

SMART 7: recent updates to the protein domain annotation

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Comparative Protein Structure Modeling Using Modeller. <i>Current Protocols in Bioinformatics</i> , 2006, 15, Unit-5.6.	25.8	2,858
2	Molecular Characterization and Comparative Sequence Analysis of Defense-Related Gene, <i>Oryza rufipogon</i> Receptor-Like Protein Kinase 1. <i>International Journal of Molecular Sciences</i> , 2012, 13, 9343-9362.	1.8	5
3	A Window into Domain Amplification Through Piccolo in Teleost Fish. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1325-1339.	0.8	4
4	Heterotrimeric G-protein Signaling Is Critical to Pathogenic Processes in <i>Entamoeba histolytica</i> . <i>PLoS Pathogens</i> , 2012, 8, e1003040.	2.1	25
5	Plasma Membrane Cyclic Nucleotide Gated Calcium Channels Control Land Plant Thermal Sensing and Acquired Thermotolerance. <i>Plant Cell</i> , 2012, 24, 3333-3348.	3.1	280
6	Sequence and Expression of <i>per</i> , <i>tim1</i> , and <i>cry2</i> Genes in the Madeira Cockroach <i>Rhyarobia maderae</i> . <i>Journal of Biological Rhythms</i> , 2012, 27, 453-466.	1.4	19
7	Epigenetic control of alternative mRNA processing at the imprinted <i>Herc3/Nap115</i> locus. <i>Nucleic Acids Research</i> , 2012, 40, 8917-8926.	6.5	44
8	Comparative Analysis of Zinc Finger Proteins Involved in Plant Disease Resistance. <i>PLoS ONE</i> , 2012, 7, e42578.	1.1	167
9	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	3.2	216
10	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2012, 41, D808-D815.	6.5	3,816
11	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
12	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012, 22, 2008-2017.	2.4	1,341
13	Designing orthogonal signaling pathways: How to fit in with the surroundings. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5140-5141.	3.3	5
14	Identification of the <i>cglC</i> , <i>cglD</i> , <i>cglE</i> , and <i>cglF</i> Genes and Their Role in Cell Contact-Dependent Gliding Motility in <i>Myxococcus xanthus</i> . <i>Journal of Bacteriology</i> , 2012, 194, 1940-1949.	1.0	34
15	cDNA Cloning and Expression Analysis of Pattern Recognition Proteins from the Chinese Oak Silkworm, <i>Antheraea pernyi</i> . <i>Insects</i> , 2012, 3, 1093-1104.	1.0	4
16	Synthesis and biological actions of diphosphoinositol phosphates (inositol pyrophosphates), regulators of cell homeostasis. <i>Biological Chemistry</i> , 2012, 393, 979-998.	1.2	73
17	Cyclic Di-GMP Phosphodiesterases <i>RmdA</i> and <i>RmdB</i> Are Involved in Regulating Colony Morphology and Development in <i>Streptomyces coelicolor</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4642-4651.	1.0	39
18	Computational Modelling of Linear Motif-Mediated Protein Interactions. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1553-1561.	1.0	11

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19	Leucine-Rich Repeat (LRR) Domains Containing Intervening Motifs in Plants. <i>Biomolecules</i> , 2012, 2, 288-311.	1.8	74
20	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012, 8, 581.	3.2	29
21	The PtdIns3Pâ€Binding Protein Phafin 2 Mediates Epidermal Growth Factor Receptor Degradation by Promoting Endosome Fusion. <i>Traffic</i> , 2012, 13, 1547-1563.	1.3	27
22	Multiplex Targeted Sequencing Identifies Recurrently Mutated Genes in Autism Spectrum Disorders. <i>Science</i> , 2012, 338, 1619-1622.	6.0	1,133
23	The auxiliary protein complex <scp>SaePQ</scp> activates the phosphatase activity of sensor kinase <scp>SaeS</scp> in the <scp>SaeRS</scp> twoâ€component system of <i><scp>S</scp>taphylococcus aureus</i>. <i>Molecular Microbiology</i> , 2012, 86, 331-348.	1.2	74
24	Computational tools for viral metagenomics and their application in clinical research. <i>Virology</i> , 2012, 434, 162-174.	1.1	59
25	Fife, a Drosophila Piccolo-RIM Homolog, Promotes Active Zone Organization and Neurotransmitter Release. <i>Journal of Neuroscience</i> , 2012, 32, 17048-17058.	1.7	42
26	Amino acid substitutions in the N-terminus, cord and Î±-helix domains improved the thermostability of a family 11 xylanase XynR8. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 1279-1288.	1.4	24
27	A new twist to coiled coil. <i>FEBS Letters</i> , 2012, 586, 2717-2722.	1.3	20
28	CancerProView: A graphical image database of cancer-related genes and proteins. <i>Genomics</i> , 2012, 100, 81-92.	1.3	2
29	PTMcode: a database of known and predicted functional associations between post-translational modifications in proteins. <i>Nucleic Acids Research</i> , 2012, 41, D306-D311.	6.5	116
30	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
31	Thiol-Based Photocycle of the Blue and Teal Light-Sensing Cyanobacteriochrome Tlr1999. <i>Biochemistry</i> , 2012, 51, 3050-3058.	1.2	68
32	Distant plant homologues: donâ€™t throw out the baby. <i>Trends in Plant Science</i> , 2012, 17, 126-128.	4.3	3
33	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
34	Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. <i>FEBS Letters</i> , 2012, 586, 2631-2637.	1.3	43
35	Distribution of the SELMA Translocon in Secondary Plastids of Red Algal Origin and Predicted Uncoupling of Ubiquitin-Dependent Translocation from Degradation. <i>Eukaryotic Cell</i> , 2012, 11, 1472-1481.	3.4	58
36	Identifying structural domains of proteins using clustering. <i>BMC Bioinformatics</i> , 2012, 13, 286.	1.2	11

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37	A genome-wide identification and analysis of the basic helix-loop-helix transcription factors in the ponerine ant, <i>Harpegnathos saltator</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 165.	3.2	18
38	Extracytoplasmic function (ECF) sigma factor σ^{F} is involved in <i>Caulobacter crescentus</i> response to heavy metal stress. <i>BMC Microbiology</i> , 2012, 12, 210.	1.3	29
39	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
40	Interactions of an <i>Arabidopsis</i> RanBPM homologue with LisH-CTLH domain proteins revealed high conservation of CTLH complexes in eukaryotes. <i>BMC Plant Biology</i> , 2012, 12, 83.	1.6	29
41	MESSA: MEta-Server for protein Sequence Analysis. <i>BMC Biology</i> , 2012, 10, 82.	1.7	43
42	A rising tide of blue-absorbing biliprotein photoreceptors – characterization of seven such bilin-binding GAF domains in <i>Nostoc</i> sp. PCC 7120. <i>FEBS Journal</i> , 2012, 279, 4095-4108.	2.2	63
43	CDD: conserved domains and protein three-dimensional structure. <i>Nucleic Acids Research</i> , 2012, 41, D348-D352.	6.5	766
44	ABC transporters of antimicrobial peptides in Firmicutes bacteria – phylogeny, function and regulation. <i>Molecular Microbiology</i> , 2012, 86, 1295-1317.	1.2	113
45	Mutations in Multidomain Protein MEGF8 Identify a Carpenter Syndrome Subtype Associated with Defective Lateralization. <i>American Journal of Human Genetics</i> , 2012, 91, 897-905.	2.6	72
46	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
47	Identification, basic characterization and evolutionary analysis of differentially spliced mRNA isoforms of human YAP1 gene. <i>Gene</i> , 2012, 509, 215-222.	1.0	86
48	An improved understanding of TNFL/TNFR interactions using structure-based classifications. <i>Trends in Biochemical Sciences</i> , 2012, 37, 353-363.	3.7	31
49	Molecular cloning and characterization of an IKK homologue from amphioxus (<i>Branchiostoma</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.0	7
50	Genome-wide identification, classification and expression analysis of genes encoding putative fasciclin-like arabinogalactan proteins in Chinese cabbage (<i>Brassica rapa</i> L.). <i>Molecular Biology Reports</i> , 2012, 39, 10541-10555.	1.0	34
51	Identification of Sare0718 As an Alanine-Activating Adenylation Domain in Marine Actinomycete <i>Salinispora arenicola</i> CNS-205. <i>PLoS ONE</i> , 2012, 7, e37487.	1.1	5
52	GASP/WFIKKN Proteins: Evolutionary Aspects of Their Functions. <i>PLoS ONE</i> , 2012, 7, e43710.	1.1	8
53	The Rice B-Box Zinc Finger Gene Family: Genomic Identification, Characterization, Expression Profiling and Diurnal Analysis. <i>PLoS ONE</i> , 2012, 7, e48242.	1.1	120
54	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 0, , .	0.1	21

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55	The Investigation of Gene Regulation and Variation in Human Cancers and Other Diseases. , 2012, , .		0
56	Functional assignment of metagenomic data: challenges and applications. Briefings in Bioinformatics, 2012, 13, 711-727.	3.2	150
57	Identification and characterization of the vitellogenin receptor in <i>Macrobrachium rosenbergii</i> and its expression during vitellogenesis. Molecular Reproduction and Development, 2012, 79, 478-487.	1.0	39
58	Mutations in EZH2 Cause Weaver Syndrome. American Journal of Human Genetics, 2012, 90, 110-118.	2.6	253
59	Characterization of Farmington virus, a novel virus from birds that is distantly related to members of the family Rhabdoviridae. Virology Journal, 2013, 10, 219.	1.4	14
60	Evolution of RNA interference proteins dicer and argonaute in Basidiomycota. Mycologia, 2013, 105, 1489-1498.	0.8	42
61	Molecular characterization of a peritrophic membrane protein from the silkworm, <i>Bombyx mori</i> . Molecular Biology Reports, 2013, 40, 1087-1095.	1.0	4
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63	Proteolytic processing of the <i>Yersinia pestis</i> YapG autotransporter by the omptin protease Pla and the contribution of YapG to murine plague pathogenesis. Journal of Medical Microbiology, 2013, 62, 1124-1134.	0.7	10
64	Molecular characterization of the full-length L and M RNAs of Tomato yellow ring virus, a member of the genus <i>Tospovirus</i> . Virus Genes, 2013, 46, 487-495.	0.7	16
65	Architecture and regulation of HtrA-family proteins involved in protein quality control and stress response. Cellular and Molecular Life Sciences, 2013, 70, 761-775.	2.4	99
66	Horizontal gene transfer of epigenetic machinery and evolution of parasitism in the malaria parasite <i>Plasmodium falciparum</i> and other apicomplexans. BMC Evolutionary Biology, 2013, 13, 37.	3.2	32
67	P2RP: a web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. BMC Genomics, 2013, 14, 269.	1.2	69
68	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . BMC Genomics, 2013, 14, 75.	1.2	222
69	Phylogenetic analysis of the Argonaute protein family in platyhelminths. Molecular Phylogenetics and Evolution, 2013, 66, 1050-1054.	1.2	12
70	Niakha virus: A novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. Virology, 2013, 444, 80-89.	1.1	26
71	Classification and evolutionary analysis of the basic helix-loop-helix gene family in the green anole lizard, <i>Anolis carolinensis</i> . Molecular Genetics and Genomics, 2013, 288, 365-380.	1.0	12
72	Transcriptome-wide identification of R2R3-MYB transcription factors in barley with their boron responsive expression analysis. Molecular Genetics and Genomics, 2013, 288, 141-155.	1.0	87

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73	Functional analysis of the carS gene of <i>Fusarium fujikuroi</i> . <i>Molecular Genetics and Genomics</i> , 2013, 288, 157-173.	1.0	17
74	Identification of MDP (muramyl dipeptide)-binding key domains in NOD2 (nucleotide-binding and Tj ETQq1 1 0.784314 rgBT /Overlook 1007-1023.	0.9	20
75	Application of Genome-Scale Metabolic Models in Metabolic Engineering. <i>Industrial Biotechnology</i> , 2013, 9, 203-214.	0.5	26
76	Tethering preferences of domain families co-occurring in multi-domain proteins. <i>Molecular BioSystems</i> , 2013, 9, 1708.	2.9	1
78	Sequencing and expression analysis of CD3 β and CD3 ϵ chains in mandarin fish, <i>Siniperca chuatsi</i> . <i>Chinese Journal of Oceanology and Limnology</i> , 2013, 31, 106-117.	0.7	8
79	Regulation of a truncated isoform of AMP-activated protein kinase α (AMPK α) in response to hypoxia in the muscle of Pacific oyster <i>Crassostrea gigas</i> . <i>Journal of Comparative Physiology B: Biochemical, Systemic, and Environmental Physiology</i> , 2013, 183, 597-611.	0.7	35
80	Drug Discovery and Development via Synthetic Biology. , 2013, , 183-206.		9
81	Insights into the structure–function relationship of disease resistance protein HCTR in maize (<i>Zea</i>) Tj ETQq1 1 0.784314 rgBT /Overlook 2013, 45, 50-64.	1.3	9
82	Recessive Cancer Genes Engage in Negative Genetic Interactions with Their Functional Paralogs. <i>Cell Reports</i> , 2013, 5, 1519-1526.	2.9	19
83	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
84	PPM-Dom: A novel method for domain position prediction. <i>Computational Biology and Chemistry</i> , 2013, 47, 8-15.	1.1	3
85	Guardians of the actin monomer. <i>European Journal of Cell Biology</i> , 2013, 92, 316-332.	1.6	62
86	Isolation and characterization of a carrot nucleolar protein with structural and sequence similarity to the vertebrate PESCADILLO protein. <i>Plant Science</i> , 2013, 208, 83-92.	1.7	0
87	The circling mutant <i>Pcdh15</i> is a new mouse model for hearing loss. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2013, 751-752, 29-35.	0.4	2
88	A strain-specific segment of the RNA-dependent RNA polymerase of grapevine fanleaf virus determines symptoms in <i>Nicotiana</i> species. <i>Journal of General Virology</i> , 2013, 94, 2803-2813.	1.3	40
89	SMG1 is an ancient nonsense-mediated $\langle scp \rangle$ mRNA $\langle /scp \rangle$ decay effector. <i>Plant Journal</i> , 2013, 76, 800-810.	2.8	58
90	Molecular Regulation of Antibiotic Biosynthesis in <i>Streptomyces</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 112-143.	2.9	611
91	Pheromone Evolution, Reproductive Genes, and Comparative Transcriptomics in Mediterranean Earthworms (Annelida, Oligochaeta, Hormogastridae). <i>Molecular Biology and Evolution</i> , 2013, 30, 1614-1629.	3.5	24

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92	Genome-wide identification and expression analysis of MAPK and MAPKK gene family in <i>Malus domestica</i> . <i>Gene</i> , 2013, 531, 377-387.	1.0	92
93	Monitoring the immune response to vaccination with an inactivated vaccine associated to bovine neonatal pancytopenia by deep sequencing transcriptome analysis in cattle. <i>Veterinary Research</i> , 2013, 44, 93.	1.1	36
94	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 202.	3.2	51
95	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
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97	SLiMScape: a protein short linear motif analysis plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2013, 14, 224.	1.2	19
98	Phylogenetic and transcriptional analysis of an expanded bZIP transcription factor family in <i>Phytophthora sojae</i> . <i>BMC Genomics</i> , 2013, 14, 839.	1.2	30
99	Molecular Phylogeny, Homology Modeling, and Molecular Dynamics Simulation of Race-Specific Bacterial Blight Disease Resistance Protein (xa5) of Rice: A Comparative Agriproteomics Approach. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 423-438.	1.0	9
100	The <sc>Div</sc>, <sc>CbrA</sc> and <sc>PleC</sc> system controls <sc>Div</sc> phosphorylation and symbiosis in <i><sc>S</sc>inorhizobium meliloti</i>. <i>Molecular Microbiology</i> , 2013, 90, 54-71.	1.2	68
101	Cloning and characterization of serpin-like genes from the striped rice stem borer, <i>Chilo suppressalis</i> . <i>Genome</i> , 2013, 56, 359-366.	0.9	6
102	Genetic determinants of swimming motility in the squid light organ symbiont <i><sc>V</sc>ibrio fischeri</i>. <i>MicrobiologyOpen</i> , 2013, 2, 576-594.	1.2	58
103	Essential Role of the E3 Ubiquitin Ligase NOPPERABO1 in Schizogenous Intercellular Space Formation in the Liverwort <i>Marchantia polymorpha</i> Â. <i>Plant Cell</i> , 2013, 25, 4075-4084.	3.1	50
104	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
105	Cc.snf5, a gene encoding a putative component of the SWI/SNF chromatin remodeling complex, is essential for sexual development in the agaricomycete <i>Coprinopsis cinerea</i> . <i>Fungal Genetics and Biology</i> , 2013, 50, 82-89.	0.9	20
106	PolA1, a Putative DNA Polymerase I, Is Coexpressed with PerR and Contributes to Peroxide Stress Defenses of Group A <i>Streptococcus</i> . <i>Journal of Bacteriology</i> , 2013, 195, 717-725.	1.0	22
107	Divergence of Erv1-Associated Mitochondrial Import and Export Pathways in Trypanosomes and Anaerobic Protists. <i>Eukaryotic Cell</i> , 2013, 12, 343-355.	3.4	42
108	P_{ll} signal transduction proteins: nitrogen regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2013, 37, 251-283.	3.9	178
109	The chicken SLAM family. <i>Immunogenetics</i> , 2013, 65, 63-73.	1.2	8

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110	Synthase-dependent exopolysaccharide secretion in Gram-negative bacteria. <i>Trends in Microbiology</i> , 2013, 21, 63-72.	3.5	206
111	A primer in macromolecular linguistics. <i>Biopolymers</i> , 2013, 99, 203-217.	1.2	13
112	Prediction of protein domain boundaries from inverse covariances. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 253-260.	1.5	13
113	Predictions of protein-RNA interactions. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2013, 3, 161-175.	6.2	19
114	All Repeats Are Not Equal: A Module-Based Approach to Guide Repeat Protein Design. <i>Journal of Molecular Biology</i> , 2013, 425, 1826-1838.	2.0	32
115	Long-Range Effects and Functional Consequences of Stabilizing Mutations in the Ankyrin Repeat Domain of β -Casin. <i>Journal of Molecular Biology</i> , 2013, 425, 902-913.	2.0	10
116	Regulation of RNA interference by Hsp90 is an evolutionarily conserved process. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 2673-2681.	1.9	12
117	The many roles of the conserved eukaryotic Paf1 complex in regulating transcription, histone modifications, and disease states. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 116-126.	0.9	120
118	The structure of TON1937 from archaeon <i>Thermococcus onnurineus</i> NA1 reveals a eukaryotic HEAT-like architecture. <i>International Journal of Biological Macromolecules</i> , 2013, 61, 433-438.	3.6	3
119	Genome-wide analysis and identification of stress-responsive genes of the NAM1/ATAF1,2/CUC2 transcription factor family in apple. <i>Plant Physiology and Biochemistry</i> , 2013, 71, 11-21.	2.8	81
120	Identification and characterisation of a highly divergent geminivirus: Evolutionary and taxonomic implications. <i>Virus Research</i> , 2013, 177, 35-45.	1.1	76
121	Single-Molecule FRET Reveals the Native-State Dynamics of the β -Casin Ankyrin Repeat Domain. <i>Journal of Molecular Biology</i> , 2013, 425, 2578-2590.	2.0	25
122	Molecular cloning of the alpha subunit of complement component C8 (CpC8 α) of whitespotted bamboo shark (<i>Chiloscyllium plagiosum</i>). <i>Fish and Shellfish Immunology</i> , 2013, 35, 1993-2000.	1.6	12
123	Identification and characterization of TLR7, TLR8a2, TLR8b1 and TLR8b2 genes in Atlantic salmon (<i>Salmo salar</i> L.). <i>Journal of Fish Diseases</i> , 2013, 36, 107-114.	1.0	48
124	The NS16 protein of aquareovirus-C is a fusion-associated small transmembrane (FAST) protein, and its activity can be enhanced by the nonstructural protein NS26. <i>Virus Research</i> , 2013, 171, 129-137.	1.1	42
125	Genome-wide identification and analysis of the aldehyde dehydrogenase (ALDH) gene superfamily in apple (<i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2013, 71, 268-282.	2.8	36
126	The <i>Drosophila</i> Selectin Furrowed Mediates Intercellular Planar Cell Polarity Interactions via Frizzled Stabilization. <i>Developmental Cell</i> , 2013, 26, 455-468.	3.1	32
127	Experimental and bioinformatic investigation of the proteolytic degradation of the C-terminal domain of a fungal tyrosinase. <i>Journal of Inorganic Biochemistry</i> , 2013, 121, 37-45.	1.5	20

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128	<i>Arabidopsis</i> RING Peroxins are E3 Ubiquitin Ligases that Interact with Two Homologous Ubiquitin Receptor Proteins ^F . <i>Journal of Integrative Plant Biology</i> , 2013, 55, 108-120.	4.1	56
129	Using Analyses of Amino Acid Coevolution to Understand Protein Structure and Function. <i>Methods in Enzymology</i> , 2013, 523, 191-212.	0.4	13
130	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
131	ADAR-Related Activation of Adenosine-to-Inosine RNA Editing During Regeneration. <i>Stem Cells and Development</i> , 2013, 22, 2254-2267.	1.1	13
132	PPIevo : Protein-protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013, 102, 237-242.	1.3	131
133	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
134	Identification of Cyclic Nucleotide Gated Channels Using Regular Expressions. <i>Methods in Molecular Biology</i> , 2013, 1016, 207-224.	0.4	23
135	Partial venom gland transcriptome of a <i>Drosophila</i> parasitoid wasp, <i>Leptopilina heterotoma</i> , reveals novel and shared bioactive profiles with stinging Hymenoptera. <i>Gene</i> , 2013, 526, 195-204.	1.0	54
136	Single-Stranded DNA-Binding Proteins: Multiple Domains for Multiple Functions. <i>Structure</i> , 2013, 21, 1074-1084.	1.6	100
137	An Extracellular Interactome of Immunoglobulin and LRR Proteins Reveals Receptor-Ligand Networks. <i>Cell</i> , 2013, 154, 228-239.	13.5	207
138	Molecular characterization of calcineurin B from the non-virulent <i>Trypanosoma rangeli</i> kinetoplastid indicates high gene conservation. <i>Molecular Biology Reports</i> , 2013, 40, 4901-4912.	1.0	4
139	Systematic characterization of hypothetical proteins in <i>Synechocystis</i> sp. PCC 6803 reveals proteins functionally relevant to stress responses. <i>Gene</i> , 2013, 512, 6-15.	1.0	26
140	A genome-wide analysis of the RNA helicase gene family in <i>Solanum lycopersicum</i> . <i>Gene</i> , 2013, 513, 128-140.	1.0	26
143	Deubiquitylases From Genes to Organism. <i>Physiological Reviews</i> , 2013, 93, 1289-1315.	13.1	350
144	An In-silico Genomic Survey to Annotate Genes Coding for Early Development-Relevant Signaling Molecules in the Pearl Oyster, <i>Pinctada fucata</i> . <i>Zoological Science</i> , 2013, 30, 877.	0.3	14
145	Viral Metagenome Annotation Pipeline. , 2013, , 1-12.		1
146	Breast-cancer anti-estrogen resistance 4 (BCAR4) encodes a novel maternal-effect protein in bovine and is expressed in the oocyte of humans and other non-rodent mammals. <i>Human Reproduction</i> , 2013, 28, 430-441.	0.4	15
147	Elucidating Human Phosphatase-Substrate Networks. <i>Science Signaling</i> , 2013, 6, rs10.	1.6	145

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980	Structural and functional annotation of PR/SET Domain (PRDM) protein family: In-silico study elaborating role of PRDM12 mutation in congenital insensitivity to pain. <i>Computational Biology and Chemistry</i> , 2020, 89, 107382.	1.1	2

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988	Identification, evolution, expression, and docking studies of fatty acid desaturase genes in wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2020, 21, 778.	1.2	31
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1005	The Draft Genome of Red Lechwe, <i>Kobus lechwe lechwe</i> . <i>Frontiers in Genetics</i> , 2020, 11, 582638.	1.1	0
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1012	Identification, annotation of Mucin genes in channel catfish (<i>Ictalurus punctatus</i>) and their expression after bacterial infections revealed by RNA-seq analysis. <i>Aquaculture Research</i> , 2020, 51, 2020-2028.	0.9	2
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1079	Genome-wide identification and expression analysis of LBD transcription factor genes in Moso bamboo (<i>Phyllostachys edulis</i>). <i>BMC Plant Biology</i> , 2021, 21, 296.	1.6	24
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1091	Genome-wide investigation and comparative analysis of <scp>MATE</scp> gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus</i> Tj ETQq0 0 0 rGT /Overlock10 Tf 50 137 Td (bre	1.6	23
1092	Genome-wide identification and analysis of the heat shock transcription factor family in moso bamboo (<i>Phyllostachys edulis</i>). <i>Scientific Reports</i> , 2021, 11, 16492.	1.6	23
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