

InterPro, progress and status in 2005

Nucleic Acids Research

33, D201-D205

DOI: [10.1093/nar/gki106](https://doi.org/10.1093/nar/gki106)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Functional Profiling: From Microarrays via Cell-Based Assays to Novel Tumor Relevant Modulators of the Cell Cycle. <i>Cancer Research</i> , 2005, 65, 7733-7742.	0.9	19
2	A Comprehensive Software Suite for the Analysis of cDNAs. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 179-188.	6.9	1
3	Screening for rapidly evolving genes in the ectomycorrhizal fungus <i>Paxillus involutus</i> using cDNA microarrays. <i>Molecular Ecology</i> , 2005, 15, 535-550.	3.9	33
4	Minimum information requested in the annotation of biochemical models (MIRIAM). <i>Nature Biotechnology</i> , 2005, 23, 1509-1515.	17.5	553
5	A comparative genomic view of clostridial sporulation and physiology. <i>Nature Reviews Microbiology</i> , 2005, 3, 969-978.	28.6	295
6	How many genomics targets can a portfolio afford?. <i>Drug Discovery Today</i> , 2005, 10, 1057-1063.	6.4	45
7	Computing chemistry on the web. <i>Drug Discovery Today</i> , 2005, 10, 1497-1500.	6.4	193
8	Predicting protein druggability. <i>Drug Discovery Today</i> , 2005, 10, 1675-1682.	6.4	260
9	The druggable genome: an update. <i>Drug Discovery Today</i> , 2005, 10, 1607-1610.	6.4	415
10	Automatic annotation of protein function. <i>Current Opinion in Structural Biology</i> , 2005, 15, 267-274.	5.7	107
11	The PD-(D/E)XK superfamily revisited: identification of new members among proteins involved in DNA metabolism and functional predictions for domains of (hitherto) unknown function. <i>BMC Bioinformatics</i> , 2005, 6, 172.	2.6	84
12	Discover protein sequence signatures from protein-protein interaction data. <i>BMC Bioinformatics</i> , 2005, 6, 277.	2.6	20
13	Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity. <i>BMC Bioinformatics</i> , 2005, 6, S20.	2.6	65
14	The EH1 motif in metazoan transcription factors. <i>BMC Genomics</i> , 2005, 6, 169.	2.8	67
15	The prediction of protein function at CASP6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 201-213.	2.6	35
17	Recognition of Unknown Conserved Alternatively Spliced Exons. <i>PLoS Computational Biology</i> , 2005, 1, e15.	3.2	44
18	Mating Type Loci of <i>Sporisorium reilianum</i> : Novel Pattern with Three a and Multiple b Specificities. <i>Eukaryotic Cell</i> , 2005, 4, 1317-1327.	3.4	97
19	Mining sequence annotation databanks for association patterns. <i>Bioinformatics</i> , 2005, 21, iii49-iii57.	4.1	32

#	ARTICLE	IF	CITATIONS
20	Glycerophosphocholine-dependent Growth Requires Gde1p (YPL110c) and Git1p in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 36110-36117.	3.4	64
21	The evolutionary computation approach to motif discovery in biological sequences. , 2005, , .		25
22	The MicrobesOnline Web site for comparative genomics. <i>Genome Research</i> , 2005, 15, 1015-1022.	5.5	176
23	Scooby-domain: prediction of globular domains in protein sequence. <i>Nucleic Acids Research</i> , 2005, 33, W160-W163.	14.5	29
24	Proteomic analysis of a eukaryotic cilium. <i>Journal of Cell Biology</i> , 2005, 170, 103-113.	5.2	933
25	Annotating the Human Proteome. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 435-440.	3.8	24
26	GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. <i>Bioinformatics</i> , 2005, 21, 3669-3671.	4.1	16
27	MAO: a Multiple Alignment Ontology for nucleic acid and protein sequences. <i>Nucleic Acids Research</i> , 2005, 33, 4164-4171.	14.5	23
28	Channel Formation by CarO, the Carbapenem Resistance-Associated Outer Membrane Protein of <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 4876-4883.	3.2	111
29	InterProScan: protein domains identifier. <i>Nucleic Acids Research</i> , 2005, 33, W116-W120.	14.5	2,556
30	Proteomic Analysis of <i>Schistosoma mansoni</i> Cercarial Secretions. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1862-1875.	3.8	175
31	Identification and characterization of a novel peritrophic matrix protein, Ae-Aper50, and the microvillar membrane protein, AEG12, from the mosquito, <i>Aedes aegypti</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2005, 35, 947-959.	2.7	64
32	How accurately can we discriminate G-protein-coupled receptors as 7-tms TM protein sequences from other sequences?. <i>Biochemical and Biophysical Research Communications</i> , 2005, 338, 1542-1546.	2.1	10
33	Investigation of protein functions through data-mining on integrated human transcriptome database, H-Invitational database (H-InvDB). <i>Gene</i> , 2005, 364, 99-107.	2.2	18
34	Proteomic resources: Integrating biomedical information in humans. <i>Gene</i> , 2005, 364, 13-18.	2.2	14
35	Identification of full genes and proteins of MCM9, a novel, vertebrate-specific member of the MCM2-8 protein family. <i>Gene</i> , 2005, 362, 51-56.	2.2	50
36	Analysis of glycoside hydrolase family 98: Catalytic machinery, mechanism and a novel putative carbohydrate binding module. <i>FEBS Letters</i> , 2005, 579, 5466-5472.	2.8	15
37	Searching for hypothetical proteins: Theory and practice based upon original data and literature. <i>Progress in Neurobiology</i> , 2005, 77, 90-127.	5.7	171

#	ARTICLE	IF	CITATIONS
38	A compendium of <i>Caenorhabditis elegans</i> regulatory transcription factors: a resource for mapping transcription regulatory networks. <i>Genome Biology</i> , 2005, 6, R110.	9.6	175
39	Sequence and structural analysis of BTB domain proteins. <i>Genome Biology</i> , 2005, 6, R82.	9.6	575
40	Evolutionary conservation of domain-domain interactions. <i>Genome Biology</i> , 2006, 7, R125.	9.6	96
41	The gain and loss of genes during 600 million years of vertebrate evolution. <i>Genome Biology</i> , 2006, 7, R43.	9.6	332
42	The <i>Methanosarcina barkeri</i> Genome: Comparative Analysis with <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> Reveals Extensive Rearrangement within Methanosarcinal Genomes. <i>Journal of Bacteriology</i> , 2006, 188, 7922-7931.	2.2	158
43	Reconstruction of a Functional Human Gene Network, with an Application for Prioritizing Positional Candidate Genes. <i>American Journal of Human Genetics</i> , 2006, 78, 1011-1025.	6.2	456
44	Protein Family Expansions and Biological Complexity. <i>PLoS Computational Biology</i> , 2006, 2, e48.	3.2	193
45	Bioinformatics database infrastructure for biotechnology research. <i>Journal of Biotechnology</i> , 2006, 124, 629-639.	3.8	15
46	Proteomic characterization of transient expression and secretion of a stress-related metalloprotease in high cell density culture of <i>Bacillus megaterium</i> . <i>Journal of Biotechnology</i> , 2006, 126, 313-324.	3.8	16
47	<i>C. elegans</i> : an invaluable model organism for the proteomics studies of the cholesterol-mediated signaling pathway. <i>Expert Review of Proteomics</i> , 2006, 3, 439-453.	3.0	15
48	ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. <i>Nucleic Acids Research</i> , 2006, 34, W362-W365.	14.5	1,428
49	Comparative proteomic analysis of high cell density cultivations with two recombinant <i>Bacillus megaterium</i> strains for the production of a heterologous dextransucrase. <i>Proteome Science</i> , 2006, 4, 19.	1.7	19
50	The Cecropin Superfamily of Toxic Peptides. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006, 11, 94-103.	1.0	28
51	Searching WormBase for Information about <i>Caenorhabditis elegans</i> . , 2006, Chapter 1, Unit 1.8.		3
52	Prediction and classification of protein functions. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 145-151.	4.0	16
53	MaGe: a microbial genome annotation system supported by synteny results. <i>Nucleic Acids Research</i> , 2006, 34, 53-65.	14.5	375
54	TRANSFAC(R) and its module TRANSCompel(R): transcriptional gene regulation in eukaryotes. <i>Nucleic Acids Research</i> , 2006, 34, D108-D110.	14.5	2,015
55	A profile-based protein sequence alignment algorithm for a domain clustering database. , 2006, , .		0

#	ARTICLE	IF	CITATIONS
56	Automated protein function prediction--the genomic challenge. Briefings in Bioinformatics, 2006, 7, 225-242.	6.5	307
57	The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. Bioinformatics, 2006, 22, 195-201.	4.1	6,515
58	MELDB: A database for microbial esterases and lipases. FEBS Letters, 2006, 580, 2736-2740.	2.8	20
59	Reconstruction and in silico analysis of the MAPK signaling pathways in the human blood fluke, <i>Schistosoma japonicum</i> . FEBS Letters, 2006, 580, 3677-3686.	2.8	24
60	Global Survey of Organ and Organelle Protein Expression in Mouse: Combined Proteomic and Transcriptomic Profiling. Cell, 2006, 125, 173-186.	28.9	429
61	Opsins and clusters of sensory G-protein-coupled receptors in the sea urchin genome. Developmental Biology, 2006, 300, 461-475.	2.0	153
62	Sea urchin Forkhead gene family: Phylogeny and embryonic expression. Developmental Biology, 2006, 300, 49-62.	2.0	192
63	Update of the NAD(P)H:quinone oxidoreductase (NQO) gene family. Human Genomics, 2006, 2, 329.	2.9	146
64	BN++ – A Biological Information System. Journal of Integrative Bioinformatics, 2006, 3, 148-161.	1.5	17
65	TRANSPATH(R): an information resource for storing and visualizing signaling pathways and their pathological aberrations. Nucleic Acids Research, 2006, 34, D546-D551.	14.5	157
66	ChimerDB—a knowledgebase for fusion sequences. Nucleic Acids Research, 2006, 34, D21-D24.	14.5	34
67	Transcriptional activators in yeast. Nucleic Acids Research, 2006, 34, 955-967.	14.5	84
68	Using the Ensembl Genome Server to Browse Genomic Sequence Data. Current Protocols in Bioinformatics, 2006, 16, Unit 1.15.	25.8	14
69	Structure of the conserved hypothetical protein MAL13P1.257 from <i>Plasmodium falciparum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 180-185.	0.7	9
70	Exploring dynamics of protein structure determination and homology-based prediction to estimate the number of superfamilies and folds. , 2006, 6, 6.		23
71	Reconstruction of central carbon metabolism in <i>Sulfolobus solfataricus</i> using a two-dimensional gel electrophoresis map, stable isotope labelling and DNA microarray analysis. Proteomics, 2006, 6, 1518-1529.	2.2	52
72	Functional analysis of the nuclear proteome of human A549 alveolar epithelial cells by HPLC-high resolution 2-D gel electrophoresis. Proteomics, 2006, 6, 2656-2672.	2.2	36
73	Reconstructing protein complexes: From proteomics to systems biology. Proteomics, 2006, 6, 4724-4731.	2.2	18

#	ARTICLE	IF	CITATIONS
74	Pilot study of the Human Proteome Organisation Brain Proteome Project: Applying different 2-DE techniques to monitor proteomic changes during murine brain development. <i>Proteomics</i> , 2006, 6, 4899-4913.	2.2	31
75	Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , 2006, 6, 5059-5075.	2.2	23
76	Functional grouping based on signatures in protein termini. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 996-1004.	2.6	5
77	Structure determination of a new protein from backbone-centered NMR data and NMR-assisted structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 480-489.	2.6	7
78	I-conotoxin superfamily revisited. <i>Journal of Peptide Science</i> , 2006, 12, 679-685.	1.4	9
79	Comparative analysis of regulatory transcription factors in <i>Schizosaccharomyces pombe</i> and budding yeasts. <i>Yeast</i> , 2006, 23, 929-935.	1.7	12
80	ABCdb: an online resource for ABC transporter repertoires from sequenced archaeal and bacterial genomes. <i>FEMS Microbiology Letters</i> , 2006, 256, 333-339.	1.8	37
81	Prediction of coenzyme specificity in dehydrogenases/ reductases. A hidden Markov model-based method and its application on complete genomes. <i>FEBS Journal</i> , 2006, 273, 1177-1184.	4.7	50
82	Revisiting the prediction of protein function at CASP6. <i>FEBS Journal</i> , 2006, 273, 2977-2983.	4.7	15
83	Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006, 8, 1183-1189.	10.3	33
84	Creating hierarchical models of protein families based on Expressed Sequence Tags: The "Sprockets" analysis pipeline. <i>Analytica Chimica Acta</i> , 2006, 564, 123-132.	5.4	0
85	Functional annotation prediction: All for one and one for all. <i>Protein Science</i> , 2006, 15, 1557-1562.	7.6	33
86	Cataloging the Relationships Between Proteins: A Review of Interaction Databases. <i>Molecular Biotechnology</i> , 2006, 34, 69-94.	2.4	6
87	Gramene: a bird's eye view of cereal genomes. <i>Nucleic Acids Research</i> , 2006, 34, D717-D723.	14.5	177
88	Conversion of MapMan to Allow the Analysis of Transcript Data from Solanaceous Species: Effects of Genetic and Environmental Alterations in Energy Metabolism in the Leaf. <i>Plant Molecular Biology</i> , 2006, 60, 773-792.	3.9	115
89	Identification and analysis of genes expressed in the adult filarial parasitic nematode <i>Dirofilaria immitis</i> . <i>International Journal for Parasitology</i> , 2006, 36, 829-839.	3.1	15
90	Immunome: A reference set of genes and proteins for systems biology of the human immune system. <i>Cellular Immunology</i> , 2006, 244, 87-89.	3.0	63
91	A Screen for Cohesion Mutants Uncovers Ssl3, the Fission Yeast Counterpart of the Cohesin Loading Factor Scc4. <i>Current Biology</i> , 2006, 16, 875-881.	3.9	68

#	ARTICLE	IF	CITATIONS
92	Emerging roles of pseudokinases. Trends in Cell Biology, 2006, 16, 443-452.	7.9	475
93	Annotating the genome of Medicago truncatula. Current Opinion in Plant Biology, 2006, 9, 122-127.	7.1	47
94	Identification and evolutionary analysis of novel exons and alternative splicing events using cross-species EST-to-genome comparisons in human, mouse and rat. BMC Bioinformatics, 2006, 7, 136.	2.6	30
95	Domain-based small molecule binding site annotation. BMC Bioinformatics, 2006, 7, 152.	2.6	25
96	Amplification of the Gene Ontology annotation of Affymetrix probe sets. BMC Bioinformatics, 2006, 7, 159.	2.6	6
97	The effects of multiple features of alternatively spliced exons on the K A /K S ratio test. BMC Bioinformatics, 2006, 7, 259.	2.6	8
98	A new measure for functional similarity of gene products based on Gene Ontology. BMC Bioinformatics, 2006, 7, 302.	2.6	597
99	MACSIMS : multiple alignment of complete sequences information management system. BMC Bioinformatics, 2006, 7, 318.	2.6	38
100	Java GUI for InterProScan (IIPS): A tool to help process multiple InterProScans and perform ortholog analysis. BMC Bioinformatics, 2006, 7, 462.	2.6	7
101	Fly-DPI: database of protein interactomes for D. melanogaster in the approach of systems biology. BMC Bioinformatics, 2006, 7, S18.	2.6	11
102	Phylogenomic analysis of vertebrate thrombospondins reveals fish-specific paralogues, ancestral gene relationships and a tetrapod innovation. BMC Evolutionary Biology, 2006, 6, 33.	3.2	29
103	A wing expressed sequence tag resource for Bicyclus anynana butterflies, an evo-devo model. BMC Genomics, 2006, 7, 130.	2.8	85
104	Phylogenomic analysis of the GIY-YIG nuclease superfamily. BMC Genomics, 2006, 7, 98.	2.8	102
105	ExtraTrain: a database of Extragenic regions and Transcriptional information in prokaryotic organisms. BMC Microbiology, 2006, 6, 29.	3.3	47
106	Incorporating genetic analyses into birth defects cluster investigations: Strategies for identifying candidate genes. Birth Defects Research Part A: Clinical and Molecular Teratology, 2006, 76, 798-810.	1.6	8
107	An experimental metagenome data management and analysis system. Bioinformatics, 2006, 22, e359-e367.	4.1	81
108	A Hidden Markov Model Approach to Model Protein Sequence and Structural Information: Identification of Helix-Turn-Helix DNA-Binding Motif. , 0, , .		0
109	A RecA-mediated exon profiling method. Nucleic Acids Research, 2006, 34, e97-e97.	14.5	5

#	ARTICLE	IF	CITATIONS
110	Protein classification using ontology classification. Bioinformatics, 2006, 22, e530-e538.	4.1	44
111	The integrated microbial genomes (IMG) system. Nucleic Acids Research, 2006, 34, D344-D348.	14.5	355
112	FLIGHT: database and tools for the integration and cross-correlation of large-scale RNAi phenotypic datasets. Nucleic Acids Research, 2006, 34, D479-D483.	14.5	34
113	VMD: a community annotation database for oomycetes and microbial genomes. Nucleic Acids Research, 2006, 34, D379-D381.	14.5	28
114	pSTIING: a 'systems' approach towards integrating signalling pathways, interaction and transcriptional regulatory networks in inflammation and cancer. Nucleic Acids Research, 2006, 34, D527-D534.	14.5	44
115	Phytome: a platform for plant comparative genomics. Nucleic Acids Research, 2006, 34, D724-D730.	14.5	35
116	The SWISS-MODEL Repository: new features and functionalities. Nucleic Acids Research, 2006, 34, D315-D318.	14.5	454
117	The Mouse Functional Genome Database (MfunGD): functional annotation of proteins in the light of their cellular context. Nucleic Acids Research, 2006, 34, D568-D571.	14.5	15
118	SIMAP: the similarity matrix of proteins. Nucleic Acids Research, 2006, 34, D252-D256.	14.5	44
119	EMBL Nucleotide Sequence Database: developments in 2005. Nucleic Acids Research, 2006, 34, D10-D15.	14.5	83
120	The UCSC Archaeal Genome Browser. Nucleic Acids Research, 2006, 34, D407-D410.	14.5	107
121	The UCSC Genome Browser Database: update 2006. Nucleic Acids Research, 2006, 34, D590-D598.	14.5	1,156
122	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
123	ProKware: integrated software for presenting protein structural properties in protein tertiary structures. Nucleic Acids Research, 2006, 34, W89-W94.	14.5	2
124	TACT: Transcriptome Auto-annotation Conducting Tool of H-InvDB. Nucleic Acids Research, 2006, 34, W345-W349.	14.5	5
125	â€˜Genome designâ€™ model and multicellular complexity: golden middle. Nucleic Acids Research, 2006, 34, 5906-5914.	14.5	34
126	A systematic approach to infer biological relevance and biases of gene network structures. Nucleic Acids Research, 2006, 34, e6-e6.	14.5	15
127	Integration of Biological Data with Semantic Networks. Current Bioinformatics, 2006, 1, 273-290.	1.5	6

#	ARTICLE	IF	CITATIONS
128	Panzea: a database and resource for molecular and functional diversity in the maize genome. Nucleic Acids Research, 2006, 34, D752-D757.	14.5	89
129	INVHOGEN: a database of homologous invertebrate genes. Nucleic Acids Research, 2006, 34, D349-D353.	14.5	4
130	Fungal Genomic Annotation. Applied Mycology and Biotechnology, 2006, , 123-142.	0.3	21
131	The DIMA web resource—exploring the protein domain network. Bioinformatics, 2006, 22, 997-998.	4.1	19
132	The Dictyostelium Kinome—Analysis of the Protein Kinases from a Simple Model Organism. PLoS Genetics, 2006, 2, e38.	3.5	150
133	Prioritizing Genomic Drug Targets in Pathogens: Application to Mycobacterium tuberculosis. PLoS Computational Biology, 2006, 2, e61.	3.2	133
134	A scalable method for integration and functional analysis of multiple microarray datasets. Bioinformatics, 2006, 22, 2890-2897.	4.1	127
135	Alternatively and Constitutively Spliced Exons Are Subject to Different Evolutionary Forces. Molecular Biology and Evolution, 2006, 23, 675-682.	8.9	55
136	Human-specific insertions and deletions inferred from mammalian genome sequences. Genome Research, 2006, 17, 16-22.	5.5	58
137	The proteome: structure, function and evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 441-451.	4.0	18
138	Towards genome-scale structure prediction for transmembrane proteins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 465-475.	4.0	33
139	Identification of function-associated loop motifs and application to protein function prediction. Bioinformatics, 2006, 22, 2237-2243.	4.1	41
140	Integrating biological data through the genome. Human Molecular Genetics, 2006, 15, R81-R87.	2.9	16
141	Research Article: Biochemical detection, pharmacological inhibition, and phylogenetic analysis of Caenorhabditis elegans metalloproteases. Bios, 2006, 77, 113-126.	0.0	1
142	Analysis of protein sequence and interaction data for candidate disease gene prediction. Nucleic Acids Research, 2006, 34, e130-e130.	14.5	138
143	A Network-based Analysis of Polyanion-binding Proteins Utilizing Yeast Protein Arrays. Molecular and Cellular Proteomics, 2006, 5, 2263-2278.	3.8	15
144	Functional Interpretation of Microarray Experiments. OMICS A Journal of Integrative Biology, 2006, 10, 398-410.	2.0	74
145	BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. Nucleic Acids Research, 2006, 34, W472-W476.	14.5	240

#	ARTICLE	IF	CITATIONS
146	Development and Implementation of the PSI MI Standard for Molecular Interaction. , 2006, , .		1
147	Identification of cell cycle regulators in Mycobacterium tuberculosis by inhibition of septum formation and global transcriptional analysis. Microbiology (United Kingdom), 2006, 152, 1789-1797.	1.8	89
148	Crystal Structure of TDP-Fucosamine Acetyltransferase (WecD) from Escherichia coli , an Enzyme Required for Enterobacterial Common Antigen Synthesis. Journal of Bacteriology, 2006, 188, 5606-5617.	2.2	27
149	L-Tartaric acid synthesis from vitamin C in higher plants. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5608-5613.	7.1	176
150	The Escherichia coli Proteome: Past, Present, and Future Prospects. Microbiology and Molecular Biology Reviews, 2006, 70, 362-439.	6.6	147
151	SCOPPI: a structural classification of protein-protein interfaces. Nucleic Acids Research, 2006, 34, D310-D314.	14.5	142
152	Genomic Organization, Differential Expression, and Interaction of SQUAMOSA Promoter-Binding-Like Transcription Factors and microRNA156 in Rice. Plant Physiology, 2006, 142, 280-293.	4.8	595
153	ProtoBee: Hierarchical classification and annotation of the honey bee proteome. Genome Research, 2006, 16, 1431-1438.	5.5	17
154	Energetic Consequences of Nitrite Stress in Desulfovibrio vulgaris Hildenborough, Inferred from Global Transcriptional Analysis. Applied and Environmental Microbiology, 2006, 72, 4370-4381.	3.1	92
155	MODOMICS: a database of RNA modification pathways. Nucleic Acids Research, 2006, 34, D145-D149.	14.5	216
156	Domain Architecture Comparison for Multidomain Homology Identification. Journal of Computational Biology, 2007, 14, 496-516.	1.6	34
157	The tiny eukaryote Ostreococcus provides genomic insights into the paradox of plankton speciation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7705-7710.	7.1	563
158	A Network-based Analysis of Polyanion-binding Proteins Utilizing Human Protein Arrays. Journal of Biological Chemistry, 2007, 282, 10153-10163.	3.4	24
159	GreenPhylDB: a database for plant comparative genomics. Nucleic Acids Research, 2007, 36, D991-D998.	14.5	70
160	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. Nucleic Acids Research, 2007, 36, D528-D533.	14.5	179
161	Being Pathogenic, Plastic, and Sexual while Living with a Nearly Minimal Bacterial Genome. PLoS Genetics, 2007, 3, e75.	3.5	176
162	IntAct--open source resource for molecular interaction data. Nucleic Acids Research, 2007, 35, D561-D565.	14.5	701
163	Genome browsing with Ensembl: a practical overview. Briefings in Functional Genomics & Proteomics, 2007, 6, 202-219.	3.8	31

#	ARTICLE	IF	CITATIONS
164	Challenges and Solutions in Proteomics. <i>Current Genomics</i> , 2007, 8, 21-28.	1.6	12
165	Specificity and Evolvability in Eukaryotic Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2007, 3, e25.	3.2	111
166	Characterization of Protein Hubs by Inferring Interacting Motifs from Protein Interactions. <i>PLoS Computational Biology</i> , 2007, 3, e178.	3.2	51
167	A Primer on Python for Life Science Researchers. <i>PLoS Computational Biology</i> , 2007, 3, e199.	3.2	58
168	EVEREST: a collection of evolutionary conserved protein domains. <i>Nucleic Acids Research</i> , 2007, 35, D241-D246.	14.5	20
169	FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. <i>Nucleic Acids Research</i> , 2007, 35, W91-W96.	14.5	248
170	SNAPPI-DB: a database and API of Structures, iNterfaces and Alignments for Protein-Protein Interactions. <i>Nucleic Acids Research</i> , 2007, 35, D580-D589.	14.5	58
171	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	14.5	444
172	The SUPERFAMILY database in 2007: families and functions. <i>Nucleic Acids Research</i> , 2007, 35, D308-D313.	14.5	216
173	EMBL Nucleotide Sequence Database in 2006. <i>Nucleic Acids Research</i> , 2007, 35, D16-D20.	14.5	136
174	Expanded protein information at SGD: new pages and proteome browser. <i>Nucleic Acids Research</i> , 2007, 35, D468-D471.	14.5	69
175	MiST: a microbial signal transduction database. <i>Nucleic Acids Research</i> , 2007, 35, D386-D390.	14.5	103
176	GeneSpeed: protein domain organization of the transcriptome. <i>Nucleic Acids Research</i> , 2007, 35, D674-D679.	14.5	9
177	Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. <i>Plant Physiology</i> , 2007, 144, 1642-1653.	4.8	17
178	Michigan Molecular Interactions (MiMI): putting the jigsaw puzzle together. <i>Nucleic Acids Research</i> , 2007, 35, D566-D571.	14.5	98
179	PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. <i>Nucleic Acids Research</i> , 2007, 35, D247-D252.	14.5	333
180	Evolutionary analysis of enzymes using Chisel. <i>Bioinformatics</i> , 2007, 23, 2961-2968.	4.1	1
181	CFGP: a web-based, comparative fungal genomics platform. <i>Nucleic Acids Research</i> , 2007, 36, D562-D571.	14.5	76

#	ARTICLE	IF	CITATIONS
182	CancerGenes: a gene selection resource for cancer genome projects. Nucleic Acids Research, 2007, 35, D721-D726.	14.5	158
183	A Web-enabled Database of Human Gene Expression Controlled Annotations for Gene List Functional Evaluation. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 394-7.	0.5	4
184	WebMOTIFS: automated discovery, filtering and scoring of DNA sequence motifs using multiple programs and Bayesian approaches. Nucleic Acids Research, 2007, 35, W217-W220.	14.5	41
185	ESTpass: a web-based server for processing and annotating expressed sequence tag (EST) sequences. Nucleic Acids Research, 2007, 35, W159-W162.	14.5	30
186	Identification of the Ligands of Protein Interaction Domains through a Functional Approach. Molecular and Cellular Proteomics, 2007, 6, 333-345.	3.8	30
187	DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397.	14.5	25
188	High-Throughput Flow Cytometry-Based Assay to Identify Apoptosis-Inducing Proteins. Journal of Biomolecular Screening, 2007, 12, 510-520.	2.6	6
189	MyHits: improvements to an interactive resource for analyzing protein sequences. Nucleic Acids Research, 2007, 35, W433-W437.	14.5	185
190	Gene Ontology annotations at SGD: new data sources and annotation methods. Nucleic Acids Research, 2007, 36, D577-D581.	14.5	218
191	Automated Improvement of Domain ANnotations using context analysis of domain arrangements (AIDAN). Bioinformatics, 2007, 23, 1834-1836.	4.1	14
192	Characterising alternate splicing and tissue specific expression in the chicken from ESTs. Cytogenetic and Genome Research, 2007, 117, 268-277.	1.1	5
193	Selection of Genes and Single Nucleotide Polymorphisms for Fine Mapping Starting From a Broad Linkage Region. Twin Research and Human Genetics, 2007, 10, 871-885.	0.6	9
194	AutoPSI: a database for automatic structural classification of protein sequences and structures. Nucleic Acids Research, 2007, 36, D398-D401.	14.5	3
195	Proteolytic Adaptor for Transfer-Messenger RNA-Tagged Proteins from $\hat{\pm}$ -Proteobacteria. Journal of Bacteriology, 2007, 189, 272-275.	2.2	27
196	Structural Genomics. , 0, , 419-438.		0
197	Expressed Sequence Tags from Phytophthora sojae Reveal Genes Specific to Development and Infection. Molecular Plant-Microbe Interactions, 2007, 20, 781-793.	2.6	59
198	Inferring Protein Function from Protein Structure. , 0, , 1211-1252.		1
199	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2007, 17, Unit 1.4.	25.8	41

#	ARTICLE	IF	CITATIONS
200	Functional genomics of sulphate-reducing prokaryotes. , 2007, , 117-140.		3
201	The mouse Gene Expression Database (GXD): 2007 update. Nucleic Acids Research, 2007, 35, D618-D623.	14.5	79
202	The tify family previously known as ZIM. Trends in Plant Science, 2007, 12, 239-244.	8.8	283
203	The ancestral role of the phosphoenolpyruvateâ€“carbohydrate phosphotransferase system (PTS) as exposed by comparative genomics. Research in Microbiology, 2007, 158, 666-670.	2.1	42
204	A combined bioinformatics and chemoinformatics approach for the development of new antiparasitic drugs. Genomics, 2007, 89, 36-43.	2.9	38
205	Membrane protein prediction methods. Methods, 2007, 41, 460-474.	3.8	104
206	Suppression of the pathogen-inducible Medicago truncatula putative protease-inhibitor MtTi2 does not influence root infection by Aphanomyces euteiches but results in transcriptional changes from wildtype roots. Plant Science, 2007, 173, 84-95.	3.6	8
207	Identification by suppression subtractive hybridization and expression analysis of Medicago truncatula putative defence genes in response to Orobancha crenata parasitization. Physiological and Molecular Plant Pathology, 2007, 70, 49-59.	2.5	37
208	Phospholipid scramblases: An overview. Archives of Biochemistry and Biophysics, 2007, 462, 103-114.	3.0	203
209	Differentiation-dependent expression of Adhfe1 in adipogenesis. Archives of Biochemistry and Biophysics, 2007, 464, 100-111.	3.0	23
210	Identification of Sensory and Signalâ€“Transducing Domains in Twoâ€“Component Signaling Systems. Methods in Enzymology, 2007, 422, 47-74.	1.0	30
211	Novel Families of Toxin-like Peptides in Insects and Mammals: A Computational Approach. Journal of Molecular Biology, 2007, 369, 553-566.	4.2	41
212	Identification of a Single HNH Active Site in Type IIS Restriction Endonuclease Eco31I. Journal of Molecular Biology, 2007, 370, 157-169.	4.2	22
213	Informatics Resources for Rice Functional Genomics. , 2007, , 355-394.		2
214	Evaluating deterministic motif significance measures in protein databases. Algorithms for Molecular Biology, 2007, 2, 16.	1.2	16
215	FlyMine: an integrated database for Drosophila and Anopheles genomics. Genome Biology, 2007, 8, R129.	9.6	345
216	GOTax: investigating biological processes and biochemical activities along the taxonomic tree. Genome Biology, 2007, 8, R33.	9.6	20
217	Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. Genome Biology, 2007, 8, R15.	9.6	117

#	ARTICLE	IF	CITATIONS
218	DiscoverySpace: an interactive data analysis application. <i>Genome Biology</i> , 2007, 8, R6.	9.6	41
219	Protein Annotation at Genomic Scale: The Current Status. <i>Chemical Reviews</i> , 2007, 107, 3448-3466.	47.7	66
220	A Tool for Creating and Parallelizing Bioinformatics Pipelines. , 2007, , .		2
221	MotifNetwork: A Grid-enabled Workflow for High-throughput Domain Analysis of Biological Sequences: Implications for annotation and study of phylogeny, protein interactions, and intraspecies variation. , 2007, , .		4
222	Protein Structure Prediction Based on a Domain Clustering Database. , 2007, , .		1
223	Plant Gene and Alternatively Spliced Variant Annotator. A Plant Genome Annotation Pipeline for Rice Gene and Alternatively Spliced Variant Identification with Cross-Species Expressed Sequence Tag Conservation from Seven Plant Species. <i>Plant Physiology</i> , 2007, 143, 1086-1095.	4.8	24
224	MotifNetwork: Genome-Wide Domain Analysis using Grid-enabled Workflows. , 2007, , .		4
225	SynDB: a Synapse protein DataBase based on synapse ontology. <i>Nucleic Acids Research</i> , 2007, 35, D737-D741.	14.5	43
226	SmedGD: the Schmidtea mediterranea genome database. <i>Nucleic Acids Research</i> , 2007, 36, D599-D606.	14.5	251
227	Oncomine 3.0: Genes, Pathways, and Networks in a Collection of 18,000 Cancer Gene Expression Profiles. <i>Neoplasia</i> , 2007, 9, 166-180.	5.3	1,847
228	Molecular Concepts Analysis Links Tumors, Pathways, Mechanisms, and Drugs. <i>Neoplasia</i> , 2007, 9, 443-IN9.	5.3	124
230	InterPro and InterProScan. <i>Methods in Molecular Biology</i> , 2007, 396, 59-70.	0.9	339
231	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	5.6	736
232	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	5.6	490
233	Inferring Protein Function from Sequence. , 0, , 1087-1119.		2
234	Comparative Modeling of Drug Target Proteins. , 2007, , 215-236.		1
235	Rv3389C from <i>Mycobacterium tuberculosis</i> , a member of the (R)-specific hydratase/dehydratase family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 303-311.	2.3	16
236	Using OWL to model biological knowledge. <i>International Journal of Human Computer Studies</i> , 2007, 65, 583-594.	5.6	59

#	ARTICLE	IF	CITATIONS
237	Homology modeling of major intrinsic proteins in rice, maize and Arabidopsis: comparative analysis of transmembrane helix association and aromatic/arginine selectivity filters. BMC Structural Biology, 2007, 7, 27.	2.3	94
238	HitKeeper, a generic software package for hit list management. Source Code for Biology and Medicine, 2007, 2, 2.	1.7	10
239	SitCon: Binding site residue conservation visualization and protein sequence-to-function tool. International Journal of Quantum Chemistry, 2007, 107, 2100-2110.	2.0	0
240	Predicting protein homocysteinylation targets based on dihedral strain energy and pKa of cysteines. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1475-1483.	2.6	15
241	Diabetes-induced changes in the renal cortical proteome assessed with two-dimensional gel electrophoresis and mass spectrometry. Proteomics, 2007, 7, 1729-1742.	2.2	53
242	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast Pichia stipitis. Nature Biotechnology, 2007, 25, 319-326.	17.5	449
243	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. Molecular Psychiatry, 2007, 12, 74-86.	7.9	386
244	Comparative Analysis of Two-component Signal Transduction System in Two Streptomyces Genomes. Acta Biochimica Et Biophysica Sinica, 2007, 39, 317-325.	2.0	6
245	Genome-wide identification and analyses of the rice calmodulin and related potential calcium sensor proteins. BMC Plant Biology, 2007, 7, 4.	3.6	166
246	From genes to functional classes in the study of biological systems. BMC Bioinformatics, 2007, 8, 114.	2.6	108
247	A new advance in alternative splicing databases: from catalogue to detailed analysis of regulation of expression and function of human alternative splicing variants. BMC Bioinformatics, 2007, 8, 180.	2.6	64
248	A domain-based approach to predict protein-protein interactions. BMC Bioinformatics, 2007, 8, 199.	2.6	68
249	Motif kernel generated by genetic programming improves remote homology and fold detection. BMC Bioinformatics, 2007, 8, 23.	2.6	43
250	A topological algorithm for identification of structural domains of proteins. BMC Bioinformatics, 2007, 8, 237.	2.6	20
251	Probabilistic prediction and ranking of human protein-protein interactions. BMC Bioinformatics, 2007, 8, 239.	2.6	115
252	Automatic generation of 3D motifs for classification of protein binding sites. BMC Bioinformatics, 2007, 8, 321.	2.6	21
253	DAVID Knowledgebase: a gene-centered database integrating heterogeneous gene annotation resources to facilitate high-throughput gene functional analysis. BMC Bioinformatics, 2007, 8, 426.	2.6	510
254	Linear array of conserved sequence motifs to discriminate protein subfamilies: study on pyridine nucleotide-disulfide reductases. BMC Bioinformatics, 2007, 8, 96.	2.6	9

#	ARTICLE	IF	CITATIONS
255	Statistical analysis of genomic protein family and domain controlled annotations for functional investigation of classified gene lists. BMC Bioinformatics, 2007, 8, S14.	2.6	3
256	The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. BMC Bioinformatics, 2007, 8, S4.	2.6	36
257	Genomic and microarray analysis of aromatics degradation in Geobacter metallireducens and comparison to a Geobacter isolate from a contaminated field site. BMC Genomics, 2007, 8, 180.	2.8	87
258	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. BMC Genomics, 2007, 8, 325.	2.8	44
259	A phylogenomic analysis of the Actinomycetales mce operons. BMC Genomics, 2007, 8, 60.	2.8	207
260	Gene function in early mouse embryonic stem cell differentiation. BMC Genomics, 2007, 8, 85.	2.8	123
261	A kingdom-specific protein domain HMM library for improved annotation of fungal genomes. BMC Genomics, 2007, 8, 97.	2.8	12
262	Sel1-like repeat proteins in signal transduction. Cellular Signalling, 2007, 19, 20-31.	3.6	146
263	Mutations in the carboxyl terminal region of E2 glycoprotein of classical swine fever virus are responsible for viral attenuation in swine. Virology, 2007, 364, 371-382.	2.4	51
264	Management and Analysis of Genomic Functional and Phenotypic Controlled Annotations to Support Biomedical Investigation and Practice. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 376-385.	3.2	14
265	HB mobile element in the Drosophila melanogaster genome: Structural and functional analyses. Russian Journal of Genetics, 2007, 43, 502-512.	0.6	0
266	The EMBL Nucleotide Sequence and Genome Reviews Databases. , 2007, 406, 1-21.		14
267	A Collection of Plant-Specific Genomic Data and Resources at NCBI. , 2007, 406, 61-87.		15
268	BGI-RIS V2. , 2007, 406, 275-299.		4
269	Analysis and prediction of functionally important sites in proteins. Protein Science, 2007, 16, 4-13.	7.6	44
270	Structural and transcriptional analyses of a purine nucleotide-binding protein from Pyrococcus furiosus: a component of a novel, membrane-bound multiprotein complex unique to this hyperthermophilic archaeon. Journal of Structural and Functional Genomics, 2007, 8, 1-10.	1.2	0
271	Maintenance DNA methyltransferase (Met1) and silencing of CpG-methylated foreign DNA in Volvox carteri. Plant Molecular Biology, 2007, 63, 325-336.	3.9	22
272	Inferring the skeleton cell cycle regulatory network of malaria parasite using comparative genomic and variational Bayesian approaches. Genetica, 2007, 132, 131-142.	1.1	10

#	ARTICLE	IF	CITATIONS
273	Identification of disulfide reductases in Campylobacterales: a bioinformatics investigation. Antonie Van Leeuwenhoek, 2007, 92, 429-441.	1.7	16
274	The leucine-rich repeat structure. Cellular and Molecular Life Sciences, 2008, 65, 2307-2333.	5.4	392
275	Gene Nomenclature System for Rice. Rice, 2008, 1, 72-84.	4.0	334
276	Systematic sequence analysis and identification of tissue-specific or stress-responsive genes of NAC transcription factor family in rice. Molecular Genetics and Genomics, 2008, 280, 547-563.	2.1	411
277	Systematic characterization of the murine mitochondrial proteome using functionally validated cardiac mitochondria. Proteomics, 2008, 8, 1564-1575.	2.2	90
278	Cardiovascular GO Annotation Initiative Year 1 Report: Why Cardiovascular GO?. Proteomics, 2008, 8, 1950-1953.	2.2	15
279	Characterization of local geometry of protein surfaces with the visibility criterion. Proteins: Structure, Function and Bioinformatics, 2008, 71, 670-683.	2.6	82
280	Protein domain annotation with integration of heterogeneous information sources. Proteins: Structure, Function and Bioinformatics, 2008, 72, 461-473.	2.6	20
281	Complete Genome Sequence of the Soil Actinomycete <i>Kocuria rhizophila</i> . Journal of Bacteriology, 2008, 190, 4139-4146.	2.2	79
282	Mutations in CHD7, Encoding a Chromatin-Remodeling Protein, Cause Idiopathic Hypogonadotropic Hypogonadism and Kallmann Syndrome. American Journal of Human Genetics, 2008, 83, 511-519.	6.2	307
283	The genome of the simian and human malaria parasite Plasmodium knowlesi. Nature, 2008, 455, 799-803.	27.8	338
284	HomeoDB: a database of homeobox gene diversity. Evolution & Development, 2008, 10, 516-518.	2.0	75
285	Access to immunology through the Gene Ontology. Immunology, 2008, 125, 154-160.	4.4	33
286	JCoast – A biologist-centric software tool for data mining and comparison of prokaryotic (meta)genomes. BMC Bioinformatics, 2008, 9, 177.	2.6	58
287	Defining functional distances over Gene Ontology. BMC Bioinformatics, 2008, 9, 50.	2.6	55
288	Just how versatile are domains?. BMC Evolutionary Biology, 2008, 8, 285.	3.2	43
289	Phylogenomics of plant genomes: a methodology for genome-wide searches for orthologs in plants. BMC Genomics, 2008, 9, 183.	2.8	18
290	Fungal cytochrome P450 database. BMC Genomics, 2008, 9, 402.	2.8	134

#	ARTICLE	IF	CITATIONS
291	Protein Domain Prediction. Methods in Molecular Biology, 2008, 426, 117-143.	0.9	11
292	NetGrep: fast network schema searches in interactomes. Genome Biology, 2008, 9, R138.	9.6	34
293	Predicting gene function in a hierarchical context with an ensemble of classifiers. Genome Biology, 2008, 9, S3.	9.6	123
294	Combining guilt-by-association and guilt-by-profiling to predict <i>Saccharomyces cerevisiae</i> gene function. Genome Biology, 2008, 9, S7.	9.6	78
295	A critical assessment of <i>Mus musculus</i> gene function prediction using integrated genomic evidence. Genome Biology, 2008, 9, S2.	9.6	214
296	An en masse phenotype and function prediction system for <i>Mus musculus</i> . Genome Biology, 2008, 9, S8.	9.6	20
297	Protein bioinformatics. , 2008, , 203-222.		1
298	Expression and Microarrays. Methods in Molecular Biology, 2008, 453, 245-255.	0.9	1
299	Diet-Induced Obesity Is Linked to Marked but Reversible Alterations in the Mouse Distal Gut Microbiome. Cell Host and Microbe, 2008, 3, 213-223.	11.0	2,535
300	ConFunc—functional annotation in the twilight zone. Bioinformatics, 2008, 24, 798-806.	4.1	95
301	Impacts of protein—protein interaction domains on organism and network complexity. Genome Research, 2008, 18, 1500-1508.	5.5	42
302	K Homology Domains of the Mouse Polycystic Kidney Disease-Related Protein, Bicaudal-C (Bicc1), Mediate RNA Binding in vitro. Nephron Experimental Nephrology, 2008, 108, e27-e34.	2.2	21
303	The functional domain grouping of microtubule associated proteins. Communicative and Integrative Biology, 2008, 1, 47-50.	1.4	5
304	Maps: An integrated system for protein sequence annotation using support vector machine. Journal of the Chinese Institute of Engineers, Transactions of the Chinese Institute of Engineers, Series A/Chung-kuo Kung Ch'eng Hsueh K'an, 2008, 31, 781-790.	1.1	0
305	Genes and (Common) Pathways Underlying Drug Addiction. PLoS Computational Biology, 2008, 4, e2.	3.2	210
306	Sequence Similarity Network Reveals Common Ancestry of Multidomain Proteins. PLoS Computational Biology, 2008, 4, e1000063.	3.2	60
307	Web-based Tools for Protein Classification. Methods in Molecular Biology, 2008, 428, 349-367.	0.9	0
308	The <i>Arabidopsis</i> MUM2 Gene Encodes a Î²-Galactosidase Required for the Production of Seed Coat Mucilage with Correct Hydration Properties. Plant Cell, 2008, 19, 4007-4021.	6.6	145

#	ARTICLE	IF	CITATIONS
309	Relevance of nucleotides of the PcaU binding site from <i>Acinetobacter baylyi</i> . <i>Microbiology (United Kingdom)</i> , 2008, 152, 1447-1458.	1.8	7
310	Structure of [NiFe] Hydrogenase Maturation Protein HypE from <i>Escherichia coli</i> and Its Interaction with HypF. <i>Journal of Bacteriology</i> , 2008, 190, 1447-1458.	2.2	43
311	Intestinal Transcriptomes of Nematodes: Comparison of the Parasites <i>Ascaris suum</i> and <i>Haemonchus contortus</i> with the Free-living <i>Caenorhabditis elegans</i> . <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e269.	3.0	42
312	Run-Off Replication of Host-Adaptability Genes Is Associated with Gene Transfer Agents in the Genome of Mouse-Infecting <i>Bartonella grahamii</i> . <i>PLoS Genetics</i> , 2009, 5, e1000546.	3.5	87
313	Michigan molecular interactions r2: from interacting proteins to pathways. <i>Nucleic Acids Research</i> , 2009, 37, D642-D646.	14.5	85
314	A Novel Pathogenicity Gene Is Required in the Rice Blast Fungus to Suppress the Basal Defenses of the Host. <i>PLoS Pathogens</i> , 2009, 5, e1000401.	4.7	179
315	RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. <i>Nucleic Acids Research</i> , 2009, 37, D996-D1000.	14.5	10
316	MODOMICS: a database of RNA modification pathways. 2008 update. <i>Nucleic Acids Research</i> , 2009, 37, D118-D121.	14.5	184
317	ADAN: a database for prediction of protein-protein interaction of modular domains mediated by linear motifs. <i>Bioinformatics</i> , 2009, 25, 2418-2424.	4.1	36
318	Bioinformatic and partial functional analysis of pEspA and pEspB, two plasmids from <i>Exiguobacterium arabatum</i> sp. nov. RFL1109. <i>Plasmid</i> , 2009, 61, 52-64.	1.4	5
319	Molecular determinants archetypical to the phylum Nematoda. <i>BMC Genomics</i> , 2009, 10, 114.	2.8	11
320	Formulating and testing hypotheses in functional genomics. <i>Artificial Intelligence in Medicine</i> , 2009, 45, 97-107.	6.5	21
321	Construction and Applications of Genome-Scale in silico Metabolic Models for Strain Improvement. , 0, 355-385.		0
322	Development and use of genetic system to identify genes required for efficient low-temperature growth of <i>Psychrobacter arcticus</i> 273-4. <i>Extremophiles</i> , 2009, 13, 21-30.	2.3	29
323	Meta-basic estimates the size of druggable human genome. <i>Journal of Molecular Modeling</i> , 2009, 15, 695-699.	1.8	23
324	Full-Length Enriched cDNA Library Construction from Tissues Related to Energy Metabolism in Pigs. <i>Molecules and Cells</i> , 2009, 28, 529-536.	2.6	7
325	Molecular cloning and characterization of bile salt hydrolase in <i>Lactobacillus casei</i> Zhang. <i>Annals of Microbiology</i> , 2009, 59, 721-726.	2.6	15
326	Preliminary analysis of glutathione S-transferase homolog from <i>Lactobacillus casei</i> Zhang. <i>Annals of Microbiology</i> , 2009, 59, 727-731.	2.6	4

#	ARTICLE	IF	CITATIONS
327	Cloning and molecular characterization of a novel rolling-circle replicating plasmid, pK1S-1, from <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> K1. <i>Journal of Microbiology</i> , 2009, 47, 466-472.	2.8	5
328	Structural genomics reveals EVE as a new ASCH/PUA-related domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 760-773.	2.6	29
329	Evidence of a tick RNAi pathway by comparative genomics and reverse genetics screen of targets with known loss-of-function phenotypes in <i>Drosophila</i> . <i>BMC Molecular Biology</i> , 2009, 10, 26.	3.0	61
330	Prediction and Integration of Regulatory and Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2009, 541, 101-143.	0.9	12
331	Functional Profiling Methods in Cancer. <i>Methods in Molecular Biology</i> , 2009, 576, 363-374.	0.9	2
332	Use of Ligand Based Models for Protein Domains To Predict Novel Molecular Targets and Applications To Triage Affinity Chromatography Data. <i>Journal of Proteome Research</i> , 2009, 8, 2575-2585.	3.7	20
333	Genome analysis and genetic enhancement of tomato. <i>Critical Reviews in Biotechnology</i> , 2009, 29, 152-181.	9.0	16
334	Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network. <i>Genome Biology</i> , 2009, 10, R91.	9.6	196
335	TFCat: the curated catalog of mouse and human transcription factors. <i>Genome Biology</i> , 2009, 10, R29.	9.6	193
336	Genome Sequence Databases: Types of Data and Bioinformatic Tools. , 2009, , 211-236.		1
337	PlasmoDB: a functional genomic database for malaria parasites. <i>Nucleic Acids Research</i> , 2009, 37, D539-D543.	14.5	1,030
338	An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. <i>Nucleic Acids Research</i> , 2009, 37, 4587-4602.	14.5	400
339	Plant Genome Annotation Methods. <i>Methods in Molecular Biology</i> , 2009, 513, 263-282.	0.9	7
340	Mining the Arabidopsis and rice genomes for cyclophilin protein families. <i>International Journal of Bioinformatics Research and Applications</i> , 2009, 5, 295.	0.2	8
341	Artificial intelligence in genomic sequence, protein structure function prediction and DNA microarrays: a survey. <i>International Journal of Computational Intelligence in Bioinformatics and Systems Biology</i> , 2009, 1, 117.	0.1	0
342	Clustering sequences by overlap. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 260.	0.1	4
343	Detecting distant homologies on protozoans metabolic pathways using scientific workflows. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 256.	0.1	5
344	Mining Cytochrome b561 proteins from plant genomes. <i>International Journal of Bioinformatics Research and Applications</i> , 2010, 6, 209.	0.2	5

#	ARTICLE	IF	CITATIONS
345	Automatic, context-specific generation of Gene Ontology slims. BMC Bioinformatics, 2010, 11, 498.	2.6	33
346	Projection of gene-protein networks to the functional space of the proteome and its application to analysis of organism complexity. BMC Genomics, 2010, 11, S4.	2.8	3
347	Real-time ligand binding pocket database search using local surface descriptors. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2007-2028.	2.6	55
348	Bayesian Markov Random Field Analysis for Protein Function Prediction Based on Network Data. PLoS ONE, 2010, 5, e9293.	2.5	81
349	Design, Validation and Annotation of Transcriptome-Wide Oligonucleotide Probes for the Oligochaete Annelid Eisenia fetida. PLoS ONE, 2010, 5, e14266.	2.5	22
350	The comprehensive microbial resource. Nucleic Acids Research, 2010, 38, D340-D345.	14.5	241
351	The integrated microbial genomes system: an expanding comparative analysis resource. Nucleic Acids Research, 2010, 38, D382-D390.	14.5	237
352	Detecting novel genes with sparse arrays. Gene, 2010, 467, 41-51.	2.2	12
353	An approach for prioritizing disease-related microRNAs based on genomic data integration. , 2010, , .		20
354	Exploring Metabolic Pathway Reconstruction and Genome-Wide Expression Profiling in Lactobacillus reuteri to Define Functional Probiotic Features. PLoS ONE, 2011, 6, e18783.	2.5	147
355	Generation and Analysis of Large-Scale Data-Driven <i>Mycobacterium tuberculosis</i> Functional Networks for Drug Target Identification. Advances in Bioinformatics, 2011, 2011, 1-14.	5.7	28
356	Genome Sequence of a Mesophilic Hydrogenotrophic Methanogen Methanocella paludicola, the First Cultivated Representative of the Order Methanocellales. PLoS ONE, 2011, 6, e22898.	2.5	52
357	Genome-Wide Computational Function Prediction of Arabidopsis Proteins by Integration of Multiple Data Sources Â Â Â. Plant Physiology, 2011, 155, 271-281.	4.8	29
358	The draft genome of the parasitic nematode Trichinella spiralis. Nature Genetics, 2011, 43, 228-235.	21.4	285
359	â€œGuilt by Associationâ€•Is the Exception Rather Than the Rule in Gene Networks. PLoS Computational Biology, 2012, 8, e1002444.	3.2	183
360	Genomic basis of endosymbiont-conferred protection against an insect parasitoid. Genome Research, 2012, 22, 106-114.	5.5	91
361	A Resource of Quantitative Functional Annotation for Homo sapiens Genes. G3: Genes, Genomes, Genetics, 2012, 2, 223-233.	1.8	6
362	Article Withdrawn: GNARE: A Grid-based Server for the Analysis of User Submitted Genomes. Nucleic Acids Research, 2012, 40, e177-e177.	14.5	4

#	ARTICLE	IF	CITATIONS
363	Novel domain combinations in proteins encoded by chimeric transcripts. <i>Bioinformatics</i> , 2012, 28, i67-i74.	4.1	35
364	Genome-wide analysis of the MYB transcription factor superfamily in soybean. <i>BMC Plant Biology</i> , 2012, 12, 106.	3.6	339
365	A Novel Type III Endosome Transmembrane Protein, TEMP. <i>Cells</i> , 2012, 1, 1029-1044.	4.1	1
366	Structure- and sequence-based function prediction for non-homologous proteins. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 111-123.	1.2	27
367	Multiplicity of genes for aromatic ring-hydroxylating dioxygenases in <i>Mycobacterium</i> isolate KMS and their regulation. <i>Biodegradation</i> , 2012, 23, 585-596.	3.0	9
368	PHYLOGENETIC ANALYSES UNRAVEL THE EVOLUTIONARY HISTORY OF NAC PROTEINS IN PLANTS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1833-1848.	2.3	87
369	Catalog of <i>Erycina pusilla</i> miRNA and categorization of reproductive phase-related miRNAs and their target gene families. <i>Plant Molecular Biology</i> , 2013, 82, 193-204.	3.9	39
370	New insights into the archaeal diversity of a hypersaline microbial mat obtained by a metagenomic approach. <i>Systematic and Applied Microbiology</i> , 2013, 36, 205-214.	2.8	31
371	The genus <i>Pseudovibrio</i> contains metabolically versatile bacteria adapted for symbiosis. <i>Environmental Microbiology</i> , 2013, 15, 2095-2113.	3.8	121
372	Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure. <i>Environmental Microbiology</i> , 2013, 15, 211-226.	3.8	206
373	Two conidiation-related Zn(II)2Cys6 transcription factor genes in the rice blast fungus. <i>Fungal Genetics and Biology</i> , 2013, 61, 133-141.	2.1	51
374	Construction of Functional Linkage Gene Networks by Data Integration. <i>Methods in Molecular Biology</i> , 2013, 939, 215-232.	0.9	9
375	Species-Specific Expansion and Molecular Evolution of the 3-hydroxy-3-methylglutaryl Coenzyme A Reductase (HMGR) Gene Family in Plants. <i>PLoS ONE</i> , 2014, 9, e94172.	2.5	50
376	Mouse model phenotypes provide information about human drug targets. <i>Bioinformatics</i> , 2014, 30, 719-725.	4.1	38
377	Genome-wide analyses of DNA-binding proteins harboring AT-hook motifs and their functional roles in the rice blast pathogen, <i>Magnaporthe oryzae</i> . <i>Genes and Genomics</i> , 2014, 36, 871-881.	1.4	1
378	Comparative Modeling of Drug Target Proteins†. , 2014, , .		5
379	Permanent draft genome of <i>Rhodopirellula rubra</i> SWK7. <i>Marine Genomics</i> , 2014, 13, 11-12.	1.1	6
380	Permanent draft genome of <i>Rhodopirellula sallentina</i> SM41. <i>Marine Genomics</i> , 2014, 13, 17-18.	1.1	5

#	ARTICLE	IF	CITATIONS
381	An Orthology-Based Analysis of Pathogenic Protozoa Impacting Global Health: An Improved Comparative Genomics Approach with Prokaryotes and Model Eukaryote Orthologs. OMICS A Journal of Integrative Biology, 2014, 18, 524-538.	2.0	8
382	Virus proteins similar to human proteins as possible disturbance on human pathways. Systems and Synthetic Biology, 2014, 8, 283-295.	1.0	2
383	Genome-based vaccine design: the promise for malaria and other infectious diseases. International Journal for Parasitology, 2014, 44, 901-913.	3.1	39
384	Permanent draft genomes of the Rhodopirellula maiorica strain SM1. Marine Genomics, 2014, 13, 19-20.	1.1	5
385	Permanent draft genomes of the two Rhodopirellula europaea strains 6C and SH398. Marine Genomics, 2014, 13, 15-16.	1.1	4
386	Role of MoAND1-mediated nuclear positioning in morphogenesis and pathogenicity in the rice blast fungus, Magnaporthe oryzae. Fungal Genetics and Biology, 2014, 69, 43-51.	2.1	19
387	Permanent draft genomes of the three Rhodopirellula baltica strains SH28, SWK14 and WH47. Marine Genomics, 2014, 13, 13-14.	1.1	3
388	Evidence of recent interspecies horizontal gene transfer regarding nucleopolyhedrovirus infection of Spodoptera frugiperda. BMC Genomics, 2015, 16, 1008.	2.8	15
389	Contributions of Descriptive and Functional Genomics to Microbial Ecology. , 2015, , 831-846.		3
390	Measuring the wisdom of the crowds in network-based gene function inference. Bioinformatics, 2015, 31, 745-752.	4.1	23
391	Virtual screening: An in silico tool for interlacing the chemical universe with the proteome. Methods, 2015, 71, 44-57.	3.8	47
392	<i>Candidatus Desulfofervidus auxilii</i> , a hydrogenotrophic sulfate-reducing bacterium involved in the thermophilic anaerobic oxidation of methane. Environmental Microbiology, 2016, 18, 3073-3091.	3.8	115
393	Transcriptome-wide analysis of the MADS-box gene family in the orchid <i>Erycina pusilla</i> . Plant Biotechnology Journal, 2016, 14, 284-298.	8.3	74
394	An Approach for Zika Virus Inhibition Using Homology Structure of the Envelope Protein. Molecular Biotechnology, 2016, 58, 801-806.	2.4	30
395	TvZNF1 is a C2H2 zinc finger protein of Trichomonas vaginalis. BioMetals, 2017, 30, 861-872.	4.1	9
396	Antivirals for allosteric inhibition of Zika virus using a homology model and experimentally determined structure of envelope protein. BMC Research Notes, 2017, 10, 354.	1.4	7
397	Peanut RNA Helicase AhRH47 Sustains Protein Synthesis Under Stress and Improves Stress Adaptation in Arabidopsis. Plant Molecular Biology Reporter, 2018, 36, 58-70.	1.8	17
398	Characterization of a Protein Phosphatase Type-1 and a Kinase Anchoring Protein in Plasmodium falciparum. Frontiers in Microbiology, 2018, 9, 2617.	3.5	14

#	ARTICLE	IF	CITATIONS
399	Distinct roles of the YPEL gene family in development and pathogenicity in the ascomycete fungus <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , 2018, 8, 14461.	3.3	13
400	<i>Azospirillum brasilense</i> Az39, a model rhizobacterium with AHL-quorum-sensing capacity. <i>Journal of Applied Microbiology</i> , 2019, 126, 1850-1860.	3.1	11
401	Database on spermatozoa transcriptogram of catagorised Frieswal crossbred (Holstein Friesian X) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.1	15
402	A PAS-Containing Histidine Kinase is Required for Conidiation, Appressorium Formation, and Disease Development in the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>Mycobiology</i> , 2019, 47, 473-482.	1.7	5
403	De novo genome assembly and comparative annotation reveals metabolic versatility in cellulolytic bacteria from cropland and forest soils. <i>Functional and Integrative Genomics</i> , 2020, 20, 89-101.	3.5	4
404	Design principles of gene evolution for niche adaptation through changes in protein-protein interaction networks. <i>Scientific Reports</i> , 2020, 10, 15628.	3.3	1
405	Recent progresses of 3D printing technologies for structural energy storage devices. <i>Materials Today Nano</i> , 2020, 12, 100094.	4.6	42
406	The Genome of <i>Peronospora belbahrii</i> Reveals High Heterozygosity, a Low Number of Canonical Effectors, and TC-Rich Promoters. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 742-753.	2.6	15
407	Genome-Wide Identification, Expression Profile of the TIFY Gene Family in <i>Brassica oleracea</i> var. capitata, and Their Divergent Response to Various Pathogen Infections and Phytohormone Treatments. <i>Genes</i> , 2020, 11, 127.	2.4	31
408	Microbial genetic and transcriptional contributions to oxalate degradation by the gut microbiota in health and disease. <i>ELife</i> , 2021, 10, .	6.0	30
409	A Little Semantic Web Goes a Long Way in Biology. <i>Lecture Notes in Computer Science</i> , 2005, , 786-800.	1.3	28
410	Applying OWL Reasoning to Genomic Data. , 2007, , 225-248.		14
411	Supramolecular Signalling Complexes in the Nervous System. , 2007, 43, 185-207.		22
412	Bioinformatic Analysis of Adhesion Proteins. <i>Methods in Molecular Biology</i> , 2007, 370, 147-171.	0.9	14
413	Comparative Genome Analysis in the Integrated Microbial Genomes (IMG) System. <i>Methods in Molecular Biology</i> , 2007, 395, 35-56.	0.9	28
414	GenColors. <i>Methods in Molecular Biology</i> , 2007, , 75-96.	0.9	8
415	Computational Prediction of Domain Interactions. <i>Methods in Molecular Biology</i> , 2007, 396, 3-15.	0.9	3
416	Pfam. <i>Methods in Molecular Biology</i> , 2007, 396, 43-58.	0.9	38

#	ARTICLE	IF	CITATIONS
417	Neural Networks Predict Protein Structure and Function. <i>Methods in Molecular Biology</i> , 2008, 458, 198-225.	0.9	8
418	EST Processing: From Trace to Sequence. <i>Methods in Molecular Biology</i> , 2009, 533, 189-220.	0.9	3
419	Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2008, 453, 33-85.	0.9	3
420	In Sffamily Identification of Genes in Bacteriophage DNA. <i>Methods in Molecular Biology</i> , 2009, 502, 57-89.	0.9	25
422	Reconstructing the Topology of Protein Complexes. , 2007, , 32-46.		7
423	Mycobacterial Sigma Factors and Surface Biology. , 0, , 223-234.		4
424	Sigma Factors: Key Molecules in Mycobacterium tuberculosis Physiology and Virulence. , 0, , 135-160.		2
425	In Silico Identification of Carboxylate Clamp Type Tetratricopeptide Repeat Proteins in Arabidopsis and Rice As Putative Co-Chaperones of Hsp90/Hsp70. <i>PLoS ONE</i> , 2010, 5, e12761.	2.5	76
426	Inference of Surface Membrane Factors of HIV-1 Infection through Functional Interaction Networks. <i>PLoS ONE</i> , 2010, 5, e13139.	2.5	7
427	Scoring Protein Relationships in Functional Interaction Networks Predicted from Sequence Data. <i>PLoS ONE</i> , 2011, 6, e18607.	2.5	24
428	Time-Resolved Transcriptomics and Bioinformatic Analyses Reveal Intrinsic Stress Responses during Batch Culture of <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2011, 6, e27160.	2.5	47
429	Expression of a Finger Millet Transcription Factor, EcNAC1, in Tobacco Confers Abiotic Stress-Tolerance. <i>PLoS ONE</i> , 2012, 7, e40397.	2.5	83
430	Gene Sets for Utilization of Primary and Secondary Nutrition Supplies in the Distal Gut of Endangered Iberian Lynx. <i>PLoS ONE</i> , 2012, 7, e51521.	2.5	23
431	Zebrafish <i>spata2</i> is expressed at early developmental stages. <i>International Journal of Developmental Biology</i> , 2007, 51, 241-246.	0.6	7
432	Comparative genome analysis of proteases, oligopeptide uptake and secretion systems in <i>Mycoplasma</i> spp. <i>Genetics and Molecular Biology</i> , 2007, 30, 225-229.	1.3	17
433	Molecular analysis of an integrative conjugative element, ICEH, present in the chromosome of different strains of <i>Mycoplasma hyopneumoniae</i> . <i>Genetics and Molecular Biology</i> , 2007, 30, 256-263.	1.3	11
434	Genomic classification of protein-coding gene families. <i>WormBook</i> , 2005, , 1-23.	5.3	19
436	Alternatively Spliced Genes as Biomarkers for Schizophrenia, Bipolar Disorder and Psychosis: A Blood-Based Spliceome-Profiling Exploratory Study (Supplementary Table). <i>Current Pharmacogenomics and Personalized Medicine</i> , 2009, 7, 164-188.	0.2	44

#	ARTICLE	IF	CITATIONS
437	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
438	Multi-Level Data Integration and Data Mining in Systems Biology. , 2009, , 476-496.		1
439	Predicting Type 1 Diabetes Candidate Genes using Human Protein-Protein Interaction Networks. <i>Journal of Computer Science and Systems Biology</i> , 2009, 02, 133.	0.0	21
440	Biological Databases- Integration of Life Science Data. <i>Journal of Computer Science and Systems Biology</i> , 2012, 04, .	0.0	6
441	The Study of Food-Grade Induced Expression and Enzymatic Properties of L-Arabinose Isomerase from <i>Lactobacillus plantarum</i> WU14 with High D-Tagatose Yield. <i>Food and Nutrition Sciences</i> (Print), 2016, 07, 320-337.	0.4	3
442	Computational model for pathway reconstruction to unravel the evolutionary significance of melanin synthesis. <i>Bioinformatics</i> , 2013, 9, 94-100.	0.5	29
443	A Novel Method for Expanding Current Annotations in Gene Ontology. <i>Lecture Notes in Computer Science</i> , 2006, , 747-756.	1.3	0
444	Ontology Guided Data Integration for Computational Prioritization of Disease Genes. <i>Lecture Notes in Computer Science</i> , 2006, , 689-698.	1.3	1
445	HSPPIP: An Online Tool for Prediction of Protein-Protein Interactions in Humans. <i>Lecture Notes in Computer Science</i> , 2006, , 603-611.	1.3	0
447	Gene and Protein Sequence Databases. , 2007, , 349-372.		0
449	New Trends in the Analysis of Functional Genomic Data. <i>Mathematics in Industry</i> , 2008, , 576-580.	0.3	1
450	Online Resources for the Molecular Contextualization of Disease. <i>Methods in Molecular Medicine</i> , 2008, 141, 287-308.	0.8	0
451	Infrastructure for distributed protein annotation. , 2008, , 413-426.		0
452	Protein Data Integration Problem. <i>Studies in Computational Intelligence</i> , 2009, , 55-69.	0.9	0
453	Impact of the <i>Toxoplasma gondii</i> Genome Project. , 0, , 309-320.		0
454	Hypoallergenic Foods beyond Infant Formulas. , 0, , 285-308.		2
455	Identification of Chimeric RNAs Using RNA-Seq Reads and Protein-Protein Interactions of Translated Chimeras. <i>Methods in Molecular Biology</i> , 2020, 2079, 27-40.	0.9	0
456	Pex7 selectively imports PTS2 target proteins to peroxisomes and is required for anthracnose disease development in <i>Colletotrichum scovillei</i> . <i>Fungal Genetics and Biology</i> , 2021, 157, 103636.	2.1	3

#	ARTICLE	IF	CITATIONS
458	Extracting Features from Gene Ontology for the Identification of Protein Subcellular Location by Semantic Similarity Measurement. , 2007, , 112-118.		0
459	Genomic functional investigation through statistical analysis of protein families and domains. AMIA ... Annual Symposium proceedings, 2006, , 1020.	0.2	0
460	Assessing and combining reliability of protein interaction sources. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 433-44.	0.7	4
470	GOblet: annotation of anonymous sequence data with gene ontology and pathway terms. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	2
471	CsPOM1, a DYRK Family Kinase, Plays Diverse Roles in Fungal Development, Virulence, and Stress Tolerance in the Anthracnose Pathogen Colletotrichum scovillei. Frontiers in Cellular and Infection Microbiology, 2022, 12, 861915.	3.9	3
473	Previous Incubation of Bradyrhizobium japonicum E109 and Azospirillum argentinense Az39 (formerly) Tj ETQq1 1 0.784314 rgBT /Over Nutrition, 2022, 22, 4669-4682.	3.4	1
474	Unifying the identification of biomedical entities with the Bioregistry. Scientific Data, 2022, 9, .	5.3	9
475	The CsSTE50 Adaptor Protein in Mitogen-Activated Protein Kinase Cascades Is Essential for Pepper Anthracnose Disease of Colletotrichum scovillei. Plant Pathology Journal, 2022, 38, 593-602.	1.7	3
476	Root-Growth-Related MaTCP Transcription Factors Responsive to Drought Stress in Mulberry. Forests, 2023, 14, 143.	2.1	2
477	A new method for predicting plant proteins function based on multi label classification algorithm. , 2022, , .		0
478	De novo transcriptomic analysis of Doum Palm (Hyphaene compressa) revealed an insight into its potential drought tolerance. PLoS ONE, 2024, 19, e0292543.	2.5	0