Ramanathan Sowdhamini

List of Publications by Year
in descending order

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	Insights from the analysis of draft genome sequence of Crocus sativus L.. Bioinformation, 2022, 18, 1-13.	0.5	6
2	Srinivasan (1962â€"2021) in Bioinformatics and beyond. Bioinformatics, 2022, 38, 2377-2379.	4.1	2
3	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
4	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	0
5	LIM domain-wide comprehensive virtual mutagenesis provides structural rationale for cardiomyopathy mutations in CSRP3. Scientific Reports, 2022, 12, 3562.	3.3	7
6	Development of candidate gene-based markers and map-based cloning of a dominant rust resistance gene in cultivated groundnut (Arachis hypogaea L.). Gene, 2022, 827, 146474.	2.2	2
7	DDX24 is required for muscle fiber organization and the suppression of wound-induced Wnt activity necessary for pole re-establishment during planarian regeneration. Developmental Biology, 2022, 488, 11-29.	2.0	5
8	Computational analysis of potential candidate genes involved in the cold stress response of ten Rosaceae members. BMC Genomics, 2022, 23, .	2.8	1
9	Quaternary variations in the structural assembly ofNâ€acetylglucosamineâ€6â€phosphate deacetylase fromPasteurella multocida. Proteins: Structure, Function and Bioinformatics, 2021, 89, 81-93.	2.6	5
10	DEELIG: A Deep Learning Approach to Predict Protein-Ligand Binding Affinity. Bioinformatics and Biology Insights, 2021, 15, 117793222110303.	2.0	30
11	Disulfide-Rich Cyclic Peptides from <i>Clitoria ternatea</i> Protect against Î²-Amyloid Toxicity and Oxidative Stress in Transgenic <i>Caenorhabditis elegans</i>. Journal of Medicinal Chemistry, 2021, 64, 7422-7433.	6.4	16
12	Genome-wide survey of tyrosine phosphatases in thirty mammalian genomes. Cellular Signalling, 2021, 84, 110009.	3.6	0
13	InsectORâ€"Webserver for sensitive identification of insect olfactory receptor genes from non-model genomes. PLoS ONE, 2021, 16, e0245324.	2.5	14
14	Ligand Docking Methods to Recognize Allosteric Inhibitors for G-Protein-Coupled Receptors. Bioinformatics and Biology Insights, 2021, 15, 117793222110377.	2.0	3
15	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (Moringa oleifera). Genomics, 2020, 112, 621-628.	2.9	22
16	A knowledge-driven protocol for prediction of proteins of interest with an emphasis on biosynthetic pathways. MethodsX, 2020, 7, 101053.	1.6	4
17	Computational search for potential COVID-19 drugs from FDA-approved drugs and small molecules of natural origin identifies several anti-virals and plant products. Journal of Biosciences, 2020, 45, 1.	1.1	38
18	Transcriptomic profiling of the medicinal plant Clitoria ternatea: identification of potential genes in cyclotide biosynthesis. Scientific Reports, 2020, 10, 12658.	3.3	11

#	Article	IF	Citations
19	Distinct Evolutionary Origins of Intron Retention Splicing Events in NHX1 Antiporter Transcripts Relate to Sequence Specific Distinctions in Oryza Species. Frontiers in Plant Science, 2020, 11, 267.	3.6	16
20	Dataset for the combined transcriptome assembly of M. oleifera and functional annotation. Data in Brief, 2020, 30, 105416.	1.0	4
21	A glance into the evolution of template-free protein structure prediction methodologies. Biochimie, 2020, 175, 85-92.	2.6	24
22	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
23	EcRBPome: a comprehensive database of all known E. coli RNA-binding proteins. BMC Genomics, 2019, 20, 403.	2.8	2
24	Topology prediction of insect olfactory receptors. Current Opinion in Structural Biology, 2019, 55, 194-203.	5.7	4
25	A Functional Agonist of Insect Olfactory Receptors: Behavior, Physiology and Structure. Frontiers in Cellular Neuroscience, 2019, 13, 134.	3.7	15
26	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
27	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
28	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
29	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
30	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
31	Vaccination and immunization strategies to design Aedes aegypti salivary protein based subunit vaccine tackling Flavivirus infection. International Journal of Biological Macromolecules, 2019, 122, 1203-1211.	7.5	11
32	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. Progress in Biophysics and Molecular Biology, 2019, 145, 19-39.	2.9	15
33	Fold combinations in multi-domain proteins. Bioinformation, 2019, 15, 342-350.	0.5	8
34	Investigating the effect of key mutations on the conformational dynamics of toll€like receptor dimers through molecular dynamics simulations and protein structure networks. Proteins: Structure, Function and Bioinformatics, 2018, 86, 475-490.	2.6	9
35	Probing subtle conformational changes induced by phosphorylation and point mutations in the <scp>TIR</scp> domains of <scp>TLR</scp>2 and <scp>TLR</scp>3. Proteins: Structure, Function and Bioinformatics, 2018, 86, 524-535.	2.6	16
36	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

#	Article	IF	Citations
37	Specificity and stability of transient protein–protein interactions. Current Opinion in Structural Biology, 2017, 44, 77-86.	5.7	20
38	Molecular mechanisms and structural features of cardiomyopathy-causing troponin T mutants in the tropomyosin overlap region. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11115-11120.	7.1	31
39	Integrative modelling of TIR domain-containing adaptor molecule inducing interferon-β (TRIF) provides insights into its autoinhibited state. Biology Direct, 2017, 12, 9.	4.6	10
40	Bioinformatics comparisons of RNA-binding proteins of pathogenic and non-pathogenic Escherichia coli strains reveal novel virulence factors. BMC Genomics, 2017, 18, 658.	2.8	3
41	Three-dimensional Modelling of the Voltage-gated Sodium Ion Channel from Anopheles gambiae Reveals Spatial Clustering of Evolutionarily Conserved Acidic Residues at the Extracellular Sites. Current Neuropharmacology, 2017, 15, 1062-1072.	2.9	1
42	RStrucFam: a web server to associate structure and cognate RNA for RNA-binding proteins from sequence information. BMC Bioinformatics, 2016, 17, 411.	2.6	9
43	A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. Journal of Biomolecular Structure and Dynamics, 2016, 34, 1979-1986.	3.5	5
44	Genome-wide survey and phylogeny of S-Ribosylhomocysteinase (LuxS) enzyme in bacterial genomes. BMC Genomics, 2016, 17, 742.	2.8	12
45	Identification of Complete Repertoire of *Apis florea* Odorant Receptors Reveals Complex Orthologous Relationships with *Apis mellifera*. Genome Biology and Evolution, 2016, 8, 2879-2895.	2.5	37
46	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. Nucleic Acids Research, 2016, 44, D410-D414.	14.5	4
47	Transcriptional regulatory networks in *Arabidopsis thaliana* during single and combined stresses. Nucleic Acids Research, 2016, 44, 3147-3164.	14.5	62
48	Genome-wide survey of putative RNA-binding proteins encoded in the human proteome. Molecular BioSystems, 2016, 12, 532-540.	2.9	21
49	Interpreting functional effects of coding variants: challenges in proteome-scale prediction, annotation and assessment. Briefings in Bioinformatics, 2016, 17, 841-862.	6.5	23
50	Molecular modelling of human 5-hydroxytryptamine receptor (5-HT$_{2A}$) and virtual screening studies towards the identification of agonist and antagonist molecules. Journal of Biomolecular Structure and Dynamics, 2016, 34, 952-970.	3.5	33
51	Rapid and enhanced remote homology detection by cascading hidden Markov model searches in sequence space. Bioinformatics, 2016, 32, 338-344.	4.1	5
52	An *in silico* 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
53	An Approach to Function Annotation for Proteins of Unknown Function (PUFs) in the Transcriptome of Indian Mulberry. PLoS ONE, 2016, 11, e0151323.	2.5	40
54	Molecular Dynamics Simulations and Structural Analysis to Decipher Functional Impact of a Twenty Residue Insert in the Ternary Complex of Mus musculus TdT Isoform. PLoS ONE, 2016, 11, e0157286.	2.5	9

#	Article	IF	Citations
55	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. PLoS ONE, 2016, 11, e0159627.	2.5	5
56	PIMA: Protein-Protein Interactions in Macromolecular Assembly - a web server for its Analysis and Visualization. Bioinformation, 2016, 12, 9-11.	0.5	19
57	PPCheck: A Webserver for the Quantitative Analysis of Protein-Protein Interfaces and Prediction of Residue Hotspots. Bioinformatics and Biology Insights, 2015, 9, BBI.S25928.	2.0	61
58	SInCRe—structural interactome computational resource for <i>Mycobacterium tuberculosis</i>. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav060.	3.0	10
59	Energetic Calculations to Decipher pH-Dependent Oligomerization and Domain Swapping of Proteins. PLoS ONE, 2015, 10, e0127716.	2.5	4
60	Computational Approaches for Decoding Select Odorant-Olfactory Receptor Interactions Using Mini-Virtual Screening. PLoS ONE, 2015, 10, e0131077.	2.5	19
61	NrichD database: sequence databases enriched with computationally designed protein-like sequences aid in remote homology detection. Nucleic Acids Research, 2015, 43, D300-D305.	14.5	12
62	Genome sequencing of herb Tulsi (Ocimum tenuiflorum) unravels key genes behind its strong medicinal properties. BMC Plant Biology, 2015, 15, 212.	3.6	80
63	Enriching the annotation of Mycobacterium tuberculosis H37Rv proteome using remote homology detection approaches: Insights into structure and function. Tuberculosis, 2015, 95, 14-25.	1.9	9
64	Collation and analyses of DNA-binding protein domain families from sequence and structural databanks. Molecular BioSystems, 2015, 11, 1110-1118.	2.9	5
65	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
66	Mechanistic Heterogeneity in Contractile Properties of α-Tropomyosin (TPM1) Mutants Associated with Inherited Cardiomyopathies. Journal of Biological Chemistry, 2015, 290, 7003-7015.	3.4	41
67	DOCKSCORE: a webserver for ranking protein-protein docked poses. BMC Bioinformatics, 2015, 16, 127.	2.6	33
68	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
69	Structural Interface Parameters Are Discriminatory in Recognising Near-Native Poses of Protein-Protein Interactions. PLoS ONE, 2014, 9, e80255.	2.5	9
70	POEAS: Automated Plant Phenomic Analysis Using Plant Ontology. Bioinformatics and Biology Insights, 2014, 8, BBI.S19057.	2.0	6
71	ECMIS: computational approach for the identification of hotspots at protein-protein interfaces. BMC Bioinformatics, 2014, 15, 303.	2.6	14
72	Distribution, classification, domain architectures and evolution of prolyl oligopeptidases in prokaryotic lineages. BMC Genomics, 2014, 15, 985.	2.8	15

#	Article	IF	Citations
73	Sequence search and analysis of gene products containing RNA recognition motifs in the human genome. BMC Genomics, 2014, 15, 1159.	2.8	10
74	LenVarDB: database of length-variant protein domains. Nucleic Acids Research, 2014, 42, D246-D250.	14.5	4
75	Insights on pH-dependent conformational changes of mosquito odorant binding proteins by molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1742-1751.	3.5	10
76	Filling-in Void and Sparse Regions in Protein Sequence Space by Protein-Like Artificial Sequences Enables Remarkable Enhancement in Remote Homology Detection Capability. Journal of Molecular Biology, 2014, 426, 962-979.	4.2	15
77	Decoding the structural events in substrate‐gating mechanism of eukaryotic prolyl oligopeptidase using normal mode analysis and molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1428-1443.	2.6	20
78	DOR â€" a Database of Olfactory Receptors â€" Integrated Repository for Sequence and Secondary Structural Information of Olfactory Receptors in Selected Eukaryotic Genomes. Bioinformatics and Biology Insights, 2014, 8, BBI.S14858.	2.0	19
79	Structural updates of alignment of protein domains and consequences on evolutionary models of domain superfamilies. BioData Mining, 2013, 6, 20.	4.0	0
80	Oligomerisation status and evolutionary conservation of interfaces of protein structural domain superfamilies. Molecular BioSystems, 2013, 9, 1652.	2.9	72
81	Comparative analyses of stress-responsive genes in Arabidopsis thaliana: insight from genomic data mining, functional enrichment, pathway analysis and phenomics. Molecular BioSystems, 2013, 9, 1888.	2.9	26
82	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. Plant and Cell Physiology, 2013, 54, e8-e8.	3.1	130
83	Comparative Genomics of Odorant Binding Proteins in Anopheles gambiae, Aedes aegypti, and Culex quinquefasciatus. Genome Biology and Evolution, 2013, 5, 163-180.	2.5	112
84	Genome-wide survey of DNA-binding proteins in Arabidopsis thaliana : analysis of distribution and functions. Nucleic Acids Research, 2013, 41, 7212-7219.	14.5	14
85	Improved Detection of Remote Homologues Using Cascade PSI-BLAST: Influence of Neighbouring Protein Families on Sequence Coverage. PLoS ONE, 2013, 8, e56449.	2.5	10
86	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
87	Improved performance of sequence search approaches in remote homology detection. F1000Research, 2013, 2, 93.	1.6	2
88	Rebelling for a Reason: Protein Structural â€œOutliersâ€. PLoS ONE, 2013, 8, e74416.	2.5	5
89	An alignment-free domain architecture similarity search (ADASS) algorithm for inferring homology between multi-domain proteins. Bioinformation, 2013, 9, 491-499.	0.5	11
90	PASS2 version 4: An update to the database of structure-based sequence alignments of structural domain superfamilies. Nucleic Acids Research, 2012, 40, D531-D534.	14.5	17

#	Article	IF	Citations
91	Re-visiting protein-centric two-tier classification of existing DNA-protein complexes. BMC Bioinformatics, 2012, 13, 165.	2.6	8
92	Functional repertoire, molecular pathways and diseases associated with 3D domain swapping in the human proteome. Journal of Clinical Bioinformatics, 2012, 2, 8.	1.2	12
93	PrionHome: A Database of Prions and Other Sequences Relevant to Prion Phenomena. PLoS ONE, 2012, 7, e31785.	2.5	22
94	3DSwap: curated knowledgebase of proteins involved in 3D domain swapping. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar042-bar042.	3.0	28
95	3dswap-pred: Prediction of 3D Domain Swapping from Protein Sequence Using Random Forest Approach. Protein and Peptide Letters, 2011, 18, 1010-1020.	0.9	26
96	Critical assessment of structure-based sequence alignment methods at distant relationships. Briefings in Bioinformatics, 2011, 12, 163-175.	6.5	12
97	Structural Analysis of Prolyl Oligopeptidases Using Molecular Docking and Dynamics: Insights into Conformational Changes and Ligand Binding. PLoS ONE, 2011, 6, e26251.	2.5	27
98	PASS2. International Journal of Knowledge Discovery in Bioinformatics, 2011, 2, 53-66.	0.8	4
99	Insights from the analysis of conserved motifs and permitted amino acid exchanges in the human, the fly and the worm GPCR clusters. Bioinformation, 2011, 7, 15-20.	0.5	4
100	TM-MOTIF: an alignment viewer to annotate predicted transmembrane helices and conserved motifs in aligned set of sequences. Bioinformation, 2011, 7, 214-221.	0.5	4
101	HORIBALFRE program: Higher Order Residue Interactions Based ALgorithm for Fold REcognition. Bioinformation, 2011, 7, 352-359.	0.5	0
102	Primary Structural Documentation of the Major Urinary Protein of the Indian Commensal Rat (Rattus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.9	8
103	In silico point mutation and evolutionary trace analysis applied to nicotinic acetylcholine receptors in deciphering ligand-binding surfaces. Journal of Molecular Modeling, 2010, 16, 1651-1670.	1.8	6
104	Identification of functionally diverse lipocalin proteins from sequence information using support vector machine. Amino Acids, 2010, 39, 777-783.	2.7	11
105	Insights into Protein Sequence and Structure-Derived Features Mediating 3D Domain Swapping Mechanism using Support Vector Machine Based Approach. Bioinformatics and Biology Insights, 2010, 4, BBI.S4464.	2.0	13
106	Phylogenetic Analysis and Selection Pressures of 5-HT Receptors in Human and Non-human Primates: Receptor of an Ancient Neurotransmitter. Journal of Biomolecular Structure and Dynamics, 2010, 27, 581-598.	3.5	21
107	100 ns Molecular Dynamics Simulations to Study Intramolecular Conformational Changes in Bax. Journal of Biomolecular Structure and Dynamics, 2010, 28, 71-83.	3.5	82
108	Molecular modeling and docking studies of human 5-hydroxytryptamine 2A (5-HT2A) receptor for the identification of hotspots for ligand binding. Molecular BioSystems, 2009, 5, 1877.	2.9	34

#	Article	IF	Citations
109	Length Variations amongst Protein Domain Superfamilies and Consequences on Structure and Function. PLoS ONE, 2009, 4, e4981.	2.5	36
110	Analysis of the impact of ERK5, JNK, and P38 kinase cascades on each other: A systems approach. Bioinformation, 2009, 3, 244-249.	0.5	3
111	Computational prediction and analysis of impact of the cross-talks between JNK and P38 kinase cascades. Bioinformation, 2009, 3, 250-254.	0.5	11
112	CUSP: an algorithm to distinguish structurally conserved and unconserved regions in protein domain alignments and its application in the study of large length variations. BMC Structural Biology, 2008, 8, 28.	2.3	16
113	PURE: A webserver for the prediction of domains in unassigned regions in proteins. BMC Bioinformatics, 2008, 9, 281.	2.6	11
114	STIF: Identification of stress-upregulated transcription factor binding sites in Arabidopsis thaliana. Bioinformation, 2008, 2, 431-437.	0.5	24
115	Evolutionary analysis of PHLPP1 gene in humans and non-human primates. Bioinformation, 2008, 2, 471-474.	0.5	1
116	Sequence and structural analyses of interleukin-8-like chemokine superfamily. In Silico Biology, 2008, 8, 307-30.	0.9	4
117	Genome inventory and analysis of nuclear hormone receptors in Tetraodon nigroviridis. Journal of Biosciences, 2007, 32, 43-50.	1.1	16
118	IWS: Integrated Web Server for protein sequence and structure analysis. Bioinformation, 2007, 2, 86-90.	0.5	5
119	A novel meta-cleavage product hydrolase from Flavobacterium sp. ATCC27551. Biochemical and Biophysical Research Communications, 2006, 351, 675-681.	2.1	15
120	Domain architectural census of eukaryotic gene products containing O-protein phosphatases. Gene, 2006, 366, 246-255.	2.2	5
121	SSToSS--sequence-structural templates of single-member superfamilies. In Silico Biology, 2006, 6, 311-9.	0.9	3
122	Enhanced structure prediction of gene products containing class III adenylyl cyclase domains. In Silico Biology, 2006, 6, 351-62.	0.9	3
123	Genome wide survey of G protein-coupled receptors in Tetraodon nigroviridis. BMC Evolutionary Biology, 2005, 5, 41.	3.2	31
124	Cross genome phylogenetic analysis of human and Drosophila G protein-coupled receptors: application to functional annotation of orphan receptors. BMC Genomics, 2005, 6, 106.	2.8	52
125	Comparative analysis of different competitive antagonists interaction with NR2A and NR2B subunits of N-methyl-D-aspartate (NMDA) ionotropic glutamate receptor. Journal of Molecular Modeling, 2005, 11, 489-502.	1.8	6
126	Native and modeled disulfide bonds in proteins: Knowledge-based approaches toward structure prediction of disulfide-rich polypeptides. Proteins: Structure, Function and Bioinformatics, 2005, 58, 866-879.	2.6	23

#	Article	IF	Citations
127	DIAL: a web-based server for the automatic identification of structural domains in proteins. Nucleic Acids Research, 2005, 33, W130-W132.	14.5	25
128	Structural Consequences of D481N/K483Q Mutation at Glycine Binding Site of NMDA Ionotropic Glutamate Receptors: A Molecular Dynamics Study. Journal of Biomolecular Structure and Dynamics, 2005, 22, 399-410.	3.5	6
129	FASSM: enhanced function association in whole genome analysis using sequence and structural motifs. In Silico Biology, 2005, 5, 425-38.	0.9	4
130	GenDiS: Genomic Distribution of protein structural domain Superfamilies. Nucleic Acids Research, 2004, 33, D252-D255.	14.5	16
131	Improvement of alignment accuracy utilizing sequentially conserved motifs. BMC Bioinformatics, 2004, 5, 167.	2.6	12
132	PASS2: an automated database of protein alignments organised as structural superfamilies. BMC Bioinformatics, 2004, 5, 35.	2.6	34
133	Improvement of comparative modeling by the application of conserved motifs amongst distantly related proteins as additional restraints. Journal of Molecular Modeling, 2004, 10, 69-75.	1.8	4
134	Evolutionary trace analysis of ionotropic glutamate receptor sequences and modeling the interactions of agonists with different NMDA receptor subunits. Journal of Molecular Modeling, 2004, 10, 305-316.	1.8	10
135	Conserved spatially interacting motifs of protein superfamilies: Application to fold recognition and function annotation of genome data. Proteins: Structure, Function and Bioinformatics, 2004, 54, 657-670.	2.6	19
136	Regions of minimal structural variation among members of protein domain superfamilies: application to remote homology detection and modelling using distant relationships. FEBS Letters, 2004, 569, 31-36.	2.8	17
137	Fold prediction and comparative modeling of Bdm1: a probable α/β hydrolase associated with hot water epilepsy. Journal of Molecular Modeling, 2003, 9, 3-8.	1.8	20
138	Structural determinants of binding and specificity in transforming growth factor-receptor interactions. Proteins: Structure, Function and Bioinformatics, 2001, 45, 408-420.	2.6	11
139	Knowledge-Based Protein Modeling. Critical Reviews in Biochemistry and Molecular Biology, 1994, 29, 1-68.	5.2	206
140	Molecular recognition in protein families: A database of aligned three-dimensional structures of related proteins. Biochemical Society Transactions, 1993, 21, 597-604.	3.4	53
141	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