

Ramanathan Sowdhamini

List of Publications by Year in descending order

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141
papers

2,530
citations

236925

25
h-index

276875

41
g-index

152
all docs

152
docs citations

152
times ranked

3443
citing authors

#	ARTICLE	IF	CITATIONS
1	Knowledge-Based Protein Modeling. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1994, 29, 1-68.	5.2	206
2	STIFDB2: An Updated Version of Plant Stress-Responsive Transcription Factor DataBase with Additional Stress Signals, Stress-Responsive Transcription Factor Binding Sites and Stress-Responsive Genes in Arabidopsis and Rice. <i>Plant and Cell Physiology</i> , 2013, 54, e8-e8.	3.1	130
3	Comparative Genomics of Odorant Binding Proteins in <i>Anopheles gambiae</i> , <i>Aedes aegypti</i> , and <i>Culex quinquefasciatus</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 163-180.	2.5	112
4	100 ns Molecular Dynamics Simulations to Study Intramolecular Conformational Changes in Bax. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 28, 71-83.	3.5	82
5	Genome sequencing of herb Tulsi (<i>Ocimum tenuiflorum</i>) unravels key genes behind its strong medicinal properties. <i>BMC Plant Biology</i> , 2015, 15, 212.	3.6	80
6	Oligomerisation status and evolutionary conservation of interfaces of protein structural domain superfamilies. <i>Molecular BioSystems</i> , 2013, 9, 1652.	2.9	72
7	Transcriptional regulatory networks in <i>Arabidopsis thaliana</i> during single and combined stresses. <i>Nucleic Acids Research</i> , 2016, 44, 3147-3164.	14.5	62
8	PPCheck: A Webserver for the Quantitative Analysis of Protein-Protein Interfaces and Prediction of Residue Hotspots. <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S25928.	2.0	61
9	Molecular recognition in protein families: A database of aligned three-dimensional structures of related proteins. <i>Biochemical Society Transactions</i> , 1993, 21, 597-604.	3.4	53
10	Cross genome phylogenetic analysis of human and <i>Drosophila</i> G protein-coupled receptors: application to functional annotation of orphan receptors. <i>BMC Genomics</i> , 2005, 6, 106.	2.8	52
11	Mechanistic Heterogeneity in Contractile Properties of β -Tropomyosin (TPM1) Mutants Associated with Inherited Cardiomyopathies. <i>Journal of Biological Chemistry</i> , 2015, 290, 7003-7015.	3.4	41
12	An Approach to Function Annotation for Proteins of Unknown Function (PUFs) in the Transcriptome of Indian Mulberry. <i>PLoS ONE</i> , 2016, 11, e0151323.	2.5	40
13	Computational search for potential COVID-19 drugs from FDA-approved drugs and small molecules of natural origin identifies several anti-virals and plant products. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	38
14	Identification of Complete Repertoire of <i>Apis florea</i> Odorant Receptors Reveals Complex Orthologous Relationships with <i>Apis mellifera</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2879-2895.	2.5	37
15	Length Variations amongst Protein Domain Superfamilies and Consequences on Structure and Function. <i>PLoS ONE</i> , 2009, 4, e4981.	2.5	36
16	PASS2: an automated database of protein alignments organised as structural superfamilies. <i>BMC Bioinformatics</i> , 2004, 5, 35.	2.6	34
17	Molecular modeling and docking studies of human 5-hydroxytryptamine 2A (5-HT2A) receptor for the identification of hotspots for ligand binding. <i>Molecular BioSystems</i> , 2009, 5, 1877.	2.9	34
18	DOCKSCORE: a webserver for ranking protein-protein docked poses. <i>BMC Bioinformatics</i> , 2015, 16, 127.	2.6	33

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19	Molecular modelling of human 5-hydroxytryptamine receptor (5-HT _{2A}) and virtual screening studies towards the identification of agonist and antagonist molecules. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 952-970.	3.5	33
20	Genome wide survey of G protein-coupled receptors in <i>Tetraodon nigroviridis</i> . <i>BMC Evolutionary Biology</i> , 2005, 5, 41.	3.2	31
21	Molecular mechanisms and structural features of cardiomyopathy-causing troponin T mutants in the tropomyosin overlap region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11115-11120.	7.1	31
22	DEELIG: A Deep Learning Approach to Predict Protein-Ligand Binding Affinity. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110303.	2.0	30
23	Interface residues of transient protein-protein complexes have extensive intra-protein interactions apart from inter-protein interactions. <i>Biology Direct</i> , 2019, 14, 1.	4.6	29
24	3DSwap: curated knowledgebase of proteins involved in 3D domain swapping. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar042-bar042.	3.0	28
25	Structural Analysis of Prolyl Oligopeptidases Using Molecular Docking and Dynamics: Insights into Conformational Changes and Ligand Binding. <i>PLoS ONE</i> , 2011, 6, e26251.	2.5	27
26	3dswap-pred: Prediction of 3D Domain Swapping from Protein Sequence Using Random Forest Approach. <i>Protein and Peptide Letters</i> , 2011, 18, 1010-1020.	0.9	26
27	Comparative analyses of stress-responsive genes in <i>Arabidopsis thaliana</i> : insight from genomic data mining, functional enrichment, pathway analysis and phenomics. <i>Molecular BioSystems</i> , 2013, 9, 1888.	2.9	26
28	DIAL: a web-based server for the automatic identification of structural domains in proteins. <i>Nucleic Acids Research</i> , 2005, 33, W130-W132.	14.5	25
29	A glance into the evolution of template-free protein structure prediction methodologies. <i>Biochimie</i> , 2020, 175, 85-92.	2.6	24
30	STIF: Identification of stress-upregulated transcription factor binding sites in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2008, 2, 431-437.	0.5	24
31	Native and modeled disulfide bonds in proteins: Knowledge-based approaches toward structure prediction of disulfide-rich polypeptides. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 58, 866-879.	2.6	23
32	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. <i>Briefings in Bioinformatics</i> , 2016, 17, 841-862.	6.5	23
33	PrionHome: A Database of Prions and Other Sequences Relevant to Prion Phenomena. <i>PLoS ONE</i> , 2012, 7, e31785.	2.5	22
34	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (<i>Moringa oleifera</i>). <i>Genomics</i> , 2020, 112, 621-628.	2.9	22
35	Phylogenetic Analysis and Selection Pressures of 5-HT Receptors in Human and Non-human Primates: Receptor of an Ancient Neurotransmitter. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 27, 581-598.	3.5	21
36	Genome-wide survey of putative RNA-binding proteins encoded in the human proteome. <i>Molecular BioSystems</i> , 2016, 12, 532-540.	2.9	21

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37	Fold prediction and comparative modeling of Bdm1: a probable $\hat{I}\pm/\hat{I}^2$ hydrolase associated with hot water epilepsy. <i>Journal of Molecular Modeling</i> , 2003, 9, 3-8.	1.8	20
38	Decoding the structural events in substrate- \hat{E} gating mechanism of eukaryotic prolyl oligopeptidase using normal mode analysis and molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1428-1443.	2.6	20
39	Specificity and stability of transient protein- \hat{E} protein interactions. <i>Current Opinion in Structural Biology</i> , 2017, 44, 77-86.	5.7	20
40	Conserved spatially interacting motifs of protein superfamilies: Application to fold recognition and function annotation of genome data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 657-670.	2.6	19
41	DOR \hat{E} a Database of Olfactory Receptors \hat{E} Integrated Repository for Sequence and Secondary Structural Information of Olfactory Receptors in Selected Eukaryotic Genomes. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S14858.	2.0	19
42	Computational Approaches for Decoding Select Odorant-Olfactory Receptor Interactions Using Mini-Virtual Screening. <i>PLoS ONE</i> , 2015, 10, e0131077.	2.5	19
43	PIMA: Protein-Protein Interactions in Macromolecular Assembly - a web server for its Analysis and Visualization. <i>Bioinformatics</i> , 2016, 12, 9-11.	0.5	19
44	Regions of minimal structural variation among members of protein domain superfamilies: application to remote homology detection and modelling using distant relationships. <i>FEBS Letters</i> , 2004, 569, 31-36.	2.8	17
45	PASS2 version 4: An update to the database of structure-based sequence alignments of structural domain superfamilies. <i>Nucleic Acids Research</i> , 2012, 40, D531-D534.	14.5	17
46	GenDiS: Genomic Distribution of protein structural domain Superfamilies. <i>Nucleic Acids Research</i> , 2004, 33, D252-D255.	14.5	16
47	Genome inventory and analysis of nuclear hormone receptors in <i>Tetraodon nigroviridis</i> . <i>Journal of Biosciences</i> , 2007, 32, 43-50.	1.1	16
48	CUSP: an algorithm to distinguish structurally conserved and unconserved regions in protein domain alignments and its application in the study of large length variations. <i>BMC Structural Biology</i> , 2008, 8, 28.	2.3	16
49	Probing subtle conformational changes induced by phosphorylation and point mutations in the $\langle scp \rangle$ TIR $\langle /scp \rangle$ domains of $\langle scp \rangle$ TLR $\langle /scp \rangle$ 2 and $\langle scp \rangle$ TLR $\langle /scp \rangle$ 3. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 524-535.	2.6	16
50	Distinct Evolutionary Origins of Intron Retention Splicing Events in NHX1 Antiporter Transcripts Relate to Sequence Specific Distinctions in <i>Oryza</i> Species. <i>Frontiers in Plant Science</i> , 2020, 11, 267.	3.6	16
51	Disulfide-Rich Cyclic Peptides from <i>Clitoria ternatea</i> Protect against \hat{I}^2 -Amyloid Toxicity and Oxidative Stress in Transgenic <i>Caenorhabditis elegans</i> . <i>Journal of Medicinal Chemistry</i> , 2021, 64, 7422-7433.	6.4	16
52	A novel meta-cleavage product hydrolase from <i>Flavobacterium</i> sp. ATCC27551. <i>Biochemical and Biophysical Research Communications</i> , 2006, 351, 675-681.	2.1	15
53	Distribution, classification, domain architectures and evolution of prolyl oligopeptidases in prokaryotic lineages. <i>BMC Genomics</i> , 2014, 15, 985.	2.8	15
54	Filling-in Void and Sparse Regions in Protein Sequence Space by Protein-Like Artificial Sequences Enables Remarkable Enhancement in Remote Homology Detection Capability. <i>Journal of Molecular Biology</i> , 2014, 426, 962-979.	4.2	15

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55	A Functional Agonist of Insect Olfactory Receptors: Behavior, Physiology and Structure. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 134.	3.7	15
56	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 145, 19-39.	2.9	15
57	Genome-wide survey of DNA-binding proteins in <i>Arabidopsis thaliana</i> : analysis of distribution and functions. <i>Nucleic Acids Research</i> , 2013, 41, 7212-7219.	14.5	14
58	ECMIS: computational approach for the identification of hotspots at protein-protein interfaces. <i>BMC Bioinformatics</i> , 2014, 15, 303.	2.6	14
59	InsectORâ€”Webserver for sensitive identification of insect olfactory receptor genes from non-model genomes. <i>PLoS ONE</i> , 2021, 16, e0245324.	2.5	14
60	Insights into Protein Sequence and Structure-Derived Features Mediating 3D Domain Swapping Mechanism using Support Vector Machine Based Approach. <i>Bioinformatics and Biology Insights</i> , 2010, 4, BBI.S4464.	2.0	13
61	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	2.6	13
62	Improvement of alignment accuracy utilizing sequentially conserved motifs. <i>BMC Bioinformatics</i> , 2004, 5, 167.	2.6	12
63	Critical assessment of structure-based sequence alignment methods at distant relationships. <i>Briefings in Bioinformatics</i> , 2011, 12, 163-175.	6.5	12
64	Functional repertoire, molecular pathways and diseases associated with 3D domain swapping in the human proteome. <i>Journal of Clinical Bioinformatics</i> , 2012, 2, 8.	1.2	12
65	NrichD database: sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. <i>Nucleic Acids Research</i> , 2015, 43, D300-D305.	14.5	12
66	Genome-wide survey and phylogeny of S-Ribosylhomocysteinase (LuxS) enzyme in bacterial genomes. <i>BMC Genomics</i> , 2016, 17, 742.	2.8	12
67	Structural determinants of binding and specificity in transforming growth factor-receptor interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 408-420.	2.6	11
68	PURE: A webserver for the prediction of domains in unassigned regions in proteins. <i>BMC Bioinformatics</i> , 2008, 9, 281.	2.6	11
69	Identification of functionally diverse lipocalin proteins from sequence information using support vector machine. <i>Amino Acids</i> , 2010, 39, 777-783.	2.7	11
70	Vaccination and immunization strategies to design <i>Aedes aegypti</i> salivary protein based subunit vaccine tackling Flavivirus infection. <i>International Journal of Biological Macromolecules</i> , 2019, 122, 1203-1211.	7.5	11
71	Transcriptomic profiling of the medicinal plant <i>Clitoria ternatea</i> : identification of potential genes in cyclotide biosynthesis. <i>Scientific Reports</i> , 2020, 10, 12658.	3.3	11
72	Computational prediction and analysis of impact of the cross-talks between JNK and P38 kinase cascades. <i>Bioinformation</i> , 2009, 3, 250-254.	0.5	11

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73	An alignment-free domain architecture similarity search (ADASS) algorithm for inferring homology between multi-domain proteins. <i>Bioinformatics</i> , 2013, 9, 491-499.	0.5	11
74	Evolutionary trace analysis of ionotropic glutamate receptor sequences and modeling the interactions of agonists with different NMDA receptor subunits. <i>Journal of Molecular Modeling</i> , 2004, 10, 305-316.	1.8	10
75	Improved Detection of Remote Homologues Using Cascade PSI-BLAST: Influence of Neighbouring Protein Families on Sequence Coverage. <i>PLoS ONE</i> , 2013, 8, e56449.	2.5	10
76	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. <i>BMC Genomics</i> , 2014, 15, 1159.	2.8	10
77	Insights on pH-dependent conformational changes of mosquito odorant binding proteins by molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1742-1751.	3.5	10
78	SInCRea€”structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
79	Integrative modelling of TIR domain-containing adaptor molecule inducing interferon- γ (TRIF) provides insights into its autoinhibited state. <i>Biology Direct</i> , 2017, 12, 9.	4.6	10
80	Structural Interface Parameters Are Discriminatory in Recognising Near-Native Poses of Protein-Protein Interactions. <i>PLoS ONE</i> , 2014, 9, e80255.	2.5	9
81	Enriching the annotation of <i>Mycobacterium tuberculosis</i> H37Rv proteome using remote homology detection approaches: Insights into structure and function. <i>Tuberculosis</i> , 2015, 95, 14-25.	1.9	9
82	RStrucFam: a web server to associate structure and cognate RNA for RNA-binding proteins from sequence information. <i>BMC Bioinformatics</i> , 2016, 17, 411.	2.6	9
83	Investigating the effect of key mutations on the conformational dynamics of toll-like receptor dimers through molecular dynamics simulations and protein structure networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 475-490.	2.6	9
84	Molecular Dynamics Simulations and Structural Analysis to Decipher Functional Impact of a Twenty Residue Insert in the Ternary Complex of <i>Mus musculus</i> TdT Isoform. <i>PLoS ONE</i> , 2016, 11, e0157286.	2.5	9
85	Primary Structural Documentation of the Major Urinary Protein of the Indian Commensal Rat (<i>Rattus</i>) Tj ETQq1 1 0,784314 rgBT /Ove	0,9	0,9
86	Re-visiting protein-centric two-tier classification of existing DNA-protein complexes. <i>BMC Bioinformatics</i> , 2012, 13, 165.	2.6	8
87	Fold combinations in multi-domain proteins. <i>Bioinformatics</i> , 2019, 15, 342-350.	0.5	8
88	LIM domain-wide comprehensive virtual mutagenesis provides structural rationale for cardiomyopathy mutations in CSRP3. <i>Scientific Reports</i> , 2022, 12, 3562.	3.3	7
89	Comparative analysis of different competitive antagonists interaction with NR2A and NR2B subunits of N-methyl-D-aspartate (NMDA) ionotropic glutamate receptor. <i>Journal of Molecular Modeling</i> , 2005, 11, 489-502.	1.8	6
90	Structural Consequences of D481N/K483Q Mutation at Glycine Binding Site of NMDA Ionotropic Glutamate Receptors: A Molecular Dynamics Study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005, 22, 399-410.	3.5	6

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91	In silico point mutation and evolutionary trace analysis applied to nicotinic acetylcholine receptors in deciphering ligand-binding surfaces. <i>Journal of Molecular Modeling</i> , 2010, 16, 1651-1670.	1.8	6
92	POEAS: Automated Plant Phenomic Analysis Using Plant Ontology. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S19057.	2.0	6
93	Insights from the analysis of draft genome sequence of <i>Crocus sativus</i> L.. <i>Bioinformatics</i> , 2022, 18, 1-13.	0.5	6
94	Domain architectural census of eukaryotic gene products containing O-protein phosphatases. <i>Gene</i> , 2006, 366, 246-255.	2.2	5
95	Collation and analyses of DNA-binding protein domain families from sequence and structural databanks. <i>Molecular BioSystems</i> , 2015, 11, 1110-1118.	2.9	5
96	A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1979-1986.	3.5	5
97	Rapid and enhanced remote homology detection by cascading hidden Markov model searches in sequence space. <i>Bioinformatics</i> , 2016, 32, 338-344.	4.1	5
98	Quaternary variations in the structural assembly of N-acetylglucosamine-6-phosphate deacetylase from <i>Pasteurella multocida</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 81-93.	2.6	5
99	Rebelling for a Reason: Protein Structural "Outliers". <i>PLoS ONE</i> , 2013, 8, e74416.	2.5	5
100	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. <i>PLoS ONE</i> , 2016, 11, e0159627.	2.5	5
101	IWS: Integrated Web Server for protein sequence and structure analysis. <i>Bioinformatics</i> , 2007, 2, 86-90.	0.5	5
102	DDX24 is required for muscle fiber organization and the suppression of wound-induced Wnt activity necessary for pole re-establishment during planarian regeneration. <i>Developmental Biology</i> , 2022, 488, 11-29.	2.0	5
103	Improvement of comparative modeling by the application of conserved motifs amongst distantly related proteins as additional restraints. <i>Journal of Molecular Modeling</i> , 2004, 10, 69-75.	1.8	4
104	LenVarDB: database of length-variant protein domains. <i>Nucleic Acids Research</i> , 2014, 42, D246-D250.	14.5	4
105	Energetic Calculations to Decipher pH-Dependent Oligomerization and Domain Swapping of Proteins. <i>PLoS ONE</i> , 2015, 10, e0127716.	2.5	4
106	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. <i>Nucleic Acids Research</i> , 2016, 44, D410-D414.	14.5	4
107	Topology prediction of insect olfactory receptors. <i>Current Opinion in Structural Biology</i> , 2019, 55, 194-203.	5.7	4
108	A knowledge-driven protocol for prediction of proteins of interest with an emphasis on biosynthetic pathways. <i>MethodsX</i> , 2020, 7, 101053.	1.6	4

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109	Dataset for the combined transcriptome assembly of <i>M. oleifera</i> and functional annotation. Data in Brief, 2020, 30, 105416.	1.0	4
110	PASS2. International Journal of Knowledge Discovery in Bioinformatics, 2011, 2, 53-66.	0.8	4
111	Insights from the analysis of conserved motifs and permitted amino acid exchanges in the human, the fly and the worm GPCR clusters. Bioinformatics, 2011, 7, 15-20.	0.5	4
112	TM-MOTIF: an alignment viewer to annotate predicted transmembrane helices and conserved motifs in aligned set of sequences. Bioinformatics, 2011, 7, 214-221.	0.5	4
113	FASSM: enhanced function association in whole genome analysis using sequence and structural motifs. In Silico Biology, 2005, 5, 425-38.	0.9	4
114	Sequence and structural analyses of interleukin-8-like chemokine superfamily. In Silico Biology, 2008, 8, 307-30.	0.9	4
115	An <i>in silico</i> approach towards the identification of novel inhibitors of the TLR-4 signaling pathway. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1345-1362.	3.5	3
116	Bioinformatics comparisons of RNA-binding proteins of pathogenic and non-pathogenic <i>Escherichia coli</i> strains reveal novel virulence factors. BMC Genomics, 2017, 18, 658.	2.8	3
117	Genome-wide survey of remote homologues for protein domain superfamilies of known structure reveals unequal distribution across structural classes. Molecular Omics, 2018, 14, 266-280.	2.8	3
118	Genome-Wide Search for Tyrosine Phosphatases in the Human Genome Through Computational Approaches Leads to the Discovery of Few New Domain Architectures. Evolutionary Bioinformatics, 2019, 15, 117693431984028.	1.2	3
119	Analysis of short interproton distances in proline peptides as a guide in the interpretation of nuclear Overhauser effects. Collection of Czechoslovak Chemical Communications, 1988, 53, 2801-2809.	1.0	3
120	Mechanistic Basis Of Peptide-Protein Interaction In AtPep1-PEPR1 Complex In <i>Arabidopsis thaliana</i> . Protein and Peptide Letters, 2015, 22, 618-627.	0.9	3
121	Analysis of the impact of ERK5, JNK, and P38 kinase cascades on each other: A systems approach. Bioinformatics, 2009, 3, 244-249.	0.5	3
122	Ligand Docking Methods to Recognize Allosteric Inhibitors for G-Protein-Coupled Receptors. Bioinformatics and Biology Insights, 2021, 15, 117793222110377.	2.0	3
123	DSDBASE 2.0: updated version of DiSulphide dataBASE, a database on disulphide bonds in proteins. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	3
124	SSToSS–sequence-structural templates of single-member superfamilies. In Silico Biology, 2006, 6, 311-9.	0.9	3
125	Enhanced structure prediction of gene products containing class III adenylyl cyclase domains. In Silico Biology, 2006, 6, 351-62.	0.9	3
126	EcRBPome: a comprehensive database of all known <i>E. coli</i> RNA-binding proteins. BMC Genomics, 2019, 20, 403.	2.8	2

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127	PASS2 version 6: a database of structure-based sequence alignments of protein domain superfamilies in accordance with SCOPe. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	2
128	Improved performance of sequence search approaches in remote homology detection. F1000Research, 2013, 2, 93.	1.6	2
129	Srinivasan (1962â€“2021) in Bioinformatics and beyond. Bioinformatics, 2022, 38, 2377-2379.	4.1	2
130	Development of candidate gene-based markers and map-based cloning of a dominant rust resistance gene in cultivated groundnut (<i>Arachis hypogaea</i> L.). Gene, 2022, 827, 146474.	2.2	2
131	Genome-Wide Analysis of Domain-Swap Predicted Products in the Genome of Anti-Stress Medicinal Plant: <i>Ocimum tenuiflorum</i> . Bioinformatics and Biology Insights, 2019, 13, 117793221882136.	2.0	1
132	Specialized structural and functional roles of residues selectively conserved in subfamilies of the pleckstrin homology domain family. FEBS Open Bio, 2019, 9, 1848-1859.	2.3	1
133	A High Throughput Exome Sequencing Approach To Analyse Events Within a Good Responder CML Patient Under Imatinib At Diagnosis and Under Remission. Blood, 2013, 122, 5161-5161.	1.4	1
134	Evolutionary analysis of PHLPP1 gene in humans and non-human primates. Bioinformation, 2008, 2, 471-474.	0.5	1
135	Three-dimensional Modelling of the Voltage-gated Sodium Ion Channel from <i>Anopheles gambiae</i> Reveals Spatial Clustering of Evolutionarily Conserved Acidic Residues at the Extracellular Sites. Current Neuropharmacology, 2017, 15, 1062-1072.	2.9	1
136	Computational analysis of potential candidate genes involved in the cold stress response of ten Rosaceae members. BMC Genomics, 2022, 23, .	2.8	1
137	Structural updates of alignment of protein domains and consequences on evolutionary models of domain superfamilies. BioData Mining, 2013, 6, 20.	4.0	0
138	GenDiS database update with improved approach and features to recognize homologous sequences of protein domain superfamilies. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	0
139	Genome-wide survey of tyrosine phosphatases in thirty mammalian genomes. Cellular Signalling, 2021, 84, 110009.	3.6	0
140	HORIBALFRE program: Higher Order Residue Interactions Based ALgorithm for Fold REcognition. Bioinformation, 2011, 7, 352-359.	0.5	0
141	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	0