

Narayanaswamy Srinivasan

List of Publications by Year in descending order

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Version: 2024-02-01

170
papers

4,190
citations

159585

30
h-index

144013

57
g-index

195
all docs

195
docs citations

195
times ranked

6177
citing authors

#	ARTICLE	IF	CITATIONS
1	Pseudokinases repurpose flexibility signatures associated with the protein kinase fold for noncatalytic roles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 747-764.	2.6	2
2	Identification, functional characterization, assembly and structure of ToxIN type III toxin-antitoxin complex from <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2022, 50, 1687-1700.	14.5	4
3	DSDBASE 2.0: updated version of DiSulphide dataBASE, a database on disulphide bonds in proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
4	Comparison of side-chain dispersion in protein structures determined by cryo-EM and X-ray crystallography. <i>IUCr</i> , 2022, 9, 98-103.	2.2	4
5	Profiles of Natural and Designed Protein-Like Sequences Effectively Bridge Protein Sequence Gaps: Implications in Distant Homology Detection. <i>Methods in Molecular Biology</i> , 2022, 2449, 149-167.	0.9	2
6	Understanding structural variability in proteins using protein structural networks. <i>Current Research in Structural Biology</i> , 2022, 4, 134-145.	2.2	6
7	Signatures of conserved and unique molecular features in Afrotheria. <i>Scientific Reports</i> , 2021, 11, 1011.	3.3	2
8	Rewards of divergence in sequences, 3-D structures and dynamics of yeast and human spliceosome SF3b complexes. <i>Current Research in Structural Biology</i> , 2021, 3, 133-145.	2.2	4
9	Hypervariability of accessible and inaccessible conformational space of proteins. <i>Current Research in Structural Biology</i> , 2021, 3, 229-238.	2.2	5
10	Protein Structure, Dynamics and Assembly: Implications for Drug Discovery. , 2021, , 91-122.		1
11	Conformational Strain Indicated by Ramachandran Angles for the Protein Backbone Is Only Weakly Related to the Flexibility. <i>Journal of Physical Chemistry B</i> , 2021, 125, 2597-2606.	2.6	7
12	D614G substitution at the hinge region enhances the stability of trimeric SARS-CoV-2 spike protein. <i>Bioinformatics</i> , 2021, 17, 439-445.	0.5	7
13	Transient association between proteins elicits alteration of dynamics at sites far away from interfaces. <i>Structure</i> , 2021, 29, 371-384.e3.	3.3	5
14	Master Blaster: an approach to sensitive identification of remotely related proteins. <i>Scientific Reports</i> , 2021, 11, 8746.	3.3	0
15	Identification of Potential Binders of Mtb Universal Stress Protein (Rv1636) Through an in silico Approach and Insights Into Compound Selection for Experimental Validation. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 599221.	3.5	10
16	NOD: a web server to predict New use of Old Drugs to facilitate drug repurposing. <i>Scientific Reports</i> , 2021, 11, 13540.	3.3	2
17	SIRT6 transcriptionally regulates fatty acid transport by suppressing PPAR β . <i>Cell Reports</i> , 2021, 35, 109190.	6.4	35
18	“All That Glitters Is Not Gold”: High-Resolution Crystal Structures of Ligand-Protein Complexes Need Not Always Represent Confident Binding Poses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6830.	4.1	6

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19	Comparative Analysis of Structural and Dynamical Features of Ribosome Upon Association With mRNA Reveals Potential Role of Ribosomal Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 654164.	3.5	4
20	Sequence Divergence and Functional Specializations of the Ancient Spliceosomal SF3b: Implications in Flexibility and Adaptations of the Multi-Protein Complex. <i>Frontiers in Genetics</i> , 2021, 12, 747344.	2.3	1
21	Unity and diversity among viral kinases. <i>Gene</i> , 2020, 723, 144134.	2.2	2
22	Discrete analyses of protein dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2988-3002.	3.5	20
23	Genome-wide and structural analyses of pseudokinases encoded in the genome of <i>Arabidopsis thaliana</i> provide functional insights. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1620-1638.	2.6	9
24	Manoeuvring protein functions and functional levels by structural excursions. , 2020, , 77-104.		2
25	Molecular and Structural Basis of Cross-Reactivity in <i>M. tuberculosis</i> Toxin Antitoxin Systems. <i>Toxins</i> , 2020, 12, 481.	3.4	10
26	Artificial protein sequences enable recognition of vicinal and distant protein functional relationships. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1688-1700.	2.6	1
27	Potent HCV NS3 Protease Inhibition by a Water-Soluble Phyllanthin Congener. <i>ACS Omega</i> , 2020, 5, 11553-11562.	3.5	3
28	Mutations in SARS-CoV-2 viral RNA identified in Eastern India: Possible implications for the ongoing outbreak in India and impact on viral structure and host susceptibility. <i>Journal of Biosciences</i> , 2020, 45, 1.	1.1	117
29	Data set of intrinsically disordered proteins analysed at a local protein conformation level. <i>Data in Brief</i> , 2020, 29, 105383.	1.0	4
30	Repurposing drugs against the main protease of SARS-CoV-2: mechanism-based insights supported by available laboratory and clinical data. <i>Molecular Omics</i> , 2020, 16, 474-491.	2.8	33
31	A structural entropy index to analyse local conformations in intrinsically disordered proteins. <i>Journal of Structural Biology</i> , 2020, 210, 107464.	2.8	13
32	How good are comparative models in the understanding of protein dynamics?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 874-888.	2.6	4
33	Mechanism of CcdA-Mediated Rejuvenation of DNA Gyrase. <i>Structure</i> , 2020, 28, 562-572.e4.	3.3	15
34	Influence of Disease-Causing Mutations on Protein Structural Networks. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 620554.	3.5	23
35	Structural and dynamical aspects of evolutionarily conserved protein-protein complexes. , 2020, , 3-31.		0
36	In silico prediction of protein flexibility with local structure approach. <i>Biochimie</i> , 2019, 165, 150-155.	2.6	15

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37	NU-6027 Inhibits Growth of Mycobacterium tuberculosis by Targeting Protein Kinase D and Protein Kinase G. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	34
38	Stereochemical Assessment of (Ï†,Ï†) Outliers in Protein Structures Using Bond Geometry-Specific Ramachandran Steric-Maps. Structure, 2019, 27, 1875-1884.e2.	3.3	17
39	Chandrasekharan Ramakrishnan (1939â€“2019): The student behind the Ramachandran map. Protein Science, 2019, 28, 1920-1922.	7.6	0
40	Structural variations within proteins can be as large as variations observed across their homologues. Biochimie, 2019, 167, 162-170.	2.6	4
41	Interface residues of transient protein-protein complexes have extensive intra-protein interactions apart from inter-protein interactions. Biology Direct, 2019, 14, 1.	4.6	29
42	Bioinformatic and mutational studies of related toxinâ€“antitoxin pairs in Mycobacterium tuberculosis predict and identify key functional residues. Journal of Biological Chemistry, 2019, 294, 9048-9063.	3.4	27
43	In Silico Modeling of FDA-Approved Drugs for Discovery of Anticandida Agents: A Drug-Repurposing Approach. , 2019, , 463-526.		8
44	Mycobacterium tuberculosis Rv0366c-Rv0367c encodes a non-canonical PezAT-like toxin-antitoxin pair. Scientific Reports, 2019, 9, 1163.	3.3	16
45	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
46	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. Source Code for Biology and Medicine, 2019, 14, 5.	1.7	14
47	Repurposing Drugs Based on Evolutionary Relationships Between Targets of Approved Drugs and Proteins of Interest. Methods in Molecular Biology, 2019, 1903, 45-59.	0.9	4
48	Longâ€range molecular dynamics show that inactive forms of Protein Kinase A are more dynamic than active forms. Protein Science, 2019, 28, 543-560.	7.6	9
49	Fold combinations in multi-domain proteins. Bioinformatics, 2019, 15, 342-350.	0.5	8
50	An Augmented Pocketome: Detection and Analysis of Small-Molecule Binding Pockets in Proteins of Known 3D Structure. Structure, 2018, 26, 499-512.e2.	3.3	38
51	Heterologous Expression, Purification and Characterization of an Oligopeptidase A from the Pathogen Leptospira interrogans. Molecular Biotechnology, 2018, 60, 302-309.	2.4	3
52	Clustering of multiâ€domain protein sequences. Proteins: Structure, Function and Bioinformatics, 2018, 86, 759-776.	2.6	2
53	A natural small molecule inhibitor corilagin blocks HCV replication and modulates oxidative stress to reduce liver damage. Antiviral Research, 2018, 150, 47-59.	4.1	38
54	Use of designed sequences in protein structure recognition. Biology Direct, 2018, 13, 8.	4.6	5

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55	Recognition of sites of functional specialisation in all known eukaryotic protein kinase families. PLoS Computational Biology, 2018, 14, e1005975.	3.2	4
56	Same but not alike: Structure, flexibility and energetics of domains in multi-domain proteins are influenced by the presence of other domains. PLoS Computational Biology, 2018, 14, e1006008.	3.2	41
57	Specificity and stability of transient protein-protein interactions. Current Opinion in Structural Biology, 2017, 44, 77-86.	5.7	20
58	Structure determination of contaminant proteins using the MarathonMR procedure. Journal of Structural Biology, 2017, 197, 372-378.	2.8	7
59	Comparison of <i>Leptospira interrogans</i> and <i>Leptospira biflexa</i> genomes: analysis of potential leptospiral-host interactions. Molecular BioSystems, 2017, 13, 883-891.	2.9	6
60	Deciphering common recognition principles of nucleoside mono/di and tri-phosphates binding in diverse proteins via structural matching of their binding sites. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1699-1712.	2.6	3
61	Detection and Characterization of Bacterial Proteinases Using Zymography. Methods in Molecular Biology, 2017, 1626, 103-114.	0.9	4
62	Resolving protein structure-function-binding site relationships from a binding site similarity network perspective. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1319-1335.	2.6	14
63	Design, Synthesis, and Experimental Validation of Peptide Ligands Targeting Mycobacterium tuberculosis If Factors. Biochemistry, 2017, 56, 2209-2218.	2.5	0
64	Sendai virus recruits cellular villin to remodel actin cytoskeleton during fusion with hepatocytes. Molecular Biology of the Cell, 2017, 28, 3801-3814.	2.1	6
65	Recognition of a structural domain (RWDBD) in Gcn1 proteins that interacts with the RWD domain containing proteins. Biology Direct, 2017, 12, 12.	4.6	6
66	Seeing but not believing: the structure of glycerol dehydrogenase initially assumed to be the structure of a survival protein from <i>Salmonella typhimurium</i> . Acta Crystallographica Section D: Structural Biology, 2017, 73, 609-617.	2.3	6
67	Exploring anti-malarial potential of FDA approved drugs: an in silico approach. Malaria Journal, 2017, 16, 290.	2.3	16
68	Identification of a novel epitope in the C terminus of hepatitis C virus-E2 protein that induces potent and cross-reactive neutralizing antibodies. Journal of General Virology, 2017, 98, 962-976.	2.9	6
69	Knowledge-based prediction of protein backbone conformation using a structural alphabet. PLoS ONE, 2017, 12, e0186215.	2.5	12
70	Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. Biology Direct, 2016, 11, 27.	4.6	3
71	Comparative analyses of quaternary arrangements in homo-oligomeric proteins in superfamilies: Functional implications. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1190-1202.	2.6	3
72	Structure-function studies of <i>HNF1A</i> (<i>MODY3</i>) gene mutations in South Indian patients with monogenic diabetes. Clinical Genetics, 2016, 90, 486-495.	2.0	32

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73	Conservation of structural fluctuations in homologous protein kinases and its implications on functional sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 957-978.	2.6	7
74	Cover Image, Volume 84, Issue 7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, C1-C1.	2.6	0
75	Editorial overview: Theory and simulation. <i>Current Opinion in Structural Biology</i> , 2016, 37, iv-v.	5.7	0
76	Classification of Protein Kinases Influenced by Conservation of Substrate Binding Residues. <i>Methods in Molecular Biology</i> , 2016, 1415, 301-313.	0.9	1
77	Use of evolutionary information in the fitting of atomic level protein models in low resolution cryo-EM map of a protein assembly improves the accuracy of the fitting. <i>Journal of Structural Biology</i> , 2016, 195, 294-305.	2.8	9
78	Determination of crystal structures of proteins of unknown identity using a marathon molecular replacement procedure: structure of <i>Stenotrophomonas maltophilia</i> phosphate-binding protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1081-1089.	2.3	10
79	Structural and mechanistic insights into human splicing factor SF3b complex derived using an integrated approach guided by the cryo-EM density maps. <i>RNA Biology</i> , 2016, 13, 1025-1040.	3.1	5
80	Protein sequence design and its applications. <i>Current Opinion in Structural Biology</i> , 2016, 37, 71-80.	5.7	10
81	Improving the Accuracy of Fitted Atomic Models in Cryo-EM Density Maps of Protein Assemblies Using Evolutionary Information from Aligned Homologous Proteins. <i>Methods in Molecular Biology</i> , 2016, 1415, 193-209.	0.9	4
82	Homology-Based Prediction of Potential Protein-Protein Interactions between Human Erythrocytes and <i>Plasmodium falciparum</i> . <i>Bioinformatics and Biology Insights</i> , 2015, 9, BBI.S31880.	2.0	21
83	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	3.0	8
84	Evolutionary and structural analyses of heterodimeric proteins composed of subunits with same fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1766-1786.	2.6	1
85	SInCR structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav060.	3.0	10
86	Weak conservation of structural features in the interfaces of homologous transient protein-protein complexes. <i>Protein Science</i> , 2015, 24, 1856-1873.	7.6	7
87	Protein flexibility in the light of structural alphabets. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 20.	3.5	71
88	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
89	The beta hairpin structure within ribosomal protein S5 mediates interplay between domains II and IV and regulates HCV IRES function. <i>Nucleic Acids Research</i> , 2015, 43, 2888-2901.	14.5	33
90	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

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91	A Gaussian network model study suggests that structural fluctuations are higher for inactive states than active states of protein kinases. <i>Molecular BioSystems</i> , 2015, 11, 1079-1095.	2.9	7
92	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
93	Recognizing drug targets using evolutionary information: implications for repurposing FDA-approved drugs against <i>Mycobacterium tuberculosis</i> H37Rv. <i>Molecular BioSystems</i> , 2015, 11, 3316-3331.	2.9	20
94	De-DUFing the DUFs: Deciphering distant evolutionary relationships of Domains of Unknown Function using sensitive homology detection methods. <i>Biology Direct</i> , 2015, 10, 38.	4.6	34
95	Typical and atypical domain combinations in human protein kinases: functions, disease causing mutations and conservation in other primates. <i>RSC Advances</i> , 2015, 5, 25132-25148.	3.6	6
96	Structure-Based Phylogenetic Analysis of the Lipocalin Superfamily. <i>PLoS ONE</i> , 2015, 10, e0135507.	2.5	36
97	Hybrid and Rogue Kinases Encoded in the Genomes of Model Eukaryotes. <i>PLoS ONE</i> , 2014, 9, e107956.	2.5	3
98	CLAP: A web-server for automatic classification of proteins with special reference to multi-domain proteins. <i>BMC Bioinformatics</i> , 2014, 15, 343.	2.6	11
99	Correlation between local structural dynamics of proteins inferred from NMR ensembles and evolutionary dynamics of homologues of known structure. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 751-758.	3.5	6
100	From workstations to workbenches: Towards predicting physicochemically viable protein-protein interactions across a host and a pathogen. <i>IUBMB Life</i> , 2014, 66, 759-774.	3.4	10
101	Ramachandran analysis of conserved glycol residues in homologous proteins of known structure. <i>Protein Science</i> , 2014, 23, 843-850.	7.6	6
102	Accurate prediction of interfacial residues in two-domain proteins using evolutionary information: Implications for three-dimensional modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1219-1234.	2.6	7
103	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
104	The relationship between classification of multi-domain proteins using an alignment-free approach and their functions: a case study with immunoglobulins. <i>Molecular BioSystems</i> , 2014, 10, 1082.	2.9	8
105	Chemical specificity and conformational flexibility in proteinase-inhibitor interaction: Scaffolds for promiscuous binding. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 151-157.	2.9	0
106	An overview of recent advances in structural bioinformatics of protein-protein interactions and a guide to their principles. <i>Progress in Biophysics and Molecular Biology</i> , 2014, 116, 141-150.	2.9	65
107	Re-analysis of cryoEM data on HCV IRES bound to 40S subunit of human ribosome integrated with recent structural information suggests new contact regions between ribosomal proteins and HCV RNA. <i>RNA Biology</i> , 2014, 11, 891-905.	3.1	14
108	Investigations of Ramachandran disallowed conformations in protein domain families. <i>International Journal of Biological Macromolecules</i> , 2014, 63, 119-125.	7.5	14

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109	Small molecule inhibitors of HCV replication from Pomegranate. Scientific Reports, 2014, 4, 5411.	3.3	59
110	Understanding the role of domain-domain linkers in the spatial orientation of domains in multi-domain proteins. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1467-1480.	3.5	35
111	Structural Insights into <i>Saccharomyces cerevisiae</i> Msh4-Msh5 Complex Function Using Homology Modeling. PLoS ONE, 2013, 8, e78753.	2.5	17
112	Repertoire of Protein Kinases Encoded in the Genome of <i>Takifugu rubripes</i> . Comparative and Functional Genomics, 2012, 2012, 1-12.	2.0	3
113	Roles of residues in the interface of transient protein-protein complexes before complexation. Scientific Reports, 2012, 2, 334.	3.3	30
114	Cascaded walks in protein sequence space: use of artificial sequences in remote homology detection between natural proteins. Molecular BioSystems, 2012, 8, 2076.	2.9	9
115	Structural and molecular basis of interaction of HCV non-structural protein 5A with human casein kinase 1 α and PKR. BMC Structural Biology, 2012, 12, 28.	2.3	13
116	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. BMC Structural Biology, 2012, 12, 6.	2.3	19
117	Protein-Protein Interactions in Clathrin Vesicular Assembly: Radial Distribution of Evolutionary Constraints in Interfaces. PLoS ONE, 2012, 7, e31445.	2.5	1
118	Extent of Structural Asymmetry in Homodimeric Proteins: Prevalence and Relevance. PLoS ONE, 2012, 7, e36688.	2.5	56
119	Targeted Modifications in Adeno-Associated Virus Serotype (AAV)- 8 Capsid Improves Its Hepatic Gene Transfer Efficiency in Vivo. Blood, 2012, 120, 2045-2045.	1.4	0
120	Stability of domain structures in multi-domain proteins. Scientific Reports, 2011, 1, 40.	3.3	96
121	AlignHUSH: Alignment of HMMs using structure and hydrophobicity information. BMC Bioinformatics, 2011, 12, 275.	2.6	11
122	Identification of Local Conformational Similarity in Structurally Variable Regions of Homologous Proteins Using Protein Blocks. PLoS ONE, 2011, 6, e17826.	2.5	6
123	A short survey on protein blocks. Biophysical Reviews, 2010, 2, 137-145.	3.2	107
124	Prediction of protein-protein interactions in dengue virus coat proteins guided by low resolution cryoEM structures. BMC Structural Biology, 2010, 10, 17.	2.3	14
125	Classification of Protein Kinases on the Basis of Both Kinase and Non-Kinase Regions. PLoS ONE, 2010, 5, e12460.	2.5	31
126	Novel insertion and deletion mutants of RpoB that render <i>Mycobacterium smegmatis</i> RNA polymerase resistant to rifampicin-mediated inhibition of transcription. Microbiology (United Kingdom), 2010, 156, 1565-1573.	1.8	14

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127	A Framework for Classification of Prokaryotic Protein Kinases. PLoS ONE, 2010, 5, e10608.	2.5	20
128	Recognition of Interaction Interface Residues in Low-Resolution Structures of Protein Assemblies Solely from the Positions of Cl± Atoms. PLoS ONE, 2009, 4, e4476.	2.5	8
129	Structure-Based Phylogeny as a Diagnostic for Functional Characterization of Proteins with a Cupin Fold. PLoS ONE, 2009, 4, e5736.	2.5	54
130	Classification of Nonenzymatic Homologues of Protein Kinases. Comparative and Functional Genomics, 2009, 2009, 1-17.	2.0	8
131	Molecular and Structural Basis of Drift in the Functions of Closely-Related Homologous Enzyme Domains: Implications for Function Annotation Based on Homology Searches and Structural Genomics. In Silico Biology, 2009, 9, S41-S55.	0.9	6
132	How effective is the data on co-occurrence of domains in multi-domain proteins in prediction of protein-protein interactions?. , 2009, , .		1
133	Evolutionary Divergence of Plasmodium falciparum: Sequences, Protein- Protein Interactions, Pathways and Processes. Infectious Disorders - Drug Targets, 2009, 9, 257-271.	0.8	9
134	Analysis of the protein kinome of <i>Entamoeba histolytica</i>. Proteins: Structure, Function and Bioinformatics, 2008, 71, 995-1006.	2.6	47
135	Comparative kinomics of human and chimpanzee reveal unique kinship and functional diversity generated by new domain combinations. BMC Genomics, 2008, 9, 625.	2.8	9
136	A data integration approach to predict host-pathogen protein-protein interactions: application to recognize protein interactions between human and a malarial parasite. In Silico Biology, 2008, 8, 235-50.	0.9	29
137	Structural Compromise of Disallowed Conformations in Peptide and Protein Structures. Protein and Peptide Letters, 2007, 14, 672-682.	0.9	14
138	PIC: Protein Interactions Calculator. Nucleic Acids Research, 2007, 35, W473-W476.	14.5	802
139	Strategies for the effective identification of remotely related sequences in multiple PSSM search approach. Proteins: Structure, Function and Bioinformatics, 2007, 67, 789-794.	2.6	12
140	Comparison of sequence-based and structure-based phylogenetic trees of homologous proteins: Inferences on protein evolution. Journal of Biosciences, 2007, 32, 83-96.	1.1	32
141	Analysis on sliding helices and strands in protein structural comparisons: A case study with protein kinases. Journal of Biosciences, 2007, 32, 921-928.	1.1	0
142	Genome-wide comparative analyses of domain organisation of repertoires of protein kinases of Arabidopsis thaliana and Oryza sativa. Gene, 2006, 380, 1-13.	2.2	42
143	MuPSSM: a database of multiple position-specific scoring matrices of protein domain families. Nucleic Acids Research, 2006, 34, D243-D246.	14.5	29
144	Cascade PSI-BLAST web server: a remote homology search tool for relating protein domains. Nucleic Acids Research, 2006, 34, W143-W146.	14.5	17

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145	Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. BMC Genomics, 2005, 6, 129.	2.8	65
146	Interaction preferences across protein-protein interfaces of obligatory and non-obligatory components are different. BMC Structural Biology, 2005, 5, 15.	2.3	84
147	Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. Bioinformatics, 2005, 21, 2821-2826.	4.1	27
148	Assessment of a Rigorous Transitive Profile Based Search Method to Detect Remotely Similar Proteins. Journal of Biomolecular Structure and Dynamics, 2005, 23, 283-298.	3.5	22
149	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. Nucleic Acids Research, 2005, 33, W126-W129.	14.5	9
150	KinG: a database of protein kinases in genomes. Nucleic Acids Research, 2004, 32, 153D-155.	14.5	75
151	SUPFAM: a database of sequence superfamilies of protein domains. BMC Bioinformatics, 2004, 5, 28.	2.6	36
152	Enhanced functional and structural domain assignments using remote similarity detection procedures for proteins encoded in the genome of Mycobacterium tuberculosis H37Rv. Journal of Biosciences, 2004, 29, 245-259.	1.1	8
153	A genomic perspective of protein kinases in Plasmodium falciparum. Proteins: Structure, Function and Bioinformatics, 2004, 58, 180-189.	2.6	147
154	Interaction interfaces of protein domains are not topologically equivalent across families within superfamilies: Implications for metabolic and signaling pathways. Proteins: Structure, Function and Bioinformatics, 2004, 58, 339-353.	2.6	27
155	Structural Modes of Stabilization of Permissive Phosphorylation Sites in Protein Kinases: Distinct Strategies in Ser/Thr and Tyr Kinases. Journal of Molecular Biology, 2004, 339, 1025-1025.	4.2	0
156	Structural Modes of Stabilization of Permissive Phosphorylation Sites in Protein Kinases: Distinct Strategies in Ser/Thr and Tyr Kinases. Journal of Molecular Biology, 2004, 339, 1025-1039.	4.2	134
157	Recognition of remotely related structural homologues using sequence profiles of aligned homologous protein structures. In Silico Biology, 2004, 4, 445-60.	0.9	3
158	Tolerance to the substitution of buried apolar residues by charged residues in the homologous protein structures. Proteins: Structure, Function and Bioinformatics, 2003, 53, 783-791.	2.6	6
159	Survey for g-proteins in the prokaryotic genomes: Prediction of functional roles based on classification. Proteins: Structure, Function and Bioinformatics, 2003, 52, 585-597.	2.6	25
160	Effective detection of remote homologues by searching in sequence dataset of a protein domain fold. FEBS Letters, 2003, 552, 225-230.	2.8	9
161	SUPFAM--a database of potential protein superfamily relationships derived by comparing sequence-based and structure-based families: implications for structural genomics and function annotation in genomes. Nucleic Acids Research, 2002, 30, 289-293.	14.5	40
162	The repertoire of protein kinases encoded in the draft version of the human genome: atypical variations and uncommon domain combinations. Genome Biology, 2002, 3, research0066.1.	9.6	42

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163	Influence of solvent molecules on the stereochemical code of glycyyl residues in proteins. Proteins: Structure, Function and Bioinformatics, 2002, 49, 326-334.	2.6	4
164	Lipopolysaccharide phosphorylating enzymes encoded in the genomes of Gram-negative bacteria are related to the eukaryotic protein kinases. Protein Science, 2002, 11, 1580-1584.	7.6	24
165	PALI—a database of Phylogeny and ALLignment of homologous protein structures. Nucleic Acids Research, 2001, 29, 61-65.	14.5	88
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