genes in <i>Camelus bactrianus</i> by whole transcriptome sequencing. <i>FEBS Open Bio</i> , 2022, 12, 864-876.	1.0	0
2930	Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle <i>Pollicipes pollicipes</i> . <i>GigaScience</i> , 2022, 11, .	3.3	8
2931	Genome-wide identification of CAMTA gene family members in rice (<i>Oryza sativa</i> L.) and in silico study on their versatility in respect to gene expression and promoter structure. <i>Functional and Integrative Genomics</i> , 2022, 22, 193-214.	1.4	9
2932	Genome Analysis of the Broad Host Range Necrotroph <i>Nalanthamala psidii</i> Highlights Genes Associated With Virulence. <i>Frontiers in Plant Science</i> , 2022, 13, 811152.	1.7	1
2933	Genome-wide analysis of sucrose synthase family in soybean and their expression in response to abiotic stress and seed development. <i>PLoS ONE</i> , 2022, 17, e0264269.	1.1	2
2934	Identification and regulatory network analysis of SPL family transcription factors in <i>Populus euphratica</i> Oliv. heteromorphic leaves. <i>Scientific Reports</i> , 2022, 12, 2856.	1.6	7
2935	Genome-Wide Analyses of Aspartic Proteases on Potato Genome (<i>Solanum tuberosum</i>): Generating New Tools to Improve the Resistance of Plants to Abiotic Stress. <i>Plants</i> , 2022, 11, 544.	1.6	4
2936	The genome of <i>Hibiscus hamabo</i> reveals its adaptation to saline and waterlogged habitat. <i>Horticulture Research</i> , 2022, 9, uhac067.	2.9	12
2937	ATGPred-FL: sequence-based prediction of autophagy proteins with feature representation learning. <i>Amino Acids</i> , 2022, 54, 799-809.	1.2	3
2938	Understanding the Evolution of Mitochondrial Genomes in the Green Macroalgal Genus <i>Ulva</i> (Ulvoophyceae, Chlorophyta). <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	3
2939	Chromosome-Level Genome Assembly for <i>Acer pseudosieboldianum</i> and Highlights to Mechanisms for Leaf Color and Shape Change. <i>Frontiers in Plant Science</i> , 2022, 13, 850054.	1.7	7
2940	Genome-Wide Survey and Development of the First Microsatellite Markers Database (AnCorDB) in <i>Anemone coronaria</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3126.	1.8	13
2941	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2022, 50, 3155-3168.	6.5	34

#	ARTICLE	IF	CITATIONS
2942	Transcriptome analysis of the bivalve <i>Placuna placenta</i> mantle reveals potential biomineralization-related genes. <i>Scientific Reports</i> , 2022, 12, 4743.	1.6	6
2943	A Systematic Phylogenomic Classification of the Multidrug and Toxic Compound Extrusion Transporter Gene Family in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, 774885.	1.7	8
2944	Genome-wide transcriptional profiling and functional analysis reveal miR-330-MAPK15 axis involving in cellular responses to deoxynivalenol exposure. <i>Chemosphere</i> , 2022, 298, 134199.	4.2	3
2945	High Molecular Weight Kininogen: A Review of the Structural Literature. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13370.	1.8	15
2946	A comprehensive analysis of <i>NAC</i> gene family in <i>Oryza sativa japonica</i> : a structural and functional genomics approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 856-870.	2.0	3
2947	Genome-wide characterization, evolution, structure, and expression analysis of the F-box genes in <i>Caenorhabditis</i> . <i>BMC Genomics</i> , 2021, 22, 889.	1.2	6
2948	Integrated Analysis of the ceRNA Network and M-7474 Function in Testosterone-Mediated Fat Deposition in Pigs. <i>Genes</i> , 2022, 13, 668.	1.0	2
2949	Genome-Wide Screening of Transposable Elements in the Whitefly, <i>Bemisia tabaci</i> (Hemiptera: Tj ETQq1 1 0.784314 rgBT /Overlock 10 396.	1.0	5
2950	The Importance of Weakly Co-Evolving Residue Networks in Proteins is Revealed by Visual Analytics. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	2
2951	Simple, efficient and thorough shotgun proteomic analysis with PatternLab V. <i>Nature Protocols</i> , 2022, 17, 1553-1578.	5.5	26
2952	Lentil allergens identification and quantification: An update from omics perspective. <i>Food Chemistry Molecular Sciences</i> , 2022, 4, 100109.	0.9	3
3128	Distinctive signatures of pathogenic and antibiotic resistant potentials in the hadal microbiome. <i>Environmental Microbiomes</i> , 2022, 17, 19.	2.2	6
3130	Human Protein-isoaspartate O-Methyltransferase Domain-Containing Protein 1 (PCMTD1) Associates with Cullin-RING Ligase Proteins. <i>Biochemistry</i> , 2022, 61, 879-894.	1.2	2
3131	Transcriptome annotation reveals minimal immunogenetic diversity among Wyoming toads, <i>Anaxyrus baxteri</i> . <i>Conservation Genetics</i> , 2022, 23, 669-681.	0.8	2
3132	Functional dissection of human mitotic genes using CRISPR-Cas9 tiling screens. <i>Genes and Development</i> , 2022, 36, 495-510.	2.7	2
3133	Whole-Transcriptome Analysis Reveals Long Noncoding RNAs Involved in Female Floral Development of Hickory (<i>Carya cathayensis</i> Sarg.). <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
3134	Validation of a random <i>Vibrio parahaemolyticus</i> genomic library by selection of quinolone resistance in a heterologous host. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	0
3135	SRC homology 3 domains: multifaceted binding modules. <i>Trends in Biochemical Sciences</i> , 2022, 47, 772-784.	3.7	11

#	ARTICLE	IF	CITATIONS
3136	DomBpred: Protein Domain Boundary Prediction Based on Domain-Residue Clustering Using Inter-Residue Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 912-922.	1.9	2
3137	Genome Assembly and Evolutionary Analysis of the Mandarin Duck <i>Aix galericulata</i> Reveal Strong Genome Conservation among Ducks. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	1
3138	Plasmodium manipulates the expression of host long non-coding RNA during red blood cell intracellular infection. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	8
3139	Catching a Walker in the ActDNA Partitioning by ParA Family of Proteins. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	8
3140	Antioxidant potential of <i>Pediococcus pentosaceus</i> strains from the sow milk bacterial collection in weaned piglets. <i>Microbiome</i> , 2022, 10, .	4.9	16
3141	High-throughput analysis of lncRNA in cows with naturally infected <i>Staphylococcus aureus</i> mammary gland. <i>Animal Biotechnology</i> , 0, , 1-9.	0.7	0
3142	A consensus view of the proteome of the last universal common ancestor. <i>Ecology and Evolution</i> , 2022, 12, .	0.8	10
3144	The landscape of isoform switches in sepsis: a multicenter cohort study. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
3145	Development of a High Oleic Cardoon Cell Culture Platform by SAD Overexpression and RNAi-Mediated FAD2.2 Silencing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3146	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	3.4	26
3147	Transcriptional Basis for Haustorium Formation and Host Establishment in Hemiparasitic <i>Psittacanthus schiedeanus</i> Mistletoes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
3149	Genome-Wide Study of Hsp90 Gene Family in Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.) and Their Imperative Roles in Response to Cold Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3150	Genetic determinants of lung cancer: Understanding the oncogenic potential of somatic missense mutations. <i>Genomics</i> , 2022, , 110401.	1.3	6
3151	Systematic Analysis of NB-ARC Gene Family in Rice and Functional Characterization of GNP12. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
3152	The Long Read Transcriptome of Rice (<i>Oryza sativa</i> ssp. <i>japonica</i> var. <i>Nipponbare</i>) Reveals Novel Transcripts. <i>Rice</i> , 2022, 15, .	1.7	2
3153	Comparative physiology and transcriptome analysis reveals that chloroplast development influences silver-white leaf color formation in <i>Hydrangea macrophylla</i> var. <i>maculata</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	1
3154	Genome wide and evolutionary analysis of heat shock protein 70 proteins in tomato and their role in response to heat and drought stress. <i>Molecular Biology Reports</i> , 2022, 49, 11229-11241.	1.0	3
3155	Transcriptome comparison for identification of pigmentation-related genes in different color varieties of Siamese fighting fish <i>Betta splendens</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, , 101014.	0.4	1

#	ARTICLE	IF	CITATIONS
3156	Conserved and lineage-specific hypothetical proteins may have played a central role in the rise and diversification of major archaeal groups. <i>BMC Biology</i> , 2022, 20, .	1.7	4
3157	Transcriptome analysis revealed the roles of long non-coding RNA and mRNA in the bursa of Fabricius during pigeon (<i>Columba livia</i>) development. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	3
3158	Comparative Transcriptome Analysis Reveals Gene Expression Differences in Eggplant (<i>Solanum</i>) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 6	1.9	3
3159	Identification and Analysis of Long Non-Coding RNAs Related to UV-B-Induced Anthocyanin Biosynthesis During Blood-Fleshed Peach (<i>Prunus persica</i>) Ripening. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
3160	The gill transcriptome of threatened European freshwater mussels. <i>Scientific Data</i> , 2022, 9, .	2.4	10
3161	Characterizing isoform switching events in esophageal adenocarcinoma. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 29, 749-768.	2.3	5
3162	Transformer Neural Networks for Protein Family and Interaction Prediction Tasks. <i>Journal of Computational Biology</i> , 2023, 30, 95-111.	0.8	3
3163	Possible Contribution of Alternative Transcript Isoforms in Mature Biofilm Growth Phase of <i>Candida glabrata</i> . <i>Indian Journal of Microbiology</i> , 2022, 62, 583-601.	1.5	1
3164	Whole transcriptome analyses and comparison reveal the metabolic differences between oxidative and glycolytic skeletal muscles of yak. <i>Meat Science</i> , 2022, 194, 108948.	2.7	3
3165	A cytosolic thiouridylase gene MoCTU2 in <i>Magnaporthe oryzae</i> is important for vegetative hyphal growth, conidiation, and responses to rapamycin and high temperature. <i>Physiological and Molecular Plant Pathology</i> , 2022, 121, 101886.	1.3	0
3166	Genome-wide identification, classification, and expression profiling of serine esterases and other esterase-related proteins in the tobacco hornworm, <i>Manduca sexta</i> . <i>Insect Science</i> , 2023, 30, 338-350.	1.5	2
3167	Two siblings with GAPO syndrome: a novel missense variant in ANTXR1. <i>Clinical Dysmorphology</i> , 2022, 31, 191-195.	0.1	0
3168	Identification of Novel Multi-Omics Expression Landscapes and Meta-Analysis of Landscape-Based Competitive Endogenous RNA Networks in ALDH+ Lung Adenocarcinoma Stem Cells. <i>BioMed Research International</i> , 2022, 2022, 1-20.	0.9	1
3169	Proteomic analysis of phytopathogenic fungus <i>Macrophomina phaseolina</i> identify known and novel mycelial proteins with roles in growth and virulence. <i>Journal of Proteins and Proteomics</i> , 2022, 13, 149-157.	1.0	1
3170	Genome-Wide Identification and Characterization of Heat Shock Protein 20 Genes in Maize. <i>Life</i> , 2022, 12, 1397.	1.1	3
3171	Substrate specificity of branched chain amino acid aminotransferases: The substitution of glycine to serine in the active site determines the substrate specificity for Î±-ketoglutarate. <i>Frontiers in Catalysis</i> , 0, 2, .	1.8	0
3172	A High-Quality Genome of <i>Rhizoctonia solani</i> , a Devastating Fungal Pathogen with a Wide Host Range. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 954-958.	1.4	5
3173	Enzymatic properties and biological activity of resuscitation-promoting factor B of <i>Rhodococcus</i> sp. (GX12401). <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1

#	ARTICLE	IF	CITATIONS
3174	Transcriptional regulation underlying the temperature response of embryonic development rate in the winter moth. <i>Molecular Ecology</i> , 0, , .	2.0	2
3175	Genome-Wide Identification and Transcriptome Analysis of DUF642 Gene Family in Wheat. <i>Botanical Research</i> , 2022, 11, 630-640.	0.0	0
3177	Genome-Wide Identification and Characterization of YUCCA Gene Family in <i>Mikania micrantha</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 13037.	1.8	4
3179	In silico functional annotation of hypothetical proteins from the <i>Bacillus paralicheniformis</i> strain Bac84 reveals proteins with biotechnological potentials and adaptational functions to extreme environments. <i>PLoS ONE</i> , 2022, 17, e0276085.	1.1	5
3180	Bioinformatic approaches for studying the microbiome of fermented food. <i>Critical Reviews in Microbiology</i> , 2023, 49, 693-725.	2.7	9
3181	Nutrient regulation of lipochitooligosaccharide recognition in plants via NSP1 and NSP2. <i>Nature Communications</i> , 2022, 13, .	5.8	18
3182	Transcriptome analysis reveals the proline metabolic pathway and its potential regulation TF-hub genes in salt-stressed potato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3183	Gene Expression in the Developing Seed of Wild and Domesticated Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13351.	1.8	3
3184	Genomic insights into phage-host interaction in the deep-sea chemolithoautotrophic <i>Campylobacterota</i> , <i>Nitratiruptor</i> . <i>ISME Communications</i> , 2022, 2, .	1.7	1
3185	Genome-wide identification of RsGRAS gene family reveals positive role of RsSHRc gene in chilling stress response in radish (<i>Raphanus sativus</i> L.). <i>Plant Physiology and Biochemistry</i> , 2022, 192, 285-297.	2.8	2
3186	An integrative analysis of lncRNAs and mRNAs highlights the potential roles of lncRNAs in the process of follicle selection in Taihang chickens. <i>Theriogenology</i> , 2023, 195, 122-130.	0.9	1
3187	Identification of CAMTA Gene Family in <i>Heimia myrtifolia</i> and Expression Analysis under Drought Stress. <i>Plants</i> , 2022, 11, 3031.	1.6	1
3188	Revealing the Regulatory Mechanism of lncRNA-LMEP on Melanin Deposition Based on High-Throughput Sequencing in Xichuan Chicken Skin. <i>Genes</i> , 2022, 13, 2143.	1.0	4
3189	Discovery, Structure, and Mechanism of a Class II Sesquiterpene Cyclase. <i>Journal of the American Chemical Society</i> , 2022, 144, 22067-22074.	6.6	15
3190	Insights on variant analysis in silico tools for pathogenicity prediction. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	17
3191	Investigating isoform switching in <i>RHBDF2</i> and its role in neoplastic growth in breast cancer. <i>PeerJ</i> , 0, 10, e14124.	0.9	1
3192	Mining key genes related to root morphogenesis through genome-wide identification and expression analysis of RR gene family in citrus. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3195	Genome-Wide Identification and Expression Analysis of the PME and PME1 Gene Families in <i>Diospyros kaki</i> : A Bioinformatics Study. <i>Horticulturae</i> , 2022, 8, 1159.	1.2	3

#	ARTICLE	IF	CITATIONS
3197	Unsupervised Machine Learning Organization of the Functional Dark Proteome of Gram-Negative "Superbugs": Six Protein Clusters Amenable for Distinct Scientific Applications. <i>ACS Omega</i> , 2022, 7, 46131-46145.	1.6	0
3200	Characterization and genomic analysis of a novel halovirus infecting <i>Chromohalobacter beijerinckii</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
3201	Differentially expressed long noncoding RNAs in RAW264.7 macrophages during <i>Brucella</i> infection and functional analysis on the bacterial intracellular replication. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
3202	Draft genome sequencing and secretome profiling of <i>Sclerotinia sclerotiorum</i> revealed effector repertoire diversity and allied broad-host range necrotrophy. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
3203	Looking for the mechanism of arsenate respiration of <i>Fusibacter</i> sp. strain 3D3, independent of ArrAB. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3204	Overexpression of a DUF740 family gene (LOC_Os04g59420) imparts enhanced climate resilience through multiple stress tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3205	<i>coth</i> Genes Are Necessary for Normal Spore Formation and Virulence in <i>Mucor lusitanicus</i> . <i>MBio</i> , 2023, 14, .	1.8	10
3206	RNA sequencing and transcriptome analyses reveal differentially expressed genes in the defensive glands of the medicinal beetle <i>Blaps rhynchopetera</i> . <i>Entomological Research</i> , 2023, 53, 12-28.	0.6	1
3207	Comparative genome analysis reveals high-level drug resistance markers in a clinical isolate of <i>Mycobacterium fortuitum</i> subsp. <i>fortuitum</i> MF GZ001. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	1
3208	Identification of aluminum-resistant miRNAs and lncRNAs in <i>Vitis quinquangularis</i> and exploration of the related aluminum-tolerance mechanisms. <i>Environmental and Experimental Botany</i> , 2023, 206, 105194.	2.0	2
3209	Genome-Wide Identification, Evolutionary and Functional Analyses of WRKY Family Members in <i>Ginkgo biloba</i> . <i>Genes</i> , 2023, 14, 343.	1.0	5
3210	Identification and Functional Prediction of Long Non-Coding RNA in Longissimus Dorsi Muscle of Queshan Black and Large White Pigs. <i>Genes</i> , 2023, 14, 197.	1.0	3
3211	Advancement in Machine Learning: A Strategic Lookout from Cancer Identification to Treatment. <i>Archives of Computational Methods in Engineering</i> , 0, , .	6.0	1
3212	Rational Design of Profile HMMs for Sensitive and Specific Sequence Detection with Case Studies Applied to Viruses, Bacteriophages, and Casposons. <i>Viruses</i> , 2023, 15, 519.	1.5	1
3213	Genome-wide identification of the geranylgeranyl pyrophosphate synthase (GGPS) gene family involved in chlorophyll synthesis in cotton. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
3214	Identification and Characterization of Long Non-Coding RNAs Involved in Sex-Related Gene Regulation in Kelp <i>Saccharina japonica</i> . <i>Journal of Ocean University of China</i> , 2023, 22, 755-765.	0.6	1
3215	liUGT71B2 catalyzes lignan glycosylation in <i>Isatis indigotica</i> with substrates specificity. <i>Industrial Crops and Products</i> , 2023, 195, 116483.	2.5	3
3216	Environmental viromes reveal global virosphere of deep-sea sediment RNA viruses. <i>Journal of Advanced Research</i> , 2024, 56, 87-102.	4.4	1

#	ARTICLE	IF	CITATIONS
3217	Genome-guided approaches and evaluation of the strategies to influence bioprocessing assisted morphological engineering of <i>Streptomyces</i> cell factories. <i>Bioresource Technology</i> , 2023, 376, 128836.	4.8	2
3218	Differential expression of the AP2/EREBP gene family in the contrasting genotypes of maize provides insights of abiotic stress tolerance. <i>Cereal Research Communications</i> , 2023, 51, 835-850.	0.8	2
3219	Genome Size Changes by Duplication, Divergence, and Insertion in <i>Caenorhabditis</i> Worms. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	0
3220	Zinc/iron-regulated transporter-like protein gene family in <i>Theobroma cacao</i> L: Characteristics, evolution, function and 3D structure analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3221	Transposon-derived transcription factors across metazoans. <i>Frontiers in Cell and Developmental Biology</i> , 0, 11, .	1.8	2
3223	Parthenocarpy-related genes induced by naphthalene acetic acid in oil palm interspecific O × C [<i>Elaeis oleifera</i> (Kunth) Cortés × <i>Elaeis guineensis</i> Jacq.] hybrids. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0
3224	Functional and structural diversification of incomplete phosphotransferase system in cellulose-degrading clostridia. <i>ISME Journal</i> , 2023, 17, 823-835.	4.4	1
3225	Two Novel <i>Bursaphelenchus xylophilus</i> Kunitz Effector Proteins Using Different Infection and Survival Strategies to Suppress Immunity in Pine. <i>Phytopathology</i> , 2023, 113, 539-548.	1.1	0
3226	Integrated Analysis of Transcriptome Expression Profiles Reveals miRNA-326-Regulated Porcine Chondrocyte Differentiation. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7257.	1.8	1
3227	Surface ID: A Geometry-aware System for Protein Molecular Surface Comparison. <i>Bioinformatics</i> , 0, , .	1.8	0
3302	Application of computation in the study of biosynthesis of phytochemicals. , 2024, , 321-355.		0