

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	PIC: Protein Interactions Calculator. <i>Nucleic Acids Research</i> , 2007, 35, W473-W476.	14.5	802
2	Conformations of disulfide bridges in proteins. <i>International Journal of Peptide and Protein Research</i> , 1990, 36, 147-155.	0.1	164
3	A genomic perspective of protein kinases in <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 180-189.	2.6	147
4	Structural Modes of Stabilization of Permissive Phosphorylation Sites in Protein Kinases: Distinct Strategies in Ser/Thr and Tyr Kinases. <i>Journal of Molecular Biology</i> , 2004, 339, 1025-1039.	4.2	134
5	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
6	An evaluation of the performance of an automated procedure for comparative modelling of protein tertiary structure. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 501-512.	2.1	111
7	A short survey on protein blocks. <i>Biophysical Reviews</i> , 2010, 2, 137-145.	3.2	107
8	Stability of domain structures in multi-domain proteins. <i>Scientific Reports</i> , 2011, 1, 40.	3.3	96
9	PALI—a database of Phylogeny and ALLignment of homologous protein structures. <i>Nucleic Acids Research</i> , 2001, 29, 61-65.	14.5	88
10	Interaction preferences across protein-protein interfaces of obligatory and non-obligatory components are different. <i>BMC Structural Biology</i> , 2005, 5, 15.	2.3	84
11	KinG: a database of protein kinases in genomes. <i>Nucleic Acids Research</i> , 2004, 32, 153D-155.	14.5	75
12	Protein flexibility in the light of structural alphabets. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 20.	3.5	71
13	Diversity in domain architectures of Ser/Thr kinases and their homologues in prokaryotes. <i>BMC Genomics</i> , 2005, 6, 129.	2.8	65
14	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
15	Small molecule inhibitors of HCV replication from Pomegranate. <i>Scientific Reports</i> , 2014, 4, 5411.	3.3	59
16	Extent of Structural Asymmetry in Homodimeric Proteins: Prevalence and Relevance. <i>PLoS ONE</i> , 2012, 7, e36688.	2.5	56
17	Structure-Based Phylogeny as a Diagnostic for Functional Characterization of Proteins with a Cupin Fold. <i>PLoS ONE</i> , 2009, 4, e5736.	2.5	54
18	Analysis of the protein kinome of <i>Entamoeba histolytica</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 995-1006.	2.6	47

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19	The repertoire of protein kinases encoded in the draft version of the human genome: atypical variations and uncommon domain combinations. <i>Genome Biology</i> , 2002, 3, research0066.1.	9.6	42
20	Genome-wide comparative analyses of domain organisation of repertoires of protein kinases of <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> . <i>Gene</i> , 2006, 380, 1-13.	2.2	42
21	Same but not alike: Structure, flexibility and energetics of domains in multi-domain proteins are influenced by the presence of other domains. <i>PLoS Computational Biology</i> , 2018, 14, e1006008.	3.2	41
22	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. <i>Nucleic Acids Research</i> , 2002, 30, 289-293.	14.5	40
23	An Augmented Pocketome: Detection and Analysis of Small-Molecule Binding Pockets in Proteins of Known 3D Structure. <i>Structure</i> , 2018, 26, 499-512.e2.	3.3	38
24	A natural small molecule inhibitor corilagin blocks HCV replication and modulates oxidative stress to reduce liver damage. <i>Antiviral Research</i> , 2018, 150, 47-59.	4.1	38
25	SUPFAM: a database of sequence superfamilies of protein domains. <i>BMC Bioinformatics</i> , 2004, 5, 28.	2.6	36
26	Structure-Based Phylogenetic Analysis of the Lipocalin Superfamily. <i>PLoS ONE</i> , 2015, 10, e0135507.	2.5	36
27	Understanding the role of domain--domain linkers in the spatial orientation of domains in multi-domain proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1467-1480.	3.5	35
28	SIRT6 transcriptionally regulates fatty acid transport by suppressing PPAR β . <i>Cell Reports</i> , 2021, 35, 109190.	6.4	35
29	Conformational characteristics of asparaginyl residues in proteins. <i>International Journal of Peptide and Protein Research</i> , 1994, 44, 112-122.	0.1	34
30	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
31	NU-6027 Inhibits Growth of <i>Mycobacterium tuberculosis</i> by Targeting Protein Kinase D and Protein Kinase G. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	34
32	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
33	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
34	Comparison of sequence-based and structure-based phylogenetic trees of homologous proteins: Inferences on protein evolution. <i>Journal of Biosciences</i> , 2007, 32, 83-96.	1.1	32
35	Structure--function studies of <i>HNFI1A</i> (<i>MODY3</i>) gene mutations in South Indian patients with monogenic diabetes. <i>Clinical Genetics</i> , 2016, 90, 486-495.	2.0	32
36	Classification of Protein Kinases on the Basis of Both Kinase and Non-Kinase Regions. <i>PLoS ONE</i> , 2010, 5, e12460.	2.5	31

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37	Roles of residues in the interface of transient protein-protein complexes before complexation. <i>Scientific Reports</i> , 2012, 2, 334.	3.3	30
38	MuPSSM: a database of multiple position-specific scoring matrices of protein domain families. <i>Nucleic Acids Research</i> , 2006, 34, D243-D246.	14.5	29
39	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
40	A data integration approach to predict host-pathogen protein-protein interactions: application to recognize protein interactions between human and a malarial parasite. <i>In Silico Biology</i> , 2008, 8, 235-50.	0.9	29
41	Interaction interfaces of protein domains are not topologically equivalent across families within superfamilies: Implications for metabolic and signaling pathways. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 339-353.	2.6	27
42	Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. <i>Bioinformatics</i> , 2005, 21, 2821-2826.	4.1	27
43	Bioinformatic and mutational studies of related toxin-antitoxin pairs in <i>Mycobacterium tuberculosis</i> predict and identify key functional residues. <i>Journal of Biological Chemistry</i> , 2019, 294, 9048-9063.	3.4	27
44	Survey for g-proteins in the prokaryotic genomes: Prediction of functional roles based on classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 585-597.	2.6	25
45	Lipopolysaccharide phosphorylating enzymes encoded in the genomes of Gram-negative bacteria are related to the eukaryotic protein kinases. <i>Protein Science</i> , 2002, 11, 1580-1584.	7.6	24
46	Influence of Disease-Causing Mutations on Protein Structural Networks. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 620554.	3.5	23
47	Assessment of a Rigorous Transitive Profile Based Search Method to Detect Remotely Similar Proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2005, 23, 283-298.	3.5	22
48	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
49	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
50	Specificity and stability of transient protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2017, 44, 77-86.	5.7	20
51	Discrete analyses of protein dynamics. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2988-3002.	3.5	20
52	A Framework for Classification of Prokaryotic Protein Kinases. <i>PLoS ONE</i> , 2010, 5, e10608.	2.5	20
53	Comparison of tertiary structures of proteins in protein-protein complexes with unbound forms suggests prevalence of allostery in signalling proteins. <i>BMC Structural Biology</i> , 2012, 12, 6.	2.3	19
54	Structural interpretation of site-directed mutagenesis and specificity of the catalytic subunit of protein kinase CK2 using comparative modelling. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 119-127.	2.1	18

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55	Cascade PSI-BLAST web server: a remote homology search tool for relating protein domains. <i>Nucleic Acids Research</i> , 2006, 34, W143-W146.	14.5	17
56	Structural Insights into <i>Saccharomyces cerevisiae</i> Msh4-Msh5 Complex Function Using Homology Modeling. <i>PLoS ONE</i> , 2013, 8, e78753.	2.5	17
57	Stereochemical Assessment of (ϕ , ψ) Outliers in Protein Structures Using Bond Geometry-Specific Ramachandran Steric-Maps. <i>Structure</i> , 2019, 27, 1875-1884.e2.	3.3	17
58	Exploring anti-malarial potential of FDA approved drugs: an in silico approach. <i>Malaria Journal</i> , 2017, 16, 290.	2.3	16
59	<i>Mycobacterium tuberculosis</i> Rv0366c-Rv0367c encodes a non-canonical PezAT-like toxin-antitoxin pair. <i>Scientific Reports</i> , 2019, 9, 1163.	3.3	16
60	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
61	In silico prediction of protein flexibility with local structure approach. <i>Biochimie</i> , 2019, 165, 150-155.	2.6	15
62	Mechanism of CcdA-Mediated Rejuvenation of DNA Gyrase. <i>Structure</i> , 2020, 28, 562-572.e4.	3.3	15
63	Structural Compromise of Disallowed Conformations in Peptide and Protein Structures. <i>Protein and Peptide Letters</i> , 2007, 14, 672-682.	0.9	14
64	Prediction of protein-protein interactions in dengue virus coat proteins guided by low resolution cryoEM structures. <i>BMC Structural Biology</i> , 2010, 10, 17.	2.3	14
65	Novel insertion and deletion mutants of RpoB that render <i>Mycobacterium smegmatis</i> RNA polymerase resistant to rifampicin-mediated inhibition of transcription. <i>Microbiology (United Kingdom)</i> , 2010, 156, 1565-1573.	1.8	14
66	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
67	Investigations of Ramachandran disallowed conformations in protein domain families. <i>International Journal of Biological Macromolecules</i> , 2014, 63, 119-125.	7.5	14
68	Resolving protein structure-function-binding site relationships from a binding site similarity network perspective. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1319-1335.	2.6	14
69	iPBAvizu: a PyMOL plugin for an efficient 3D protein structure superimposition approach. <i>Source Code for Biology and Medicine</i> , 2019, 14, 5.	1.7	14
70	Structural and molecular basis of interaction of HCV non-structural protein 5A with human casein kinase II α and PKR. <i>BMC Structural Biology</i> , 2012, 12, 28.	2.3	13
71	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
72	A structural entropy index to analyse local conformations in intrinsically disordered proteins. <i>Journal of Structural Biology</i> , 2020, 210, 107464.	2.8	13

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73	Strategies for the effective identification of remotely related sequences in multiple PSSM search approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 789-794.	2.6	12
74	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
75	Knowledge-based prediction of protein backbone conformation using a structural alphabet. <i>PLoS ONE</i> , 2017, 12, e0186215.	2.5	12
76	AlignHUSH: Alignment of HMMs using structure and hydrophobicity information. <i>BMC Bioinformatics</i> , 2011, 12, 275.	2.6	11
77	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
78	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
79	SInCRE structural interactome computational resource for <i>Mycobacterium tuberculosis</i> . Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
80	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
81	Protein sequence design and its applications. <i>Current Opinion in Structural Biology</i> , 2016, 37, 71-80.	5.7	10
82	Molecular and Structural Basis of Cross-Reactivity in <i>M. tuberculosis</i> Toxin-Antitoxin Systems. <i>Toxins</i> , 2020, 12, 481.	3.4	10
83	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
84	Effective detection of remote homologues by searching in sequence dataset of a protein domain fold. <i>FEBS Letters</i> , 2003, 552, 225-230.	2.8	9
85	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. <i>Nucleic Acids Research</i> , 2005, 33, W126-W129.	14.5	9
86	Comparative kinomics of human and chimpanzee reveal unique kinship and functional diversity generated by new domain combinations. <i>BMC Genomics</i> , 2008, 9, 625.	2.8	9
87	Cascaded walks in protein sequence space: use of artificial sequences in remote homology detection between natural proteins. <i>Molecular BioSystems</i> , 2012, 8, 2076.	2.9	9
88	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
89	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
90	Long-range molecular dynamics show that inactive forms of Protein Kinase A are more dynamic than active forms. <i>Protein Science</i> , 2019, 28, 543-560.	7.6	9

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91	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
92	Evolutionary Divergence of <i>Plasmodium falciparum</i> : Sequences, Protein- Protein Interactions, Pathways and Processes. <i>Infectious Disorders - Drug Targets</i> , 2009, 9, 257-271.	0.8	9
93	Enhanced functional and structural domain assignments using remote similarity detection procedures for proteins encoded in the genome of <i>Mycobacterium tuberculosis</i> H37Rv. <i>Journal of Biosciences</i> , 2004, 29, 245-259.	1.1	8
94	Recognition of Interaction Interface Residues in Low-Resolution Structures of Protein Assemblies Solely from the Positions of C α Atoms. <i>PLoS ONE</i> , 2009, 4, e4476.	2.5	8
95	Classification of Nonenzymatic Homologues of Protein Kinases. <i>Comparative and Functional Genomics</i> , 2009, 2009, 1-17.	2.0	8
96	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
97	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	3.0	8
98	In Silico Modeling of FDA-Approved Drugs for Discovery of Anticandida Agents: A Drug-Repurposing Approach. , 2019, , 463-526.		8
99	Fold combinations in multi-domain proteins. <i>Bioinformatics</i> , 2019, 15, 342-350.	0.5	8
100	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
101	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
102	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
103	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
104	Structure determination of contaminant proteins using the MarathonMR procedure. <i>Journal of Structural Biology</i> , 2017, 197, 372-378.	2.8	7
105	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
106	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
107	Tolerance to the substitution of buried apolar residues by charged residues in the homologous protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 783-791.	2.6	6
108	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. <i>In Silico Biology</i> , 2009, 9, S41-S55.	0.9	6

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109	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
110	Ramachandran analysis of conserved glycol residues in homologous proteins of known structure. <i>Protein Science</i> , 2014, 23, 843-850.	7.6	6
111	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
112	Comparison of <i>Leptospira interrogans</i> and <i>Leptospira biflexa</i> genomes: analysis of potential leptospiral-host interactions. <i>Molecular BioSystems</i> , 2017, 13, 883-891.	2.9	6
113	Sendai virus recruits cellular villin to remodel actin cytoskeleton during fusion with hepatocytes. <i>Molecular Biology of the Cell</i> , 2017, 28, 3801-3814.	2.1	6
114	Recognition of a structural domain (RWDBD) in Gcn1 proteins that interacts with the RWD domain containing proteins. <i>Biology Direct</i> , 2017, 12, 12.	4.6	6
115	Seeing but not believing: the structure of glycerol dehydrogenase initially assumed to be the structure of a survival protein from <i>Salmonella typhimurium</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 609-617.	2.3	6
116	Identification of a novel epitope in the C terminus of hepatitis C virus-E2 protein that induces potent and cross-reactive neutralizing antibodies. <i>Journal of General Virology</i> , 2017, 98, 962-976.	2.9	6
117	“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
118	Identification of Local Conformational Similarity in Structurally Variable Regions of Homologous Proteins Using Protein Blocks. <i>PLoS ONE</i> , 2011, 6, e17826.	2.5	6
119	Understanding structural variability in proteins using protein structural networks. <i>Current Research in Structural Biology</i> , 2022, 4, 134-145.	2.2	6
120	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
121	Use of designed sequences in protein structure recognition. <i>Biology Direct</i> , 2018, 13, 8.	4.6	5
122	Hypervariability of accessible and inaccessible conformational space of proteins. <i>Current Research in Structural Biology</i> , 2021, 3, 229-238.	2.2	5
123	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
124	Influence of solvent molecules on the stereochemical code of glycol residues in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 49, 326-334.	2.6	4
125	Detection and Characterization of Bacterial Proteinases Using Zymography. <i>Methods in Molecular Biology</i> , 2017, 1626, 103-114.	0.9	4
126	Structural variations within proteins can be as large as variations observed across their homologues. <i>Biochimie</i> , 2019, 167, 162-170.	2.6	4

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127	Repurposing Drugs Based on Evolutionary Relationships Between Targets of Approved Drugs and Proteins of Interest. <i>Methods in Molecular Biology</i> , 2019, 1903, 45-59.	0.9	4
128	Data set of intrinsically disordered proteins analysed at a local protein conformation level. <i>Data in Brief</i> , 2020, 29, 105383.	1.0	4
129	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
130	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
131	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
132	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
133	Recognition of sites of functional specialisation in all known eukaryotic protein kinase families. <i>PLoS Computational Biology</i> , 2018, 14, e1005975.	3.2	4
134	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
135	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
136	Repertoire of Protein Kinases Encoded in the Genome of <i>Takifugu rubripes</i> . <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-12.	2.0	3
137	Hybrid and Rogue Kinases Encoded in the Genomes of Model Eukaryotes. <i>PLoS ONE</i> , 2014, 9, e107956.	2.5	3
138	Computational recognition and analysis of hitherto uncharacterized nucleotide cyclase-like proteins in bacteria. <i>Biology Direct</i> , 2016, 11, 27.	4.6	3
139	Comparative analyses of quaternary arrangements in homo-oligomeric proteins in superfamilies: Functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1190-1202.	2.6	3
140	Deciphering common recognition principles of nucleoside mono/di and tri-phosphates binding in diverse proteins via structural matching of their binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1699-1712.	2.6	3
141	Heterologous Expression, Purification and Characterization of an Oligopeptidase A from the Pathogen <i>Leptospira interrogans</i> . <i>Molecular Biotechnology</i> , 2018, 60, 302-309.	2.4	3
142	Potent HCV NS3 Protease Inhibition by a Water-Soluble Phyllanthin Congener. <i>ACS Omega</i> , 2020, 5, 11553-11562.	3.5	3
143	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
144	Recognition of remotely related structural homologues using sequence profiles of aligned homologous protein structures. <i>In Silico Biology</i> , 2004, 4, 445-60.	0.9	3

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145	Clustering of multi-domain protein sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 759-776.	2.6	2
146	Unity and diversity among viral kinases. <i>Gene</i> , 2020, 723, 144134.	2.2	2
147	Manoeuvring protein functions and functional levels by structural excursions. , 2020, , 77-104.		2
148	Signatures of conserved and unique molecular features in Afrotheria. <i>Scientific Reports</i> , 2021, 11, 1011.	3.3	2
149	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
150	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
151	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
152	How effective is the data on co-occurrence of domains in multi-domain proteins in prediction of protein-protein interactions?. , 2009, , .		1
153	Protein-Protein Interactions in Clathrin Vesicular Assembly: Radial Distribution of Evolutionary Constraints in Interfaces. <i>PLoS ONE</i> , 2012, 7, e31445.	2.5	1
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